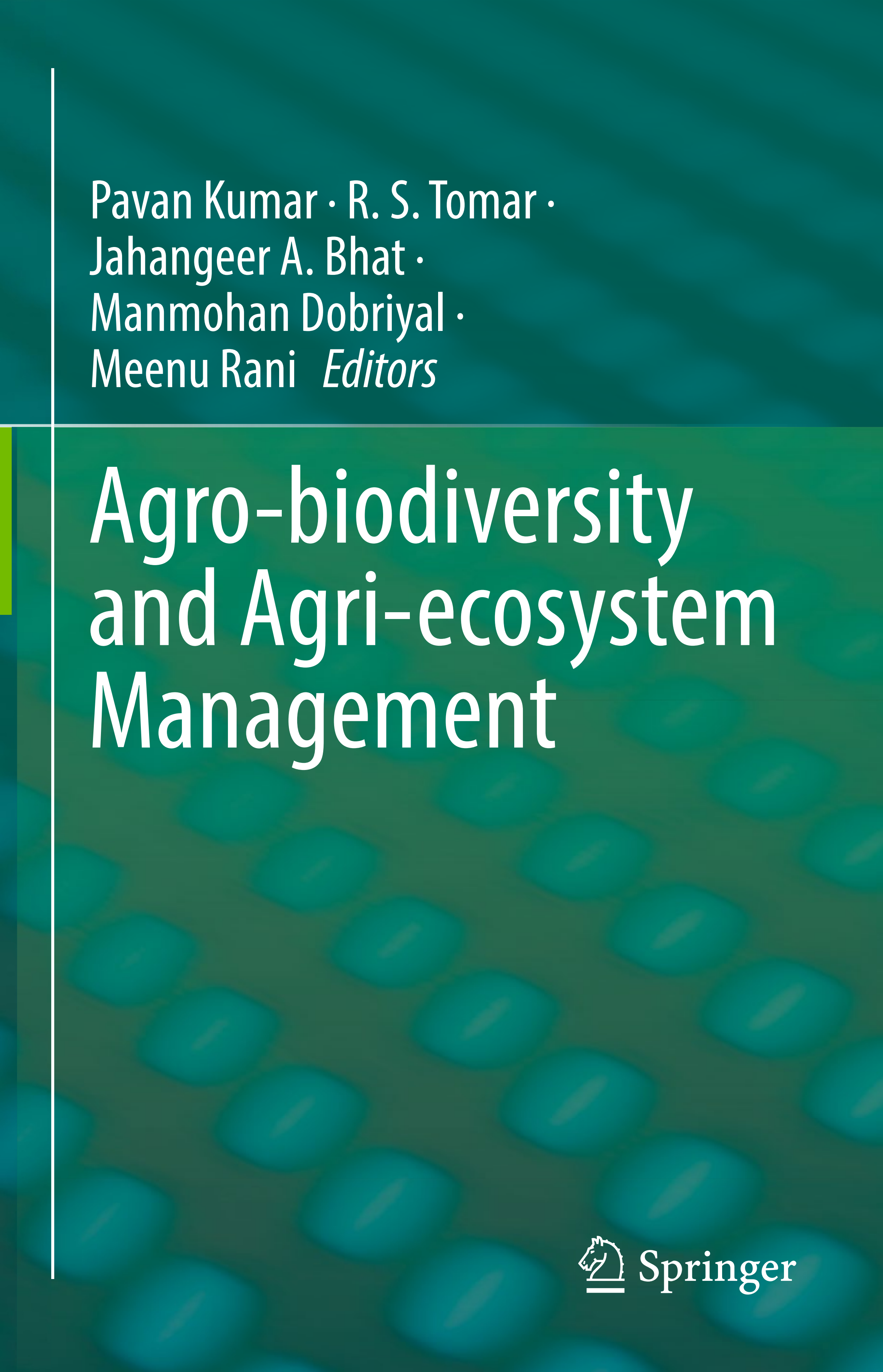

Pavan Kumar · R. S. Tomar ·
Jahangeer A. Bhat ·
Manmohan Dobriyal ·
Meenu Rani *Editors*

Agro-biodiversity and Agri-ecosystem Management

Springer

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Foreword

रानी लक्ष्मी बाई केन्द्रीय कृषि विश्वविद्यालय
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डॉ अरविन्द कुमार
कुलपति
Dr Arvind Kumar
Vice-Chancellor

In order to maintain agro-biodiversity and agri-ecosystem management, researcher scientists have continuously been involved in finding solutions due to its wide impact on human and environmental systems. The present-day challenges, due to rapid climate change, are immense primarily due to an imbalance in the biodiversity and ecosystem which not only necessitates maintenance of desired balance but also restoration of biodiversity. Agro-biodiversity and agri-ecosystem can be tracked using recent research and development processes required in the maintenance of local diversity at the genetic, species and ecosystem levels.

The present book includes distinct chapters with blueprint and strategies that can be applied to conserve agro-biodiversity and agri-ecosystem using the role of range grasses, carbon sequestration potential and identifying the relationships between climate resilience, climate change and adaptability. The contents on advanced molecular tools and techniques have facilitated and fastened the process of identifying the problems in agricultural systems associated with the rapidly changing climatic conditions and also enriched knowledge on advanced tools and techniques like artificial intelligence, big data analysis, and information technology that can be used to conserve agro-biodiversity.

I congratulate the editors, the authors of chapters and the publisher for selecting a very important topic on agro-biodiversity and agro-ecosystem management which will serve as a source of knowledge and benefit researchers, particularly biologists, environmentalists and other stakeholders involved in the maintenance of sound ecosystem health.

Arvind Kumar

Rani Lakshmi Bai
Central Agricultural University
Jhansi, Uttar Pradesh, India
November 10, 2021

Foreword

नरेन्द्र सिंह तोमर
NARENDRA SINGH TOMAR

कृषि एवं किसान कल्याण मंत्री
भारत सरकार
कृषि भवन, नई दिल्ली
MINISTER OF AGRICULTURE & FARMERS WELFARE
GOVERNMENT OF INDIA
KRISHI BHAWAN, NEW DELHI

Agro-biodiversity and agri-ecosystem comprise a diverse variety within and between living creatures including plants, animals and microorganisms, considered to be essential for the food and nutritional security. Agricultural production occupies about one-third of the land area across the globe, and overexploitation of the natural resources has not only resulted in the degradation of land and water bodies but also impaired the precious ecosystem. Consequently, protecting and conserving the agro-biodiversity is inevitable and poses a major challenge before researchers, environmentalists, social workers and policy makers.

This book aims to elucidate various approaches and strategies for conservation and restoration of agro-biodiversity and agri-ecosystem, using advanced agricultural production and management techniques. The understanding of relationships between climate resilience, climate change and adaptability along with carbon sequestration potential will further create awareness of their key role towards agricultural production and subsequently sustainable use of resources. Modern tools and techniques can be used for the precise and efficient approach in addressing the relevant issues pertaining to the conservation and management of agro-biodiversity. The use of molecular approaches like genome sequencing, genome editing, CRISPR-Cas, and transgenics at genetic level, in association with bioinformatics tools and computer programmes based on artificial intelligence, big data analysis, and information technology will play a crucial role in not only mapping but also conserving agro-biodiversity and agri-ecosystem.

I compliment the editors, the authors of chapters and the publisher for highlighting current issues in the form of a book which shall serve as a guide by providing valuable information, immensely useful in the conservation and restoration of biodiversity and agro-ecosystem management.

Narendra Singh Tomar

Minister of Agriculture and
Farmers Welfare, Government of India
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About the Editors

Pavan Kumar is an Assistant Professor (Wildlife Management) in the Department of Forest Biology and Tree Improvement, College of Horticulture and Forestry, Rani Lakshmi Bai Central Agricultural University, Jhansi, U.P., India. He obtained his Ph.D. degrees from the Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi. He did his B.Sc. (Botany) and M. Sc. (Environmental Science) from Banaras Hindu University, Varanasi, India, and subsequently obtained a master's degree in Remote Sensing (M. Tech) from Birla Institute of Technology, Mesra Ranchi, India. His current research interests include Resilient Agriculture and Climate Change studies. He was a recipient of Innovation China National academy award for remote sensing. Dr. Kumar has published 50 research papers in international journals and authored several books. He has visited countries like the USA, France, the Netherlands, Italy, China, Indonesia, Brazil and Malaysia for various academic/ scientific assignments, workshop and conferences. Dr. Kumar is a member of International Associations for Vegetation Science, USA, and Institution of Geospatial and Remote Sensing, Malaysia.

R. S. Tomar is a Faculty in the College of Horticulture and Forestry, Rani Lakshmi Bai Central Agricultural University, Jhansi, U.P., India. He worked in his Ph.D. degrees at Indian Agricultural Research Institute, New Delhi. He did his B.-Sc. (Biochemistry) and M. Sc. (Biotechnology) from Jiwaji University, Gwalior, India. His research area includes molecular breeding of rice, wheat, soybean and lentil. He developed mapping populations, i.e. RILs, and identified QTLs and putative candidate genes for drought tolerance in wheat, pyramiding of rust resistance genes in wheat using conventional and molecular breeding approaches. He also worked on International Genome Sequencing projects (IWGSP) on Wheat, Mango and *P. sojae*. Recently, he worked as Scientist on "National Certification System for Tissue Culture Raised Plants (NCS-TCP) such as banana, guava, bamboo, date palm and apple on Genetic Fidelity" at ICAR-NIPB, Pusa Campus, New Delhi. Dr. Tomar is Fellow of Indian Society of Genetics & Plant Breeding, New Delhi, and Executive Council Member of NESA, New Delhi. He has been awarded with Eminent Scientist, Distinguished Scientist, Young Biotechnologist Award, Young Scientist and Scientist of the Year Award by various scientific organisations.

He is the editor in chief of *International Journal of Agricultural Sciences* (IJAS) and *NESA Newsletter* and editorial board member and reviewer of many renowned international journals. Dr. Tomar has published more than 50 research papers in national and international journals and authored several books. He has visited countries like Belgium and Canada for various academic/scientific assignments.

Jahangeer A. Bhat, Ph.D. is a former head of the Department of Forestry, College of Agriculture, Fisheries and Forestry, Fiji National University, Republic of Fiji Islands. Dr. Jahangeer has worked as a counsellor, mentor, and coordinator for forestry academic programmes. He has been instrumental in developing HE and TVET streams of forestry and allied programmes and worked closely for accreditation with the Fiji Higher Education Commission and forestry stakeholders. Before joining Fiji National University, he worked for H. N. B. Garhwal University, Srinagar, India, and has 12 years of research and 9 years of teaching experience with a publication record of more than 70, including research articles, review papers, conference papers, and books of national and international repute. Dr. Jahangeer reviews research articles for several scientific journals and has handled research projects in his capacity as Principal Investigator and Co-Principal Investigator. His major interests lie in emerging issues in forestry including conservation of biodiversity, traditional knowledge of plants, and sustainable management of forest resources. His focus of research is vegetation ecology, ethnobotany, and evaluation of ecosystem services, forest plant biodiversity, climate change, and sociocultural issues in forestry. Dr. Jahangeer is currently working for College of Horticulture and Forestry, Rani Lakshmi Bai Central Agricultural University, Jhansi, India.

Manmohan Dobriyal A Professional Forester graduated in Forestry followed by by post graduation and Doctoral degrees at different institutes like GB Pant University, Pantnagar, TNAU, Coimbatore, and Forest Research Institute, Dehradun. He was faculty in different institutes like DCAST, Dehradun; DIBNS, Dehradun, Uttrakhand; CoHF, MPUAT, Udaipur/AU, Kota, Rajasthan as Assistant Professor (Forestry). He also serves as Associate Professor & Head, Department of Silviculture & Agroforestry at CoF, NAU, Navsari, Gujarat. Currently He is Professor and Head, Forestry at CoHF, Rani Lakshmi Bai Central Agricultural University. He has more than 19 years of experience in Forestry Research and Teaching and extension. His specialisation is Forest ecology & Environment/Silviculture, Non-Wood Forest Products (Medicinal and Aromatic Plants) Agroforestry, Biodiversity conservation and Ecosystem services. He published more than 100 papers and articles in referred journals and attended various conferences, operated research projects apart from guiding many PG & PhD students. His goal is to work for the development of the Forestry sector and to give recognition to our Trees, Forests & Nature reserves which harbour the rich biodiversity for the benefit of the mankind.

Meenu Rani is a researcher in the Department of Geography, Kumaun University, Nainital, Uttarakhand, India. Dr. Rani received her M.Tech degree in Remote Sensing from Birla Institute of Technology, Ranchi, India. She has a working experience in the major disciplines of agriculture and forestry while working with Haryana Space Application Centre, Indian Council of Agricultural Research and GB Pant National Institute of Himalayan Environment and Sustainable Development. Dr. Rani has authored several peer-reviewed scientific research papers and presented works at many national and international conferences in the USA, Italy and China. She has been awarded with various fellowships from the International Association for Ecology, Future Earth Coast and SCAR Scientific Research Programme. She was awarded early career scientists achievement in 2017 at Columbia University, New York, USA.

Part I

General

Introduction to Agro-Biodiversity and Agri-Ecosystem in the Twenty-First Century

1

Aishwarya and Pavan Kumar

Abstract

Sustainable natural resources are one of the major challenges for ecosystem agro-biodiversity. The monitoring of ecosystem agro-biodiversity is in increasing demand in the national and international growth sector. Many professional researchers and academicians working towards sustainable management of natural resources management and nature resource conservation are confronted with the task of agro-biodiversity monitoring yet have a background distant from agro-biodiversity sciences. Agricultural biodiversity is an important subset of biodiversity. Agricultural biodiversity is the key results of the interaction among the genetic resources, environment and management systems, as well as practices used by global diverse peoples and therefore the use of land and other resources for production in different ways. Agro-biodiversity Index plays an important role for monitoring framework and informs food systems policy.

Keywords

Agro-biodiversity · ABDI · Agri-ecosystem · Natural resources management

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1.1 Agro-Biodiversity and Agri-Ecosystem

Mara country is an agricultural country. For centuries, human civilizations have been giving important place to agriculture. Ancient agriculture was completely based on traditional knowledge. Humans have developed many methods of agriculture through centuries of experiments (McDaniel et al. 2014; Beillouin et al. 2019; Stomph et al. 2020). The relationship of agriculture with nature is very old. After the adoption of modern agriculture in our country, our biodiversity, biodiversity, natural resources, environment, and ecology have been harmed to a great extent. In order to provide food to the growing population, through the Green Revolution, chemical fertilizers were used in more and more quantities in the fields. Along with this, the use of toxic chemicals for disease and pest control in crops increased, as a result of which the residues of chemical elements are directly affecting the ground water and air and human life directly and indirectly through crops (Raseduzzaman and Jensen 2017; Renard and Tilman 2019; IFPRI 2019).

Agricultural biodiversity or agro-biodiversity is not only backbone of sustainable agriculture but also essential components of different farming systems, viz., horticulture, agro-forestry, fisheries, poultry, and other crops and cropping systems. Agricultural biodiversity is the foundation of feasible horticultural increases including various parts of cultivating frameworks like crops, agro-forestry, crops and trimming frameworks, plantations, livestock, fisheries, poultry, and so on (Almekinders et al. 1995; Brookfield and Padoch 1994). It gives food and raw materials for product's manufacturing, for example, cotton for textile industry, wood as fuel and construction material, plants and roots utilized for nutrition, medicinal, and biofuels source and with occupations and earnings, together with those got from resource cultivating.

Agro-biodiversity is viewed as the biodiversity's subset of which involves the variability and diversity of plants, microorganisms, and preservation of genetic resources and animals by means of in situ and ex situ conservation associated to agricultural sector. With the use of modern resources in the fields, the farmer is gradually becoming dependent on the market. The farmer has become completely dependent on the market for seeds, chemical fertilizers, and disease and pest control for farming (Doolittle 1984; Guo et al. 1996; Koziell 1998). The debt burden on the farmers is increasing due to the high expenditure on farming. Due to the excessive use of chemical fertilizers and pesticides, not only does the production cost increase in farming, but chemical fertilizers gradually reduce the fertility of the field and the effect of pesticides on insects and diseases also decreases. Due to the high production of the same type of crops, there is also a decrease in the market price, and farmers do not get proper economic benefits, due to which the farmer is becoming financially weak. There are a total 170 pesticides registered in our country. Out of which 64% pesticides are used in agriculture. It is estimated that of the total pesticide use 45.5% is in cotton, 22.8% in paddy, and 6.4% in wheat. Farmers are taking loans from banks or moneylenders due to the increasing production value from the purchase of agricultural machinery, chemical fertilizers, and pesticides used in modern farming. Even after spending more, when the farmer is not able to get the expected production and profit, then he is not able to repay the loan on time (Netting 1996; Padoch and de Jong 1992; Pimentel et al. 1992). In such a situation, the farmer either mortgages his land or sells the land to deposit the loan installment. It has even been seen that the farmer is getting rid of debt by selling his body parts or is finally embracing death in case of failure to repay the loan. The environmental balance is deteriorating day by day due to excessive use of chemicals. The fertility of the land is decreasing and the land is becoming barren. Due to the use of more chemicals, beneficial insects are getting destroyed, and the outbreak of harmful insects is increasing in the crops. Whereas on the other hand the biodiversity, with the increasing use of single crop, developed and hybrid seeds, biodiversity is decreasing day by day. Agro-ecology is the systematic study of environmental processes related to agricultural production systems. It also emphasizes the development of measures to reduce the environmental harm caused by agriculture whether it is pollution, or damage to forests and wildlife, or any other adverse effect (Thrupp 1998; UNEP 1998; Wood and Lenné 1997).

1.2 NITI Aayog Policy in India

International experts at a conference organized by NITI Aayog on 29 May supported efforts to substantially promote agro-ecological and natural farming approaches in India. Presenting his views to senior international and national experts and policy makers, Union Agriculture Minister Shri Narendra Singh Tomar said, “Natural farming is our indigenous system based on cow dung and urine, biomass, mulch and soil aeration. In the next 5 years, we intend to reach 20 lakh hectares in any form of organic farming including natural farming, of which 1.2 million hectares is under Bhartiya Prakritik Krishi Padhati (BPKP)”.

He said that Paramparagat Krishi Vikas Yojana, launched in 2015 to promote organic farming among small and marginal farmers, has covered 7 lakh hectares and 8 lakh farmers in the last 4 years. He said that Andhra Pradesh, Karnataka, Himachal Pradesh, and Kerala have adopted natural farming on a large scale. In Andhra Pradesh alone, 2 lakh hectares of land has been brought under natural farming under this scheme. Forming the basis for the first-of-its-kind online high-level roundtable conference in India, Dr. Rajiv Kumar, Vice Chairman, NITI Aayog, asked whether agro-ecology and natural farming would be “preventing excessive and unnecessary use of water, farmer indebtedness, will contribute towards reducing greenhouse gases while supporting farmers’ incomes and their ability to adapt to climate change,” setting the high standards required for transformation and renewal of agriculture in India.

Organic farming is a cultural system of autonomy based on the optimal use of organic or organic natural resources, without using no chemical, synthetic, or genetically modified organisms (GMOs) and fertilizers to obtain organic food without deteriorate the quality of land and environment. All this in a sustainable, balanced, and maintainable manner. The main objective of organic agriculture is obtaining healthy food of high nutritional quality and obtained through sustainable

Fig. 1.1 ABDI approach to Agro-biodiversity Index

processes, without the presence of chemical synthesis substances. This type of agriculture is a global system of production management, which enhances the health of agro-ecology, including biological diversity, biological cycles, and soil biological activity. Agro-biodiversity Index (ABDI) also plays a very vital role in a food systems approach to collating agro-biodiversity data aimed at enabling policy makers, non-governmental organizations, civil society leaders, and businesses to understand relationships between dimensions of agro-biodiversity across the food system, compare agro-biodiversity use and conservation across countries, and identify priority interventions to enhance agro-biodiversity for more sustainable food systems (Fig. 1.1).

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Part II

Agro Biodiversity Conservation and Challenges

2

An Assessment of Forest Diversity: Challenges and Management

Pranab Pal

Abstract

Forests have played a critical role in enriching human life's social, economic, and religious facets in several ways, both materialistic and psychological. India is one of the world's most diverse woodland habitats. Forests are valued at 20% (i.e., 3.28 million sq. km of the total land in India). Forests should be handled for the advantage of the highest number in the long term. The existence of canopies explains how forests accumulate nitrogen from the atmosphere and survive without much fertilization, unlike the agricultural fields. And organisms like insects, birds, mammals, etc. add to the biodiversity of trees and forests. India's woodland cover rose from 640,319 sq. km (i.e., 11.2%) in 1987 to 712,249 sq. km in 2019. In this paper, a detailed assessment of forest diversity is provided by dividing it into three segments: mangroves' significant role in affecting the woodland diversity considering it as one of the most important sources of biodiversity on the planet; wildfire is the oldest and most widespread threat in forests since it claims to threaten not just the forest resources but also the fauna and flora of the whole regime, severely disrupting biodiversity; and finally, how trees boost the environment and hence the effect of climate change on the overall destruction of forests. Due to this around 90% of the large stocks of predatory fish are gone. India is home to approximately 300 amphibian species, and about 60% of these species in India is endemic. Around 20–25% of global greenhouse gas emissions are liable for deforestation and 30% of topographical zone is influenced through land debasement. The Intergovernmental Science-Policy Forum on Biodiversity and Ecosystem Services has (IPBES) reported that 1,000,000 species are at present risk of elimination. Biodiversity's misfortune is attributable to a few reasons, but the methods by far the most guilty parties are natural decimation as

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well as over-exploitation of biodiversity, powered by our detonating numbers and undefended usage. Plastic has gotten irreplaceable during the COVID-19 pandemic, driving atmosphere champions. India creates 9.4 million tons of plastic waste each year (approx 26,000 tons for every day). Only 5.6 million is reused, even as about 3.8 million tons are gone uncollected. Sea life biologists have cautioned that by 2050 there will be extra plastic in the Earth's oceans than fish. The four types of marine turtles that happen in India's beachfront alongside marine climate are completely jeopardized. The World Conservation Union (IUCN) states that the effects of outsider intrusive species are tremendous, unpretentious, and typically irreversible. They might be as harmful toward local species alongside biological systems on a worldwide scale of the misfortune and corruption of environments. The world is currently losing a concerning rate of ten billion trees each year. Because of these consolidated impacts of environmental change and anthropogenic activities, about 42% of the 260,553 km^2 of elephant natural surroundings is eradicated. Lately, rhino numbers have dropped drastically because of poaching for their horn which is valued inside Asian nations. And about 50% of all mammalian and bird species could go extinct in the next 200–300 years. Air defilement is one of the most distinguishably loathsome scourges to have biased India. Hence, this chapter primarily focuses on most ecosystems are under threat from several factors, and each new consequence adds to the stress already felt by ecosystems and their wildlife.

Keywords

Deforestation · Human pressure · Climate change · Forest fire · Sustainability

2.1 Introduction

Nature works persistently as per its laws, yet man abuses it continually in various ways and on various occasions. Nature tells the man that there isn't anything on the planet that isn't liable to change. Nature has given a warning that even the entire world might be (Choubey 2019) pulverized in a not so distant future. Practically every time, we neglect to evaluate, or even factor in, the natural expense of such cataclysms. Forests are basic territories for biodiversity, and they are likewise basic for the arrangement of a wide scope of biological system benefits that are critical to human prosperity. The tree has numerous advantages for the whole existence of our planet. Trees tower gloriously into the air where they retain carbon and deliver oxygen, a cycle that allows the very existence of (Berlyn 2020) aerobic life forms like people to exist. Their underlying foundations infiltrate profoundly into the dirt where they reuse supplements around the rhizosphere. Trees cover only around 33% of the earth's surface, but they are responsible for roughly 66% of the planet's carbon capture through the photosynthetic cycle.

Desertification and land debasement is one of the greatest ecological dangers that the world network is looking at in present-day times. The risky impact is clear all over the place. Switching land corruption and its results while quickening positive accomplishments for individuals and environments to convey Sustainable Development Goals involve prime significance. Every year, the world loses 12 million hectares of land (Ojha 2019) enough to create 20 million tons of food grains because of overexploitation and climatic varieties. If we talk about the calamitous results of land corruption and desertification of India, the image appears to be exceptionally somber. Approximately 30% of nations' entire geological territory is influenced by land contamination. The explanation behind deforestation and debasement could be because of (FSI 2017) redirection of forest land for non-ranger service reasons, infringements, and other biotic and regular aggravations in woods.

Today, over 1,000,000 species are very nearly annihilated, undermining worldwide food security, generally because of environmental misfortune and land debasement. Land corruption working couples with environmental change and biodiversity misfortune may compel up to 700 million individuals to move by 2050. Desertification land corruption and dry spell are immense difficulties. According to experts, India's population is projected to increase by 1.7 billion by 2050, and it was one of the first countries to agree on the 2030 Sustainable Development Target. India's CO_2 emissions will increase from 2.3 gigatonnes (Gt) per year currently to over 4.8 Gt in 2050 (Tripathi and Powell 2020) with 3.3 Gt per year coming from coal use alone. As reported by the IUCN Red List of Endangered Species, 41% of amphibians, 25% of reptiles, 34% of conifers, 13% of birds, 31% of sharks and fishes, 33% of coral reefs, and 27% of crustaceans are threatened with extinction.

Amphibians are the first terrestrial vertebrates to have evolved on earth nearly 350 million years ago. They colonized virtually (Vasudevan et al. 2010) all habitats in the terrestrial biome. Indian amphibians pose a serious challenge to their life. Habitat degradation and fragmentation for growth and monoculture plantation are significant threats to forest species. Carbon capture through afforestation, reforestation, and forest conservation is one of the cheapest options (Rawat 2019) today for carbon sequestration. Additionally 20% of the world's 380,000 plant species are by the side of risk of extinction, making plants more endangered than birds, according to the first global report (Gilbert 2010) on the status of plant biodiversity. Fresh National Correspondence to the United Nations Framework Convention on Climate Change (UNFCCC) indicates that our forests account for around 12% of our national emissions. Globally, it is estimated that 22% of the forests found in developing (GEE, UNDP 2006) countries are managed by local communities. Conservation of habitats, mitigation of climate change, conservation of international waters, prevention of habitat loss, and removal of chronic organic contaminants are global environmental goals with local community need – issues that have been tackled in various ways across the world, based on the specific economic, cultural, political, and environmental circumstances of the countries involved.

2.2 Recapitulation of Forest Diversity

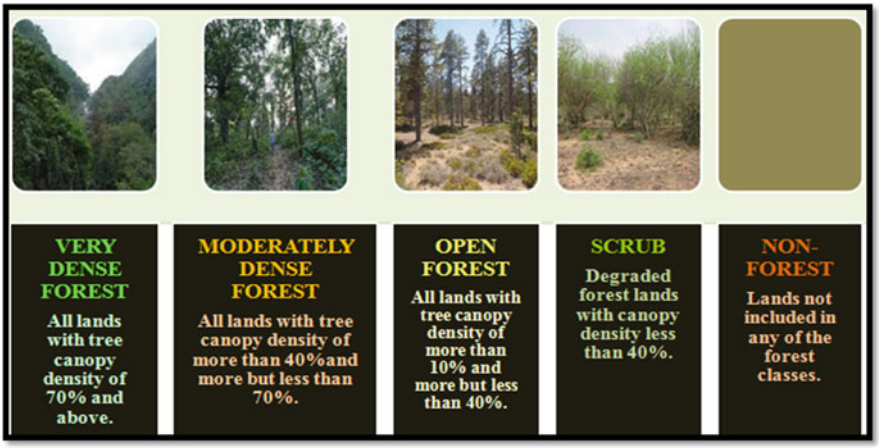
Since the cause of life in the topographical past, assorted biological systems have developed on earth which are overseeing the atmosphere and are the principal geological elements of our planet earth. Woodlands are fundamental for life on earth. 300,000,000 individuals overall live in timberlands, and 1.6 billion depend (WWF 2019) on them for their occupations. India is invested with different woodland types extending from tropical damp evergreen timberlands within the upper east as well as the southwest on the way to tropical dry thistle forests in focal and western India. Woodland is the second biggest land use in India close to agribusiness. The current woodland status of the world is the consequence of these changes, both characteristic and anthropogenic. The assortment of physiographic and climatic conditions has credited India with rich biodiversity.

Biogeographically, India is arranged at the tri-intersection of three domains, to be specific, Afro-tropical, Indo-Malayan, and Palaeo-icy domains. Forests are home to 80% of the world's earthly biodiversity. The most organically differing and complex woodlands on earth are tropical rainforests, where precipitation is plentiful and temperatures are in every case warm. Timberlands assume a basic part in moderating environmental switch since they absorb carbon dioxide and other ozone harming substances that would some way or another be free in the air and add to continuous changes in atmosphere designs. After independence as well, the forests of the nation stayed under colossal tension because of different variables. Lantana is one of the ten most reprehensible obtrusive species in the world and a form of high concern in India. The inquiry also brings attention to the 300,000 km^2 of forest area (an additional 44% of forest area) across India which is compromised by the Lantana strike, which means that there is a high chance (Rastogi 2020) of biodiversity misfortune due to Lantana intrusions in these regions.

1. *Very Dense Forest (VDF)*: with canopy the density of more than 70%.
2. *Moderately Dense Forest (MDF)*: canopy density 40–70%.
3. *Open Forest(OF)*: canopy the density between 10 and 40%.
4. *Scrub*: Degraded forest lands by way of canopy density less than 10%.
5. *Non-forest*: Lands not mentioned within some of the above classes (includes water) (Fig. 2.1).

The complete woodland front of the nation according to India State of Forest Report 2009 is 690,899 sq.km which establish 21.02% of the topographical zone of the nation. Of this 83,510 sq.km (2.54%) is extremely thick woods, the (Fig. 2.2) reasonably thick woodland comprises 319,012 sq.km (9.71%), and open forests establish 288,377 sq.km (8.77%). The mangrove spread in the (FSI 2011, 2013, 2017) nation is 4639 sq.km which is 0.14% of the complete geological territory. The absolute increment in woods and tree spread which together make up the nation's green spread – somewhere in the range of 2017 and 2019 – was 5188 sq.km.

The absolute weight on India's forests is exceptionally high due to the high populace. The fast development in the economy of the nation over the most recent



VERY DENSE FOREST
All lands with tree canopy density of 70% and above.

MODERATELY DENSE FOREST
All lands with tree canopy density of more than 40%and more but less than 70%.

OPEN FOREST
All lands with tree canopy density of more than 10% and more but less than 40%.

SCRUB
Degraded forest lands with canopy density less than 40%.

NON-FOREST
Lands not included in any of the forest classes.

Fig. 2.1 Types of forest cover. Source: FSI

multi decade has put extra requests on forests for foundation development. Forest assumes a significant function in the nation's biological solidness and financial turn of events. The public woodland strategy in India, since 1952, has defined an objective of bringing 33% of the region of the nation under timberland spread. India targets keeping up at least 33% of the nation's geological region under woods and tree spread. The extent of various wood thickness classes is portrayed in the pie outline in rate terms. According to FSI, the primary purpose behind the woods spread increment was because of the adjustment in the zone of the trees outside the woodlands. The woodlands of the planet earth were nonstop on change because of advancement. The current wood's status in the world is the aftereffect of the changes, both common and anthropogenic.

Concurring examination between 2015 and 2020, the pace of deforestation was assessed by the side of ten million hectares for every year, down (The State of the World's Forests 2020) from 16 million hectares for each year since 1990s. Agriculture and development keep on being the principal driver (Table 2.1) of deforestation as well as woodland debasement with the related loss of forests biodiversity. Appropriation of the woods spread over the globe is reliant on numerous variables, fundamentally topographical attributes, for example, elevation, geography/soil type, and atmosphere. Atmosphere conditions, for example, the temperature and the precipitation, are vital factors in deciding the woods dissemination. In terms of the level of land under woodland spread, South America is on the top, having almost 50% of its territory mass under timberland and in terms of per capita forests zone. As of December 2019, an aggregate of 20,334 tree species had been remembered for the IUCN Red List of Threatened Species (IUCN 2018), of which 8056 were surveyed as internationally undermined (Critically Endangered, Endangered, or Vulnerable) (Table 2.2).

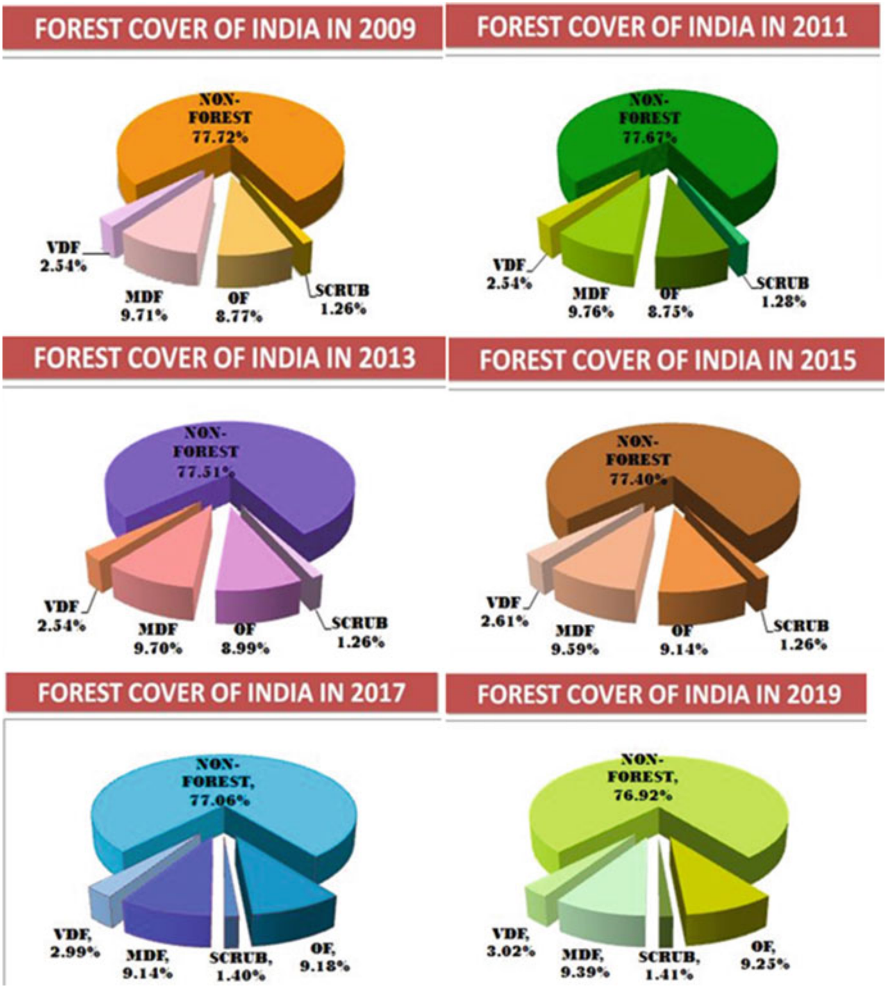


Fig. 2.2 Forest cover assessment. Source: FSI

Table 2.1 World forest area by region (Source: FFDM, NIDM)

Sl.no	Name of the region	Percentage (%)
1.	Africa	23
2.	Asia	19
3.	Europe	45
4.	Caribbean	30
5.	North and Central America	33
6.	South America	49
7.	Oceania	23

Table 2.2 Management of mangrove sites in India

Sl. no	Name of the state	Mangrove sites
1.	West Bengal	Sundarbans
2.	Odisha	Bhitarkanika, Mahanadi, Subarnarekha, Devi, Dhamra, mangrove genetic resources Centre, Chilka
3.	Andhra Pradesh	Coringa, east Godavari, Krishna
4.	Tamil Nadu	Pichavaram, Muthupet, Ramna, Pulicat, Kazhuveli
5.	Andaman and Nicobar	North Andaman's, Nicobar
5.	Kerala	Vembanad, Kannur
6.	Karnataka	Coondapur, Dakshina Kannada/Honnavar, Karwar, Mangalore Forest division
7.	Goa, Maharashtra	Achra-Ratnagiri, Devgarh-Vijay Durg, Veldur, Kundalika-Revdanda, Mumbra-diva, Vikroli, Shreevardhan, Vaitarna, Vasai-Manori, Malvan
8.	Gujarat	Gulf of Kachchh, gulf of Khambhat, dumas-Ubhrat

Over 1400 tree species are surveyed as fundamentally jeopardized and in earnest need of protection activity. As per a study The United Nations Trillion Tree Campaign has been dispatched to encourage (Crowther 2020) individuals all around the globe to reestablish trees. We have to help an enormous worldwide development to secure and reestablish the world's timberlands. This is an open door for us all to get included. This advantages us all.

2.2.1 Mangrove Habitats

The term "mangrove" is used to refer to a whole community of trees and shrubs. But the trees designated as mangroves are not closely related: they belong to several different plant families. Mangroves are salt-tolerant tropical and subtropical plants (TNAU 2016) in intertidal regions of the planet. The unique areas in which these plants occur are referred to as "mangrove habitats." Mangrove woods stabilize the coastline, minimizing erosion caused by storm surges, currents, waves, and tides. The complex root structure of mangroves also makes these forests attractive to fish and other species looking for food and protection from predators. Indonesia, Thailand, and Mexico are locations with especially large areas of mangrove forest. Mangroves internationally spread (Fig. 2.3) a territory of just around 152,000 sq.km in 123 tropical and sub-tropical countries and regions.

According to the FSI, India's mangroves cover 4975 km^2, or 0.15% of the country's topographical zone. Mangrove timberlands are biodiversity hotspots, and mangroves in India are the ideal pristine objections to see nature's endowments. Mangroves are available worldwide on different shorelines between roughly 250 N and 250S scope. Mangroves offer ideal habitats for many terrestrial and marine species, carbon sinks, and natural barriers against storm (www.

Fig. 2.3 Mangrove forests in India

mangrovesforthefuture.org) surges and coastal erosion. Mangroves provide invaluable services but have been declining worldwide because of anthropogenic and different dangers. Mangroves are critically desirable sites that take care of shrimp and fish areas. In addition, they limit storm damage. Despite their high economic value, mangroves are often harvested for timber and charcoal production and cleared for progress. In recent years, mangroves have been gradually cleared for rice production and commercial shrimp hatcheries, while South East Asia, in fact, as much as 15% of the mangrove land has been cleared for aquaculture purposes. About 35% of the world's mangrove forests have been lost, and 40% of mangrove native vertebrates are faced with extinction. Mangrove ecosystems are inhabited by a variety of salt-tolerant inter-tidal halophytic plants and innumerable amount of invertebrate and vertebrate fauna. Maybe, the most significant mangrove woods (Fig. 2.4) in India is the Sunderbans, and its popular occupant, the Bengal swamp tiger, the most desired wild felines in this aspect of the world. The total area under the mangrove ecosystem in India is about 0.8 million ha.

The important genera include Rhizophora, Ceriops, Bruguiera, Derris, Xylocarpus, Sonneratia, Acanthus, Avicennia, Heritiera, Nypa, Phoenix, etc. These are generally evergreen with thick leaves and sunken stomata. The trees primarily belong to the family *Rhizophoraceae*, *Verbenaceae*, and *Sonneratiaceae. Pneumatophores* also are a common adaptation in many species. Mangroves are a vital forest habitat, as can be seen in some of the mangrove plants, such as Bruguiera cylindrical and Sonneratia acida, which are on the verge of expansion. About 35,000 hectares of mangroves have been destroyed in India due to shrimp cultivation. Estimates of mangrove diversity suggest that there are 16–24 families and 54–75 species worldwide. The world's largest mangrove species was discovered in America (http://www.fao.org/forestry/mangroves).

The Educational Science as well as Cultural Body of the United Nations (UNESCO) supports the conservation of mangroves by means of drawing every one of its strength through its several programs to protect mangrove ecosystems in the vein of man along with the Biosphere Programme, the International Hydrological Programme, the Intergovernmental Oceanographic Commission, and the Local and Indigenous Information Structures Initiative Mangroves which are all listed in the

Fig. 2.4 Significance of mangrove

Biosphere Reserves, World Heritage Sites, and UNESCO World Heritage Sites geo parks.

According to mangroves management, there are 38 mangrove sites listed for extensive protection and management. It leads to the development of awareness, management, and protection of mangrove habitats around the world. To protect the genetic diversity of mangroves, the National Mangroves Genetic Resource Center has been established in Bhitarkanika in Odisha where the maximum number of mangrove species of the country is present in a single area. Mangroves are among the oldest as well as most creative wetland forests of our earth. Mangroves provide priceless services but have been declining worldwide as a consequence of anthropogenic as well as additional threats. Thus, while mangrove forests have a significant role to play for more valuable ecological resources, the scientific conservation of mangrove forests requires time not only for human well-being, but also for coastal biodiversity.

2.2.2 Perils of Wildfire

Wild hearth place is the maximum not unusual place danger to forest, and fires are as vintage because of the woodland itself. They pose a primary danger now no longer handiest to the woodland resources, however additionally to the whole regime, to the fauna and flora, and to the bio-range and ecology and surroundings of the region. The wood gets combined with the dry, senescent leaves in the fall, when there has been no rain for months, and the twinges of the may burst into the place with the slightest spark. The Himalayan forests, in particular Garhwal Himalayas, have been burning frequently over the last few summers, with the region's tremendous loss of vegetation. Several 37,059 fires were observed within 2018 using (Fig. 2.5) the MODIS (Moderate Resolution Imaging Spectro-Radiometer) sensor data.

Over 30,000 forest fires were registered in India in 2019; experts suggest that fire management (Srivastava 2020a, b) should concentrate on prevention, not containment, and that tribal populations should be targeted for successful management. Humans are responsible for around 95% of forest fires in India, primarily through the fostering of new grass flushes, the gathering of tiny forest things, and the use of land for shifting cultivation. Land capital, including carbon contained in biomass every year, and large tracts of woodland are threatened by fires of varying severity and size. According to forest inventory data, 54.40 per cent of forests in India are subject to sporadic fires, 7.49 per cent (Satendra and Kaushik 2014).

It is destroyed every year due to forest fires, which negatively affect the movement of goods and services greater than 6 feet (1.8 m) wide from the wooded area.

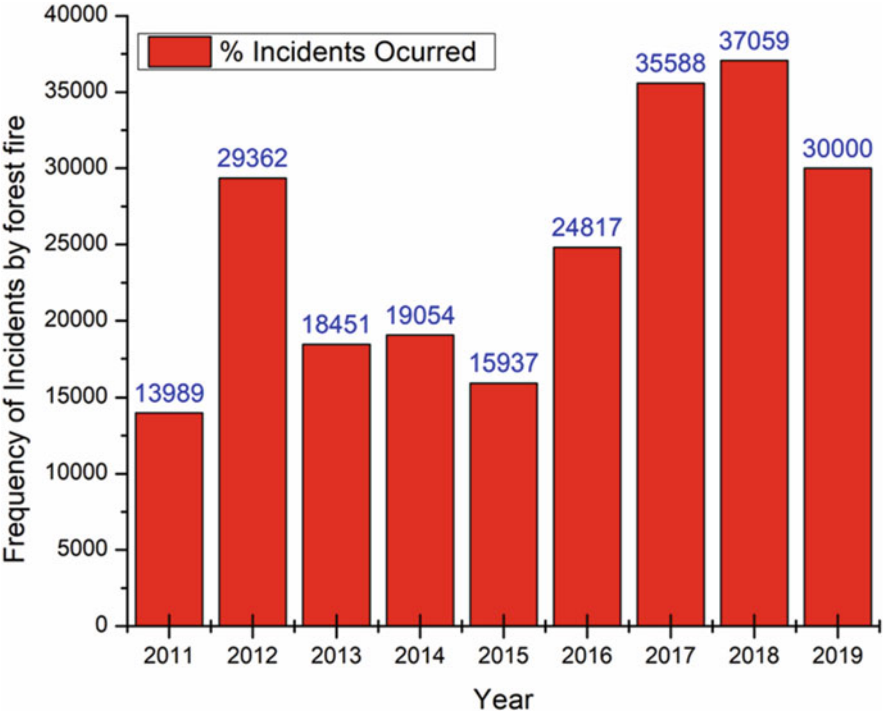


Fig. 2.5 Forest fire incidents in India (Source: FSI)

Fig. 2.6 Forest fire area in Uttarakhand and Assam

These shootings regularly arrive at the extents of significant fire and are now and then started by ignition and warmth from surface and ground fires. Different anthropogenic elements join to cause uncontrolled flames. Flames of shifting power and degree can influence a large number of hectares of woodland consistently, genuinely affecting the variable on supplement cycling and working of a biological system.

According to the data, the majority of the fires occurred in Uttarakhand, India, in 2019, with the Kumaon district (681) leading the way, followed by the Garhwal area (367), and the untamed life safe-havens and public parks (51) accounting for 938.77 hectares, 360.11 hectares, and 70.41 hectares of timberland, respectively (Fig. 2.6). Some timberland biological systems have developed in light of successive (Srivastava 2020a, b) fires from regular causes; however, most are helpless to the harmful impacts of fierce blaze. Every year, several hectares of the world's trees are lost by fire, causing monetary misfortune, environmental damage, and the loss of human life much like wild greenery. The ongoing Australian bushfires in 2019 ought to have pushed India to more readily get ready. A few animal types (more than one billion animal groups) have been affected severely by Australia's flames. Among the fowls, the Kangaroo Island Glossy Black Cockatoo, which happens just on Kangaroo Island, has endured the flames. These have likewise worn out its natural surroundings. There's another marsupial called the Kangaroo Island Dunnart.

Its environment has been totally scorched. In this way, the loss of these species has implied worldwide misfortunes since they happen no place else. Losing such species implies it will recuperate after the flames. The flames are consuming large areas of these trees, and the woodlands in the northeastern and central sections of India, as well as the country's central regions, have the most fire-prone areas. Almost a third of the timberland in Mizoram is classified as "extremely fire-prone".

In India, 65% of the provincial family depend (Hegde 2017) on kindling for cooking. Around 1,000,000 passings are accounted for yearly brought about by the exhaust of kindling for cooking. So as to spare forests from fire, it is important to receive the most recent procedures for putting out fires. The fires are a clear indication of climate change as well as they are taking place across the world. A portion of the fire concealment methods is to create three-meter wide fire paths around the fringe of the fire, reverse discharges, game plan of water shower, fire retardant synthetic substances ought to be splashed from the back tank and if conceivable by helicopters. There must be a prepared staff of firemen to control the fire.

2.3 Repercussions of Climate Change on Forest Diversity

Forests play an important role in climate change mitigation through acting as "sinks," absorbing as well as storing carbon from the atmosphere into biomass in addition to soil; other than when cleared or degraded, they are too noteworthy sources of greenhouse gas emissions. Forests are therefore significant components of climate change adaptation strategies. Without direct managing interventions, climate change is probable to jeopardize forest ecosystem health, pliability, efficiency, biodiversity, as well as carbon storage along with forest degradation in addition to thrashing which will continue to contribute to climate change, fascinating 2.6 billion tonnes of carbon dioxide every year, in relation to one-third of the carbon dioxide released from fossil fuel combustion.

Many studies suggested that the Himalayan range was in the midst of nearly all sensitive regions to climate change. Since the 1950s, the cold arid zone in Himachal Pradesh witnessed a pointed rise of about 10^{C} in mean temperature. On the other hand, this massive holding structure also ensures that as trees are burned down, there is a large collision. As per the Global Risk Report (GRR), by the World Economic Forum, the repercussions (Down To Earth 2020) of climate change are conspicuously harder as well as more rapidly than expected. Environmental risks now pinnacle the risks agenda. Deforestation accounts for about 20% of all greenhouse gas emissions rather than the entire transport industry in the country. Around the same time, the capacity to eradicate trees is diminished as forests are destroyed. Since deforestation and habitat depletion have such a major effect on climate change, minimizing forest losses can have many advantages for both wildlife and humans.

This includes cutting greenhouse gas emissions, carbon sequestration, providing other ecosystem services, and (WWF, UK) preserving intact, working ecosystems that have the greatest chance of resisting climate change. Forests have a significant effect on climate change by affecting the level of carbon dioxide in the atmosphere. When trees expand, carbon is eliminated from the atmosphere and consumed (Digests 2001) in wood, leaves, and soil. Adaptation and mitigation are two main approaches to climate change. Mitigation tackles the causes of climate change and adjusts the impacts. In the forestry industry, adaptation includes improvements in management strategies designed to reduce the vulnerability of trees to climate change and measures designed to reduce people's vulnerability to climate change. Forest conservation measures may be classified under four major categories: reduction of deforestation emissions; reduction of forest depletion emissions; enhancement of forest carbon sinks; and replacement of items. Forests are also sources of GHG emissions from greenhouse gases, primarily CO_2.

Deforestation and habitat depletion account for an estimated 17% of global (GHG) pollution. A report conducted by the United Nations for Disaster Risk Reduction (UNDRR) stated that India is in the third place after China and the

Table 2.3 Human cost of disasters (Source: UNDRR)

Sl.no	Disaster impact	1980–1999	2000–2019
1.	Reported disasters	4212	7348
2.	Total deaths	1.19 million	1.23 million
3.	Total affected	3.25 billion	4.03 billion
4.	Economic loses	$1.6 trillion	$3 trillion

USA to register the largest number of (TOI 2019) natural disasters. Extreme weather events – floods, storms, landslides, heat waves, drought, and wildfire – accounted for almost 91% of all 7348 natural disasters in the last 20 years (2000–2019) as compared to 4212 recorded (Table 2.3) between 1980 and 1999. The UNDRR also warned that global warming is causing more climate-related disasters, the frequency of which has increased by more than 83% in the last two decades compared to the previous two. There are significant risks to human life and property, including air pollution, influenza, earthquakes, drought, and climate change. Climate change and increased climate instability have both overt and indirect (FAO 2013) impacts on forests and forest-dependent residents. Biodiversity depletion or degradation has significant consequences for climate change.

According to climate change researchers, almost 49 million more individuals (Mahapatra and Jeevan 2018) will be pushed out of the workforce by 2020 at the cost of famine. India, being a developing country, would be affected by climate change in an unforeseen way. India, as an extra developed nation, will also face an unpredictable climate change effect. Climate change can have a number of effects on the distribution of woodland habitats and populations, and impacts on the structure and structure of habitats. Changing climate has a direct impact on the cost of water, energy supply, environmental protection, and mine closure techniques (Down To Earth 2018).

2.4 Challenges as an Outcome of Forest Degradation

Because woodland trees are the cornerstones of forest ecosystems, their existence is essential for some floral and faunal relationships in these biological systems. There is indeed pressure on woodland land resulting from the extraction of assets by businesses and infringement for the purpose of enhancing farming. The rising clashes between monitoring forests for producing environment administrations and redirection for formative undertaking present perhaps the greatest test in dealing with the woods assets. Since people started cutting trees, 40% of Earth’s tree spread has been obliterated. Up to 20% of ozone harming substance outflows every year is because of timberland spread misfortune. It is projected that demand in wood is rising faster from 58 million cubic meters in 2005 to 153 million cubic meters in 2020.

The annual production of the woodland stock can only gracefully contain 70 million cubic meters of timber, constraining us on the way to bring in hardwood lumber as of different countries. While actualizing these green plans, India faces colossal difficulties. Timberlands in India are now exposed to numerous stresses (Ravindra Nath 2012) including over-extraction, bug flare-ups, domesticated animals brushing, forest fires, and other anthropogenic weights. Environmental warming has a valid effect on the endurance of cultivated saplings. The extension of dry lands and desertification is another tremendous test that should be dealt with legal intercessions. There is a need for participatory afforestation models to integrate knowledge on local communities and better conservation of forest resource. Woods are the most important form of social development. The sages calculated the scientific and profound energy of the forest, living next to trees and streams of water. However, as problems with the advancement of creativity and self-assurance are incalculable, we should minimize them together.

2.5 Conclusion

We are battling to shield woodlands around the world from deforestation and corruption showing them a way to reclamation. Woodlands help settles the atmosphere, continue a variety of life, give financial chance, and are the wellspring of culture for some Indigenous Peoples. However, woodlands and other basic environments are yet to be determined, as there is expanding strain to change timberlands over to croplands, fields, and manors. At present, there are profoundly deficient securities against exercises that corrupt the estimation of woods. The current woods ought to be secured. The times of misuse have pulverized and debased a great part of the Earth's common timberlands. We've just lost a portion of our woodland land around the world.

Over the planet from the Amazon to Canada and Indonesia, huge territories are being corrupted to a great extent because of impractical modern exercises. Essentially, for the development of towns and urban communities, woodlands have been cleared, and this cycle proceeds right up 'til the present time causing the loss of forests spread. The need to secure those woodlands that remain is more earnest than any other time. Losing these essential biological systems is uprooting networks, undermining the territories of uncommon and imperiled species, and regurgitating ozone-depleting substances into the environment. Supportable woodland executives, reforestation, agro ranger service, empowering plant-based eating regimens, establishing biodiversity protection zones, and creating forest cover belts that store carbon play a central role in our future.

The Earth's greening can be accredited on the way to both reforestation and agricultural activity. The assessment of the ecological as well as genetic diversity of the Himalayan conifers is important for the assessment of budding responses to changing climate circumstances. Conservation plans for large temperate medicinal plants must be established. The effect of climate change on insects and diseases in the Himalayas must also be measured. In addition to prevention, concerted efforts are required to establish successful adaptation strategies. Land reforestation is very important in alleviating the current challenge of greenhouse gases, climate change, and habitat loss. All the way through these efforts, we focus on the top of creating a sustainable future. Administrations underlined the seriousness of thrifty forests to check the annihilation emergency as well as battle environmental change. Nature secures consideration of us if we acquire consideration of it. We must work hard to ensure what is left in order to keep a strategic distance from new consequences.

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Agrobiodiversity, Status, and Conservation Strategies

3

Kavita Singh

Abstract

Agrobiodiversity is a critical subset of biodiversity and significant from the perspective of biodiversity conservation. India is one of the megadiverse countries that holds around 8% of the global biodiversity and has 18% of the world's livestock. The country also has around 91,000 animal species and 46,000 plant species and which is 7% and 6.5% of the global flora and fauna, respectively. A large portion of the Indian residents is dependent on natural ecosystems for fuel, food, water, and medicine. Agrobiodiversity comprises the world's diversity of genetic resources (species used for food, fiber, fuel, fodder, pharmaceuticals, varieties, breeds). Moreover, it encompasses the diversity of non-harvested species that support production (pollinators, predators, soil microorganisms, etc.) and the diversity of the agroecosystems. In addition to being essential for environmental stability, agrobiodiversity is also crucial for local economic development and livelihood. The locals' dependence on agrobiodiversity is even more significant in areas without government-managed forests or protected areas. In India, the gene pool of native species of crops and cattle remained unnoticed for a long time. Around 140 native species of cattle are on the verge of extinction. The National Gene Bank has more than 300,000 samples of indigenous plants which are no longer cultivated. Many crops are grown, but only a few are consumed in large quantities, causing food security and health issues. Agrobiodiversity management has been analyzed in this chapter to provide conservation options, processes, methods, and good practices to help create a shared understanding of agrobiodiversity and conservation. In situ, ex situ, and on-farm conservation practices need priority, and their strengthening and

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integration with the overall conservation plans of the Central government are required.

Keywords

Agrobiodiversity · Conservation · Crop · Environment · Genetic resources · Economic

3.1 Introduction

3.1.1 Agrobiodiversity Terminology

Agriculture is a subset of biodiversity in general, as illustrated in Fig. 3.1 (FAO 1999). Agricultural biodiversity, also branded as agrobiodiversity, is a broad term that encompasses "the variety and variability of animal species, plants, and microorganisms at the genetic, species, and ecological levels that stabilize the ecosystem structures, functions, and processes in and around production processes, and that could provide food and non-food farm commodities" (FAO 1999). The significant agrobiodiversity constituents are as follows: centers of origin of cultivated species and varieties. It encompasses (1) harvested crop types, progenitors of cultivated plants and animal breeds, and their non-domesticated species; (2) non-harvested species such as microbes and pollinators that sustain agro-sylvan ecosystems; and (3) non-harvested species in the environment that contribute to the operation of food production ecosystems. The diversity of agrobiodiversity is also attributable to the interplay of culturally different ethnic groups through time and space on the breeding and selection of the progenitors of farmed species. It comprises the diversity and diversity of plants, animals, and microbes, which assist in functioning and maintain the agroecosystems' essential functions, including its processes and structures, ensuring agricultural production and food security (FAO 1999).

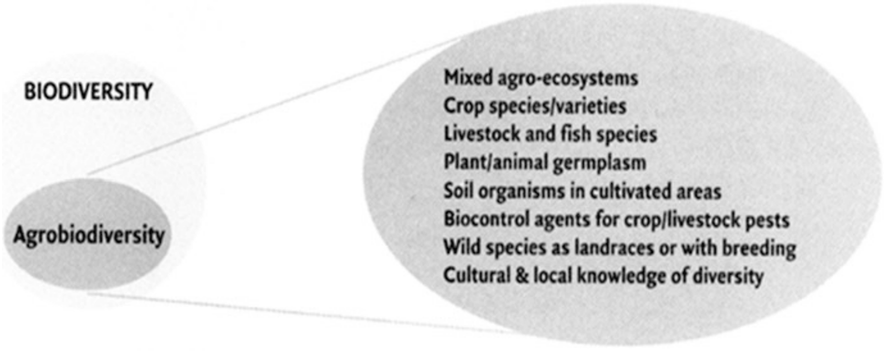

Fig. 3.1 Agrobiodiversity is a subset of biodiversity (FAO 1999)

It is critical for the sustainability of food systems and diets. Its management may help provide food, nutrition, and livelihoods security, and it is crucial for climatic adaptation and mitigation (Frison et al. 2011). An analysis of 172 case studies and project reports worldwide reveals that agricultural biodiversity adds to resilience in various ways, many of which are coupling in nature. These behaviors are explored to discover markers of resilience in agricultural landscapes using the social-ecological system's hypothesis as a conceptual framework (Mijatović et al. 2013).

3.1.2 Status of Biodiversity in India

Agriculture, including forestry, range management, and sustenance of plant biodiversity, has been the core of Indian civilization that dates back to several millenniums. The enormous plant diversity arising from India's varied soil, environment, and altitude variations has resulted in various crop species and varieties suiting to different domestic and commercial needs. This unique position of India has been well taken into account in the shield of Plant Varieties and Farmers' Rights Act 2001.

India, the birthplace of agrobiodiversity, is one of the world's largest 12 mega diversity nations and is widely regarded as a hub of crop plant domestication. India has been renowned for millennia for its cultures and the convergence of human migrations drawn to the lush Indo-Gangetic plains. Through selection and adaptations, ancient agricultural societies have cultivated and created a rich array of crop plants from this abundant variety from time immemorial. India's physiographic features and climatic patterns range from the highest snow-capped mountain ranges in the Himalayas to the moist tropics of the Western Ghats and from the maximum rainfall in Cherrapunji in Meghalaya to one of the lowest rainfall areas in the Thar desert.

India contains approximately 45,000 plant and fungus species, accounting for 11% of the globe's flora. India is abundant in endemic species, which account for 33% of the country's flora. India is one of the world's top 10 species-rich countries, with a high rate of endemism (MOEFCC 2017). The biodiversity hotspots (Mittermeier et al. 2004) as seen in Fig. 3.2 are as follows: (1) Himalaya: This word refers to the whole of India's Himalayan region (Bhutan, China, Pakistan, Tibet, Nepal, and Myanmar). (2) Indo-Burma: This includes all of north-eastern India excluding Assam and the Andaman and Nicobar Islands (and Myanmar, Thailand, Vietnam, Laos, Cambodia, and southern China). (3) The Western Ghats and Sri Lanka: This region includes the whole Western Ghats (and Sri Lanka). Sunderland: The Nicobar Islands (Singapore, Brunei, Philippines, Indonesia, Malaysia).

Moreover, it also has 25 micro hotspots of flora, 16 forest types, 251 subtypes, 166 crop plants, and around 320 wild relatives of cultivated plants originated in India. The region has 21 agro-ecological regions (Nayar 1996). Within the spectrum of crop species and wild relatives, there are thousands of varieties, cultivars, landraces, and ecotypes in India (Nayar et al. 2009). In India, crop species and

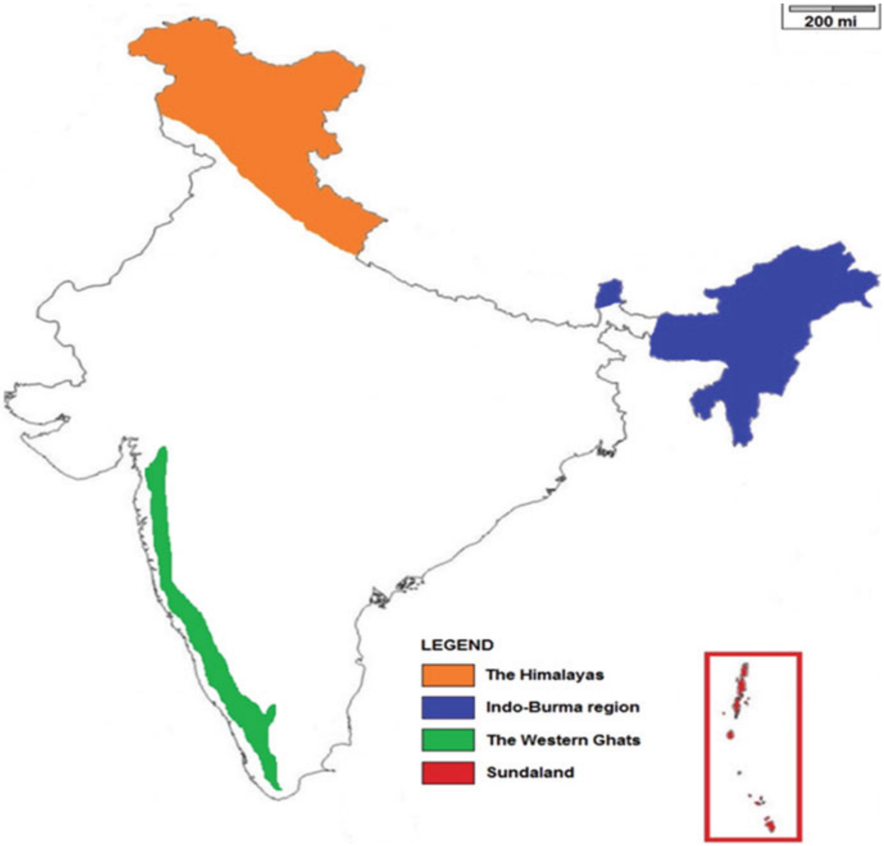

Fig. 3.2 India is part of four biodiversity hotspots (MOEFCC 2017)

wild relatives exist in thousands of variations, cultivars, landraces, and ecotypes. Indian farming cultures have developed and sustained an incredible array of crops throughout millennia to fit various habitats and ecological constraints. The Task Force suggested the following 22 agrobiodiversity hotspot regions in India based on their richness of agrobiodiversity, i.e., crop varieties, crop species, wild relatives of various crop species cultivated, social relevance and ancientness of agriculture, wild crop species occurring in the region, number of domesticated species, and exclusivity of agroecosystems (Nayar et al. 2009):

(1) Cold Desert Region, (2) Western Himalayan Region, (3) Eastern Himalayan Region, (4) Brahmaputra Valley Region, (5) Khasia-Jaintia-Garo Hills Region, (6) North-Eastern Hill Region, (7) Arid Western Region, (8) Malwa Plateau and Central Highlands Region, (9) Kathiawar Region, (10) Bundelkhand Region, (11) Upper Gangetic Plains Region, (12) Lower Gangetic Plains Region, (13) Gangetic Delta Region, (14) Chotanagpur Region, (15) Bastar Region, (16) Koraput Region, (17) Southern Eastern Ghats Region, (18) Kaveri Region,

(19) Deccan Region, (20) Konkan Region, (21) Malabar Region, and (22) Islands Region (Andaman and Nicobar Islands, Lakshadweep).

3.2 Agrobiodiversity Hotspots of India

3.2.1 Cold Desert Region

Cold desert's geographical location and range are Jammu and Kashmir (Ladakh, Leh (Nubra valley)) and Himachal Pradesh (Lahaul Spiti).

Its agrobiodiversity in terms of crops:

Cereals: Barley (*Hordeum vulgare*), wheat (*Triticum aestivum*); pseudocereal: buckwheat (*Fagopyrum esculentum*).

Vegetables: Bell pepper (*Capsicum frutescens*), cauliflower (*B.oleracea* var. botrytis), cabbage (*B. oleracea* var. *capitata*), onion (*A. cepa*), pea (*P. sativum*), potato (*S. tuberosum*), tomato (*Lycopersicon esculentum*).

Fruits: Apple (*Malus domestica*), apricot (*Prunus armeniaca*), seabuckthorn (*Hippophae rhamnoides).*

Medicinal plants: *Atropa acuminata, Dioscorea deltoidea, Ephedra gerardiana, Mentha longifolia, Podophyllum hexandrum, Saussurea bracteata*.

3.2.2 Western Himalayan Region

Western Himalayan region's geographical location and range are Jammu and Kashmir (Jammu, Kathua, Kupwara, Udhampur, Phulwama, Srinagar, Anantnag, Badgam, Doda), Himachal Pradesh (Bilaspur, Kullu, Mandi, Shimla, Chamba, Kinnaur, Solan, Una, Hamirpur, Kangra), and Uttarakhand (Almora, Dehradun, Nainital, Garhwal, Hardwar, Pithorgarh, Udhamsingh Nagar, Uttarkashi, Rudraprayag, Tewri-Garhwal, Bageshwar, Chamoli, Champawat).

Its agrobiodiversity in terms of crops:

Cereals: Maize (Z. mays), barley (H. vulgare), oat (A. sativa), ragi (Eleusine coracana), rice (O. sativa), wheat (T. aestivum), amaranth (Amaranthus hypocondriacus).

Millets: Foxtail millets (Setaria italica); buckwheat (Fagopyrum emarginatum).

Legumes: Chick pea (C. arietinum), black gram (V. mungo), French bean (Phaseolus vulgaris), horse gram (Macrotyloma uniflorus), lentil (Lens culinaris), ricebean (Vigna umbellata), soybean (Glycine max), mustard (Brassica juncea).

Vegetables: Brussels sprouts (B. oleracea var. gemmifera), chilli (Capsicum annuum), cabbage (Brassica oleracea var. capitata), cauliflower (B. oleracea var. botrytis).

Fruit: Apple (Malus domestica).

Tuber: Potato (Solanum tuberosum).

Spices: Saffron (Crocus sativus).

Sugar-yielding crops: Sugarcane (Saccharum officinarum).

Beverage: Tea (Camellia sinensis).

3.2.3 Eastern Himalayan Region

Eastern Himalayan region's geographical location and range are Sikkim, Arunachal Pradesh, and West Bengal (Darjeeling).

Its agrobiodiversity in terms of crops:

Cereals: Maize (*Z. m*ays), barley (*H. vulgare*), wheat (*T. aestivum*), rice (*O. sativa*) Pseudocereals: Amaranth (*Amaranthus hypocondriacus*), buckwheat (*Fagopyrum esculentum*).

Millets: Proso millet (*P. miliaceum*), finger millet (*E. coracana*).

Legumes: Adjukibean (*Vigna angularis*), blackgram (*Vigna mungo*), chenopodium (*Chenopodium album*), ricebean (*Vigna umbellata*), swordbean (*Canavalia gladiata*).

Vegetables: Brussels sprouts (*B. oleracea* var. gemmifera), cabbage (*B. olerace*a var. capitata), cauliflower (*B. oleracea* var. botrytis), dolichos (*Lablab purupureus*), soybean (*Glycine m*ax), winged bean (*Psophocarpus tetragonolobus).*

Fruits: Banana (*Musa acuminata*), chebulic myrobalan (*Terminalia chebula*), citron (*Citrus medica*), fig (*Ficus carica*), kiwi (*Actinidia strigosa*), lemon (*Citrus limon*), mandarin (*Citrus reticulata*), mango (*Mangifera indica*, *M. sylvatica*), peach (*Prunus domestica*).

Tuber: White yam (*Dioscorea alata*), yam (*Amorphophallus bulbifera*), taro (*Colocasia esculenta*).

Spices: Bengal cardamom (*Amomum aromaticum*), black pepper (*P. nigrum*), cinnamon (*Cinnamomum bejholgota*), cardamom (*E. cardamomum*), galanga (*Alpinia galanga*), ginger (*Z. officinale*), long pepper (*Piper longum*), niger (*Guizotia abyssinica*), perilla (*Perilla frutescens*), turmeric (*Curcuma longa*).

Oilseeds: Sesame (*Sesamum indicum*).

Fibre: Jute (*Corchorus olitorius*), mesta (*Hibiscus cannabinus*), tree cotton (*Gossypium arboreum*).

Sugar-yielding crops: Sugarcane (*Saccharum officinarum*).

Beverages: Tea (*Camellia sinensis*).

3.2.4 Brahmaputra Valley

Brahmaputra Valley's geographical location and range are Assam (Bongaigaon, Barpeta, Dhubri, Kokrajhar, Nalbari, Goalpara, Golaghat, Kamrup, Morigaon, Nagaon, Darrang, Sonitpur, Dibrugarh, Dhemaji, Jorhat, Lakhimpur, Sibsagar, and Tinsukia).

Crops:

Cereals: Maize (*Z. mays*), rice (*O. sativa*), wheat (*T. aestivum*).

Millets: Finger millet (*E. coracana*), foxtail millet (*S. italica*).

Legumes: Pigeon pea (*C. cajan*), black gram (*V. mungo*).

Vegetables: Bitter gourd (*Momordica charantia*), brinjal (*Solanum melongena*), luffa (*Luffa aegyptiaca, Luffa graveolens*).

Fruits: Coconut (*Cocos nucifera*), lemon (*Citrus limon*), mango (*Mangifera indica*), plantain (*Musa acuminata*), pineapple (A*nanas comosus*), pumello (*Citrus maxima*).

Tubers: Elephant-foot yam (*Amorphophallus bulbifer*), white yam (*Dioscorea alata*), taro (*Colocasia esculenta*).

Spices: Arecanut (*Areca catechu*), Bengal cardamom (*Ammomum aromaticum*).

3.2.5 Khasia-Jaintia- Garo Hill

Meghalaya (East Garo Hills, South Garo Hills, East Khasi Hills, West Garo Hills, West Khasi Hills, Jaintia Hills, and Ri-Bhoi).

Crops:

Cereals: Maize (*Z. mays*), rice (*O. sativa*).

Millets: Soft-shelled forms (*Coix lacryma-jobi*).

Legumes: Rice bean (*Vigna umbellata*).

Vegetables: Bitter gourd (*Momordica charantia*), brinjal (*Solanum melongena*), Brussels sprouts (*B. oleracea* var. gemmifera), cauliflower (*B. oleracea* var. botrytis), cabbage (*B. oleracea* var. capitata), cucumber (*Cucumis sativus*), ridged gourd (*Luffa acutangula*), snake gourd (*Trichosanthes cucumeriana* var. anguina, T. cucumeriana var. cucumeriana), sponge gourd (*Luffa aegyptiaca*), tomato (*Lycopersicon esculentum*).

Fruits: Banana (*Musa acuminata*), mango ginger (*Curcuma amada*), pineapple (*ananas comosus*).

Tuber: Potato (*Solanum tuberosum*).

Fiber: Cotton (*Gossypium hirsutum*).

Jute: (*Corchorus capsularis*).

Spices: Ginger (*Zingiber officianale*), pepper (*Piper nigrum*).

3.2.6 Northeast Hills

Manipur (Bisnupur, Imphal (East), Imphal (West), Thoubal, Tamenglong, Ukhrul, Chandel, Senapati, Ukhrul,), Nagaland (Kohima, Dimapur, Phek, Mokokchung, Mon, Tuensang, Wokha, Zunheboto), Mizoram (Aizwal, Lunglei, Champhal, Kolasib, Lawngtlai, Marnit, Chhimtuipui, Serchhip), and Tripura (North Tripura, South Tripura, West Tripura, and Dhalai).

Crops:

Cereals: Barley (*H. vulgare*), rice (*O. sativa*), maize (*Z. mays*), sorghum (*S. bicolor*) Pseudocereals: Amaranth (*A. hypocondriacus*).

Millets: Foxtail millet (*S. italica*), finger millet (*E. coracana*), soft-shelled forms (*Coix lacryma-jobi*).

Legumes: Mustard (*Brassica juncea*), rice bean (*Vigna umbellata*), pigeon pea (*Cajanus cajan*).

Vegetables: Brussels sprouts (*B. oleracea* var. gemmifera), brinjal (*Solanum melongena*), carrot (*Daucus carota*), cauliflower (*B. oleracea* var. botrytis), cabbage (*B.. oleracea* var. capitata), chenopodium (*Chenopodium album*), chilli (*Capsicum annuum*), cucumber (*Cucumis sativus*), spinach (*S. oleracea*), onion (*A. cepa*), tomato (*L. esculentum*).

Fruits: Banana (*Musa acuminata*), kudzu vine (*Pueraria edulis*), melon (*Cucumis melo*), pineapple (*Ananas comosus*).

Spices: Ginger (*Zingiber officianale*).

Fiber: Jute (*Corchorus olitorius*).

Beverages: Coffee (*Coffea arabica*), tea (*Camellia sinensis*).

3.2.7 Arid Western Region

Rajasthan (Churu, Hanumangarh, Ganganagar, Sikar, Nagaur, Pali, Jalore, Sirohi, Jodhpur, Udaipur, Dungarpur, and Jhunjhunu, part of Jaisalmer, Bikaner).

Crops:

Cereals: Maize (*Z. mays*), sorghum (*S. bicolor*), wheat (*Triticum aestivum*), rice (*O. sativa*).

Millets: Pearl millet (*P. americanum*).

Legumes: Cowpea (*V. unguiculata*), chickpea (*Cicer arietinum*), clusterbean (*Cyamopsis tetragonolobus*), green gram (*V. radiata*), black gram (*V. mungo*), moth bean (*Vigna aconitifolia*), sponge gourd (*Luffa aegyptiaca*).

Oilseeds: Rapeseed, taramira (*Brassica napus*), sesame (*Sesamum indicum*).

Forage legume: *Crotalaria burhia*.

Fodder grasses: *Cenchrus ciliaris*, C. *setigerus*, *Chrysopogon fulvus*, *Lasiurus scindicus*, *Sorghum halepense*.

3.2.8 Malwa Plateau and Central Highlands

Madhya Pradesh (Bhopal, Indore, Jabalpur, Shadol; Sehore, Shajapur, Raisen, Ujjain, Mandasaur, Rajgarh, Hoshangabad, Mandla, Narsinghpur, Umaria).

Crops:

Cereals: Barley (*Hordeum vulgar*e), maize (*Z. mays*), sorghum (*S. bicolor*), wheat (*T. aestivum*), rice (*O. sativa*).

Millets: Foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*), kodo millet (*Paspalum scrobiculatum*), proso millet (*Panicum miliare*), pearl millet (*Pennisetum americanum*).

Legumes: Chickpea (*Cicer arietinum*), cowpea (*V. unguiculata*), black gram (*V. mungo*), garden pea (*P. sativum*), green gram (*V. radiata*), horse gram (*Macrotyloma uniflorus*), lentil (*Lens culinaris*), pigeon pea (*Cajanus cajan*).

Vegetables: Musk melon (*Cucumis melo* var. culta), melon (*Cucumis melo* var. agrestis), soybean (*Glycine max*).

Fruit: Watermelon (*Citrullus lanatus*).

Medicinal plants: Opium (*Papaver somniferum*).

Oilseeds: Groundnut (*Arachis hypogaea*), linseed (*Linum usitatissimum*), mustard (*Brassica juncea*), niger (*Guizotia abyssinica*), safflower (*Carthamus tinctorius*), sesame (*Sesamum indicum*).

Spices: Coriander (*Coriandrun sativum*), cumin (*Cuminum cyminum*), marijuana (*Cannabis sativus*).

3.2.9 Kathiawar Region

Gujarat (Ahemadabad, Amreli,Banaskantha, Bhavnagar, Bharuch, Jamnagar, Surendranagar, Rajkot, Porbandar, Junagarh, Surat, Navsari, Valsad, Anand).

Crops:

Cereals: Barley (*H. vulgare*), maize (*Z. mays*), rice (*O. sativa*), sorghum (*S. bicolor*), wheat (*Triticum aestivum*).

Pseudocereals: Amaranth (*amaranthus hypocondriacu*s).

Millets: Foxtail millet (*Setaria italica*), finger millet (*E. coracana*), pearl millet (*Pennisetum glaucum*), kodo millet (*P. scrobiculatum*), proso millet (*Panicum miliaeceum*).

Legumes: Black gram (*V. mungo*), cowpea (*V. unguiculata*), chickpea (*Cicer arietinum*), cluster bean (*Cyamopsis tetragonolobus*), moth bean (*Vigna aconitifolia*), green gram (*V. radiata*), mustard (*Brassica juncea*), pigeon pea (*C. cajan*).

Vegetables: Bitter gourd (*M. charantia*), brinjal (*Solanum melongena*), bottle gourd (*L. siceraria*), chilli (*Capsicum annuum*), okra (*abelmoschus esculentus*).

Fruit: Guava (*Psidium guajava*), jamun (*Syzygium cuminii*), mango (*Mangifera indica*).

Spices: Cumin (*Cuminum cyminum*).

Oilseeds: Sesamum (*Sesamum indicum*), castor (*Ricinus communis*), cotton (*Gossypium herbaceum*), groundnut (A*rachis hypogaea*).

Forages legumes and grasses: *Alhagi pseudalhagi*, *Cenchrus biflorus*, *C. ciliaris*, *Chloris villosa*, *Cynodon dactylon*, *Dactyloctenium aegypticum*, *D. scindicum*, *Eleusine compressa*, *Eragrostis ciliaris*, *Indigofera oblongifolia*, *Medicago sativa*, *Sorghum halpense*.

Sugar-yielding crops: Sugarcane (*Saccharum officinarum*).

Narcotics: Tobacco (*Nicotiana tabacum*).

3.2.10 Bundelkhand Region

Uttar Pradesh (Jhansi, Banda, Chitrakoot, Damoh, Datia, Hamirpur, Jalaun, Lalitpur) and Madhya Pradesh (Damoha, Datia, Panna, Sagar, Tikamagarh Chattarpur, Rewa, Sidhi, Satna).

Crops:

Cereals: Barley (*H. vulgare*), wheat (*T. aestivum*).

Millets: Pearl millet (*Pennisetum glaucum*), sorghum (*S. bicolor*), chickpea (*Cicer arietinum*).

Legumes: Mung bean (*V. radiata*), soybean (*Glycine m*ax), urd bean (*V. mungo*), pigeon pea (*C. cajan*).

Fruit: Watermelon (*Citrullus lanatus*).

Vegetables: Bitter gourd (*Momordica charantia*), cucumber (*Cucumis sativus*), muskmelon (*Cucumis callosus*), okra (*abelmoschus esculentus*), snake gourd (*Trichosanthes cucumeriana*. Var. anguina).

Oilseeds: Groundnut (*arachis hypogaea*), linseed (*Linum usitatissimum*), rapeseed (*Brassica napus*), mustard (*Brassica juncea*), niger (*Guizotia abyssinica*), safflower (*Carthamus tinctorius*), sesame (*Sesamum indicum*).

Fiber: Cotton (*Gossypium herbaceum*).

3.2.11 Upper Gangetic Plains

Central Uttar Pradesh (Hardoi, Sitapur, Barabanki, Lucknow, Unnao, Rae Bareilly, Kanpur, Kannuj) and North-eastern Uttar Pradesh (Maharajganj, Gorakhpur, Sidharatnagar, Sant Kabir Nagar, Kushinagar, Deoaria, Basti).

Crops:

Cereals: Maize (*Z. mays*), sorghum (*S. bicolor*), rice (*O. sativa*), wheat (*T. aestivum*) Pseudocereals: Amaranth (*Amaranthus hypocondriacus*), buckwheat (*Fagopyrum esculentu*m) Millets: Kodo millet (*Paspalum scrobiculatum*), pearl millet, garden pea (*Pisum sativum*), lentil (*Lens culinaris*), green gram (*V. radiata*), pigeon pea (*C.s cajan*).

Vegetables: Ash gourd (*Benincasa hispida*), Brussels sprouts (*B. oleracea* var. gemmifera), cauliflower (*B.oleracea* var. botrytis), cabbage (*B. oleracea* var. capitata), bitterguard (*Momordica dioica*), *Luffa echinata*, ridged gourd (*Luffa acutangula*), round gourd (*Citrullus fistulosus*), *Solanum incanum.*

Fruits: Water chestnut (*Trapa natans* var. bispinosa).

Oilseeds: Black mustard (*Brassica nigra*), safflower (*Carthamus tinctorius*), mustard (*Brassica tournifortii*), sesame (*Sesamum indicum*).

Spices: Fenugreek (*Trigonella foenum-graceum*).

Fiber: *Corchorus trilocularis.*

Sugar-yielding crops: Sugarcane (*Saccharum officinarum*)

3.2.12 Lower Gangetic Plain

North Bihar (The Paschim Champaran, Purbi Champaran, Gopalganj, Siwan, Sitamarhi, Muzaffarapur, Sasaram, Buxar, Bhjojpur, Patna, Bhabua, Rohatas, Jhanabad, Vaishali, Samastipur, Darbangha, Madhubani, Sheohar, Madhupura).

Crops:

Cereals: Barley (*Hordeum vulgare*), maize (*Zea mays*), rice (*Oryza sativa*), sorghum (S*orghum bicolo*r), wheat (*Triticum aestivum*).

Pseudocereals: Amaranth (*Amaranthus hypocondriacus*).

Millets: Finger millet (*Eleusine coracana*), foxtail millet (*Setaria italica*), kodo millet (*Paspalum scrobiculatum*), proso millet (*Panicum milliare*).

Legumes: Black mustard (*B. nigra*), mustard (*Brassica juncea*), rape seed (*Brassica napu*s), black gram (*Vigna mungo*), chickpea (*Cicer arietinum*), green gram (*V. radiata*), cowpea (*Vigna unguiculata*), pigeon pea (*C. cajan*), ricebean (*Vigna umbellata*), lentil (*Lens culinaris*).

Vegetables: Brussels sprouts (*B. oleracea* var. gemmifera), chilli (*Capsicum annuum*), cabbage (*Brassica. oleracea* var. capitata).

Fruit: Mango (*Mangifera indica*), water chestnut (*Trapa natans* var. bispinosa).

Tuber: Potato (*Solanum tuberosum*).

Oilseeds: Cotton (*Gossypium herbaceum*), safflower (*Carthamus tinctorius*).

3.2.13 Gangetic Delta

West Bengal (Howrah, North 24 Parganas, Hooghly, Nadia, Birbhum, Bardhaman, South 24 Parganas, and Murshidabad).

Crops:

Cereals: Barley (*Hordeum vulgare*), rice (*O. sativa*), maize (*Z. mays*), sorghum (*S. bicolor*), wheat (*T. aestivum*).

Pseudocereals: Amaranth (*Amaranthus hypocondriacus*).

Millets: Finger millet (*E. coracana*), kodo millet (*P. scrobiculatum*), foxtail millet (*S. italica*).

Legumes: Chickpea (*C. arietinum*), pigeon pea (*C. cajan*), green gram (*V. radiata*).

Vegetables: Bitter gourd (*Momordica charantia*), Brassica (*Brassica oleracea*, *B. oleracea*, *B. oleracea*), chilli (*Capsicum annuum*), cucumber (*Cucumis sativus*), karonda (*Carissa carandas*), Luffa (Luffa aegyptiaca), musk melon (*Cucumis melo)*, winged bean (*Psophocarpus tetragonolobus*).

Fruits: Pomello (*Citrus maxima*).

Tuber: Elephant-foot yam (*Amorphophallus bulbifer*, *A. campanulatus*), potato (*Solanum tuberosum*), taro (*Colocasia esculenta*, *C. fallax*).

Oilseeds: Sunflower (*Helianthus annuus*).

Fiber: Jute (*Corchorus capsularis*).

Beverages: Tea (*Camellia sinensis*).

Sugar-yielding crops: Sugarcane (*S. officinarum*).

Narcotics: Tobacco (*N. tabacum*).

3.2.14 Chota Nagpur Region

Jharkhand (Palamau, Ranchi, Lohardaga, Hazaribhag, Singhbhum, Gumla, and Santhal Pargana. Orissa: Mayurbhanj).

Crops:

Cereals: Maize (*Zea mays*), rice (*O. sativa*), sorghum (*S. bicolor*).

Pseudocereals: Amaranth (*Amaranthus hypocondriacus*).

Millets: Finger millet (*Eleusine coracana*).

Legumes: Horse gram (*M. uniflorum*), moth bean (*Vigna aconitifolia*), pegion pea (*Cajanus cajan*), rice bean (*Vigna umbellata*).

Vegetable: Bottle gourd (*Lagenaria siceraria*), Brassica (*Brassica oleracea*, Brinjal (*Solanum melongena*), cucumber (*Cucumis sativus*), kundri (*Coccinia indica*).

Fruit: Pineapple (*Ananas comosus*).

Tubers: Taro (*Colocasia esculenta*), yam (*Dioscorea esculenta*).

Spices: Ginger (*Zingiber officinalis*).

3.2.15 Bastar Region

Chhattisgarh (Bastar, Bilaspur, Durg, Raipur, Jashpur, Kabirdham, Kanker, Korba, Koria, Mahasamu, Kondaigoan, Rajnandgoan).

Crops:

Cereals: Sorghum (*S. bicolor*), rice (*O. sativa*), wheat (*T. aestivum*).

Pseudocereals: Amaranth (*Amaranthus* spp.)

Millets: Barnyard millet (*Echinochloa frumentacea*), finger millet (*E. coracana*), kodo millet (*P. biculatum*), little millet (*P. sumatrense*).

Legumes: Black gram (*V.mungo*), chickpea (*Cicer arietinum*), green gram (*V. radiata*), moth bean (*V. aconitifolia*), mustard (*Brassica juncea*), pigeon pea (*Cajanus cajan*).

Vegetables: Bottle gourd (*L. sicerarea*), brinjal (*S. melongena*), chickling pea (*Lathyrus sativus)*, dolichos bean (*Lablab purpureus*), kundri (*Coccinia indi*ca), pumpkin (*Cucurbita pepo*), okra (*Abelmoschus esculentus*), winged bean (*Psophocarpus tetragonolobus*).

Tubers: Yam (*Dioscorea bulbifera*), sugarcane (*Saccharum officinarum*).

3.2.16 Koraput Region

Orissa (Gajpati, Kalahandi, Koraput, Malkangiri, Jeypore, Bolangir, Sonabeda, Nabrangpur, Rayagada) and Andhra Pradesh (Srikakulam, Vishkhapatnam, Vizianagram).

Crops:

Cereals: Maize (*Z. mays*), rice (*O. sativa*), sorghum (*S. bicolor*).

Pseudocereals: Amaranth (*Amaranthus hypocondriacus*).

Millets: Finger millet (*E. coracana*), foxtail millet (*S. italica*), kodo millet (*Paspalum scrobiculatum*), little millet (*P. sumatrense*), pearl millet (*P. americana*).

Legumes: Black gram (*V. mungo*), chickpea (*C. arietinum*), cowpea (*V. unguiculata*), green gram (*V. radiata*), horse gram (*M. uniflorum*), pigeon pea (*Cajanus cajan*), ricebean (*Vigna umbellata*).

Vegetables: Bitter gourd (*M. charantia*), brinjal (*S. melongena*), cabbage (*B. oleracea* var. capitata), cauliflower (*B. oleracea* var. botrytis), chilli (*Capsicum annuum*), cucumber (*Cucumis sativus*), dolichos (*Lablab purpureus*), melon (*Cucumis melo* var. agrestis), pumpkin (*Cucurbita pepo*), ridged gourd (*Luffa acutangula*), soybean (*Glycine max*), sponge gourd (*Luffa aegyptiaca*).

Fruit: Banana (*Musa sapientum*).

Tubers: Yam (*Dioscorea alata*), sweet potato (*Ipomoea batata*).

Oilseeds: Castor (*Ricinus communis*), niger (*Guizotia abysinica*), sesame (*Sesamum indicum*).

Spices: Pepper (*Piper nigrum*).

3.2.17 Southern Eastern Ghats

Andhra Pradesh (Chitoor, Cuddapah, Kurnool Ananthpur) and Karnataka (Bellary, Raichur, Kolar).

Crops:

Cereals: Rice (*O. sativa*), sorghum (*S. bicolor*), wheat (*T. aestivum*).

Millets: Pearl millet (*Pennisetum glaucum*).

Legumes: Chickpea (*Cicer arietinum*), field bean (*Lablab purpureus* var. lignosus), green gram (*V. radiata*), groundnut (*A. hyogaea*), horse gram (*M. uniflorum*), pigeon pea (*Cajanus cajan*).

Vegetables: Brinjal (*Solanum melongena*), okra (*A. esculentus*), onion (*allium cepa*).

Fruits: Citrus (*Citrus aurantifolia*), karonda (*Carissa carandas*), mango (*Mangifera indica*), pomello (*Citrus maxima*).

Oilseeds: Cotton (*Gossypium arboreum*), Levant cotton (*Gossypium herbaceum*), mustard (*Brassica juncea*), niger (*Guizotia abyssinica*), sesame (*Sesamum indicum*).

Fiber: Sunnhemp (*Crotalaria juncea*).

3.2.18 Kaveri Region

Tamil Nadu (Chengai Anna, North Arcot, South Arcot, Ambedkar, Thiuvannamalai, Thiruarur, Salem, Vellore, Tiruchirapalli, Dharmapuri, Pudukottai, Kanchipuram, Namakkal, Karur, and Dindigal)

Crops:

Cereals: Rice (*O. sativa*), sorghum (*S. bicolor*).

Millets: Finger millet (*E. coracana*), foxtail millet (*S. italica*), kodo millet (*P. scrobiculatum*), pearl millet (*Pennisetum glaucum*).

Legumes: Chickpea (*Cicer arietinum*), green gram (*V. radiata*), horse gram (*M. uniflorum*), pigeonpea (*Cajanus cajan*).

Vegetables: Canavalia (*Canavalia ensiformis*).

Fruit: Banana (*Musa sapientum*), cucumber (*Cucumis sativus*), gherkin (*Cucumis anguria*), mango (*M. indica*), musk melon (*C. melo*), water melon (*C. lanatus*), tamarind (*T. indica*).

Tubers: Elephant-foot yam (*Amorphophalus paeonifolius*), potato yam (*Dioscorea bulbifera*), sweet potato (*Ipomoea batatas*), yam (*Dioscorea alata*).

Spices: *Curcuma latifolia*, palmyra (*Borassus flabellifer*), tapioca (*Manihot esculentum*).

Oilseeds: Cotton (*Gossypium hirsutum*), groundnut (*Arachis hypogaea*).

3.2.19 Deccan Plateau

Maharashtra (Jalna, Hingoli, Pharbhani, Beed, Nanded, Latur, Osmanabad, Solapur, Sangli, Gondia, Gadchiroli Andhra Pradesh: Adilabad, Karimnagar, Warangal, Khammam Karnataka: Bidar, Gulbarga).

Crops:

Cereals: Barley (*Hordeum vulgare*), maize (*Zea mays*), rice (*Oryza sativa*), sorghum (*S. bicolor*), wheat (*T. aestivum*).

Millets: Barnyard millet (*E. frumentacea*), finger millet (*E. coracana*), foxtail millet (*S. italica*), little millet (*P. sumatrense*), pearl millet (*Pennisetum americanum*), proso millet (*Panicum milliare*).

Legumes: Black gram (*V. mungo*), chickpea (*C. arietinum*), cowpea (*V. unguiculata*), green gram (*V. radiata*), pigeonpea (*Cajanus cajan*), pillipesara (*Vigna trilobata*), ricebean (*Vigna umbellata*).

Vegetables: Bitter gourd (*Momordica charantia*), chilli (*Capsicum annuum*), cucumber (*C. sativus*), musk melon (*Cucumis melo*), ridged gourd (*Luffa acutangula*), sponge gourd (*Luffa aegyptiaca*).

Fruit: Jamun (*Syzygium cuminii*).

Oilseeds: Brassica (*Brassica juncea*), groundnut (*Arachis hypogaea*), niger (*Guizotia abyssinica*), safflower (*Carthamus tinctorius*), sesame (*Sesamum indicum*).

Fibre: Cotton (*Gossypium arboreum*, *G. herbaceum*), dry land Jute (*Corchorus antichorus*).

3.2.20 Konkan Region

Maharashtra (Raigad, Mumbai, Thane, part of Pune, Satara, Ratnagiri, Sindhudurg, and Kolhapur districts), Goa (North Goa, South Goa), and Karnataka (Uttar Kannada).

Crops:

Cereals: Rice (*O. sativa*), sorghum (*S. bicolor*), wheat (*T. aestivum*).

Millets: Finger millet (*E. coracana*), foxtail millet (*S. italica*), pearl millet (*Pennisetum glaucum*), proso millet (*P. miliare*).

Legumes: Black gram (*V. mungo*), cow pea (*V. unguiculata*), green gram (*V. radiata*), horse gram (*M. uniflorum*), pegion pea (*Cajanus cajan*).

Vegetable: Bottle gourd (*Lagenaria siceraria*), brinjal (*Solanum melongena*), Brussels sprouts (*B. oleracea* var. gemmifera), cabbage (*B.. oleracea* var. capitata, cauliflower (*B.oleracea va*r. botrytis), chilli (*Capsicum annuum*), cucumber (*Cucumis sativus*), kundri (*Coccinia indica*), ladyfinger (*A. esculentus*), pumpkin (*C. pepo*), ridged gourd (*L. acutangula*), snake gourd (*T. cucumeriana* var. anguina), tomato (*Lycopersicon esculentum*), winter squash (*Cucurbita maxima*).

Fruits: Arecanut (*Areca catechu*), banana (*Musa acuminata*, *M. sapientum*), cashewnut (*Anacardium occidentale*), coconut (*C. nucifera*), jackfruit (*A. heterophyllus*), mango (*M. indica*), pineapple (*A. comosus*).

Tubers: Elephant-foot yam (*Amorphophallus commutatus*), tapioca (*Manihot esculentum*), taro (*Colocasia esculenta*), yam (*Dioscorea bulbifer*, *Dioscorea esculenta*).

Spices: Ginger (*Zingiber officinale*).

3.2.21 Malabar Region

Kerala (Idukki, Kasargod, Wayanad, Kannur, Malappuram, Palakkad, Thrissur, Ernakulam, Alappuza, Kollam, Pathanamthitta Kottayam, Kozikode, Thiruvananthapuram), Karnataka: (Dakshin Kannada, Udipi, Kodagu) and Tamil Nadu (Nilgiris, Kanyakumari).

Crops:

Cereals: Rice (*Oryza sativa*), sorghum (*Sorghum bicolor*).

Legumes: French bean (*Phaseolus vulgaris*), moth bean (*Vigna aconitifolia*), ricebean (*Vigna umbellata*).

Vegetable: Bitter gourd (*M. charantia*), brinjal (*S. melongena*), cucumber (*C. sativus*), Lablab bean (*Lablab purpureus*), musk melon (*Cucumis melo*), okra (*Abelmoschus esculentus*), ridged gourd (*Luffa acutangula* var. acutangula, *L. acutangula* var. amara), snake gourd (*Trichosanthes cucumeriana* var. anguina), sponge gourd (*Luffa aegyptiaca*), sword bean (*Canavalia gladiata*).

Fruits: Arecanut (*Areca catechu*), cashewnut (*Anacardium occidentale*), coconut (*Cocos nucifera)*, jackfruit (*Artocarpus heterophyllus*), Malabar tamarind (*Garcinia gummigutta*), mango (*Mangifera indica*), plantain (*Musa sapientum*, *M. acuminata*).

Tubers: Country potato (*Coleus parviflorus*, *C. rotundifolius*), elephant-foot yam (*Amorphophallus paeonifolius*), tapioca (*Manihot esculentum*), taro (*Colocasia esculenta* var. esculenta), yam (*Dioscorea alata*, *D. bulbifera* var. sativa).

Spices: Cardamom (*Elettaria cardamomum*), cinnamon (*C. verum*, *C. malabatrum*), clove (*S. aromaticum*), ginger (*Z. officinale*, *Zingiber purpureum*), nutmeg (*M. fragrans*), pepper (*Piper nigrum*).

Oilseeds: Oil palm (*Elaeis guineensis*), sesame (*Sesamum indicum*).

Beverages: Coffee (*C. arabica*), tea (*C. sinensis*).

Latex: Rubber (*Hevea brasiliensis*).

3.2.22 Islands Region

Andamans and Nicobar Islands and Lakshdweep Islands.

Crops:

Cereals: Rice (*Oryza sativa*).

Legumes: Black gram (*V. mungo*), greengram (*V. radiata*).

Vegetables: Bitter gourd (*M. charantia*), brinjal (*S. melongen*a), cucumber (*Cucumis sativus*), okra (*Abelmoschus escultntus*), ridged gourd (*Luffa acutangula* var. acutangula, *L. acutangula* var. amara), snake gourd (*Trichosanthes cucumeriana* var. anguina), sponge gourd (*Luffa aegyptiaca*), bottle gourd (*L. siceraria*), sword bean (*Canavalia gladiat*a), pepper (*Piper nigrum*), ginger (*Zingiber officinale*).

Tubers: Tapioca (*Manihot esculenta*).

Fruits: Arecanut (*Areca catechu*), cashewnut (*Anacardium occidentale*), coconut (*C. nucifera*), jackfruit (*A. heterophyllus*), mango (*M. indica*), oil palm (*Elaeis guineensis*), pineapple (*Ananas comosus*).

Tubers: Elephant-foot yam (*A. paeoniifolius*), taro (*C. esculenta*), yam (*Dioscorea bulbifera*).

3.3 Agrobiodiversity Loss Trends

Since the early 1900s, international farmers have abandoned their many indigenous varieties and landraces, favoring genetically homogenous, high-yielding cultivars. 30% of cattle breeds are threatened with loss; six breeds each month are lost. Today, two-thirds of the earth's food is produced by only 12 plant species and 5 animal species. Animals supply about 30% of human food and agricultural needs, and 12% of the world's population subsists nearly exclusively on ruminant products. Three plant species, maize (*Z. mays*), rice (*O. sativa*), and wheat (*T. aestivum*), accounting for more than 60% of the calories and proteins acquired by humans from plants. Only 150 to 200 of the 250,000 to 300,000 edible plant species known to science are utilized by humans (Figs. 3.1, 3.2, and 3.3).

Over 90% of agricultural types have been lost from farmer's fields, and 50% of the numerous domestic animal species have been destroyed. When harvested

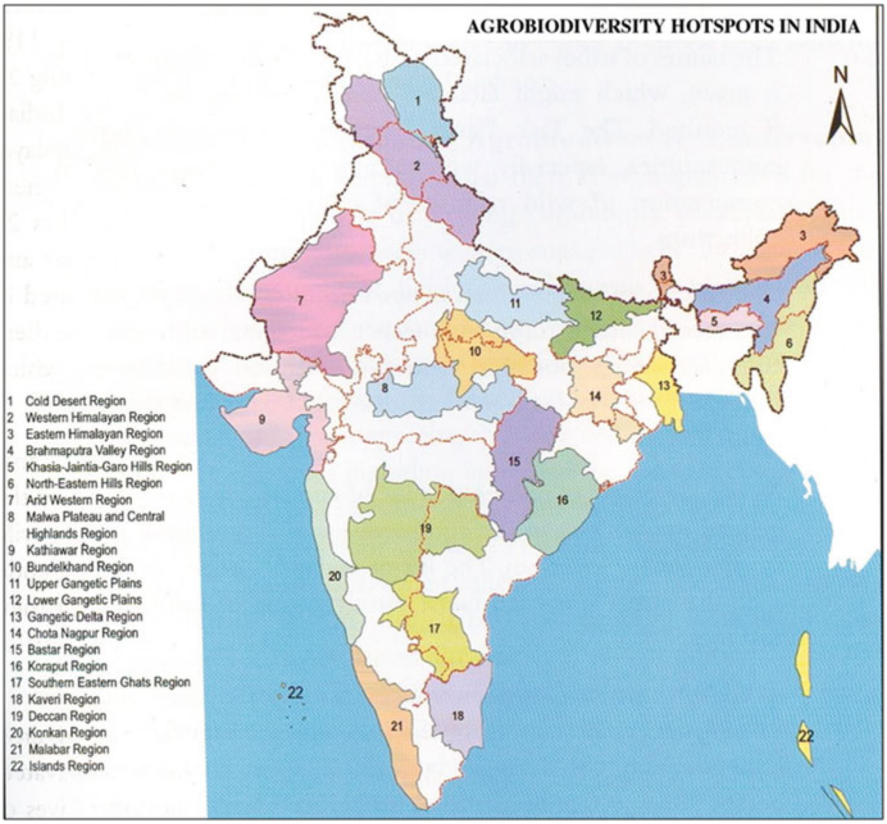

Fig. 3.3 Agrobiodiversity hotspots of India (Nayar et al. 2009)

species, variations, and breeds go extinct, a diverse variety of unharvested species also perish. In fisheries, all 17 significant fishing grounds on the planet are currently being fished at or beyond their sustainable limits, resulting in the extinction of numerous fish populations. The loss of coastal wetlands, forest cover, and other uncultivated “wild” regions and the degradation of the aquatic environment aggravate the genetic erosion of agrobiodiversity. Locally diverse food production systems, including indigenous knowledge, farmer culture, and skills, are in danger. Around 20% of the 7616 cattle breeds examined by the FAO are categorized as endangered.

Numerous factors have played a role in the decline of agrobiodiversity Fig. 3.4 shows a diagrammatic overview of the variables influencing worldwide agrobiodiversity decline. TEV is an abbreviation for total economic value. Brown et al. inspired this adaptation (Brown et al. 1993).

The decrease intensified during the twentieth century due to increasing demand from a burgeoning population and increased competitiveness for natural resources. Numerous factors contribute to the decrease of agrobiodiversity. The significant

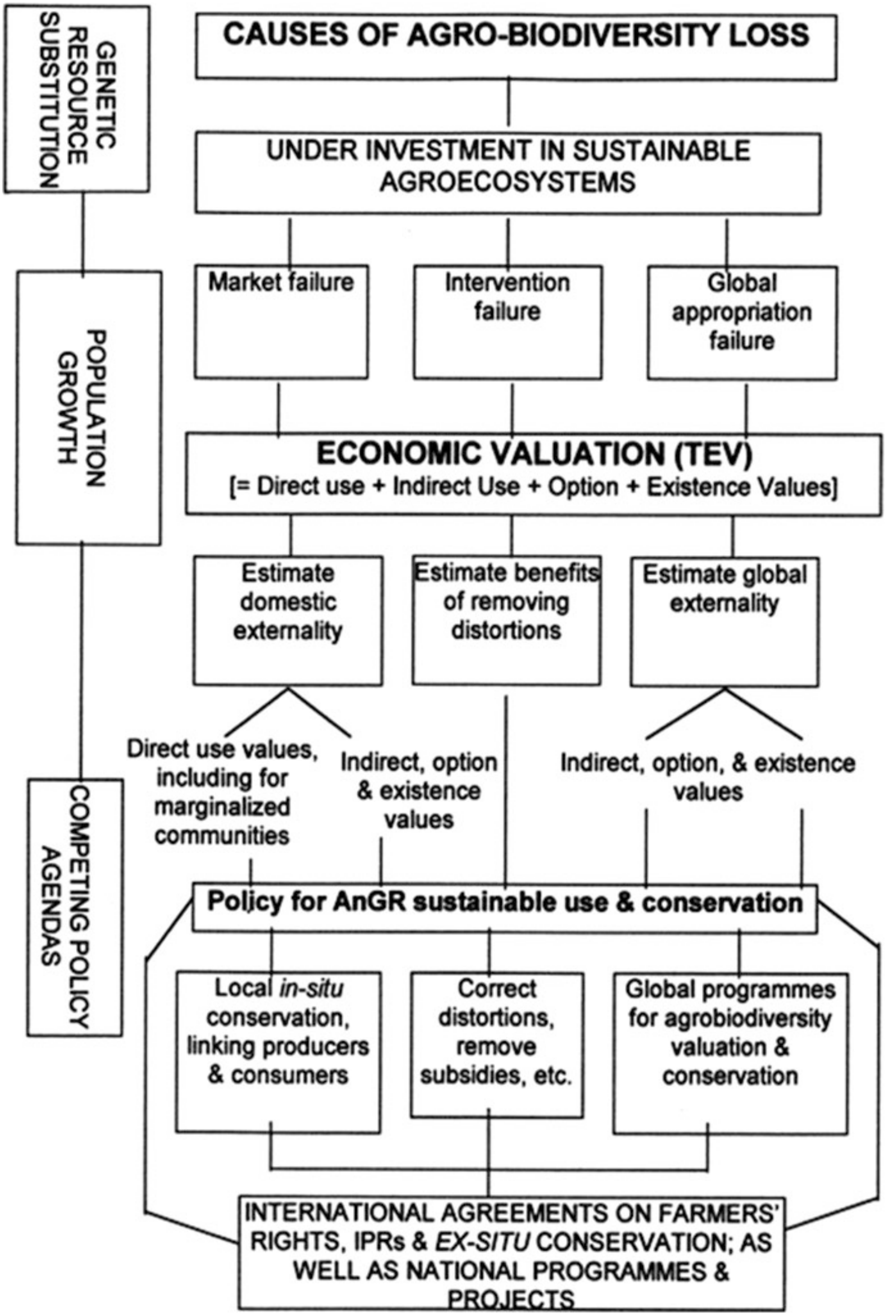

Fig. 3.4 Schematic summary of factors affecting global agrobiodiversity loss. TEV = total economic value. Source Brown et al. (1993)

factors contributing to the loss of agrobiodiversity are the rapid spreading out of the industrial and green revolutions, the globalization of the food scheme and marketing, the substitute of native varieties with improved or non-native cultivars and species, land clearing, species overexploitation, urban sprawl, environmental degradation, and overgrazing, as well as shifting agricultural systems and policies.

The fast rapid expansion and Agro-industry (Green Revolution in agriculture) was a significant factor in the spectacular loss of crop variety. Intensive cattle farming, industrial fisheries, and aquaculture are also included. Specific production methods make use of genetically modified strains and types. Monocultures produce a small number of agricultural types and few domestic animal breeds or fish and aquatic species.

The two main driving factors are the globalization of the food scheme and marketing. Industrialized patenting and other copyright regimes extended to living beings have resulted in extensive cultivation and raising fewer kinds and breeds. As a consequence, a more homogeneous, less diversified, but more spirited global market is created. As a consequence, farmer and consumer views, preferences, and living circumstances have changed; small-scale, varied food production lines that preserve livestock integration into arable production have been curtailed; crops and domestic animal breeds have been neglected, decreasing the diversity of uses for cattle; and the usage of "nurturing" has diminished.

As documented by nearly all nations, the primary cause of agricultural genetic erosion is the replacement of indigenous varieties with better or alien kinds and species. Genetic erosion often happens when newer ones replace older kinds in farmers' fields. Genes and gene combinations present in many farmer's varieties are absent from modern kinds. Often, when commercial varieties are introduced into traditional agricultural methods, the number of variations decreases. While the FAO (1996) notes the development of specific markers of genetic erosion, few systematic studies of agricultural genetic diversity loss have been conducted. Additionally, the Food and Agriculture Organization (FAO) country Reports (1996) found that almost all nations acknowledge that genetic erosion is significant.

Policies and regulatory frameworks affecting the livestock industry are not always supportive of the long-term use of animal genetic resources. Governmental subsidies, whether explicit or implicit, have often favored the growth of large-scale agriculture at the cost of smallholder systems that rely on indigenous genetic resources. Development initiatives, disease control measures, and post-disaster rehabilitation programs can jeopardize genetic diversity if they do not guarantee that the breeds employed are suitable for the local fabrication environment and the requirements of the intended beneficiaries. Adopting suitable methods for the developing world's low-external-input production systems is a significant issue. Pastoralists and smallholders are responsible for the conservation of a large segment of the world's livestock biodiversity. Their aptitude to remain in this position may need additional assistance, such as adequate access to grazing pasture. Conservation measures must not stifle production system growth or livelihood possibilities. Attaining such a balance is problematic.

3.4 Conservation of Agrobiodiversity in Agriculture

In order to explore methods for sustainable agricultural development, country typologies have been established. According to the significance of agriculture in the economy overall, the World Development Report (2008) divides nations into three categories: agriculturally based, changing, and urbanized economies (World Bank 2007). Increased productivity of smallholder farming is a crucial precondition for creating economic development and decreasing poverty and food insecurity in agricultural-based economies, including most Sub-Saharan Africa. Client-driven participatory research involving a diverse variety of stakeholders at various scales should be prioritized.

There are broadly five agrobiodiversity conservation components, and their examples are depicted in Fig. 3.5 (Joshi et al. 2020). Components are conservation strategies, methods/approaches; conservation accelerators; conservation enabling environment; conservation values; and conservation sensitizing/understanding agrobiodiversity. Figure 3.6 shows four agrobiodiversity conservation strategies and 44 methods/approaches (Joshi and Upadhya 2019). Detailed descriptions of possible biotechnological approaches and strategies for successfully controlling agricultural plant genetics are shown in Fig. 3.7 (following the research of Joshi 2017).

Sub-Saharan Africa is an excellent example of an agricultural economy. Farmers in most areas produce on marginal lands with little market access and are subject to high levels of risk from climate unpredictability, plant pest incursions, and disease outbreaks. Crop production is mainly focused on food crops for farm families. Agricultural output and input markets are underdeveloped, and agricultural productivity is poor. Although better varieties from conventional breeding programs have been extensively accepted for a few crops in certain regions, most farmers still depend on landraces for agricultural production. The usage of genetically modified cultivars is still highly restricted. Diversified farming methods and the utilization of low-yield, low-risk crops and types are essential measures these farmers utilize to

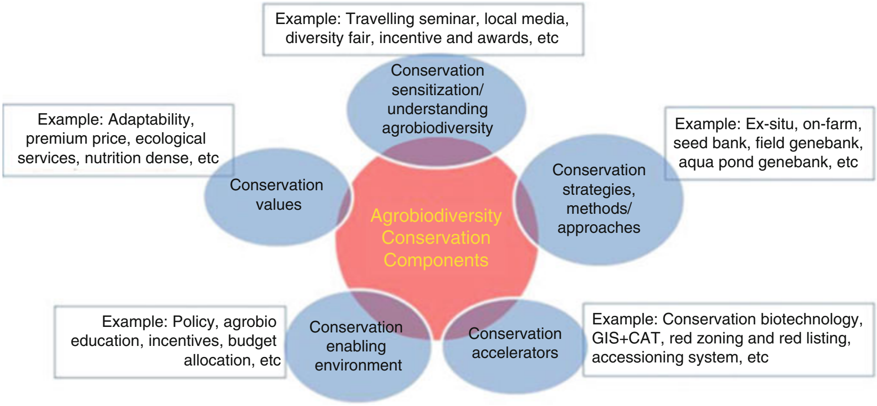

Fig. 3.5 Agrobiodiversity conservation components with examples (Joshi et al. 2020)

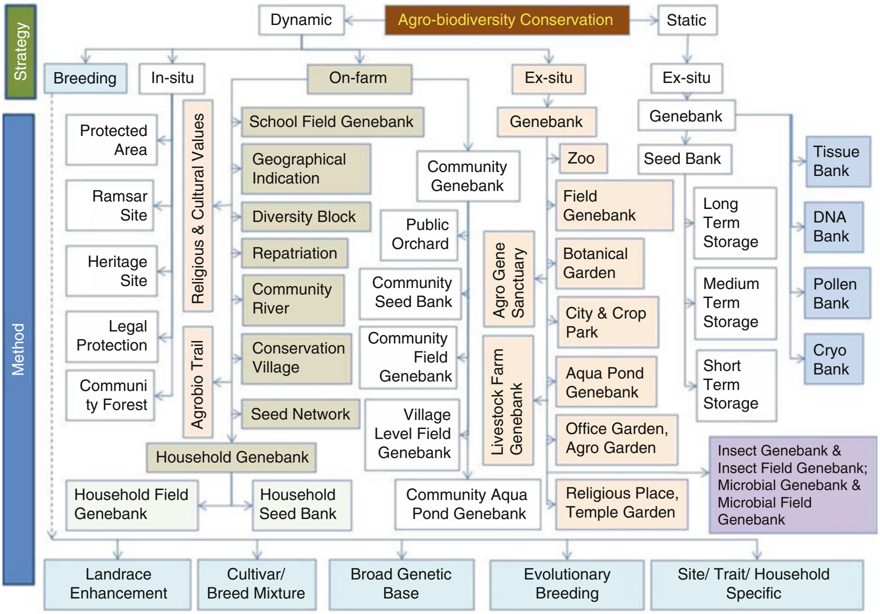

Fig. 3.6 Four agrobiodiversity conservation strategies and 44 methods and approaches (Joshi and Upadhya 2019)

mitigate the dangers they confront. Improving the productivity and profitability of smallholder agricultural systems while preserving or improving their resilience is critical for the region's long-term usage. Agriculture production and stability and net profits on sold surpluses from farming must all be improved. To achieve these objectives across various production systems and agro-ecological circumstances prevalent in agricultural-based economies, a diverse set of crop genetic resources is required.

On-farm genetic resource management programs can significantly enhance farmers' livelihoods at the local level. Farmers may combine on-farm conservation and usage programs with local infrastructure development or greater access to valuable germplasm stored in national genebanks. Farmers benefit from the programs' ongoing support for agricultural variety and environmental health. Crop resources available locally may be used to support efforts to increase crop output or secure new marketing possibilities. They may lead to sustained livelihood improvement by focusing development efforts on local resources and empowering agricultural communities. Farmers with limited resources, in particular, may profit from development efforts that do not rely on external inputs that are either expensive or unsuitable for marginal agroecosystems.

Conservation and utilization of genetic resources on farms also give farmers more control over their crops' genetic resources. Farmers and communities are recognized as the custodians of local biodiversity and the traditional knowledge to which it is

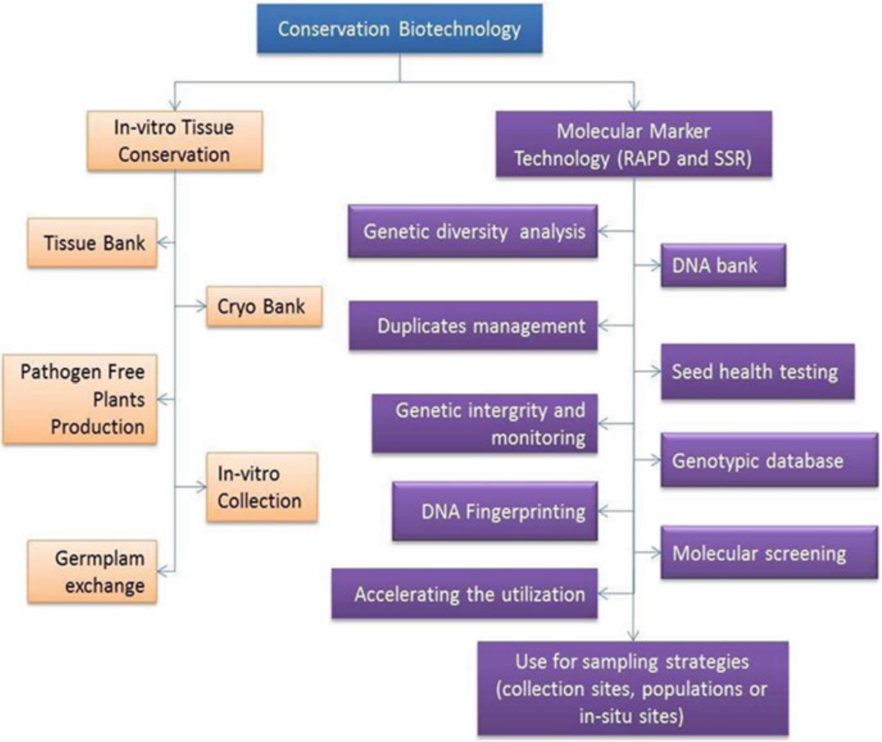

Fig. 3.7 Potential biotechnological tools and approaches for better managing agricultural plant genetic resources (Source: Joshi 2017)

connected in on-farm genetic resource management. As a result, farmers are more likely to enjoy the advantages of the genetic material they manage.

3.5 The Importance of Agrobiodiversity for the Sustainability of Agriculture

Farmers have been selecting plants for more than 10,000 years to create varieties that produce greater yields, are less vulnerable to disease, and exhibit a certain degree of regularity in ripening and germination, making harvesting simpler. Over millennia, a great diversity of agricultural crop species has evolved due to this selection of crop plants and their cultivation under various environmental circumstances, some of which were severe. In India, for example, until a few decades ago, there were up to 30,000 rice varieties available for cultivation.

These trends have been reversing over the last 150 years. Since then, there has been a decrease in the biological variety of agricultural plants. Fewer and fewer plant species are being utilized for agriculture, and just three of them (rice, maize, and wheat) report for more than 60% of the world's food manufacture. Agricultural plant species are becoming more scarce, and genetic diversity within species is diminishing as well. It is well acknowledged that plant breeding and commercial seed production have contributed significantly to decreasing genetic diversity within particular species. When it comes to any particular crop, the number of cultivars is continuously reducing, and the variations are becoming more homogenous, while some traits are being lost in the process. Because of the need to become accustomed to climate change and provide global food security, this "genetic degradation" poses a danger to the survival of the whole world population, which is particularly concerning. As a result, humanity will need whatever genetic variety it can muster to face current and future problems, some of which are yet to be discovered. Achieving a balance between the conservation of biological variety and agricultural development must be accomplished simultaneously.

Global grain output increased by almost threefold between 1950 and 2000, a period of 50 years. This rise was made possible mainly by advancements in plant breeding, extensive nitrogen fertilization, and the development of efficient herbicides for weed management. Even though this productivity gain was mainly accomplished on rich soils under optimum growing circumstances, only a tiny proportion of farmers reaped the benefits of this increase in output. A significant percentage of all farms is still comprised of smallholdings. Most of these farms do not utilize external inputs such as fertilizer or pesticides because traditional intensification methods are inappropriate for such operations. In the 1980s, this kind of farming was still used to cultivate about 60% of all agricultural land in the country. Even though this number is likely to be lower today, traditional agriculture continues to contribute to global food production and is essential to ensuring food security throughout the globe.

In order to feed the growing global population, agricultural intensification must be increased even more in the future. By 2050, it is projected that the earth's population will have increased to about 9 billion people. The ability to develop the agricultural area in order to feed this population, on the other hand, is very restricted. Agriculture must begin utilizing nutrients and energy more effectively to be sustainable; it must maintain ecosystems and their functions while preserving biodiversity, and it must be climate-friendly to be sustainable. One method of improving the production potential of conventionally cultivated lands is to diversify the species present on the farm. On the other hand, crops and their varieties anticipated to generate greater yields in less favorable locations must have characteristics that vary from those of high-yielding varieties grown on more favorable sites.

The quest for alternatives began more than 50 years ago and developed the evolutionary plant breeding technique we use today. When developing new varieties, breeders routinely use farmers' local genetically varied varieties and have evolved to be more resistant to environmental stresses. Crossbreeding is the process of bringing together seeds from several sources and recombining them via the process of selection. Evolutionary breeding using composite crossbred populations is an up-and-coming technique for agricultural intensification, especially in environmentally degraded environments and crop adaptation to climate change-induced environmental change. Participatory plant breeding is a viable strategy for ensuring the protection of agrobiodiversity while also ensuring the viability of agricultural production. The practice of breeding is not limited to breeders alone, nor does it take place only in investigational fields or labs, as is the case with traditional methods. Most of the breeding takes place on their farms, and farmers are actively engaged in the whole breeding process.

3.6 The Backbone of India's Conservation Efforts

One of the most severe environmental issues facing humanity is irreversible biodiversity loss, which eliminates animal and plant species and erodes genetic resources, endangering the human race's very existence. Biodiversity, particularly agrobiodiversity, is critical for feeding the world's millions of people. Apart from habitat loss, the most significant danger to agrobiodiversity today is the rapidly decreasing gene pool caused by genetic uniformity in high-producing cultivars. Native varieties and cultivars of our crops are vanishing from our rapidly changing farming environment, farmlands, and forests, as high-yielding types penetrate the islands of rural or tribal populations that preserve our heritage genetic resources.

According to the Stockholm Declaration adopted at the UN (United Nations) Conference on the Human Environment (June 1972), the Brundtland Commission report (on "Our Common Future") in 1987, and the First Earth Summit in Rio de Janeiro (1992), which adopted several environmental conventions, including the CBD (Convention on Biological Diversity), Climate Change, and Ozone Depletion, India, as a signatory to the conventions mentioned above, enacted national laws to protect our environment. The EPA (Environment Protection Act, 1986), the Protection of Plant Varieties and Farmers' Rights Act (2001), and the BDA (Biological Diversity Act) are only a few of our significant legislation (2002). The Rio Earth Summit was a watershed moment for sustainable development, which has evolved into a new paradigm for preserving ecosystems and integrated management approach of land, water, and living resources in India's development scenario. India is a signatory to the United Nations Millennium Development Goals and the Kyoto Protocol to the UNFCCC (United Nations Framework Convention on Climate Change). The Johannesburg Declaration (2002) on sustainable development for the welfare of marginal rural, tribal, and ethnic communities and on gender equity serves as a guide for India's new legislative initiatives on tribal welfare, grassroots Panchayat Raj institutions development, and safeguarding plant varieties and farmer's rights.

In light of the various climate change projections, and the postulated rise in earth's mean temperature of 1.4–5.8 °C and rise in sea level between 1990 and 2100, resulting in changes in rainfall patterns and poleward shifts of biomes, the possibility of drastic changes in terms of El Nino, drought, and flash floods, and ecosystem changes, there would be drastic changes in agrobiodiversity affecting agricultural production systems. As a consequence, damaged agroecosystems and species would go extinct. Experts have previously expressed concern about the melting of the Arctic and Antarctic IceCaps and the Himalayan glaciers.

3.7 Conclusion

High-yielding cultivars suffocate the agricultural cropping situation by inventory, measuring, and assessing the loss of many wild relatives, varieties, and landraces of our crop plants. Unless and until a variety of landrace is identified and recorded (certified, named, and preserved), its extinction will stay unknown. The current estimates of the incidence and decline of native landraces are far from adequate, and this problem requires scientific investigation by experts. Appropriate measures may be made to compile a Red Data Book of India's Cultivated Plants, Varieties, and Landraces.

It is essential to complement the current network of institutionalized ex situ NBPGR collections, specialized national crop institutes, and agricultural colleges with the forthcoming in situ on-farm community gene banks anticipated under agrobiodiversity hotspots. Documentation of collections such as the Green Data Book of Cultivated Plant Varieties and Landraces is required.

Agrobiodiversity has emerged as a global priority, formalized via legally binding international accords. While the benefit of agrobiodiversity is undeniable, it will also vary according to the customer (e.g., breeders, poor farmers, etc.). Measuring agrobiodiversity is a necessary but not sufficient condition for designing conservation strategies. Measurement may be accomplished in various ways and for various different units of analysis (species, varieties, genes). The techniques, units of analysis, and sample procedures to be used will depend on the conservation program's goals.

Similarly, the statistical methods available for analyzing data on agrobiodiversity are many, and the goals determine their proper use. Conservation strategies are implemented in two main categories: in situ and ex situ. While both methods are conceptually complementary, there are few instances of integrated approaches being used in practice. Each of these methods offers several benefits and drawbacks, but some are being disputed at the moment. Regardless of these obstacles, it is evident that conserving agrobiodiversity is necessary for developing sustainable agricultural systems.

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Role of Range Grasses in Conservation and Restoration of Biodiversity

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Abstract

Range grasses grow in diverse environmental conditions from extreme dry and hot conditions to cold and upland hilly areas. Range grasses have unique adaptability mechanism which makes suitable in diverse range. Because of wide availability, it is widely used in various forms by humans as well as animals as a source of food and feed. These grasses are major source of energy generated on earth and serve as multi-nutrient source. These range grasses play significant role in building economy as well as sustaining ecosystem. Due to excess degradation in the environment, huge imbalance has occurred in the ecosystem. The range grasses play an important role in conservation and restoration of biodiversity by phytoremediation, carbon sequestration, abiotic stress resistance, soil conservation, nutritional security for livestock with high fodder value, and medicinal and aromatic property. This chapter deals with various aspects of range grasses which show its importance in restoration for use in the coming future.

Keywords

Range grasses · Restoration · Conservation · Phytoremediation · Carbon sequestration

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4.1 Introduction

Grasses (Poaceae family) are most versatile monocotyledonous flowering plant group which evolved towards the end of cretaceous period. They grow at extreme climatic conditions all around the world from lush green forests to dry desert, from cold mountains to extreme hot weather (Prasad et al. 2011). It's the adaptability in these plants which makes them invincible. These grasses constitute staple food for most of the people and animals on earth and covers up to 20% of total land area (Shantz 1954). The Poaceae belongs to vast plant family and overall ranked fifth with around 780 genera and 12,000 numbers of various species (Christenhusz and Byng 2016). It includes large number of cereal crops like rice, wheat, maize, millets, and range grasses. Other than being source of food and feed, it is widely used as building material, source for biofuel, industrial application, paper manufacturing, etc.

Grasses dominated biomes called as grasslands as pampas, steppes, and prairies (Lambert 2006). Grasses are monocot, flowering plants, show rapid reproduction, and are well adapted to harsh conditions which make them crucial for livestock food security as well as suitable to grow in adverse climatic conditions. Grasses are present in the base of the food chain being the major energy producers on earth. This is the reason why these serve as a multi-nutrient resource. The roots of these grasses bind to soil and prevent erosion and preserve soil moisture and texture. These provide home and shelter to thousands of animals and insects species. The ecosystem where grasses are the primary producers is known as grassland ecosystem. Approximately 24% of Indian land is covered with grassland which can be categorized into the following sub-categories: (1) Sub-Himalayan Grasslands include fertile tarai region; (2) Montane Grasslands mean mountainous grasslands which depend on altitude, soil, slope, etc. of existing mountains, for example, *Bugyal* grasslands of Uttarakhand, *Shola* grasslands of Karnataka, and *Khajjiar* grasslands of Himachal Pradesh. Other than the abovementioned grasslands, there are coastal grassland and wetland grasslands and riverine and alluvial grasslands. In India, range grasses play an important role in building of economy as well as sustaining ecosystem. But these grasses are being overlooked because of profit-oriented development. It has resulted in degradation of the biodiversity. The detailed description of role of range grasses in conservation and restoration is as follows.

4.1.1 Phytoremediation

Phytoremediation is an eco-friendly, in situ, low-cost strategy to purify tainted soils and groundwater by the plants to absorb and detoxify the contaminant. Phytoremediation mainly takes care of various pollutants like heavy metals and radionuclides like Radium-226, Cesium-137, Strontium-90, and organic compounds. There are six basic mechanisms of phytoremediation which are as follows:

1. Rhizofiltration: It is a technique which primarily involves roots of hydroponically growing plants for water remediation. Roots either restrict these contaminants at their surface through physical adsorption or translocate them to shoot after absorption.
2. Phytoextraction: technique to remove contaminants from soil.
3. Phytotransformation or phytodegradation: It involves conversion or transformation of harmful and toxic contaminants present in contaminated soils, sediments, and water into non-harmful and non-toxic forms. Plant alters the molecular composition of contaminants either by taking them through plant metabolism or by producing specific enzymes for their degradation.
4. Phyto-stimulation or plant-assisted bioremediation: It assists in plant-mediated breakdown of contaminants by stimulating microbial activities in the root zone. It is also applicable to both soil and water.
5. Phytostabilization: It aims to retain contaminants in the soil by reducing their mobility and migration potential. Contaminants make chemical complexes either with root's exudates or get physically adsorbed in the root surface or may be sequestered within root vacuoles. Plants at the site of contamination also check soil erosion and retard flow of water thus playing a crucial role in restricting their movement through underground water percolation or any other dietary source.
6. Phytovolatilization: It involves intake and transpiration rate of contaminants, by plants. The transpiration of the contaminant can be direct by the plant. And also it is after modification by the plant and then released into the atmosphere. The process is known as evapotranspiration of plants.
7. All the phytoremediation techniques mentioned above frequently involve plant roots for the uptake of contaminants. Uptake efficiency of roots depends largely upon their genetic characteristics governing root system architecture (RSA) and type of transporters present and physical and chemical contaminants along with their concentration. Major advantages of phytoremediation over traditional technologies include its eco-friendly nature with minimal disturbance to the environment. The self-sustainable and self-manageable processes can be applied to large field areas and keeping soils in good condition after treatment. Among various plant species, grasses play significant part in phytoremediation because of characteristics like rapid growth, large biomass, and resistance to phytotoxic and genotoxic effects of contaminants as compared to herbs, shrubs, and trees.

There are several grass species both annual and perennial whose role has been reported for phytoremediation. Napier grass role in removal of cadmium from cadmium contaminated soil at Kyushu, Japan (Ishii et al. 2015). He also reported that cutting frequency of Napier grass affects uptake of cadmium as two cutting frequencies resulted in higher uptake of cadmium over single cutting. It resulted in soil Cd concentration reduction by 4.6% with two cuttings in a single year of Napier grass cultivation. Phusantisampan et al. (2016) found that the ecotype of *Vetiveria zizanioides* with large number of adventitious roots cumulate more Cd than those with lesser roots. Sylwia and Korzeniowska (2016) also compared phytoremediation potential of three grasses, *Poa pratensis*, *Lolium perenne*, and *Festuca rubra*, through pot experiment at three different concentrations of cadmium. They found that all the three grasses had bioaccumulation factor ($BF > 1$) while translocation factor ($TF < 1$) which indicated their suitability for phytostabilization over phytoextraction. The phytostabilization potential of *L. perenne* was found to be the best in comparison to other two grasses *Festuca rubra* and *P. pratensis*. Murphy et al. (2020) stated switch grass role in removing synthetic ingredient of the polycarbonate plastics and epoxy resins, i.e., Bisphenol-A (BPA), widely used in food containers, cans, and water bottles.

Utilization of grasses can surely help us in restoring contaminated land sites from heavy metals and other organic contaminants. Since root systems of grasses play a major role in phytoremediation, their detailed study is very essential for the selection of suitable grass species. Along with the root system, other factors like depth of the treatment zone, time period required to clean the contaminated site, and toxic effects of contaminants on plant species need to be considered for the successful remediation of sites.

4.2 Carbon Sequestration

Grasslands function as an intrinsic part of pasturelands and rangelands constituting nearly half of the global land area. It helps in environmental regulation, livestock feed, and soil carbon sequestration, soil health maintenance, and conservation of biological diversity (Liu et al. 2021; Ribeiro et al. 2014). Grasslands have higher amount of inherent soil organic carbon (SOC) amounting to nearly 343 Pg SOC present at 1 m depth with 0.5 Pg C year^{-1} sequestration rate. The high C sequestration potential of grasslands is due to their high underground C allocation, rhizodeposition, and root turnover. The GPP of grasslands is calculated at 31.3 and 8.5Pg C year^{-1} in tropical savannas and shrub lands and temperate grasslands, respectively. These grasslands substantially influence the global carbon (C) cycle and serve as a sink of methane (CH_4) and atmospheric carbon dioxide (CO_2). SOC is the fundamental indicator of grassland productivity and soil fertility. Also, SOC is regarded as the primary means for lowering atmospheric carbon dioxide reducing global climate change (Conant et al. 2017; Freibauer et al. 2004; Ghosh and Mahanta 2014). Therefore, understanding the potential of grassland soils for storing organic carbon is crucial for developing novel strategies to mitigate climate change and addressing the deterioration in soil health (Gray and Bishop 2016).

Depletion of terrestrial C stock (vegetation and stock) has been recorded to be 502.65×10^9tn since the start of agriculture. The fundamental C sequestration process in grasslands involves the transportation of atmospheric CO_2 to the plant biomass by photosynthetic carbon fixation and subsequent formation of stable soil organic carbon (SOC) from biomass resulting in organic mineral complex formation. During the breakdown, a small part of this biomass constitutes the soil inorganic carbon (SIC) as carbonates and bicarbonates. The pedogenic carbonates are formed by the disintegration of CO_2 into a dilute carbonic acid (Lal et al. 2018). The fundamental process of grassland C sequestration involves photosynthesis of environmental CO_2 to net primary productivity (NPP). The sequestration of NPP into the terrestrial biosphere as net ecosystem productivity (NEP) results in formation of SIC and OSC. The C sequestration in the grassland ecosystem includes augmenting the storage of SIC and SOC enhancing the NEP and NPP. Both the NEP and NPP largely depend on the optimum supply of essential plant nutrients (micro and macronutrients), water holding capacity, and stability of organo-mineral complexes (Yang et al. 2019). The SOC depends on the characteristics of the soil profile like nutrient reserves, water capacity, mineralogical composition, soil texture and depth, and landscape attributes (i.e., drainage, aspect, position, and terrain). The SOC sequestration is examined by area-specific land use and its management practices which results in positive soil/ecosystem C budget. The soil has C budget when the input biomass overcome the loss from processes like leaching, mineralization, and erosion (Lal 2018). Although there is no single universal practice for creating soil C budget, the recognition of cultural, economic, social, and biophysical factors is vital in sequestering atmospheric CO_2 into the terrestrial biosphere (Lorenz and Lal 2018).

Agroforestry like silvipasture systems augments the uptake of carbon by lengthening the growing season, enhancing soil fertility, extending the niches from which soil nutrients and water are drawn (De Stefano and Jacobson 2018; Nair et al. 2009). Silvipasture systems increase the C sequestered in trees and soil biomass. Increased and better management of agroforestry systems can effectively sequester 0.012 Tg C per year, while it is estimated that transformation of degraded grasslands of about 630 million ha can sequester 0.59 Tg C annually. The potential of the agroforestry system to sequester C has been found to vary in the range of 12 and 228 Mg/ha (Kirby and Potvin 2007). The theory behind this assumption is that the presence of trees in pasture and croplands results in abundant pruning/litter biomass which is returned to the soil by decaying roots to ameliorate the soil chemical and physical attributes (Haile et al. 2008; Singh and Gill 2014). Restoration of degraded lands increases the production areas having minimal herbage productivity, enhancing C sequestration and inputs. The better grazing management augments the development of herbaceous species. Elevated photosynthetic rates were found in the grazed mixed-grass prairie when compared to ungrazed prairie. Grazing also stimulates the aboveground production, rhizome production, tillering, root exudation, and root respiration. Livestock urination and defecation also positively influence nutrient cycling and SOC sequestration (Xiong et al. 2016). Cultivation of favorable grass species which is well suited to the existing climate, resistant to biotic and abiotic stresses, can withstand grazing, with higher biomass production can result in higher carbon inputs and more carbon sequestration.

4.3 Abiotic Stress

With the changing climatic patterns, the abiotic stresses particularly drought and heat raised the concern in agriculture. By 2050, the world population will be 9 to 10 billion, and for that 60–110% global food production will be required (Rockström et al. 2017). The continuous deforestation process and overuse of fossil fuel have raised the CO_2 level from 280 to 400 ppm and further expected to rise to 800 ppm by 2100 (Hofmann et al. 2009). This leads to extreme weather conditions as temperature fluctuations, unpredictable weather, sometimes excessive rains, or drought are few examples. It is reported that 455 of arable land is under drought condition and the arid area all around the world has increased from 17 to 27% since 1950 (Thornton et al. 2014). Salinity is another major problem in agriculture which limits crop production up to 50% (Panta et al. 2014). Most crop species are sensitive to salt stress (1.0–1.8 dS m^{-1}), but this problem is increasing in different parts of lands due to over-irrigation (Ahmad 2010). Various anthropogenic activities as overuse of synthetic and chemical fertilizer and mineral extraction lead to heavy metal pollution which is resulting in increased concentration of mercury (Hg), cadmium (Cd), arsenic (As), etc. (Manzoor et al. 2018).

Abiotic stresses like drought rise in temperature, salinity, and alkalinity all together affect plant at a specific time which minimizes plant's ability to acclimatize against such stresses (Tomar et al. 2012). Among these abiotic stresses water scarcity or deficit is most damaging and prevalent worldwide (Boyer 1982; Araus et al. 2002). Others like salinity, low temperature, and acidity are also common worldwide affecting yield and productivity.

During evolution, grasses became widespread around 55 and 70 million years ago which is now about 30–40% available in ice-free land (Kellogg 2001; Blair et al. 2014). Over the course of time, grasses adapted to those environments which were too harsh, trees, for example, in northern region where frosting low temperature controls growth of trees (Scheffer et al. 2012) and in hot regions where high temperature and low rainfall favor grasslands over woody tress (Sankaran et al. 2005). These grasses have unique capability to combat drought, temperature fluctuations, salinity, and heavy metal stress enabled by more resilient anatomical, physiological, and molecular functioning (Linder et al. 2018) (Table 4.1). The major contribution in adaption is of C_4 photosynthesis (42% of all grass species) as this leads to water use efficiency (WUE) and less photorespiration (Osborne et al. 2014). Other than that grasses modify leaf anatomy, stomatal structure with unique properties, salt glands, and low critical leaf water potential (Nunes et al. 2020).

The majority of grass families can be categorized based on evolutionary and morphologically or phenotypically distinct groups: (1) BOP (Bambusoideae, Oryzoideae, and Pooideae) and (2) PACMAD (Panicoideae, Arundinoideae, Chloridoideae, Micrairoideae, Aristidoideae, and Danthonioideae) (Grass Phylogeny Working Group II 2012).

Clades-1: BOP (Bambusoideae, Oryzoideae, and Pooideae Subfamilies)

The BOP grasses are known as grasses of cool season which grow in temperate climatic conditions with C_3 photosynthetic pathway (Schubert et al. 2019). Within this clade Bambusoideae and Oryzoideae include warm season grasses while Pooideae contains cool season grasses. The Pooideae grasses are the largest subfamily with independent frost tolerance mechanism in this subfamily (Schubert et al. 2019).

Table 4.1 List of Range Grasses with Abiotic Stress Tolerance

S. no	Common name	Scientific name	Subfamily	Adopted traits
1	Anjan grass	*Cenchrus ciliaris*	Panicoideae	Drought tolerant Trivedi (2002)
2	Motha dhaman	*Cenchrus setigerus*	Panicoideae	Drought tolerant Trivedi (2002)
3	Marvel grass	*Dichanthium annulatum*	Panicoideae	Drought and salinity tolerant Trivedi (2002)
4	Deenanath grass	*Pennisetum pedicellatum*	Panicoideae	Drought tolerant Trivedi (2002)
5	Rhodes grass	*Chloris gayana*	Chloridoideae	Drought and salinity tolerant (Trivedi 2002)
6	Golden crown grass	*Paspalum dilatatum*	Panicoideae	Drought and frost tolerant Trivedi (2002)
7	Blue grass	*Poa pratensis*	Pooideae	Winter hardiness (Trivedi 2002)
8	Para grass, Buffalo grass	*Brachiaria mutica*	Panicoideae	Resistance to water logging Trivedi (2002)
9	Blue buffel grass	*Cenchrus glaucus*	Panicoideae	Drought tolerant Trivedi (2002)
10	Rye grass	*Lolium perenne*	Pooideae	Drought tolerant (Trivedi 2002)
11	Congo signal grass	*Brachiaria brizantha*	Panicoideae	Drought tolerant Trivedi (2002)
12	Bermuda grass	*Cynodon dactylon*	Chloridoideae	Tolerance to Drought, salinity and alkalinity Trivedi (2002)
13	Sabai grass	*Eulaliopsis binata*	Panicoideae	Frost and drought tolerant Trivedi (2002)
14	Nandi grass	*Setaria sphacelata*	Panicoideae	Moderately drought tolerant Agriculture (and Food 2019)
15	Guinea grass	*Megathyrsus maximus*	Panicoideae	Drought and salinity tolerant Benabderrahim and Elfalleh (2021)
16	Sewan grass	*Lasiurus scindicus*	Panicoideae	Extremely drought tolerant: King of dessert grasses Sharma et al. (2016)
17	Tall fescue	*Festuca arundinacea*	Pooideae	Superior drought, heat, and salt tolerance Mian et al. (2008)
18	Meadow fescue	*Festuca pratensis*	Pooideae	High frost tolerance Kosmala et al. (2009)
19	Black spear grass	*Heteropogon contortus*	Panicoideae	Drought tolerant (Goergen and Daehler 2001)
20	Vetiver grass	*Vetiveria zizanioides*	Panicoideae	Drought and water logging Trivedi (2002)

Clades-2: PACMAD (Panicoideae, Arundinoideae, Chloridoideae, Micrairoideae, Aristidoideae, and Danthonioideae)
These grasses belong to warm temperate and tropical regions with C_4 photosynthesis. Majority of range grasses of this clade are salt and drought tolerant (Marks et al. 2021). Panicoideae grasses evolved under such climate which was suitable for agriculture, whereas Chloridoideae grasses evolved in arid climate. This way, Chloridoideae grasses have more potential for developing climate resilient crops (Liu and Osborne 2015).

Till date grasses are underutilized in developing crops which are more suited to changing climatic conditions with better resilience. Advanced approaches such as omics and bioinformatics can be used to understand the complex and adaptive mechanism of stress tolerance, and selected genes can be further transferred to desired crops by conventional or cisgenesis approaches.

4.4 Soil Conservation

4.4.1 Soil Physical Properties

The soil physical and chemical properties are very important parameters for the better growth of range grasses. Also the soil physical and chemical properties are governed by the grown natural grasses and grazing behavior and intensity of animal. Among all other aspects land use pattern and vegetation composition mainly affect the soil physical as well as soil chemical property. The foraging behavior of animals leads to denudation of vegetation responsible for variation in soil properties and biogeochemical changes in grassland. It is observed that soil parent material, climate condition, watering points, flora, and fauna play vital role on soil properties. The regular grazing has its own marks and traces which affect soil physical properties. Mechanical strength of soil depends on water content of soil. The deformation of soil structure is caused because of decreased water tension and internal mechanical strength. The overgrazing exerts pressure on soil resulting in poor soil physical properties. This leads to decreased grazing intensity, soil porosity, air permeability, and conductivity with poor soil functions. The dominance of range grasses in grassland have positive effects on soil water holding capacity with increase in soil organic matter content. The vegetation on grassland acts as protective mulch to mitigate the pressure of livestock and protect soil structure from deterioration. In the natural grassland plant growth and its decomposition patterns are favorable for micro-flora activity and restoration of plant cover.

4.4.2 Soil Chemical Properties

The chemical properties of soil largely depend on natural vegetation, flora, and fauna. These help in adaptation and responsiveness against changing environment. The grass family in the grassland area play pivotal role on nutrient cycle and microbial activity. The livestock excreta in the soil return chemical elements to the soil, and this way nutrient cycle is maintained. The livestock excreta composition states stocking rate, size, and digestive characteristics of microorganisms present in grassland. In grassland the soil pH is directly proportional to grazing intensity, i.e., increase in grazing result in high soil pH. The animal trampling brings carbonates deposition closer to the soil surface enriching it with water-soluble chemical constituents, i.e., Na^+ and K^+. The decrease in vegetation results in increase in evaporation rate extracting water and soluble salts from depth to the top surface of soil. Accordingly, vegetation growth decreases due the accumulation of salts in top soils. The increased vegetation cover considerably changes soil organic matter storage. The increase in soil organic matter storage by range grasses improves the soil fertility and increases the soil biological activity. Soil organic matter in grassland by playing the role of buffer helps in maintaining soluble nutrients for a longer time. The denudation of grasses results in reduction of organic matter content. In grassland soil and available grass vegetation interactions create a strong coupling in carbon and nitrogen nutrient cycles. In heavy grazed sites of grassland, losses of carbon and nitrogen alter the growth of soil microbes by reducing lower fungal and bacterial growth. Therefore, by improving grazing management practices the carbon sequestration rate could be increased. In grassland, the rate of nitrogen mineralization is controlled by its mix kind of grassy vegetation. The rate of nitrogen mineralization can be speed up by promoting good quality range grasses species with low carbon/nitrogen ratio.

4.4.3 Soil Biological Properties

Soils and their components are the most diverse ecosystem with complex webs of micro and macro fauna, flora, and other organisms. A large number of organisms exhibit soil, and it is projected that around 30% of living species spend fully or part of their life span in soil (Decaëns et al. 2006). It is estimated that each gram of soil is enriched with $1x10^9$ microorganisms and about four thousand species which include springtails, roundworms, nematodes, fungi, bacteria, archaebacteria, etc. Among these organisms, especially microorganisms such as fungi, bacteria, archaea, nematode, and insects are not identified yet. Living organisms grow and reproduce in soils. These microorganisms from microbes to moles promote both plant growth and livestock production (Kibblewhite et al. 2008), generate antibiotics (Wall et al. 2015), and maintain greenhouse gases level in the environment (Singh et al. 2010). The breakdown of organic residues from complex to simpler form helps in maintaining soil fertility and nutrients availability for plants. Most of the soil organisms are usually active at a depth of 0–15 cm in the soil surface due to presence of organic residues. The structure and function of living organisms in soil depends on organic matter, nutrient availability, depth, microclimate, and physio-chemical properties in soil.

4.4.4 Major Groups of Soil Organisms

Soil microorganisms are important in various nutrient cycles (Dengler et al. 2014). The important part of soil flora is micro flora: bacteria, algae, and fungi. Soil fauna is divided into three groups based on their body width such as microfauna (size <0.1 mm), mesofauna (0.1–2.0 mm), and marofauna (>2 mm) (Martin and Focht 1977). The microorganisms especially prokaryotes in the soil are ammonia oxidizers (Bates et al. 2011) like bacteria (Briske 2017) and fungi which feed on dead and decaying organic matter (Lynch 1987) while other live as mycorrhizas on plant roots and obtain simple sugars (Hawksworth 1991). The plant pathogenic fungi play an important role in grassland ecosystem resulting in reduced biomass production. The fungal pathogens infecting grass reduce the dominance of grass species and enhance the growth of legumes (Allan et al. 2010). The algae need sunlight and moisture for proper growth and development. They are present in huge number in soil especially soil surface. These algae present in soil belong to class Chlorophyceae. Algae are important in the grassland because of their contribution in organic matter to the soil.

4.5 Nutritional Security for Livestock/Fodder Value

One of the most common constraints to decreased livestock productivity is the lack of availability of quality feed and fodder of adequate supply. This fodder inadequacy alone is equivalent to half of the total loss in animal productivity. Besides many challenges, effect of climate change directly and indirectly threatens the availability of quality forage and feed by affecting water availability, livestock health, reproduction, and biodiversity (Thornton and Gerber 2010; Kumar et al. 2012; Halli et al. 2018). It was suggested that the cost of feed can be significantly reduced through greater use of perennial range grasses (native and introduced) because of their yield and nutritional quality under challenging environments. Therefore, we can reduce the dependency on expensive meal concentrates for economic milk production. However, tropical grasses differ widely with respect to yield and nutritional composition, leading to perform better under different ranges of climatic conditions (Table 4.2). These range grasses are the rich source of carbohydrates, and crude protein, useful as green and dry fodder, useful for silage/hay making, used as concentrates feed blocks, supply major calories to animals, also act as bedding materials, and can also supplement the water demand of livestock. In supplementation to cultivated forage crops, range grasses (either native or improved pastures) are the rich source of feed with higher metabolizable energy forage for livestock. Besides animal feed the grasses also have the potential to contribute considerably towards the reclamation of degraded ecosystems and wild life conservator.

The perennial range grasses constitute a significant component of modern-day animal husbandry. They are capable of meeting the fodder requirement effectively without adversely affecting the farmer’s economy and can match monetary returns of the best of food and commercial crops even under irrigated areas with high productivity and palatability. They can provide continuous green fodder through

Table 4.2 Fodder yield and nutritional quality of range grasses

Sl no.	Tropical grasses	Yield (t ha^{-1}) and nutritional value
1	Forest blue grass (*Bothriochloa intermedia*)	2.4–7.8 dry matter; 6.0% crude protein
2	Indian blue grass (*Bothriochloa pertusa*)	44 green fodder yield, 73% dry matter; 7.1 to 2.4% crude protein
3	Congo signal grass (*Brachiaria brizantha*)	4–120 dry matter in two cuts; 9.6–8.1% crude protein
4	Para grass (*Brachiaria mutica*)	Green fodder yield 1950–2755; 7% crude protein, 0.76% ca, and 0.49% P
5	Anjan grass (*Cenchrus ciliaris*)	6–12 dry matter, 11.0% crude protein with suitable ca and P ratio
6	Dhaman grass (*Cenchrus setigerus*)	3.9 to 7.9 dry fodder yield; 7.8% crude protein
7	Rhodes grass (*Chloris gayana*)	17–175.6 green fodder yield; 5% crude protein, 0.5% ca, and 0.3% P
8	Gusia grass (*Chrysopogon fulvus*)	4.2–10 dry fodder yield; 4.6–5.4% crude protein
9	Lawn grass (*Cynodon dactylon*)	Dry matter 4–5 (rainfed) and 30–35 (irrigated); 7–11.1% crude protein and 18.6–28.2% crude fiber
10	Marvel grass (*Dichanthium annulatum*)	2.8 to 4.5 green fodder yield per cut; 5–7% crude protein
11	Digit grass (*Digitaria decumbens*)	7–13 green fodder yield; 11.8% crude protein, 30.2% crude fiber, and 9.2% ash
12	Brown beetle grass (*Diplachne fusca*)	30–40 green fodder yield in highly alkali soil, 8.5% crude protein
13	Lampa grass (*Heteropogon contortus*)	6.4 dry fodder yield in semi-arid, 10% crude protein, 1.14% ca, and 0.19% P
14	Sewan grass (*Lasiurus scindicus*)	Dry fodder yield of 2.5–3.5 (rainfed) and 7–8.5 (irrigated), 12.8% crude protein, 27.0% crude fiber, and 12.8% ash
15	Sudan grass (*Panicum antidotale*)	20 green fodder yield (rainfed) and 50–60 (irrigated), quite high crude protein; 7.3%, low P; 0.09% and 0.39% ca
16	Guinea grass (*Panicum maximum*)	Green fodder yield of 50–60 (rainfed) and 80–100 (irrigated); 5–8% crude protein
17	Bahia grass (*Paspalum notatum*)	20–40 green fodder yield; 11–12% crude protein
18	Dinanath grass (*Pennisetum pedicellatum*)	100 green fodder yield; 7.4% crude protein; 0.42% ca and 0.21% P
19	Rat's tail grass (*Sehima nervosum*)	16 green fodder yield; 2.3–6.9% crude protein; highest ca; 0.68% and 0.05–0.18% P
20	Setaria grass (*Setaria sphacelata*)	Green fodder yield of 22.8–23.8 (rainfed) and 61.2 (irrigated); 5.3–6.9% crude protein
21	Hybrid Napier grass (*Pennisetum glaucum* × *P. purpureum*)	70–250 green fodder yield, 8.7–10.2% crude protein, 28–30.5% crude fiber and 10–11.5% ash

Table 4.3 Range grasses with their common name, botanical name, and part of plant used by cattle and ruminants

Common name	Botanical name	Plant part	Uses	References
Seymour grass, Indian blue grass, Phulwa	*Bothriochloa pertusa (L.) A. Camus*	All plant	Aromatic with a scent like ginger when it is crushed	Duke (1983)
Buffelgrass, anjan grass, African foxtail	*Cenchrus ciliaris L.*	Green, hay	Lactagogue, folk remedies for kidney pain, tumors, sores, and wounds	Duke and Wain (1981)
Birdwood grass, birdwood buffel, cow sandbur, anjan grass, dhaman, motha dhaman,	*Cenchrus setigerus*	Fodder, hay	Fodder grass	Quattrocchi (2006)
Rhodes grass	*Chloris gayana Kunth*	Silage, hay, fodder	Fodder grass	Duke (1983)
Guria grass, red false beard grass, and reddish-yellow beardgrass	*Chrysopogon fulvus*	All plant	Palatable pasture grass	Quattrocchi (2006)
West Indian lemon grass or simply lemon grass	*Cymbopogon citratus*	Leaves	Fragrant leaves dried leaves brewed into tea	Carbajal et al. (1989)
Marvel grass, Diaz bluestem, Kleberg bluestem, Hindi grass, ringed dichanthium, sheda grass	Dichanthium annulatum	Silage, hay	Forage for livestock	Cook et al. (2005)

recurrent cuttings for more than 2–3 years needing no repeated sowing or planting prove less cumbersome to growers and ensure higher monetary returns as compared to other sources of fodder. The diverse range of perennial fodder crops is available and suitable for different agro-ecosystems (Table 4.3).

4.6 Medicinal and Aromatic Property of Range Grasses

The growing demand in chemical products to feed the cattle for increased food and fodder has led to higher health risk and increased rate of metabolic functional disorders. The demands could be fulfilled using green health alternatives and other eco-friendly products such as trees, shrubs, grasses, and vines, abundantly growing in South Asia. These are environment-friendly products which can procure by promoting community-based conservation. However, there is no or very scant scientifically proven information is available in use of grasses for medicinal purpose. Besides, some of the studies have proved that the range grasses have the chemical component which makes it highly suitable for medicinal value and affect biological processes (Palombo 2006). These chemical components often play a defense role in the living body after consumption. It may possess pharmaceutical or valuable chemicals. Secondary metabolites like tannins and lignin are biologically inactive with high molecular weight and low palatability (Stepp and Moerman 2001). The diverse range of grasses have been proven to have several medicinal properties like anti-mutagenic, anti-microbial, anti-diarrheal, anti-inflammatory, anti-diabetic, anti-plasmodial, diuretic, hepato-protective, and antioxidant activities (Gebashe et al. 2019). Several secondary metabolites like steroids, phenol aldehydes (benzaldehyde derivatives and cinnamaldehyde derivatives), benzoxazinoid derivatives, chiral monoterpenes, aldehydes, fatty acids, and volatile in South African traditional medicine have been known in grass species (Kähkönen et al. 1999). The grasses constitute of several with biological activity known for therapeutic values in traditional medicine.

Cenchrus ciliaris L. an important perennial range grass species is a highly nutritious grass with its constituent properties good for pasture land in hot and dry areas. These are enriched with palatable forage and good in drought as well as wet period in the region. These grasses increase milk production in cattles due to presence of long chain hydrocarbons, carboxyl esters, amino and nitro compound, etc. along with phytochemicals such as flavonoids, steroids, and alkaloids. These components make it the grasses of high medicinal properties (Hema et al. 2010). The leaves of *Cymbopogon citratus* also known as lemon grasses are widely used as traditional medicine and as herbal supplement in various food products specially tea. The *Cymbopogon citratus* essential oil is widely popular for anti-protozoa activity against *Leishmania amazonensis (*Santin et al. 2009*)*. The leaves of lemon grass not only have unique aroma flavor, but it is commonly used as stimulant, antimicrobial, and anti-inflammatory whereas the oil is used as carminative, anti-depressant, analgesic, anti-pyretic, anti-bacterial, and anti-fungal agent (Carbajal et al. 1989). The Dichanthium annulatum (Forsk.) is widely known as “marvel grass” which is used as forage developed from seed to feed cattle (Kumar et al. 2008). The grass is also used in treating dysentery and menorrhagia (Nisar et al. 2014). Heteropogon contortus grasses have polysaccharides along with myo-inositol, galactinol, and raffinose (Blake and Richards 1970). It is a medicinally important grass with each and every part having high impact on the cattle body (Beveridce et al. 1972). *Paspalum notatum* is a rich source of nutritious constituents at seedling stages but palatability decreases with maturity.

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Molecular Approaches in Agrobiodiversity Conservation

5

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Abstract

Agriculture in the neoteric period not only deals with traditional farming practices along with rearing animals; it integrates modern techniques as well as biotechnological advances with the purpose of (a) providing food security (b) enhancing environmental quality as well as natural resources, (c) making the most efficient use of both non-renewable and on-farm resources, (d) sustaining the economic viability of farming activities, and (e) improving living standard of farmers and society as a whole. But, intensive agricultural practices and ever-changing nature of climate gradually exploit the symmetry of agrobiodiversity. Loss of genetic diversity and fragmentation of natural habitats are looking so prominent nowadays to make a stable agro-ecosystem vulnerable. Therefore, the conservation of biodiversity has been considered as a global concern, and several strategies have been implicated in understanding and conserving plant diversity throughout the world. As it is known that restoring genetic variability is the main perquisite of the survival of any living entities in their natural habitats, study of ancestral relationship along with typical breeding pattern looks so crucial. Modern biotechnological interventions (marker technology, DNA fingerprinting, RNAi, molecular farming) have already achieved ample appreciations in the field of agrobiodiversity conservation.

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Keywords

Agrobiodiversity · Genetic diversity · DNA fingerprinting · RNAi · Molecular farming

5.1 Introduction

Biological diversity refers to the variation in living systems on Earth at every possible level, from genetic make-up to ecological complexes, and encompasses the much-required evolutionary processes to sustain life. Agrobiodiversity is a subset of biological diversity, reflecting the interactions among genetic resources, the environment, and management practices by culturally diversified communities. It comprises the variation in both genetic resources (varieties, breeds) which are essential for food, fodder, fiber, fuel etc. and non-harvested species that support production (soil microorganisms, predators, pollinators), as well as maintain agro-ecosystems (agricultural, pastoral, forest, and aquatic). Agrobiodiversity is often understood at three distinct levels: (1) species diversity refers to the dissimilarity among different species; (2) genetic diversity corresponds to the variety of genes contained in plants, animals, fungi, and microorganisms; and (3) ecosystem diversity stands for all the different habitats that exist, like tropical or temperate forests, hot and cold deserts, wetlands, rivers, mountains, etc. The genetic variation within species includes wild relatives, landraces, and modern cultivars, as well as ex situ collections. This variation within a genepool allows breeders and farmers to develop new varieties that improve productivity, quality, and resistance to biotic and abiotic stresses in changing environments (Rudebjer 2009).

Genetic variation plays a key role for the survival of the plant species as well as animals in their natural habitat, influenced by climate change due to global warming, pollution, introduction of novel competitors, etc. (Khan et al. 2012). Since species either evolve or become extinct under diversified environmental challenges, genetic variation in a population reflects its evolutionary potential (Boothby 2019). Biological diversity due to genetic variation at every levels also includes several agro-ecosystems which are basically manmade ecological systems in order to provide food security to human society (Pacicco et al. 2018). Plant genetic resources (PGR) including the wild progenitors and the landrace populations are crucial sources of novel genes that allow species to withstand the unpredictable constraints due to pests, diseases, and abiotic stresses, leading to development of agrobiodiversity (Ceccarelli 2012; Kell et al. 2012). Since the hunting period of human civilization, searching and gathering wild plant species for food and livestock management, a process of domestication of crop wild relatives into crops began. Through both natural and human selection over thousands of years, such crops evolved as landraces with better adaptation in ever-changing environments throughout the globe (Hendry et al. 2017). Traditional farming systems promote genetic diversity among these landraces through the continuous process of selection on the basis of human preferences and crop performances. Modern agricultural practices, on the other hand, keep focus on high yield potential and therefore primarily aim to achieve genetic uniformity within crop varieties rather than genetic diversity among the crop plants. As genetic diversity is not well maintained in the field of modern agriculture, mono-culturing by reducing crop rotation and crop diversification must lead vulnerability of existing crop varieties to pests and diseases (Lin 2011). Gradual exploitation of genetic resources threatens the gene pool both of wild growing and of cultivated plant varieties, resulting in depletion of the natural variability (Ferni et al. 2006; Coates and Dixon 2007).

Besides environmental selection pressure, influence of human activity on the intensive agricultural practices for better yield and quality ultimately led to the degradation and imbalance of agrobiodiversity, accompanied by a loss of species and a decrease in genetic diversity (Belokurova 2010). In this scenario, conservation biology has been emerged as an interdisciplinary science focused on identifying areas with a high level of biodiversity (Gherardi et al. 2009) and intellectual, ecological, social, political, as well as cultural means of preventing, minimizing, and/or restoring diversity losses (Coates and Dixon 2007; Heywood et al. 2007). Genetic drift due to random selection of certain genes induces reduction of genetic variation and thus hinders the survival of natural population (Reed and Frankham 2003). Since gene flow among relative populations due to geographical proximity and ecological similarities provokes natural selection pressure intensely, depletion in population sizes results in rapid loss of genetic diversity (Khan et al. 2012). At present, biotechnological interventions have been used to conserve agrobiodiversity, allowing the preservation of pathogen-free material, elite plant species, and genetic diversity for short-, medium-, and long-term (Cruz-Cruz et al. 2013). Assessment of genetic diversity is becoming more accurate and efficient, when morphological, biochemical, phytochemical, and DNA-based markers are employed in the study (Khan et al. 2012). In vitro conservation in ultra-low temperature shows promising result for preserving especially the vegetatively propagated and non-orthodox seed plant species (Engelmann 2011).

5.2 Agrobiodiversity: Usefulness and Challenges

Agricultural biodiversity is not only influenced by the physical elements of the environment and biological resources, but reflects the deliberate interaction between humans and natural ecosystems (Heywood et al. 2013). Since the relationship that people have with their environment is complex and locally specific, changes in environment need to be dealt at the local scale so that remedies can be designed in ways that are culturally, socio-politically, and environmentally suited to each local context (Thomas 2011). Agricultural biodiversity also includes habitats and species outside of farming systems that benefit agro-ecosystem (Heywood and Iriondo 2003). In addition, other components of agrobiodiversity also look vital because of their contributions to ecosystem services such as pollination (Klein et al. 2007), control of greenhouse gas emissions, and soil dynamics (Frison et al. 2011).

The Convention on Biological Diversity (CBD) has defined agrobiodiversity as an important part of biological diversity that is related to food security, livestock management, and other agricultural activities at the genetic, species, and ecosystem levels for sustainable livelihood (CBD 2011). Values or usefulness of agrobiodiversity can be categorized in two groups: use-values and non-use values. Use-values may be:

(a) *Direct use-values*, which include food, fodder, shelter, ritual, medicinal, and commercialization.
(b) *Indirect use-values*, which are the benefits derived from ecosystem functions; including adaptability to marginal environments and contribution to nutrient cycling.
(c) *Option values*, which may be seen as a type of insurance value, against the occurrence of new diseases or climate change.

Non-use values, on the other hand, include the existence value, for biological communities or areas of scenic beauty when people are willing to pay to prevent a species from becoming extinct, or an area being developed (Falco 2012).

Both men and women get benefits from the direct use-values obtained from livestock management. However, men often focus on income values, obtained through commercialization of livestock products or animals, whereas for women, in many cases, the non-income values are of greater importance (Anderson 2003). For indirect use-values it is important to consider the social status obtained by managing or owning a certain resource (Rudebjer et al. 2011).

We have briefly reviewed the key factors influencing the rapid decline in agrobiodiversity as below:

1. Agricultural Intensification
   As the consequence of Green Revolution, agricultural intensification with high-input agricultural practices has been critical to meet up the needs of growing populations under ever-changing environment. But, these types of modern agricultural activities have already been found detrimental on many traditional agricultural systems, leading to a loss of genetic resources. For example, in Nepal, modern cultivars replaced landraces on three-quarters of the land area cultivated to rice between 1960 and 2000. Similarly, one-fifth of the world's livestock breeds belong to risk from the intensification of farming as the global demand for meat and other animal products increases (FAO 2007). Changing food habits in both urban and rural households has led to an overdependence on energy-rich but nutrient-poor staple crops. The lack of diversity in diets leads to malnutrition caused by a deficiency of micronutrients (vitamin A, iron, and zinc) and a steep increase in diet-related non-communicable diseases (Rudebjer et al. 2011).

2. Habitat Loss
   Population growth, agricultural expansion and intensification, and other factors are leading to substantial changes in land use that have alarming impact on global ecosystems. Habitat fragmentation due to habitat loss and land use change results in faulty sustainability for many species (Millennium Ecosystem Assessment 2005). Increase in landscape fragmentation can restrict a species' geneflow, and therefore genetic erosion in many useful wild species and crop wild relatives may occur. In addition, the pressure on marine and aquatic ecosystems is threatening fish genetic resources. Changes in the oceans due to climate change, including acidification, also pose a critical threat to marine biodiversity (CBD 2009). Loss of agrobiodiversity can also result in a substantial decrease in the resilience of farmers' agroecosystems leading to increase in farmers' vulnerability (Rudebjer et al. 2011).
3. Climate Change
   Nowadays, the loss of agrobiodiversity is believed to get rapidity at both the species and genetic level due to climate change. At the species level, biodiversity that is already endangered or vulnerable will face an increased extinction rate. Although less well documented, there will also be an impact on intra-specific genetic diversity – genes within a population – as vulnerable varieties are lost. The genetic erosion, influenced by climate change, looks serious for wild relatives of the cultivated genotypes, which may contain novel genes for plant-breeding programs to increase heat and drought tolerance to various pests and diseases. The virulence and distribution of insects and pathogens are also likely to change, increasing the risks of crop failure to smallholder farmers (Rudebjer et al. 2011).

Global agriculture with high-throughput technologies have been found contributing a huge fraction of the total anthropogenic emissions of greenhouse gases, which ultimately lead to climate disequilibrium. The most important categories of agricultural emissions are:

(a) Carbon dioxide (CO_2) emissions from burning forests, crop residues, and land.
(b) CO_2 emissions from farm machinery, facilities, processing, and transport.
(c) Methane (CH_4) emissions from rice cultivation as well as livestock management (e.g., ruminants).
(d) Release of nitrous oxide (N_2O) from popularly used nitrogenous fertilizers.

5.3 Molecular Advances to Maintain Agrobiodiversity

Conservation of agrobiodiversity can be performed by two approaches, including preservation in situ, i.e., conservation of domesticated and cultivated species in their natural habitats, and ex situ, i.e., maintaining living organisms out of their own habitats (Kirichenko et al. 2008; Belokurova 2010). Due to heavy loss of agrobiodiversity by habitat destruction, climate change, and intensive agricultural practices, both in situ and ex situ conservation strategies (see Fig. 5.1) are employed

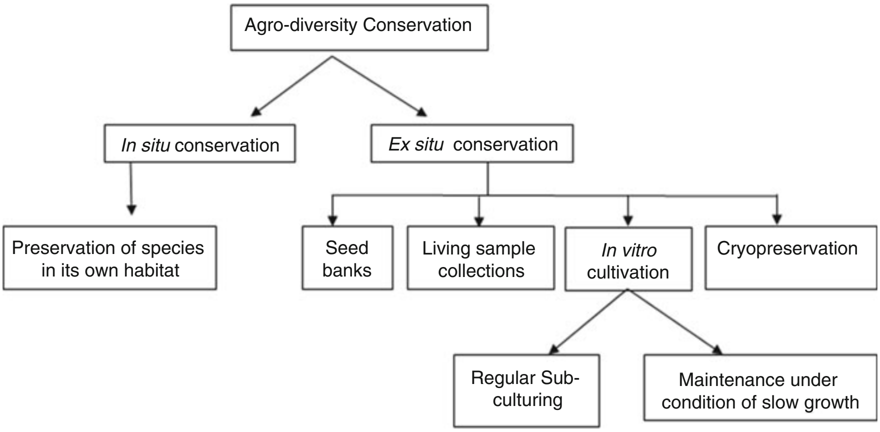

Fig. 5.1 Different approaches of agrobiodiversity conservation (Belokurova 2010)>

as complementary to each other (Cruz-Cruz et al. 2013). Conservation in situ consists of maintaining a species as a component of the natural ecosystem to which it belongs (Sarasan et al. 2006). One of the key advantages of using an in situ system is the possibility of evolutionary changes in species and populations. But, in situ conservation becomes problematic sometimes, when a significant number of wild landraces disappear due to conversion of agricultural lands into corporate sectors (Tengberg and Torheim 2007). Ex situ conservation, on the other hand, involves collection of living samples from each species and storing them outside of the conditions of natural existence in which these species evolved. The ex situ approaches enable the preservation of certain samples of genetic diversity of populations over a prolonged period of time, which better facilitates the study of anatomical, physiological, and biochemical features of a preserved material. Ex situ conservation can be accomplished both traditionally (in seed banks and in living collections under the conditions of introduction) and using more complicated approaches, such as in vitro cultivation and other advanced biotechnological interventions (Heywood and Iriondo 2003;Coates and Dixon 2007).

Modern biotechnology has already been found influencing the genetic diversity of crops and animals cultivated and managed in their natural habitats wide-spread introduction of novel species through in vitro technology. Biotechnological interventions for maintaining and restoring agrobiodiversity involve different laboratory-based technologies that are used either independently or in combination with each other. More recent technological advances, commonly referred to as "genomics," allow the implication of former technologies with minimum modifications in an (ultra)high-throughput context. As a consequence, genomics is thought to speed up the pace of (agro)biotechnological innovations in the near future (Visser and Nap 2009). Several biotechnological approaches are currently used with the target of conserving and restoring agrobiodiversity by taking care of novel traits.

Some of them, having great potential in the determination of genetic diversity, are often used in order to manage agro-ecosystem (Khan et al. 2012).

5.3.1 Marker Technology

Marker in biological system can be defined as a trait or nucleic acid sequence which is easily identifiable and reliably detects trait of interest or target gene fraction by showing polymorphism in different individuals. Apart from the morphological markers (can be seen by naked eye), biochemical as well as DNA-based genetic markers have profuse contributions in biotechnological advances for agrobiodiversity conservation.

5.3.1.1 Biochemical Markers

Use of different isozymes (different variants of the same enzymes having identical or similar functions) for the study of genetic variability within and between populations of plants and animals has huge appraisals in modern agriculture. Isozymes are generally used in taxonomy, genetic, evolutionary, and ecological studies for identification of cultivars and lines (Mondini et al. 2009).

With the advancement of modern techniques such as mass spectrometry (MS) and nuclear magnetic resonance spectrometry (NMR) combined with separation techniques, identification and structural elucidation of phytochemicals have been facilitated. These phytochemical analyses are valuable tools for taxonomic differentiation within species or for evaluating the effect of environmental factors (Khan et al. 2012). Study of metabolomics helps in distinguishing individual species within a genus (Heinrich 2008; Tianniam et al. 2010), and also discriminating the regional origins of target species (Kang et al. 2008).

5.3.1.2 Molecular Markers

DNA-based molecular markers either PCR based or non-PCR based are popularly used in the identification of plant species and their cultivars to clarify genetic variation (Kiran et al. 2010). Molecular linkage maps are now used successfully in the field of crop improvement by locating the potential genes, carrying novel traits in the plants. DNA markers are basically engaged to assess genetic diversity based on polymorphism, which is attributable to the alleles of a single gene or the homolog of a single chromosome within or between populations (Khan et al. 2012). Some potential markers, used in the evaluation of genetic diversity, are given below (Table 5.1).

5.3.2 Additional Markers

5.3.2.1 Internal Transcribed Spacer (ITS) Sequences

ITS markers work on the basis of sequence variation in different individuals. Having different rate of evolution, ITS markers are positively used in phylogenetic studies at

Table. 5.1 Different PCR-based and non-PCR-based markers used in conservation of genetic diversity

Sr. no.	Marker	Features	References
1	Random amplified polymorphic DNA (RAPD)	Very quick and easy to develop. Cost effective and easy to perform. Dominant in nature	Khan et al. 2010; Jiang 2013
2	Sequence characterized amplified region (SCAR)	Locus specific. Co-dominant in nature. Applied in the gene mapping and mostly in the marker assisted selection. Usually used to species-specific identification of vulnerable species	Roslan et al. 2017
3	Simple sequence repeat (SSR)	Used to identify structure, classification, discrimination, the relationship in individual, and population. Co-dominant marker. Considered as the best marker for detection of inter-varietal diversity and polymorphism	Matsuoka et al. 2002
4	Inter-simple sequence repeat (ISSR)	It uses the single microsatellite primer to amplify different sized inter simple sequence. Used for gene mapping, identification of variables, genetic diversity analysis, taxonomy, etc. polymorphism rate is very high among closely related species. Co-dominant in nature	Nilkanta et al. 2017
5	Restriction fragment length polymorphism (RFLP)	First molecular marker system to be used. Highly reproducible and co-dominant inheritance. Identification of genetic diseases or to identify a person who is prone to disease and also are used for the detection of the carrier for genetic disease	Emadi et al. 2010
6	Amplified fragment length polymorphism (AFLP)	No prior knowledge of the targeted DNA is required for analysis. AFLP markers are popular all over the world for use in population genetics, systematic, pathotyping, and quantitative trait loci (QTL) mapping	Saal and Wricke 2002
7	Single nucleotide polymorphism (SNP)	Universal marker for assessment of genetic variation among individuals of the same species. Genetically abundant, ubiquitous, and stable than other molecular marker types and flexible for high throughput analysis	Mammadov and Aggarwal 2012
8	Single strand conformational polymorphism (SSCPs)	Mostly multi-allelic. Usually, co-dominant and locus specific. DNA polymorphism produced by differential folding of single-stranded DNA harboring mutation	Haidong 2005

(continued)

Table. 5.1 (continued)

Sr. no.	Marker	Features	References
9	Expressed sequence tagged (EST)	An EST that appears to be unique assists to isolate new genes of beneficial agronomic traits. Used for the assessment of genetic diversity in Chinese orchid cultivars, Chinese wild almond	Tahan et al. 2009; Huang et al. 2010
10	Selective amplification of microsatellite polymorphic loci (SAMPLE)	Modified form of AFLP. SAMPLE has been reported to be more powerful than AFLP in discriminating between closely related individuals in several plant complexes, assessing genetic diversity	Singh et al. 2002; Sarwat et al. 2011

different taxonomic levels (Gulbitti-Onarici et al. 2009). Frequent insertions/deletions in the ITS sequences of nrDNA are preferred for resolving phylogenetic relationships in many plant species (Choo et al. 2009; Al-Qurainy et al. 2011), genetic diversity assessment (Mondini et al. 2009), intra-specific variation study (Haque et al. 2009), and DNA barcoding (Dong et al. 2012).

5.3.2.2 Chloroplast Spacer Sequences

The sequencing-based DNA barcode generated from nuclear and/or chloroplast DNA has been found advantageous over the polymorphic markers. The genetic differentiation in the diverse populations can easily be evaluated using specific chloroplast intergenic spacer sequences through barcoding approach (Jaakola et al. 2010).

5.3.3 DNA Microarray

Simultaneous studies on gene expression and DNA variation analysis for the identification of mutations in different populations can be carried out effortlessly by the expertise of microarray technique. It uses DNA chips to examine a multitude of loci at one time. The DNA on slide is probed with a fluorescently labelled probe and then scanned for polymorphisms. This technique is robust and high-throughput as it does not demand either agarose or polyacrylamide gels (Khan et al. 2012).

5.3.4 Plant DNA Bank

Plant DNA bank has emerged as a new molecular approach, most preferable for plant breeding, biotechnology, and biodiversity evaluation (Hodkinson et al. 2007). The DNA collections have become key resources throughout the globe especially where agro-diversity is under serious threat from multiple factors (high and low temperature, altitudes, salinity, habitat fragmentation, exposure to pollution, drought, etc.). Since analysis of DNA sequence through DNA taxonomy and DNA barcoding simplifies identification and delimitation of species, studies on phylogeny and genetic manipulation for agronomic traits in orphan crops as well as endangered species becoming so facile. The DNA bank for conservation of vast diversity of flora maintains giant DNA database which contains numerous information regarding plant family, genus, author of DNA extraction, and type of DNA product as well as marker sequences. To maximize the potential of biodiversity and efficient utilization of germplasm, ample DNA databases are available in the World Wide Web for easy access (Khan et al. 2012).

5.3.5 RNAi Technology

RNA interference (RNAi) is a potential molecular tool, used for the production of medicinal plants with novel traits as well as eradication of diseases. It provides an alternative way to inhibit specific enzyme action to check production of unwanted materials. RNAi also participates in correcting deadly mutations in populations with huge agronomic importance. This extant approach has opened new direction for crop improvement as well as biodiversity conservation by raising disease resistant, abiotic or biotic stress tolerant, and high yielding elite varieties (Younis et al. 2014).

5.3.6 Molecular Farming

Production and culture of potential pharmaceutical compounds using plant transformation strategies and transient expression system through agro-infiltration, virus infection, and molecular magnification (Obembe et al. 2011) is publicized as molecular farming or bio-farming. Since, it focuses mainly on the biosynthesis of proteins and secondary metabolites, biodiversity loss can be restrained by preserving the planting materials as well as the ultimate plant products in viable environment (Khan et al. 2012). Not only the plant-based proteins, but also the production of various vaccine, antigen, antibody, therapeutical, and nutraceutical proteins is appended to high-throughput molecular farming (Obembe et al. 2011).

Molecular farming also includes production of transgenic organisms by transferring desirable genes from various healthy lines to a single genome with the aim of improving nutritional status and growing resistance to challenging environment (Bhattacharjee 2009). Apart from the concept of “genetic contamination,” cultivation of GM (genetically modified) crops has positive effect on agrobiodiversity conservation as they are raised synthetically to withstand adverse climatic pressure. In case of animals, breeding pattern and adaptability in different geographical locations are critically evaluated and modified at genetic level to restrict diversity loss.

5.4 Conclusion

Agricultural biodiversity conveniently consummates adequate nutrition to huge global population even under the threatening of indeterminate climate change. The genetic diversity present in wild species, especially crop wild relatives, and in the cultivars of both staple and local or underutilized crops is invaluable in developing new cultivars with novel genes. Keeping the matter of agro-ecosystem conservation in mind, loss in genetic diversity as well as overall agrobiodiversity should be interdicted by all the means of modern advances in biotechnology and genetic engineering. Biotechnological approaches are nowadays looking propitious for the conservation and improvement of rare and endangered species having economic and medicinal importance. Genomics in terms of computing gene sequence similarities and common arrangements of genes (synteny) is currently found to act as the second-generation biotechnological tool by gathering beneficial information from known species phylogenetic study on other less researched taxa. Proteomics (the study of proteins) and metabolomics (the study of metabolites) can also be combined together with genomics for meta-analysis, which may simplify many conservation-related issues. Genotypic characterization through DNA fingerprinting plays an important role in developing conservation strategies such as identification of duplicates or mismatches in vindicating ex situ germplasm collections.

The conservation, restoration, and sustainable use of agrobiodiversity demand serious attention at all the academic, economic, ecological, and political levels. A sustainable system has to be built up for monitoring biotechnological interventions, by which the costs and benefits of activities can be fully assessed with the aim of declining biodiversity loss. Scientific knowledge must be deployed to integrate molecular advances with the conventional strategies for construction of a better and inclusive future, with healthy and stable environment, and consequently world peace.

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Part III

Agri Ecosystem Services and Climate Resilience

Carbon Sequestration Potential in Agricultural Systems

6

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Abstract

Carbon sequestration in agro-ecosystems offers low-cost climate mitigation strategies that can improve productivity, profitability, and sustainable development. The conventional agricultural system moved towards degenerative farming practices due to intensive and exhaustive resource exploitation, soil nutrient mining, increased cost of cultivation, and GHG emissions from the farming system. This study attempts to address the gap in knowledge and different strategies and policy orientation for regenerative farming practices to improve soil carbon sequestration. Additionally, organic input is required to enhance soil carbon sequestration, and deep-rooted crops, crop diversification, reduced tillage, water and nutrient management, agroforestry systems, and integrated farming practices are necessary steps. Further research is required for the translocation of active carbon pool to passive carbon pool. Site-specific carbon sequestration technologies should be customized to reap hire benefits by improving soil health and crop productivity.

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Keywords

Carbon sequestration · Greenhouse gases · Climate change · Regenerative agriculture · Agroforestry systems · Conservation agriculture · Carbon cycle

6.1 Introduction

Among the greenhouse gases (GHG), carbon dioxide (CO_2) is the major gas that continuously increases in the atmosphere, which imposes warming at the global level and enforces climate change. Worldwide, carbon emissions have increased significantly from the combustion of fossil fuel and industrial developments since 1900. From 1970 to 2011, CO_2 emissions have increased by about 90%. Climate change has contributed to declining agricultural production and threatened global food security (Lesk et al. 2016). Over the past few decades, yields have been reduced due to global warming (Lobell et al. 2011), and the results of modeling studies suggest that climate change will reduce food production, especially in many tropical and subtropical countries (Jarvis et al. 2011; Knox et al. 2012; Rosenzweig et al. 2014). As the fourth most significant greenhouse gas (GHG) emitter, India's total emissions account for 7% of global emissions and grow at 4.5% per year. An alarming increase in carbon-di-oxide concentration necessitates finding out strategies for reducing and capturing the CO_2 concentration from the atmosphere and mitigating the threat of global warming (Mishra et al. 2013, 2014).

Therefore, carbon capture is considered to be the most critical climate protection technology in reducing CO_2 emissions. The agriculture ecosystem is regarded as a key component in climate change mitigation because of its characteristic feature of sequestering carbon and acting as a sink for carbon storage (Mishra et al. 2014). In crops, food is being prepared by the photosynthesis process in which carbon dioxide is removed from the atmosphere and oxygen is built up that we need to breathe. Agricultural development during the past few decades has entailed the depletion of carbon stocks in soil, and these are the biggest pools of carbon and have the capability for prolonged carbon sequestration (Chaudhari et al. 2015a, b; Singh et al. 2018). IPCC also identified high-energy agricultural systems to cut carbon under climate change mitigation strategies (Watson et al. 2000; Chauhan et al. 2009; Kumar et al. 2016). Two-thirds of the terrestrial carbon is sequestered by soils and has two to three times more carbon than the atmosphere (Schmidt et al. 2011; Scharlemann et al. 2014). Carbon sequestration potential is different under different landscapes and land uses. Forests, grasslands, and rangelands sequester about 1/4 portion of the world's carbon emissions. As per the estimation, in 25 years, soils can sequester about 20 Pg C, which is more than 10% of anthropogenic emissions. The global soil carbon (C) reservoir to one-meter depth, estimated at 2500 Pg C, about 1500 Pg C is soil organic carbon (SOC), almost 3.2 times the size of the atmospheric pool and four times that of the biotic pool (Lal 2004a, b, Lal 2010; FAO 2015). Thus, several climate-smart agriculture practices are needed and promoted to enhance agricultural production and ensure food security (Lipper et al. 2014; Faurès et al. 2013; Mishra et al. 2018).

Agricultural lands can increase soil carbon stocks through various agrarian management practices by squeezing carbon from the atmosphere and stocking it in the soil as soil organic matter (Mishra et al. 2018). These practices may vary in effectiveness depending upon variability in climates, geographies, and soil types (Kumar et al. 2018). Innovative farming practices such as organic production and irrigation, conservation tillage, novel planting systems, land-use change, land restoration, and water management are ways for farmers to adapt to climate change (Paustian et al. 2016; Smith et al. 2008; Singh et al. 2018). Improved management practices have numerous benefits that may also hike the profitability, enhance fields' energy efficiency, and improve air and soil quality (Srivastava et al. 2016). The agriculture ecosystem has the twin responsibility of providing environmental services as well as food security in a sustainable way. The same carbon sequestered through conservation practices provides more productive and profitable output. The captured carbon through atmosphere and stocked up in biomass and soils are the same carbon that makes agricultural soils more productive, resulting in higher profitability for producers (Arya et al. 2018; Giri et al. 2019). More carbon content in the soil, more nutrients, and water availability to support plant growth with more resilience capacity and less requirement of fertilizers in the fields will develop sustainable agro-ecosystems. This review aims to find gaps and challenges in the present agriculture systems and the potential of carbon sequestration strategies for improving productivity, profitability, and reducing the environmental footprints.

6.2 Soil as a Source and Sink of Carbon

The soil contains approximately1,500 Gt of organic carbon (C) up to 100 cm depth and 2400 Gt C to 200 cm depth (Batjes 1996). Soil carbon reservoir exceeds the total mass of carbon in plants and atmosphere combined signifies its importance for maintenance in response to climate change. About 45% of the world's soil is subject to agricultural use (e.g., arable land and pasture), which is suppressed due to conventional farming methods (Paustian et al. 2019).

6.2.1 Carbon Cycle

What today is a part of a living thing, tomorrow will be transferred to a non-living thing, and as these atoms keep moving, the process of recycling these elements will go on between the biotic and abiotic parts of the planet. All these building blocks formulate biogeochemical cycles. The transfer of carbon between different reservoirs as it travels in the biosphere, pedosphere, geosphere, hydrosphere, and atmosphere, circulating through nature, makes up a significant movement on the planet. The carbon cycle is one of the main biogeochemical cycles as it helps

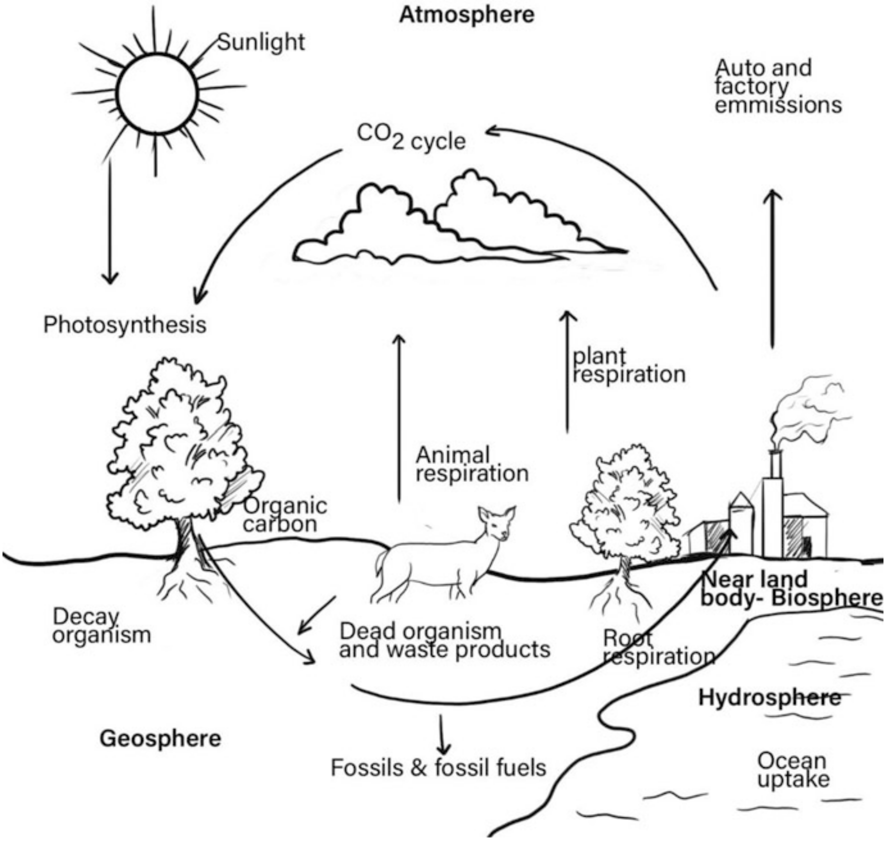

Fig. 6.1 Basics of the carbon cycle and pathways for carbon build-up in soils

regulate the global temperature and sustains a steady climate and carbon equilibrium on Earth.

The carbon cycle significantly affects the science of the oceans. All organic compounds constitute carbon, and it is also the most dominant element used in man-made and natural sources of energy, such as coal, natural gas, and oil. In the carbon cycle, the carbon is stored in sediments of rocks known as a sink for carbon released in the atmosphere during the eruption of volcanoes, the death of organisms, and several other natural processes. Similarly, carbon is often exchanged between seawater and surface oceans or stored over a long sea level. At the same time, other man-made reasons such as industrialization and transportation are sources of carbon emissions. Carbon is also exchanged during the process of photosynthesis. The cycling of carbon from biotic to abiotic component refers to carbon cycling (Fig. 6.1).

Without carbon, Earth would have been a frozen planet. With rising levels of GHGs and carbon dioxide being one of them, it significantly contributes to the heating up of our world. Deforestation, excessive burning of fossil fuels, unrestricted industrialization, and unlawful expansion of transportation alter public dependence early on for renewable energy sources such as biomass, wind, and moving water. From the time of the industrial revolution, it is noticed that the temperature has risen by one degree Fahrenheit. According to data from the ice sheet, the atmosphere has never held carbon dioxide for at least 420,000 years. Unfortunately, uninterrupted and unlawful human activities lead the carbon to be released in the atmosphere without any limit, which was previously removed from the "active pools" of the Earth's system (plants, soil, oceans, freshwater systems, and atmospheric air) that were buried deep inside the Earth.

Similarly, in the ocean, the rising level of carbon dioxide leads to ocean acidification, lowering the pH of water. The negative impact of acidification is seen on marine species and organisms who lose their ability to build their shells and skeletons. If this fast-paced gradual increment in atmospheric carbon dioxide and declining carbon sinks is not stopped, we will soon be into the throngs of worse effects of global warming.

6.2.2 Carbon Sequestration in Soil: A Carbon Trapping Mechanism

Carbon (C) sequestration in soil refers to the trapping and stocking up of CO_2 from the atmosphere into the soil in a way that extends its (MRT) mean residence time and reduces re-emission sinks (Lal et al. 2015). Among the many goals of soil C sequestration are (1) offsetting anthropogenic emissions from deforestation, combustion of fossil fuel, and cement production; (2) reducing the net increment in the concentration of atmospheric CO_2 and pool (800 PgC); (3) recovering concentration of soil organic C (SOC) (and pool) to stages above the 1.5–2.0% threshold level; (4) increasing and maintaining agronomic productivity, and advancing food and nutrient security; (5) improving the effectiveness of input usage in controlled ecosystem soils; (6) developing climate-smart soils and agro-ecosystems; and (7) reducing threats of non-point source pollution and accelerated erosion. Reduced Biomass-C inputs (i.e., roots, litterfall) and losses due to increased erosion and dissolved organic C leaching diminish SOC reserves as natural ecosystems are converted to agricultural ecosystems. Depending on the extent, intensity, and kind of deterioration, the SOC stock may be depleted by 30–75% (Lal 2004a, b). Soils prone to erosion and other degradation processes (such as loss of cohesion and structural stability, erosion, or compaction) have become more depleted of their antagonized SOC repositories. Overgrazing (Dlamini et al. 2016) and tilling worsen the depletion of the SOC stock. As a result, severely degraded and deficient soils have a higher potential capacity for SOC sequestration. There are several ways to improve soil carbon sequestration (Fig. 6.2).

Fig. 6.2 The six R's of soil carbon sequestration

6.2.2.1 Physical Mechanism

The soil aggregation process is the characteristic feature of soil that traps the carbon in soils. Smaller soil particles adhere to form bigger aggregations. The aggregation process is with the help of gluing molecules known as glomalin produced by an arbuscular mycorrhizal fungus (Six et al. 2004; Wilson et al. 2009). Aggregates can protect soil carbon for long periods if they remain stable and undisturbed.

On the other hand, tillage can swiftly disintegrate soil aggregates; soil carbon can easily be subjected to microbes and captured carbon will be utilized (Grandy and Robertson 2007).

Soil fluids and temperature significantly impact the stability and fluidity of soil organic carbon and the breakdown and mineralization processes. Temperature sensitivity differs among different fractions of soil carbon pools (e.g., labile vs. stable), and these are sensitive to cohesive and adhesive forces within organic carbon composition and between organic carbon and the soil environment (Kumar et al. 2021). Due to the ease of distribution of fresh carbon at depth and the potential release of carbon buried at depth by deep-rooted plants, a change in soil compaction from close-fitted to loose-fitted encourages mineralization of ancient soil carbon stored underneath (Kumar et al. 2020). Furthermore, increased soil aeration and significant disruption of cohesive forces that connect soil aggregates are the primary variables that encourage soil microorganisms to mineralize soil organic carbon (Chaudhari et al. 2014). Similarly, soil carbon sequestration potential can be influenced by localized and controlled processes in the soil ecosystem, such as rainfall and soil fluid infiltration, soil erosion, and solute deposition governed by soil gradient heterogeneity—all of which can influence carbon input and carbon loss rates. As a result, the binding forces between soil particles influence the aggregation, texture, and dynamics of organic carbon pools in macro-and micro-aggregates. As a result, the bulkiness of soil aggregates has a significant impact on the hydraulic properties of soil carbon solutes.

Despite being contentious, traditional observers believe that the rate of soil organic carbon mineralization is unaffected by soil size, structure, or texture (Stockmann et al. 2013). However, it has been suggested that the soil-limiting phase of organic carbon mineralization is driven by abiotic rather than biotic processes (especially microbial), named “Regulatory Gate” (Kemmitt et al. 2008). Diffusion and adsorption/desorption from soil surfaces, for example, are processes that govern carbon stocks in the soil, according to the “Regulatory Gate” hypothesis. Because soils’ carbon sequestration saturation limits are limited by inherent soil cohesion and adherence to mineral particles, this suggests that soils’ carbon sequestration capability is finite. Soil physics also helps understand the importance of abiotic carbon-protection mechanisms in the soil environment, which can help inform decisions about soils’ ability or potential to sequester carbon (Chaudhari et al. 2015a, b). Factors affecting soil carbon sequestration are mentioned in Fig. 6.3.

6.2.2.2 Chemical Mechanism: Formation of Organo-Metallic Complex

Carbon molecules can be chemically shielded from a breakdown in addition to physical protection through aggregation formation. The ability of a soil to chemically preserve carbon molecules is greatly dependent on the percentage of clay in the soil’s mineral fraction. Clay particles have a significant negative charge on their surfaces. Some of the metabolites produced by the microbial community when they metabolize carbon molecules have a strong positive charge. These molecules can form strong bonds with the clay particles when they come together, thus protecting the molecules from microorganisms. This type of chemical protection is powerful, which is why carbon and clay soils are linked worldwide (Six et al. 2002). Unfortunately, because farmers can’t change their soils’ clay composition, the possibility of such sequestration is reliant on prevailing soil resources rather than changes in management practices. However, soils with high clay content are more likely to accept soil carbon sequestration treatments. Efforts to increase soil-based carbon sequestration may therefore target and prioritize the cultivated land for clay content.

Sorption and sorptive interactions can also help to keep SOC stable. Adsorption to minerals such as phyllosilicate clays, Al-, Fe-, Mn-oxides, weak crystalline minerals, or polyvalent cations forming mineral building bridges or other organic matter are examples of these interactions. Hosking (1932) was the first to discover a link between SOC resistance to chemical oxidation and the existence of certain

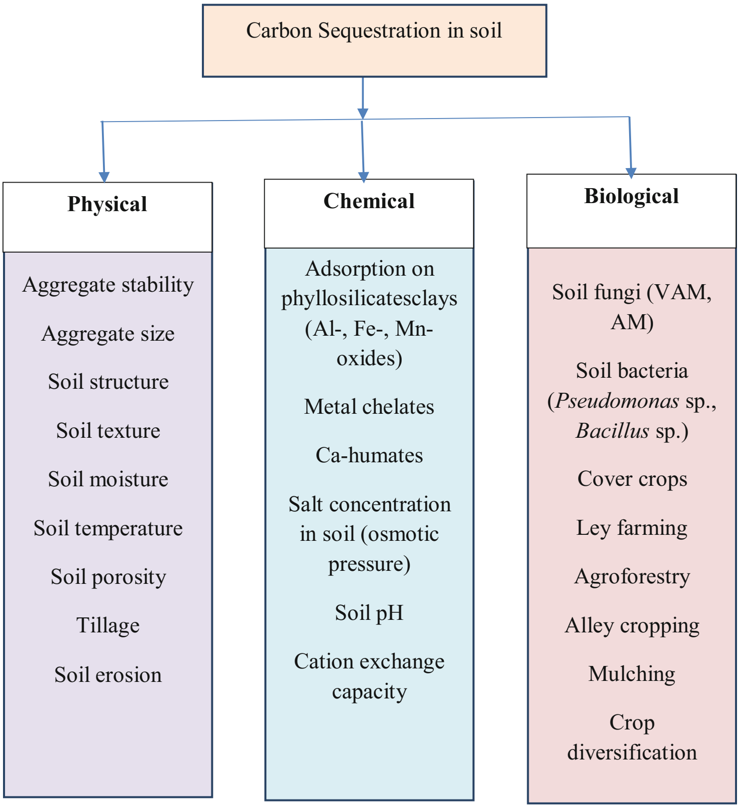

Fig. 6.3 Various physical, chemical, and biological factors affecting soil carbon sequestration

reactive mineral species. Increased SOC stocks are linked to the presence of reactive minerals or metals (Grand and Lavkulich 2011) and SOC resistance to microbial damage in incubation testing. Mineral C complexed soil organic C is of ^{14}C older age than other SOC pools (Schrumpf et al. 2013); therefore, adsorption plays a vital role in the long-term stability of SOC.

The loss of exchangeable Ca^{2+} and its replacement with exchangeable K^+ created aggregate disruption. According to Edwards and Bremner (1967), the fundamental mechanism supporting exchangeable Ca^{2+} stability is the flocculation of particles with a negative charge by outer-sphere contacts linking Ca^{2+}. It is proposed that Ca^{2+} may help in particle flocculation in the guts of earthworms belonging to certain species, resulting in "Cahumates" (Satchell 1967). Shipitalo and Protz (1989) used micromorphology and chemical pre-treatments to infer that Ca^{2+} role in particle flocculation in earthworm casts and stabilizing its microaggregates. Another method for aggregation stabilization in Ca-rich areas is the formation of complexes between Ca^{2+} and high-molecular-weight organic compounds such root mucilages or microbial polysaccharides/polymeric substances. These compounds have been demonstrated to readily complex Ca^{2+} and form gel-like structures that bind aggregates (Erktan et al. 2017). Galacturonic acids, a common root mucilage, have an excellent affinity for calcium, which causes polymer chains to link together and form an adhesive matrix (De Kerchove and Elimelech 2007). Czarnes et al. (2000) also found that these polygalacturonic acid gels increase aggregate hydrophobicity, which improves their stability throughout wetting and drying cycles.

6.2.2.3 Biological Mechanism

Soil microbes play a critical part in carbon sequestration by converting organic wastes into smaller carbon particles trapped intra-aggregate (Six et al. 2006). Mesovores (soil-dwelling insects and nematodes) are in charge of breaking down more significant bits of plant debris into tiny fragments that fungi and bacteria can digest. Soil fungus also adds to soil carbon sequestration by increasing the amount of carbon available and stabilizing the aggregates. Arbuscular Mycorrhizal Fungi (AMF) symbiotically deliver soil nutrients in exchange for simple sugars from the plants (Yanardağ et al. 2017; Govindarajulu et al. 2005). Plants utilize these nutrients effectively, increasing the carbon released into the soil through photosynthesis. AMF also creates glomalin, a sticky protein that binds soil aggregates together, protecting soil carbon (Rillig 2004). Soil bacteria also digest organic matter. Actinomycetes decompose more resistant forms of carbon, such as lignin, whereas nitrifying bacteria convert complex organic nitrogen into simpler plant-available forms. These decomposition mechanisms are critical for increasing biomass production and ensuring that carbon is transformed into stable conditions stored in soil (Six et al. 2006). Soil management for abundant soil microorganisms can greatly improve soils' potential to retain carbon by providing appropriate and diversified plant inputs and lowering tillage (Six et al. 2006).

To compensate for losses due to microbial respiration, producers modify the balance in soil carbon by changing the quantity and chemical form of carbon inputs. Following crop harvest, soil in many annual cropping systems is left bare, implying that no biomass generation occurs in that area for most of the year. Reduced yearly biomass yield means fewer carbon inputs in the soil in terms of carbon cycles, making it more difficult for farmers to compensate for year-round carbon losses. Increasing average annual biomass output through cover crops or occasional green fallows could move the carbon balance toward a gain rather than a loss (Tiemann et al. 2015a, b). Incorporate plant diversity into crop rotations and use legume cover crops, which contain carbon compounds that are likely more resistant to microbial destruction, to increase the complexity and diversity of soil carbon (Wickings et al. 2012). These approaches significantly increase the amount of aboveground biomass entering agricultural systems, but increasing belowground biomass by increasing root formation may be even more critical. Plants dominate annual farming systems with shallow root systems. According to Kell (2012), putting more attention on growing crop plants with more broad root systems could significantly increase agricultural systems' potential. The amount of biomass below ground could be improved by covering crops with deeper roots.

Biochar is a thermo-chemical combustion and carbonization product of organic feedstocks, commonly produced by pyrolysis of feedstock biomass at low oxygen concentrations and temperatures (Windeatt et al. 2014). Biochar addition to the soil as an organic supplement with long-term residence time has attracted increasing attention and interest in recent decades due to its good effects on soil chemical fertility and quality, as well as climate change mitigation (Oliveira et al. 2017). Biochar application has been shown to improve soil physical and chemical properties, water and nutrient availability and retention (Ouyang et al. 2013), the recalcitrant and labile organic C fraction, and total nitrogen (Yanardağ et al. 2017), higher soil aggregation, and porosity (Du et al. 2017) resulting in increased plant growth and productivity (Naeem et al. 2018).

6.3 Carbon Sequestration under Different Landscapes and Land Uses

Since carbon transport transfers carbon dioxide (CO_2) directly from the atmosphere to the carbon dioxide earth (C), which is highly stable, this process takes place naturally or anthropogenically. Apart from this, land intake can be broadly divided into two categories: abiotic and biotic. Abiotic sequestration strategies include injecting or trapping CO_2 into the sea, geological strata, oil resources, and coal mines. On the other hand, the biotic component involves growing and managing higher plants and microorganisms to harvest CO_2 from the atmosphere and fix this in pools of soil. Biotic extraction can be further divided based on land and marine textures. Degradation is the transfer of CO_2 from the atmosphere to biotic and pedologic carbon pools. Capturing and fixation of CO_2 is achieved through photosynthesis and its storage in dead organisms and organisms. The most important immersions in land C include soil, forests, and wetlands.

Landscapes such as forests, grasslands, and plateaus absorb about 25% of the world's carbon footprint. Carbon from plants is released into the atmosphere or carried to the ground when leaves and branches fall off or plants die. Burning fires and human activities such as deforestation can increase forest losses through carbon emissions. Oceanic sequestration involves the capture of C by photosynthetic activities of living organisms, namely, phytoplankton, which absorb CO_2 and convert C into particles of organisms deposited in the oceans. This type of sequestration reports a significant amount of about 45 PgC/year (Falkowski et al. 2000).

6.3.1 Carbon Stock in Soil Ecosystem

Direct CO_2 fixation involves its natural conversion to inorganic chemicals such as calcium and magnesium carbonates, while the way plants produce biomass through photosynthesis is called indirect sequestration. This biomass, after decomposition, is eventually transferred to the soil and disintegrated indirectly as soil organic carbon. The total amount of carbon used in the soil shows the long-term balance between carbon offset and extraction methods based on physical and biological soil boundaries. The management of abundant vegetation, forestry, land use practices, and conservation measures, including appropriate cultural practices, leads to beneficial effects on carbon sequestration in the soil. Carbon can also be trapped in the soil by accumulating humus in the surface layers, usually reaching a depth of 0.5–1 m of soil or anthropogenic activities through changes in land use or management practices (RMPs) in forests and agricultural or pastoral environments. The SOC reservoir in the soil of controlled systems is lower than that of the natural ecosystem as it is exposed to strong oxidation or mineralization, leaching, and erosion (Lal 2008). Globally, the soil has a sequestration potential of 0.4–0.8 Pg. However, the potential for soil degradation depends on several factors depending on the abiotic or biotic sequestration. The sequestration of abiotic C soil in the soil is highly dependent on clay content, soil moisture, mineralogy, topography, structural stability, and temperature regimes (Jimenez et al. 2007). Similarly, the classification of biotic C, on the other hand, depends on management practices, climate, and biological functions of soil organisms, including microflora and animals (Lal et al. 2007).

6.3.2 Carbon Stock in Forest Ecosystem

The formation of a forest in an area where there was no tree cover is known as afforestation. The reforestation of subsistence agriculture and grazing lands to combine carbon from atmospheric CO_2 into biomass is known as forestry. Carbon must not be released into the air due to forest fires or rot when trees die for this carbon sequestration to be effective. For this purpose, land set aside for trees should not be diverted to other uses, and the frequency of disturbances may need to be controlled to avoid severe disasters. Alternatively, wood from them should be consumed, for example, using biochar, bio-energy with carbon storage (BECS), landfill, or stored for use in construction, for example. Reforestation using durable trees (> 100 years) will absorb carbon dioxide for a long time and gradually release it, reducing the carbon footprint by the twenty-first century. There is enough space on Earth to plant about 1.2 billion trees. Planting and storage can contain approximately 205 million tons of carbon sequestration energy and eliminate 10 years of net CO_2 emissions (Kumar et al. 2014, 2019; Bastin et al. 2019). The Billions of Trees campaign supports this strategy. Restoring all damaged forests in the world could hold about 205 billion tons of carbon, or about two-thirds of all carbon emissions (Chazdon and Brancalion 2019). Carbon stocks in forest soils play an important role in the global carbon cycle due to their large scale, estimated at 4.1 billion hectares worldwide (Dixon and Stolper 1995). It is estimated that approximately 1240 Pg C exists in the forest ecosystem (Dixon et al. 1994). In forest habitats, carbon is stored mainly in plants and soil and at low levels in hardwood waste (Ngo et al. 2013).

Vegetation (plants) accounts for approximately 536 Pg C, and the soil is estimated to hold up to 704 Pg C. Forests maintain more than 70% of the Earth's surface SOC, and forest soil is expected to hold about 43% of carbon in the forest ecosystem to a depth of 1 m (Jobbágy and Jackson 2000). The role of forests in reducing carbon emissions into the atmosphere is multifaceted and manifold. Forests store carbon in the hard tissues and the soil environment as it grows. When forests are young, their carbon dioxide intake is very high, gradually decreasing over time. Although older forests can retain carbon for a long time, they are less productive.

Unfortunately, the high carbon content of natural forest soils is rapidly declining due to a decrease in the amount of biomass (above and below ground) returned to the soil, changes in soil moisture and temperature regimes, and the rate of organic degradation (due to differences in C:N ratio and lignin content) (Post and Kwon 2000). The reservoir of organic carbon dioxide (SOC) is depleted by 20–25% due to anthropogenic activities such as deforestation into agricultural land). Deforestation is estimated to release 1.6–1.7 Pg C per year (approximately 20% of human emissions) (Watson et al. 2000).

6.3.3 Carbon Stock in Peatlands

Peat bogs act as a carbon sink by collecting partially decomposed material that could otherwise be destroyed. Peatlands serve as carbon sink or spring depending on the weather in different parts of the world and at other times of the year (Strack et al. 2008). Bulk carbon reserves can be increased by establishing new wetlands or upgrading existing ones (Lovett and Wasser 2008).

6.3.4 Carbon Stock under Urban Forestry

Introduction of trees to new urban area which is avenue planting could promote enhancement of carbon stock. The forests of urban areas increase the amount of carbon absorbed by the cities, and carbon capture occurs during the tree's lifetime; to a lesser extent, it is commonly made and maintained. The effects of urban forests may vary depending on the type of plant used. It can therefore act as a sink and be a producer of emissions. As well as the sequestration of carbon by plants, which is difficult to measure but seems to have little effect on the amount of carbon dioxide, plants can have indirect effects on carbon by reducing energy demand (Velasco et al. 2016).

6.3.5 Carbon Stock in Wetlands

Wetland rehabilitation involves re-establishing or rehabilitating wetland's terrestrial and chemical activities). It has also been suggested to reduce climate change, and carbon dioxide fixed in this way is called blue carbon. Wetlands, especially in coastal wetlands such as mangroves, seagrass, and salt marshes, are a significant source of carbon dioxide storage; wetlands contain 20–30% of carbon dioxide, and wetlands hold only 5–8% of the Earth's crust (Mitsch et al. 2013). Studies have shown that reclaimed wetlands can be efficient CO_2 sinks. In addition to climate benefits, wetland restoration and land conservation can help conserve biodiversity, improve water quality, and help in flood control. A swamp, like trees, should be kept undisturbed for the sequestration process to work. The carbon contained in plants and mounds will be released back into the air if disturbed in any way, and the ecosystem will cease to function as a carbon sink. In addition, some wetlands can emit greenhouse gases without CO_2, such as methane, ignoring the benefits of climate change. However, it can also be challenging to quantify them according to CO_2 sequestration.

6.3.6 Carbon Stock in Agricultural Soils

According to the IPCC, agricultural soils can hold up to 1.2 billion tons of carbon a year. However, it is estimated that almost half of all agricultural soils are degraded globally, resulting in challenge of long-term carbon storage in the soil. Because agriculture covers more than one third of the world's arable land, the potential for carbon dioxide in agricultural land is enormous. Agricultural land can hold at least 10% of the current annual offset of 8–10 Gt / year (Hansen et al. 2013). Although agro-ecosystems can degrade and reduce SOC levels, carbon shortages offer the opportunity to store carbon in new ways of managing the agro-ecosystems. Carbon can also be stored in the ground as carbonates. Carbon dioxide dissolves in water and enters the soil, mixing with the minerals calcium and magnesium to produce *caliche* in the desert and on dry land thousands of years ago.

Cropland soils have lower levels of organic carbon than natural vegetation (SOC). SOC content of soils decreases by approximately 30–40% when converted from natural or natural resources, such as forests, forests, forests, steppes, and savannas (Poeplau et al. 2015). In terms of harvesting, this loss is due to the removal of carbon-containing plant material. Carbon dioxide will increase or decrease as land use changes, and this process continues until the soil reaches a new equilibrium status. Climate change could also affect deviations from this equilibrium which has a significant impact on carbon capture. Decreases in SOC content can be countered by increased carbon uptake by soil through residue retention, which can be done in various ways, such as leaving crop residues in the field, using compost as fertilizer, or rotating perennial crops. Perennials have a high amount of biomass underground, which raises the content of SOC (Poeplau et al. 2015). The soil is thought to hold more than 8580 Gigatons of organic carbon globally, almost ten times the amount in the atmosphere and is much higher than that of plants (Blakemore 2018). A well-known process for carbon sequestration could be transforming agricultural methods, as the soil can act as an efficient carbon dioxide sink, reducing up to 20% of the 2010 carbon dioxide emissions per year. Organic farming and earthworm restoration in soils can completely restrict CO_2 annual emissions of 4 Gt per year and reduce the residual emissions in the atmosphere (Biggers and Hanmer 2015).

Planting in arid areas has been proposed as a strategy to improve soil carbon storage. However, the cost of irrigating these areas using conventional fuels can outweigh any benefits of carbon sequestration. In addition, calcium and soluble bicarbonate ions are found in many areas of surface water and groundwater. CO_2 is released into the air when it is deposited into the soils. Some climate-changing gases, such as nitrous oxide and methane, are influenced by carbon sequestration and management. Changes in these gases should be considered when developing management strategies for carbon storage systems.

6.4 Agricultural Management Practices Influencing Carbon Sequestration

The existence of carbon can be seen in various forms, mainly as soil organic matter, plant biomass, and atmospheric CO_2 (Lal 2018). The terrestrial pool is the largest pool of soil organic carbon consisting of approx. 1500–1600 Pg C compared to the atmosphere, which comprises hardly 700 Pg C (Sanderman et al. 2017). Where management practices are vital for crop production and productivity, proper management practices are of at most importance for a sustainable crop production system. An improper crop management system could result in soil carbon loss due to deterioration of soil quality parameters (Lal 2008). Soil carbon is mostly sequestered as humus by the process of humification (Lal 2018). Hence, agricultural management practices tending to promote humification of soil organic carbon must be highly encouraged. Worldwide, almost 5–sixfold carbon is sequestered on the top 1–2 m of soil compared to the belowground soil or vegetation (Lal 2008). The topsoil, which is often considered surface soil, is most affected by agricultural management practices. The practices that ensure better soil health and promising crop growth and production should be prioritized as they improve the organic matter content of the soil.

More is the concentration of organic carbon higher will be its CO_2 sequestration potential. Agricultural management practices like excess use of agrochemicals, improper tillage practices, exclusion of organic matter application, and in situ crop residue burning have resulted in poor CO2 sequestration, negatively influencing soil organic carbon reserve. Recently, agricultural practices have been considered responsible for 25% of (GHGs) emission, and among the various GHGs emitted, i.e., CO_2, N_2O, and CH_4, CO_2 is regarded as the primary contributor (Smith et al. 2020). The more the carbon is emitted less it is sequestered. A prolonged atmospheric CO_2 emission has led to global warming and climate change and has influenced the soil fertility status worldwide. However, the exact magnitude of carbon emissions from the Earth to the atmosphere and biota to Earth is unknown. Various agricultural practices have been adopted with time progress, sequestering atmospheric CO_2 very efficiently over conventional approaches. Due to soil organic matter depletion, a soil carbon deficit has been created (Amelung et al. 2020). Hence, there is a scope to adopt agricultural management approaches for carbon restoration in the soil system. This section deals with causes of CO_2 loss and methods to be adopted for its efficient sequestration.

6.4.1 Impact of Excess Fertilizer Application: An Aftermath of Green Revolution

Since the Intergovernmental Panel on Climate Change (IPCC) was established by the United Nations Environment Program (UNEP) and the World Meteorological Organization (WMO) in 1988, carbon offsets in agriculture and the environment have been implicated in reducing climate change (Ingram and Fernandes 2001). Dynamics of being one of the leading countries in food production in the 1960s from a poor food country in the past, India has been through the era of Green Revolution, i.e., from 1966 to 1978 (Ladha et al. 2011). The outstanding result of increased application of mineral fertilizers as nitrogenous, phosphatic, and potassic fertilizers over food grain production fetched attention worldwide, and the mineral fertilizer application in the field of food grain production was given importance. The marginal utility of fertilizers was observed to decline with time after the Green Revolution and the lacunae were observed in the case of organic matter application.

Increased application of nitrogenous fertilizers resulted in increased GHGs emissions, especially N_2O, but on the contrary, increased application of mineral fertilizers increased soil carbon stock by the magnification of plant biomass (Lugato et al. 2018a, b). Increased plant biomass has increased soil organic carbon stock directly due to residue decomposition and fixing atmospheric CO_2 as plant biomass by photosynthesis. The stock of carbon in a given soil depends on (1) the annual amount of carbon inputs (biomass added to the soil each year) together with the rate at which the carbon inputs are transformed into SOM (composition rate) and (2) the amount of SOM which is decomposed each year (decomposition rates) (Ingram and Fernandes 2001). The harmful effect of fertilizer application on the emission of GHGs is compensated by its contribution towards soil organic carbon stock. Increased nitrogenous fertilizer application can make soil organic matter decomposition and assimilation by lowering C/N for fresh crop residues (Ladha et al. 2011; Lehman and Kleber 2015). But the knowledge regarding the extent of utilization of chemical fertilizers in crop production and its appropriate combination with various organic amendments is essential for sustainable crop production mitigating climate change (Bhattacharya et al. 2016).

6.4.2 Influence of Various Tillage Practices

Soil management practices in soil conservation approaches are considered vital for the sequestration of atmospheric carbon into the soil system. Practices are aiming at increasing soil organic matter content, i.e., residue retention, adopting high-residue crops and adopting tillage practices with minimum disturbances (Page et al. 2020). The latter is crucial in creating a suitable environment for crop establishment as tillage operations alter soil physical, chemical, and biological environment (Demenois et al. 2020). An important goal of sustainable land resources management is to expand the SOC pool by increasing passive or non-labile fraction. Conservation tillage, a common term including all tillage methods that reduce soil

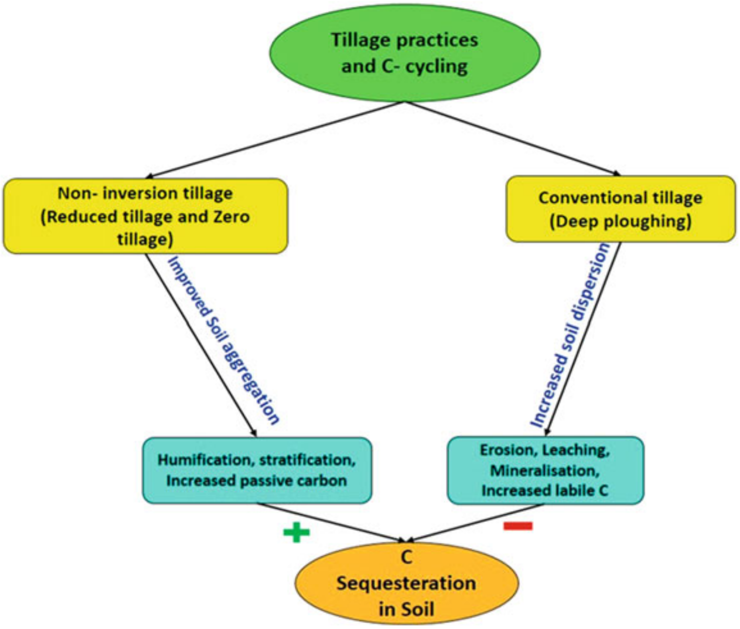

Fig. 6.4 Impact of various tillage practices on C sequestration in soil

erosion and runoff compared to conventional tillage, is known to increase the SOC content in the upper crust (Alam et al. 2014). Under conservational tillage, more carbon is sequestered because of micro-aggregation and in-depth placement of SOC in the subsoil horizons. Other practical agricultural practices associated with conservation farming increase biomass production (e.g., increased soil fertility, improved crop and crop varieties, crop closure and cultivation, improved pastures, and more focused crops) (Page et al. 2020). It is also appropriate to adopt soil and crop management systems that increase access and increase the fraction of SOC production. Because of the importance of C absorption, soil quality should be assessed according to its SOC content.

Tillage practices have a direct or indirect impact on the carbon cycle. Non-inversion tillage practices that involve zero tillage and reduced tillage improve soil aggregation and promote the humification process in soil, which on the other hand, increases the passive carbon pool. In contrast, conventional tillage practices with maximum soil disturbance due to deep ploughing lead to the disintegration of soil aggregates and passive pool reduction of soil organic carbon. Figure 6.4 represents the above concept in brief.

Nowadays, zero tillage has been preferred to conventional tillage due to its principle of minimum soil disturbance. Zero tillage is considered one of the objectives of conservation agriculture. Conservation agriculture works on three primary tenets, i.e., (1) no-tillage or minimum soil disturbance, (2) continuous coverage of soil surface by live mulch or cover crops, and (3) crop residues retention on the soil's surface. Conventional tillage aims at increasing the rate of carbon sequestration over the years. In a 13-year-long experiment in South Finland, non-inversion tillage was found beneficial over conventional tillage in carbon storage (Palojärvi et al. 2020). Similarly, in a 4-year experiment on different tillage practices (Table 6.1), i.e., Deep tillage (DT), Conventional tillage (CT), and Zero tillage (ZT), ZT resulted in the highest organic carbon content, whereas DT resulted in the lowest organic carbon content (Alam et al. 2014). A brief comparison between various tillage practices worldwide, their impact on soil health, and carbon sequestration has been presented in Table 6.1.

6.4.3 Different Crop Management Practices Influencing Sequestration of Soil Organic Carbon

6.4.3.1 Selection of Crops with Efficient C Metabolism

Earth's vegetation contains essential elements such as one tenth of the CO_2 emitted as biomass in the biogeochemical carbon cycle. Plant CO_2 can be converted into biomass or returned to the atmosphere as CO_2 by respiration (Ostle et al. 2003). The ability to assimilate and translocate atmospheric CO_2 by crops is entirely dependent on its species and genotype. Assimilation ranging from nearly 2000 Kg C ha^{-1} Y^{-1} in barley to 5000 Kg C ha^{-1} Y^{-1} on an average 4500 Kg C ha^{-1} Y^{-1} carbon is assimilated by terrestrial plants (Gherardi and Sala 2020). Due to their differential carbon metabolisms, maize is a C_4 plant that assimilates carbon more efficiently than barley, a C_3 plant (Wang et al. 2012). Among the total amount of assimilated carbon, the translocation to root comprises nearly 60%, shoot about 20–25%, and soil almost 10% (Kuzyakov and Domanski 2000; Kätterer et al. 2011). Ryegrass allocates 20% of its assimilates to soil, whereas wheat assimilates nearly 30% of its C assimilates towards the soil.

6.4.3.2 Diversification in Crop Rotation

Management of vegetal cover in agricultural soils has a direct impact on its carbon storage. Distinctly higher soil organic carbon stocks have been observed with diverse cropping systems than monocropping systems (Jarecki and Lal 2003). Various crop rotations could be maintained with many main crops, forage crops, perennial crops, and cover crops (Finney and Kaye 2017). Crop diversity in agricultural fields can be magnified in spatial and temporal scales (Tiemann et al. 2015a, b). A diverse cropping system can alter soil biological health by enhancing soil microbial population, soil physical health by better aggregate stability, and soil overall fertility by improving soil organic carbon stock throughout the soil depth, even in subsoil layers, due to the adoption of a deep-rooted cropping system (Kätterer et al. 2011; Kaiser and Kalbitz 2012). Planting deep-rooted crops and the involvement of catch crops have been considered the two most suitable crop rotation methods for sequestering carbon.

Organic carbon can be sequestered by organo-mineral aggregates even in soil subsurface with very deep vegetation through the roots, i.e., sugars, amino acids, and

Table 6.1 Impact of various tillage practices on soil health and carbon sequestration in different countries

SL	Tillage practice	Experimental period	Country	Impact on soil health	Impact on carbon sequestration	References
1	Conventional tillage	2000–2013 (13 years)	South Finland	Poor overall soil health due to reduced microbial biomass on the top soil	Organic carbon reduced at a rate of 0.4% per year	Palojärvi et al. (2020)
2	Non-inversion tillage practice	2000–2013 (13 years)	South Finland	Improved soil biological health by concentration microbial biomass of surface soil	• Vertical distribution of carbon fractions has been altered • Soil organic carbon and non- labile carbon increment.	Palojärvi et al. (2020)
3	Conservation agriculture based practices	2013–2020 (7 years)	North western India	• Greater water and nutrient acquisition • Enhanced soil macro aggregates • Higher soil organic matter in top soil	Increased SOC stock in surface soil	Mishra et al. (2016); Pooniya et al. (2021)
4	Deep tillage (DT), conventional tillage (CT) and zero tillage (ZT)	2008–2012 (4 years)	Bangladesh	• Reduction in bulk density was observed in the sequence • ZT > MT > CT > DT • Maximum available water content was observed with DT	• ZT resulted in highest organic carbon content, whereas DT resulted in lowest organic carbon content • Soil organic carbon increased by 50% from initial soil with ZT	Alam et al. (2014)
5	Continuous tillage (T), no tillage (NT), no crop residue (-S), application of crop residue (+S)	2006–2015 (9 years)	China	NT soils have higher macro aggregate content and were significantly higher in volumetric moisture content	• Higher organic carbon and C/N was observed with NT • Significant increase in accumulation rate of soil organic carbon in NT	Zhang et al. (2018)

organic acids (Lobell et al. 2011; Sokol et al. 2019). Alfa alfa (*Medicago sativa*), sunflower (*Helianthus annuus*), perennial grasses, and legume crops are few deep-rooted crop species to be adopted for sequestering atmospheric carbon. According to recent studies, the implementation of grass-clover has enhanced soil organic carbon stock nearly by 10% over two decades. The deep-rooted cropping system can assimilate 400 Kg C ha^{-1} Y^{-1} (Poffenbarger et al. 2020). Whereas according to reports, legume crops having nitrogen-fixing capacity have carbon sequestration potential limited to over 20 years of cultivation, and after that, there is much chance of emission of GHGs in the form of nitrous oxide (N_2O) (Poeplau et al. 2015; Lugato et al. 2018a, b). Therefore, knowledge regarding the nature of deep-rooted crops and their impact on soil health climate change should be considered more necessary than their adoption.

Catch crops are fast-growing crops planted to make up the gap between two main crops, often due to failure of the preceding crop (Chahal et al. 2020). Due to their adoption, a permanent vegetal cover is attained in arable lands. Crops such as grasses, legumes, and cruciferous species are considered suitable as catch crops. Due to their gap-filling over temporal scale, catch crops are responsible for additional carbon assimilation in the soil system (Kanders et al. 2017). Annual cultivation of catch crops has a carbon sequestering potential of 400 Kg C ha^{-1} Y^{-1} on an average in agricultural topsoils (Bleuler et al. 2017).

6.5 Conclusions

Global climate change impacted all the spheres where life exists. Agricultural systems are moving towards degenerative farming practices due to intensive and exhaustive resource exploitation; soil nutrient mining increased the cost of cultivation and GHG emissions from the farming system. Present research should address different strategies and policy orientations for regenerative farming practices. Organic input is required to enhance soil carbon sequestration, and deep-rooted crops, crop diversification, reduced tillage, water and nutrient management, agroforestry systems, and integrated farming practices are necessary steps. Further research is required for the translocation of active carbon pool to passive carbon pool. Site-specific carbon sequestration technologies should be customized to reap benefits by improving soil health and crop productivity.

6.6 Future Research and Dimensions

- Conventional farming practices need to be closely monitored to determine the status of soil carbon stock up to 1 cm depth.
- Conservation agriculture systems (no-tillage/reduced tillage, crop residue recycling, and crop diversification) need to be promoted for sequestering higher soil carbon.

- Further research is required on the maintenance of inorganic carbon, particularly in an arid and semi-arid climate.
- Integrated farming systems (high organic input-driven) need to be standardized at different agro-ecologies and scaled up for higher adoption.
- Climate-smart agriculture, mainly blocks plantation, bund plantation, and agroforestry system need to be promoted.

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Inter-Connectivity Between Climate Resilience, Climate Change, and Adaptability

7

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Abstract

Sustainable development requires management of various threats related to climate change and risk assessment. Because of the continuous growth in the threats like climate change, sustainability will be more difficult to achieve in many locations and populations. Although, the developmental pathways of climate resilience are pursued the interconnectivity between climate resileince, climate change, and adaptability at global level. This type of inter-connectivity would allow the generation of mutual benefits of new approaches for sustainable development. Such type of sustainable development initiates the complex interactions between climates and social and socioeconomic systems. The instructional track of climate resilience pathway was initiated with a master plan of combined mitigation and adaptation with respect to realize the goal of sustainable development by avoiding anthropogenic interference of climate change. Strategic policies on the basis of scientific studies can be very much helpful in addressing the climate mitigation. In most of the cases, the adaptation strategy of sustainable development has also involved the appropriate risk assessment. It is exclusively summarized that the procedure of climate resilience would continually need the development in the management of climate change.

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Keywords

Climate changes · Climate resilience · Adaptability · Vulnerability · Mitigation · Human-induced activity · Anthropogenic causes · Natural causes

7.1 Introduction

Climate change is one of the multidimensional issues across the world that can directly or indirectly influence the life on earth. Disturbance in the natural recourses is the major cause of the climate change. Climate change and related issues like global warming are one of the debated topics across the world since the last 40 years (Schneider and Thompson 2000). It has been believed that the human-induced activities are the major cause of climate change by increasing continuous loss in natural resources. The community across the world faces risk due to global climate change and therefore it is need of the hour to understand the nature of those threats to plan and develop adaptive mechanisms especially in areas where natural and human system would likely to be vulnerable. The United Nations Framework Convention on Climate Change (UNFCCC) used the term climate change exclusively to the activities created by humans. It is universally known that most of the climate change throughout the world is due to anthropogenic activities (IPCC 2014).

Most of the global climate change is the result of anthropogenic activities, and it is necessary to identify the anthropogenic signals against natural climate variability. The debates on climate change and adaptation towards climate resilience have been intensified in the last decade focused on the growth of greenhouse gases concentration. However, it is believed that emission of anthropogenic greenhouse gas and emission of carbon dioxide have increased since pre-industrial era due to economic and population growth and are now at peak (Houghton et al. 1996; IPCC 2014). In the last years, adaptation to climate change did not get satisfactory attention because of the various uncertainties related to impact level and timing. Therefore, occurence of certain phenomenons revals that cliamte change mitigation issues did not get much attention amongst policymakers and climate negotiators which leads to further vulnerability from climate change. The first one was to continuously increase the concentration of greenhouse gases despite the fact that climate change negotiation initiated since more than three decades. In this context, United Nations Framework Convention on Climate Change (UNFCCC) urged stakeholders across the globe to act urgently since its formation in 30 years (UNFCCC. 1992). Another one was about the seriousness of the climate change at initial level besides occurence of extreme metrological events both in terms of intensity and frequency (U.S. Global Change Research Program (USGCRP) 2018a, 2018b; World Bank 2019). Therefore, consensuses among the policymakers at a global level related to climate change mitigation and adaptation require to go hand in hand. It has been also realized that many of the countries in the world are severely affected by the climate change because of the lack of their strategic contribution.

Adaptations to climate change are mainly focused through decrease in the impact of climate change with respect to vulnerability on the earth. Vulnerability to climate change is one of the complicated phenomena that results from the climate change and related threats. The high degree of vulnerability increases the exposure of events like drought, cold, flood, etc. results the climate change and also influence the biotic populations of surrounding atmosphere (Yamin et al. 2005). To better understand about global climate change and their potential impact on the earth, Intergovernmental Panel on Climate Change (IPCC) offers the third assessment report (TAR) on the grass root level understanding concern with sensitivity, adaptability, and vulnerability of the ecological, physical, communicable, as well as social system of the climate change (IPCC 2012). The conceptual understanding of the sustainable development in response to climate change involves transformational adaptation may contribute to reduction in the risk. A number of studies recognize that not every response to climate change is associated with a significant sustainable development; some strategies may have negative impacts to the future generations across the globe (Eriksen et al. 2011).

Although the report on previous assessment including second assessment report (SAR) and special report on the regional impact on the climate change, the third assessment report (TAR) depends from them in respect to left perspectives realted to climate change (Smith et al. 2009). As compared to the previous assessment report, strategic attention has been given to the climate change adaptation, links between climate changes across the region, multiple pressures on surrounding ecosystem, sustainable development, and associated confidence level with key concluding remarks of the assessment (UNEP 2019). Based on the critical observation, most of the island states and group of countries including India, the United States, China, Russia, Brazil, Saudi Arabia, etc. are vulnerable to climate change because of the large and insignificant emission of the greenhouse gases are the vivid example at global level (CFID 2019; HC-IDC 2019).

Climate change is the unpredictable phenomenon which results as negative impact on the economic, environmental, and social aspects in the surroundings. Considering the factors that limit the ability to project current and future climate change resilience strategy across the globe indicated that most of the causes result from unpredictable changes in the ecosystem. This literate is especially focused with various causes of the climate change, adaptability, policies and practical implications for resilience activities (Biesbroek et al. 2013). Furthermore, the information shared helps policy-maker experts regarding beneficial resilience through adaptation and mitigation strategies (Uittenbroek 2016). We also focused on the adaptive barriers in terms of lack of public awareness, limited cooperation and coordination, and lack of difficulties to understand about climate information. This article also seeks to fill-up the gap between climate change and adaptation strategies in both agricultural and non-agricultural based communities throughout the world (Oulahen et al. 2018).

7.2 Factors of Climate Change

Climate change is a multidirectional issue governed by a number of environmental factors. Significant changes in the metrological events like temperature, rainfall, wind pattern, snow, and water deficit condition are the measures of climate change. The climate has been changed many times in the planet history. Climate change is the real challenge that can affect the environment and surrounding peoples across the world (Braman et al. 2010). Awareness and understanding the cause of climate change helps to raise parallel resilience. Some important factors which cause the climate change across the world are illustrated here.

7.2.1 Human-Induced Activities

Human-induced activities such as development of cultivated lands, sites, roads by removing forests, burning fossil fuels, etc. are the anthropogenic cause of the climate change on the earth surface. The activities induced by human beings release the greenhouse gases in the atmosphere. Another major cause of human-induced climate change is deforestation. When forests are cleaned for the development of infrastructure or urbanization, it causes the unprecedented increase of carbon dioxide in the atmosphere and directly affects the surface temperature of the earth (Negar and Jean 2014; Yuksel 2014). Changes in the way of land use intensification contribute to climate change by means of land degradation and desertification (IPCC 2020). Such type of change in the land use leads to cooling and warming effects on the earth and surrounding environments. The concept of land use also leads to unsustainable land management and negative economic impact on the agricultural production by accelerating climate change (David 2018).

7.2.2 Emission of Greenhouse

Emission of greenhouse gases is one of the prominent causes of climate induced by human activities (Rockstrom et al. 2017). On an estimate agricultural activity contributes more than 14% of greenhouse gases emission, most by methane formation from fermentation and application of nitrogenous fertilizers and synthetic chemicals (Poeplau et al. 2019). Emission of greenhouse gases due to large scale industrialization increases in land surface temperature is the major cause of global warming (Adnan et al. 2011). Globally, increase in the carbon dioxide emission from fuel combustion and industrialization contributes more than 78% of the total greenhouse gas emission from the last 40 years (IPCC 2014: IPCC 2020). It has been observed that over last 25 years; the global surface temperature risen continuously and resulting in the several extreme metrological events of the climate change and seasonal unpredictability too (IPCC 2018).

7.2.3 Industrial Emissions

Industries, agriculture, and food processing emit pollutants as greenhouse gasses and other harmful particles in the atmosphere as aerosols (IPCC 2020). Produced aerosols in the surrounding atmosphere affect the cloud formation, which can lead either to cooling or warming effect on their type and location (IPCC 2013). Another effect of global warming is the production of black carbon particle in the atmosphere when vegetations are burned (USGCRP 2009, 2014). Generally black carbons produced by human-induced activities are solid particles, not a gas, but it also contributes to the warming effect of the atmosphere and can directly absorb sunlight in addition to absorbing infrared radiation (Sims et al. 2017).

7.2.4 Unplanned Urbanization

Unplanned urbanization by destroying the rural agricultural sectors is one of the extreme factors of climate change. Expansion of urban area is believed to be exploitation of rural and agricultural areas. Urbanization by deforestation and by means of influencing natural resources results in the impact of environmental degradation that contributes to global warming and climate change (Muntasir and Syed 2018). However, unplanned urbanization is the direct or indirect cause of the various types of metrological events on the earth with additional risk of decrease in rural area and natural resources. Long enough and continuous urbanization also invites the migration of rural agricultural labors towards urban areas (Zhang et al. 2017). On other hand, urban expansion can enhance the warming effect in the cities and also in the surrounding areas. Such type of heat-related events can gradually decrease or increase the rainfall over the urban areas that can result in the additional risk of either drought or flood (IPCC 2018, 2020).

7.2.5 Expansion of Agricultural Areas

Expansion of agricultural areas by removing forests and green vegetation, damage of ponds and water reservoir, and other natural resources on the earth is the serious issue that can invite multidirectional climate change (Adnan et al. 2011)**.** Activities related to agricultural crop production such as use of imbalanced nitrogenous fertilizers and hazardous chemicals gradually increase the concentration of nitrous oxide and harmful chemical ions in the air and soil can also invite the events like climate change ((Ministry of Agriculture 2011). Chemicals used as fertigation, pesticides, insecticides, etc. potentially contributed to the climate change and also damage the ozone layer. Other human activities such as deep ploughing, crop residue burning, livestock rising, and filling landfills have also been considered as significant contributors to the climate change (Braman et al. 2010). It has also been observed that naturally evolved methane gas also contributes to the climate change by increase in the decomposition. On an estimate, methane gas concentration increases twice in the twentieth century by means of activities created by humans (IPCC 2020).

7.2.6 Glaciers Melting and Solar Energy

Melting of glaciers and sun energy are influenced by the natural changes that cause the anthropogenic effects across the globes. Melting of glaciers contributed to increased surface melting of ice sheet since 1993 (Peterson and Stott 2013). It has also contributed to loss of ice in arctic sea in last 40 years and increased the global ocean temperature as a component of climate change (You and Ringler 2010). The massive losses in Antarctic ice sheet and Greenland have been observed as atmospheric shrink across the world (Savage et al. 2015). On other hand, natural changes in the solar energy and sun intensity contribute to climate change up to a certain level. Such type of changes affects the sun light intensity that reaches to the earth surface (IPCC 2018). It has been also observed that the change in the solar radiation and their output affects the climate either by change in the rate of solar heat towards atmosphere to earth or by change in the proper formation of the clouds (Khavrus and Shelevytsky 2010). In addition, the sunlight intensity causes global warming because of the strongest period of the sun intensity and cooling effect due to weaker period of sun intensity of the earth (IPCC 2018).

7.3 Climate Change, Resilience, and Adaptability

Inter-connectivity between climate change and adaptation is one of the potential strategies to address global climate change. Adaptation refers to the degree of survival through adjustment in the social, ecological, and economic system in response to climatic stimulants and its impacts (Bizikova et al. 2008). Climate change resilience and adaptation has become an international issue of discussion on climate change. Numerous concepts and terms come into existence as a result of IPCC reports and dialogs by climate community. Another term “climate assessment” appears on paper and can be difficult to apply in practice in some cases. There are no any proper criteria and merit that allow to asset adaptation options across situation and location. Generation of appropriate information on present and future scenario of climate risk is the key components of climate adaptation. Efficiency of adaptation measure is also difficult to measure, and there is no single unit to measure the adaptation output. In many cases, the effectiveness of adaptation can be measured hypothetically or alternatively. Inter-connectivity between climate resilience, climate change, and adaptation is diagrammatically represented in Fig. 7.1.

Modeling capacity and data sources are also itself a type of resource on which adaptive decision has to be taken. Adaptation under adverse environmental condition is also a type of opportunity associated with atmospheric threats and climate change on the earth. The small island states and least developed countries are unable to adapt climate change because of the lack of sufficient financial resources

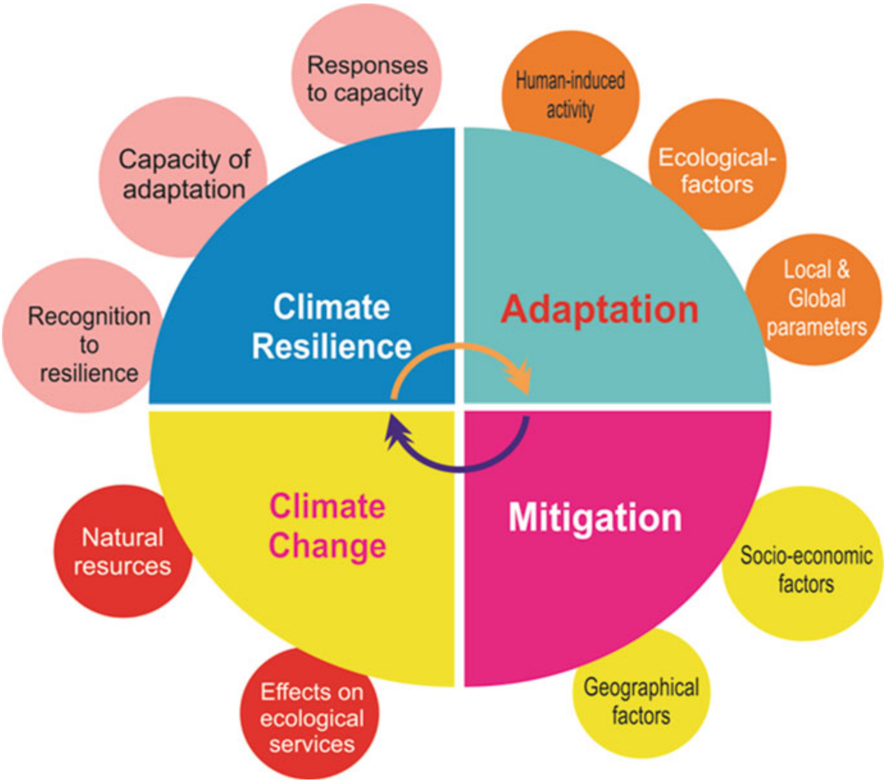

Fig. 7.1 Inter-connectivity between climate resilience, climate change, and adaptation

(Beckman 2011). On other hand, the question is how to manage investment related to global adaptation of climate change, although it would also be so more economical to adapt to climate change compared to the anticipated damage (Hallegatte et al. 2019). Overall, the adaptation for climate resilience and sustainable development are linked in the way of determinants of adaptive capacity to respond the indicator of sustainable development. The capacity building with respect to adaptation may contribute critically to both social and ecological system. Rather than the abovementioned capacity of adaptation, sustainable development framework may also require transformational changes (Lemos et al. 2013).

Climate change mitigation and adaptation is the procedure to determine the prediction of climate impact and identification of vulnerabilities. The process of mitigation and adaptation also promotes the anticipatory changes towards building resiliency other than supporting measures (Bizikova et al. 2010). Development in adaptation and mitigation strategies also requires the strength of regulations and policies and potential initiatives of climate resilience (Agrawala and van Aalst 2008). It has also been observed that the combined strength of policies, regulations, and community initiatives enhances the sustainable growth to appropriate location, insure public health and safety, and also enhance the region's capacity for resiliency (U.S. Climate Resilience Toolkit. 2016). Scientific research and expertise can help to project various types of resilience strategy with aim of sustainable development. The next generation research modeling and interdisciplinary research can also play a significant role in restoring the sustainability by managing the ecosystem. Research contribute to adaptation process with respect to climate resilience also includes excellent research and good practices for the implementation of climate modeling to anticipate future risk. Implementation of weather and climate modeling can also integrate local knowledge to develop adaptation strategies which are appropriate and eco-effective towards climate resiliency.

Finally, it is realized that the progress with climate change adaptation and mitigation towards climate resilience will not be significantly able to avoid high level of regional impact. Research on the strategy for implementation of adaptive management and risk reduction for development needs more task (Hernes 2012). Improvement in the understanding of risk relegated judgment, decision-making uncertainties and best practices in the creation of institutions will effectively integrate climate change responses for sustainable development. The transformational changes strategy is one of the considerable task for reducing the risk of climate change. It may also challenge the economic and social relation, systems, and structures that significantly contribute to climate change and vulnerability (Pelling 2010). The transformation processes are interconnected with learning, leadership, and collaboration within or across the institutions abroad. In addition, other key links associated with adaptable institutions may also able to provide wonderful platform of robust climate resilience for sustainable development (Schlitz et al. 2010). Adaptation mechanism for resilience and sustainable development is represented in Fig. 7.2.

7.4 Rural Climate Resilience

Climate change is a serious threat to the agricultural and food security in the national and international rural area. Increase in the temperature, alteration in the precipitation pattern, and other notable weather events significantly influence the productivity of cropping system mostly in the rural area (Porfirio et al. 2017). Rural climate resilience is concerned with the indigenous peoples and their surrounding ecosystem. Rural climate resilience is the global issue in most countries of the world than can be managed by adapting various types of practices at location level by the indigenous communities of the socio-ecological system (Zhang et al. 2017). A number of abiotic threats like water stress, temperature stress, global warming, and soil and water pollution are the major issues of rural peoples (Chwala 2009). Climate change and related issues on local and rural peoples have been observed at various levels and can dramatically alter the agricultural food production capacity. Climate change on the local level can also affect the people who directly depend on the local food sources and less dependent on the global food supply (Pendall et al. 2018). Strategy for saving water used for drinking and irrigation, use of early maturing crop

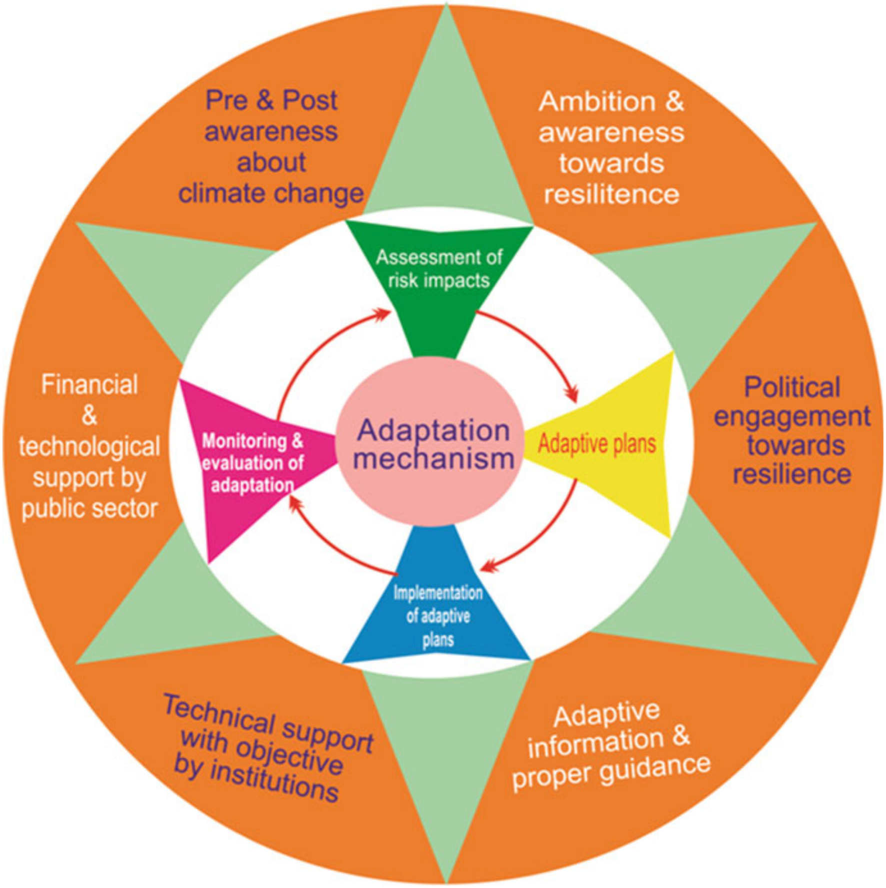

Fig. 7.2 Adaptation mechanism for climate resilience

cultivars, cultivation of drought and flood tolerance varieties of the crops, and forage and fodder storage for the animals are the primitive source of resilience in the rural areas (Barrett 2013).

Climate adaptations are the international issues for the rural peoples and numbers of adaptation plans have been implemented in the communities across the United States. Widespread of various climatic threats and hazard-mitigation planning at rural level is notable points for the health (Singh et al. 2018). Insufficient supply and improper arrangement of the nutritional and healthy food to the people of rural areas under the direct influence of climate change further increaes the vulnerability (Chaudhury et al. 2017). Almost 15% of the American population of the rural areas face limited adaptive capacity, because the challenges for rural municipalities and institutions in responding to climate change are different than those of urban areas (USGCRP 2018b).

7.5 Urban Climate Resilience

Urbanization is the considerable cause of climate change in many cities of the world. In the last several years, the issue of climate change has moved high in both well-developed and under-developed urban areas across the globe (VanDijk and Mingshun 2019). There is no any exact method on how to measure the significant level of urban resilience to climate change. Focus on the reduction of greenhouse gas emission in the urban area is one of the key practices to develop resilience (Spaans and Waterhourt 2017). Selection of initial indicators and filtering them are the primitive approach of the urban climate resilience at the local or region level. Development in the tools for monitoring progress towards climate resilience cities results in the building of urban resilience index. The urban resilience index creates inter-connectivity between urban resilience to climate change and relevant policies. Therefore, urban resilience index is the powerful tool for the decision and policy-maker to achieve the goal. In addition, urban resilience index is also able to identify the priorities to achieve high degree of urban resilience to climate change (Sharifi and Yamagata 2015).

Moreover, the search of urban resilience index has dominated all kinds of urban resilience assessment programs at various levels, such as level of community, region, city, country, and world as a whole (Mingshun et al. 2019a). The single indicator for climate resilience cannot considerable indicators to capture all the dimensions of the urban resilience. Rather than few indicators, few more indicators under monitoring crucially impart the urban resilience at certain level. The strategic task will create urban resilience index, based on the number of representative indicators and provide comprehensive information about urban resilience to climate change (Mingshun et al. 2019b).

7.6 Applications of Resilience Framework

Climate resilience framework is the novel concepts being established on the basis of the ideas related to the sustainable development under acute climatic condition. The sustainable development pathway can also contribute to resilience and adaptation and mitigation with peruse of consumption pattern through ensuring economical and social development. The idea about sustainable development evolved with main objective of strategic improvement for the populations. The implementation of resilience framework needs to be identifying appropriate actions as how can we strengthen diversity across the climate, how can we strengthen self-organization, how do we strengthen adaptiveness, and what infrastructure portfolio would be needed to resilience. Some of the potential points related to the resilience framework are illustrated here.

7.6.1 Resilience Towards Climate Change

Resilience towards climate change offers various types of contributions that can improve the environmental issues towards developing sustainable effect on the climate change. Climate resilience framework is the novel idea of establishment of multidimensional socio-ecological system (Holling 1973). The aim of resilience framework to climate change adaptation is the ability of ecological system to absorb disturbance. In this context, under-developed countries need social and ecological resilience with the idea of persistence and transformation. In addition climate resilience frameworks require the capacity of transformation that moves out of poverty towards prosperity that can be sustainable under global climatic changes. Resilience framework can be initiated at certain level to improve the various issues related to abiotic stresses. Scientific research related to climate resilience, ecological adaptation, and natural resource management have been initiated across the world (Vayda and McCay 1975).

7.6.2 Climate Resilience Pathway

The climate resilience pathway brings sustainable development with context for nations, regions, and global communities. Climate resilience pathway integrates conventional and alternative developmental pathways to meet the goal for sustainable development. The climate resilience pathway also represents trajectories that include both adaptation and mitigation for strategic management of change in the complex system (Scheffer et al. 2009). Climate resilience pathways also recognize that the action aims to reduce climate change impacts including mitigation and adaptation and also to ensure the effective risk management strategies. The climate resilience pathway should therefore continuously modified towards more adaptive and improvised management system (Edenhofer et al. 2012). The frameworks of resilience have ability of social and socio-ecological system to its components to reduce or recover from the effect of several hazardous events in timely or before adverse condition (Rockstrom et al. 2009). Rather than back works, the change was harnessed to establish new base lines with adoptive strategies for minimizing imposed changes and use them for sustainable and novel characterization (Moench and Tyler 2012).

The climate resilience pathway calls for strategic action and decision to take into account short- and long-term mitigation and adaptation. In the short-term climate adaptive strategy, society will have to adapt the climate changes linked to emissions which have strong influence on sustainable development. Considering the potential impact of climate resilience pathway sustainable development would likely become greater over time (Wilbanks and Wilbanks 2010). Novel perspectives of climate resilience, work to facilitates changes in the field of adaptive management and environmental sources (Folke 2006). Sustainable development pathway strategically contribute to climate resilience by targeting consumption pattern that ensure the economic and social development and also by reducing the harness of natural resources for maintaining the natural ecological systems (Kates 2000).

7.6.3 Modern Interpretations of Climate Resilience

The modern interpretations of climate resilience are now established as socio-economic system that can be stabilized with sustainable solutions. The second most important things of the climate resilience framework associated with attention on preventive action against the effects of climate change. Building climate resilience policies and adaptation to climate change can be treated with planned policies that work to mitigate the harm of global warming impacts on the earth (Bizikova et al. 2007). Adaptation based action may leads the opportunities to build the sustainable development through dynamic changes (Nelson et al. 2007). The most important effect of climate change occurs due to water in terms of water deficit or drought and flood or submergence. The absence of water for a long period of time, long enough to cause moisture depletion in the soil, can directly influence the crop production at a certain level. Most of the cultivated areas across the world under water deficit condition may destroy the communities and nation too. Water management and water governance system proved a key role towards building climate resilience system (Smith and Barchiesi 2009). Approaches for sustainable development through adapting government and institutional policies are diagrammatically illustrated in Fig. 7.3.

7.6.4 Smart Framework

Framework of smart and resilience climate has no limitation for improvement; and it can be improved from bottom to top level for making socio-economic development on the earth. Deforestation, disturbance of water reservoir, and industrialization are the considerable causes of climate change in most of the developed countries even in the under-developed countries. Protections of water reservoir, dense and regular tree plantation on the wasteland, and use of limited chemical during crop production are also considered as primitive awareness for climate change. Avoidance of any minute issues related to the healthy and clean environment in the present may cause severe effect on the socio-economic status of the nation in the future. So, awareness against climate change is the key point of resilience that can be easily managed by the population of a particular area by employing the various types of practices (Malhi et al. 2008). Smart framework of climate resilience is represented in Fig. 7.4.

The literature on climate resilience has also noted that one of the indirect sources of the resilience is the strength of social services. This is the critical aspects of climate resilience framework in the socio-economically disadvantaged communities of the nation. It has been empirically found that most of the places with stronger system of social security have better climate resiliency (Satterthwaite 2013). The

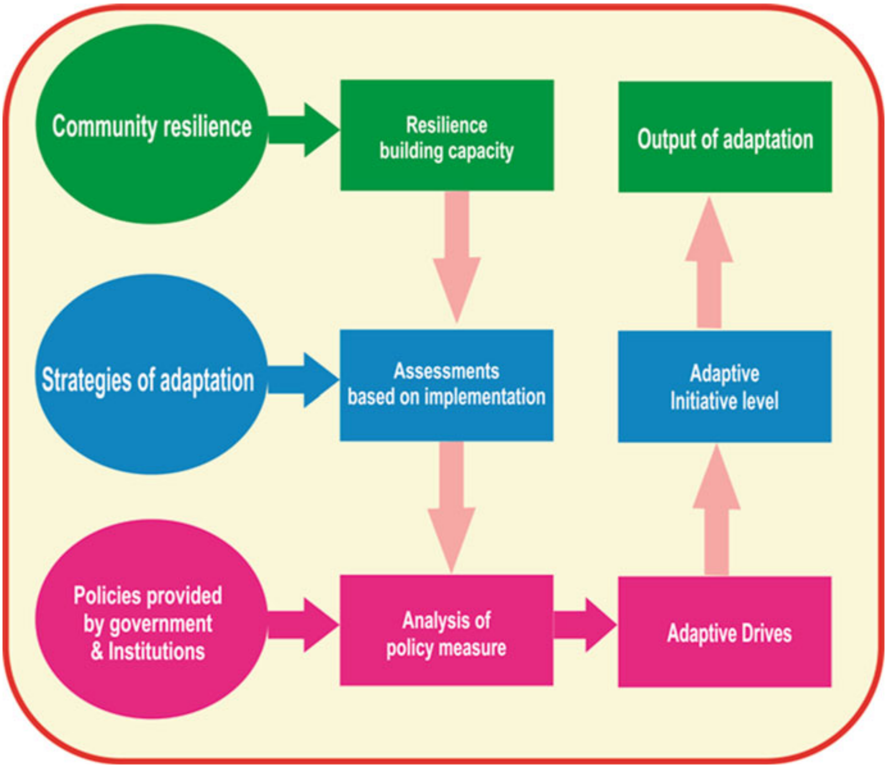

Fig. 7.3 Approaches for sustainable development through adapting various policies

remarks on the climate resilience frameworks require the strategic and stepwise improvement through creation of environmental protection and their systematic implementation in the particular region.

7.7 Conclusion

Shifting in the magnitude and timing of the various hydrometeorological events such as rainfall, flood, drought, and temperature rise with other extreme variabilities in the climate change will significantly affect natural resources, economic system and quality of ecosystem services. Moreover, the outburst of metrological events and emergence of vector-borne diseases because of climate change may pose new challenges for the global populations. In order to conclude the remarks for inertconnectivity between climate resilience, climate change, and adaptation is not simply the extension of diaster risk management. Adaptation to climate change is also not only the addressing of changes in frequency and intensity in the various types of metrological events. The effective reduction in the vulnerabilities to climate change and other natural hazards requires coordination at various levels, center of

Fig. 7.4 Smart resilience framework

governance, as well as involvement of different levels of stakeholders. To strengthen the inter-connectivity between climate resilience and adaptation to climate change, it is universally important to understand when and what level coordination is required and who should take the lead. The studies at national and international level for institutional interaction on climate risk management are strategically improving the inter-connectivity between climate resilience, climate change, and adaptation.

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Soil Organic Carbon and Total Nitrogen Stocks Under Different Land Uses in Achanakmar-Amarkantak Biosphere Reserve, India

8

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Abstract

Land use changes, essentially due to alteration from natural ecosystems into managed agro ecosystems, and subsequent deterioration in the quality of soil resources have become common phenomena in AABR. Soil reaction (pH), soil carbon, total N, available P contents, and potassium content are vital soil properties affected by such changes. This study was therefore conducted with the objective to assess the response of these vital soil chemical properties to changes in management practices arising from varying land uses (dense forest, plantation, degraded vegetation, agriculture, and agroforestry) and soil depth (0–20 and 20–40 cm). Results revealed that vital soil properties significantly ($P \leq 0.01$) responded to changes in land use and with depth. Contents of soil carbon and total N, P, K were highly significantly affected by soil depth and land use types. However, interaction of land use and soil depth is to be found significant for pH and available P. The correlation between nitrogen and carbon content of the soil is found to be positive with all depth and land use types except depth 20–40 cm in case of agroforestry land use system. Available P contents were also significantly ($P \leq 0.01$) reduced due to shift of land uses from natural forest to agricultural land uses but with soil depth and interaction effect. It can be noted that this situation is far from sustainability and has tremendous implications for productivity of the traditional low-input agriculture in the study area. This manuscript is an attempt to identify the LULC pattern and assess the carbon storage, soil organic carbon, and nitrogen stock in various land use systems in Central India along with potent productivity for natural resource management and the deficit that causes limitations in the sustainable development.

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Keywords

Available phosphorus · Crop-livestock systems · Land use change · Organic matter

8.1 Introduction

Soil is an important factor, influences the production/productivity of terrestrial planet, and plays a crucial role in the existence of different life forms, fulfilling their nutritional requirement. Soil ecosystem is the pool of plenty of macro and micro nutrients, essential for growth and development of physiognomy of plants exist on terrestrial planet. The status of the soil nutrients pool (SNP) may greatly influence with environmental and anthropogenic driving factors. Land use is a key factor governing many processes of environmental change including the soil resources. The United Nations Framework Convention on Climate Change (UNFCCC) has introduced the Land Use, Land Use Change and Forestry (LULUCF) approach, which aims at C sequestration through afforestation, reforestation, re-vegetation, and forest-crop and grassland management as a form of GHG-offset activities (Izaurralde et al. 2001; McCarl and Schneider 2001). With follow-up of this approach, in the recent years, across the globe major focus was given on the soil organic carbon (SOC) and soil total nitrogen (STN), which were highly altered with change in land use management practices. However all the nutrients more and less influence this phenomenon. SOC and soil total nitrogen (STN) can provide nutrients for plant growth and maintain good soil physical structure. Therefore, the research of SOC and STN concentration and stock is essential in increasing crop productivity and alleviating carbon emissions (Wang et al. 2016). The forest patch/fragmentation and land use land cover changes are key drivers of losses biodiversity, habitation, and ecosystem processes in tropical regions, which are intrinsically linked to composition. Soil nutrients, flora and faunal diversity, and functioning of ecosystems, which lead to the formation of varying sizes of forest patches, create isolation from dense forests and often form new forest edge (Kumar et al. 2017a, b; Thakur et al. 2019a, b; Kumar et al. 2021). It has been well observed that the SOC and STN stock of ecosystem was greatly influence with the change in land use practices (Wu et al. 2003; Gelaw et al. 2014; Gao et al. 2015 (Deforestation); Kucuker et al. 2015; Fujisaki et al. 2015 (Afforestation;(Bárcena et al. 2014; Omonode and Vyn 2006). However, nutrient status of soil not only bounded with land use changes but also affected through soil physical (Sakin 2014; Jiao et al. 2011) and chemical properties (Six and Paustian 2014). It has been well demonstrated or proved by researchers that forest ecosystems are important both ecologically and economically, and forest soil is the most fundamental terrestrial asset and natural resource (Agoumé and Birang 2009). There are certain factors like litter biomass and live biomass that directly contribute to the SNP; on the other hand inappropriate tillage operation and anthropogenic activity have negative impact on same. The SOC stocks of forest lands were higher than that in cropland in humid tropics or drought-less region (Fujisaki et al.

2015; Zhang et al. 2013). Land use in tropical areas causes significant modifications in soil properties in which agriculture has a major contribution (Pal et al. 2013), and especially cultivation of deforested land may rapidly diminish soil quality (Ayoubi et al. 2011). The conversion of natural forest to cultivated land is manifested the most in the on-site loss of SOM causing a reduction in nutrient stock, CEC, and structure stability (Hartemink et al. 2008). Beside, influence of land use on carbon content also influences the soil N cycling in tropics. There is a consistent finding that intact tropical forests have higher rates of N mineralization and nitrification than agricultural sites (Piccolo et al. 1994; Reiners et al. 1994; Neill et al. 1995, 1997), suggesting that N availability is greater (Nadelhoffer et al. 1983) where there is less human disturbance. However, soil stocks of inorganic N can be higher in agricultural sites than forest sites because of lower plant uptake (Neill et al. 1995). The change of forest land into non-forestry uses influences the emission of N_2O in the atmosphere by the so-called process de-nitrification (Keller et al. 1993; Neill et al. 1997; Verchot et al. 1999). The understanding of pattern of N_2O losses in the ecosystem is extremely desirable because it contributes in greenhouse gases as well as in ozone depletion at a large extent. These changes in land use are often localized and site specific; however their impacts collectively lead to changes in the larger global scale resulting in desertification, biodiversity loss, global warming, and ultimately change the ecosystem of the planet (Chase and Singh 2014; Kumar and Thakur 2017; Thakur 2018; Kumar et al. 2021; Thakur et al. 2021a, b). The recent study mainly focused on the objectives like estimating the nutrient status in different land use and on different depth and assessing the effects of land use changes on SNP.

8.2 Materials and Methods

8.2.1 AABR and the Study Site

The Achanakmar-Amarkantak Biosphere Reserve (AABR) is spread between 21° 15′ to 22° 58′ N latitude and 81°25′ to 82° 5′ E longitude. This covers an area of 388733.5 ha. AABR is categorized into nine different regions, namely, the dense forest (212283.5 ha), the cropland area (130,500 ha), the open forest (17,391 ha), the degraded vegetation (9414 ha), the wastelands (5222 ha), the forest blank (3266 ha), the land with/without scrub (2381 ha), the ravines land (2391 ha), and the build-up (1092 ha). In addition, water structures cover 3593 ha, and 840 ha of the area is not a part of any of the abovementioned regions. The mean daily maximum temperature of AABR ranges from 24° to 42° C whereas its mean daily minimum temperature ranges from 10° to 25° C. Relative humidity in AABR varies from 39% to 90% with an average yearly rainfall between 1322 mm and 1624.3 mm. The geology of the area is unique and varies from schist and gneisses with granite intrusions to sand stones, shale, limestone, basaltic lava, and bauxite. The composition and texture of the soil varies from sandy to loamy-clays, generally light brown to brownish, and olive green clay at some places. Red soil which is rich in iron oxide is also present. It is porous and fertile. The banks of numerous streams in the tract are rich in alluvial soil. The black cotton soil in many areas of AABR supports a large number of ecosystems and species. The site for the present study is spread over 15,100 ha with elevations ranging from 1053 to 1450 m.

8.2.2 Sampling Design and Methods

For the present study five different types of land uses are identified in AABR. These are the croplands (wheat), dense forests, plantations, degraded vegetation, and agroforestry (wheat and *Dalbergia sissoo*). Within each of the identified land uses 10 plots of sizes 20 m X 20 were set up. This made up 50 plots in total wherein each land use was replicated 10 times. Five sampling points with Z-shaped pattern in each plot were selected. The soil was excavated to a depth of 40 cm, and consolidated rock material was obtained.

Intact soil cores were sampled for a depth of 0–20 cm and 20–40 cm to estimate the stock of SOC and STN. From all the samples root particles, crop residues, and other inert material were removed manually with the help of a 2 mm sieve. After removing these particles, all samples were mixed by using quartering methods. This was followed by oven drying the material at 72 °C for 24 hours. The disturbed soil samples were used to determine the sand, silt, and clay contents, the pH value, the total phosphorus (STP), and the total potassium (STK) content. Core samples were also collected to quantify bulk density of soil at specific intervals with the help of cylinder (5 cm). In addition, pH and EC were also measured using multi-parameter.

The SOC and STN (both in Mg/ha) for each sampling site were estimated by using the following formulae (Chen et al. 2007):

$$\mathrm{SOCs} = \sum\nolimits_{i} (\mathrm{SOC}_i \times B_i \times D_i \times 8.10)$$

$$\mathrm{STNs} = \sum\nolimits_{i} (\mathrm{TN}_i \times B_i \times D_i \times 8.10)$$

where SOCs and STNs were the soil stocks of SOC and STN, respectively. SOC_i and TN_i are the carbon and nitrogen concentrations, respectively, in the i^{th} layer (gm/Kg). B_i is the bulk density of a particular layer in (g/cc) and D_i is the thickness of the core. The STP and STK were calculated by averaging all the samples of the plots.

8.2.3 Statistical Analyses

The difference in physical properties, namely, sand, silt, and clay, among different types of land uses was tested using one-way ANOVA. The bulk density, the nutrient content (STN, STP, STK, and SOC), and other chemical properties (pH and EC) of the soil are opined to vary with the type of land use and the depth of the soil. Hence, two-way ANOVA models with interaction were utilized to investigate the variation in nutrient content (STN, STP, STK, and SOC), chemical properties (pH and EC), and the bulk density. This was followed by post hoc tests for respective ANOVA models for investigating the significance of the differences between effects of pairs of land use types on different parameters (sand, silt, clay, bulk density, STN, STP, STK, SOC, pH, and EC).

The correlation between STN and SOC content was investigated for all the combination of land use and selected depths. The correlations between the parameters for nutrient content, chemical properties, and the physical properties are also investigated for each of the selected depths. The dependence of STN, STP, STK, SOC, EC, pH, bulk density, silt, sand, and clay on the bulk density and depth was modelled using regression models. All analysis was carried out in SPSS, version 16.0.

8.3 Results and Discussion

The effect of the type of land use is found to be significant on the nutrient content, the chemical properties, and the bulk density of soil (Table 8.1). The effects of selected depths are found to be significant on all the parameters. However, the interaction of land use and depth is found to be significant only in case of pH, STP, and bulk density. In addition, the one-way ANOVAs conducted for sand, silt, and clay indicated that the effect of land uses is significant (p-values <0.01 for each of sand, silt, and clay).

8.3.1 Land Use Types and STN

Pair-wise comparisons show that the difference in the STN between different pairs of land use types is significant except for the DF-AF, P-DV, P-AG, and DV-AG (Table 8.2). The average STN is estimated to be more by 36.26, 41.46, and 56.12 Kg/ha in DF when compared to P, DV, and AG, respectively (Table 8.2). The average STN in P is 35 Kg/ha less than that for AF. The STN in DV is 40.2 Kg/ha less than AF whereas it is 55 Kg/ha more in AF when compared to Ag (Table 8.2). The effect of land use and soil depth was found to be significant for all chemical properties and land use types. However the interaction of the land used and depth was significantly in case of PH and available phosphorus content. The similar trend was observed by Emiru and Gebrekidan (2013), Bijalwan et al. (2017, 2019), Thakur et al. (2017), Thakur et al. (2018), Thakur et al. (2020), Darro et al. (2020), and Kumar et al. (2017a, b). This variation can be result of loss of base farming cations.

The nitrogen contents of land use and land depth show decline trend with land use and land depth. The N content was highest in dense forest with depth of 0–20 cm. The same founding was observed by Ross et al. (1999). Concurrently, organic carbon content was profoundly affected by soil depth and land use types, however interaction with land use and soil depth not shown any significant difference. This is attributed to be continuous accumulation of dead and decay matter on surface soil. In

Table 8.1 Two-way ANOVA for different land use and depth

	Soil properties						
Parameters	STN	STP	STK	SOC	EC	pH	Bulk density
Land use	6.76 (< 0.01)	3.52 (0.01)	16.52 (< 0.01)	3.81 (0.01)	190.30 (< 0.01)	54.06 (0.000)	55.97 (< 0.01)
Depth	12.71 (< 0.01)	16.84(< 0.01)	4.67 (0.03)	102.35 (< 0.01)	82.17 (< 0.01)	49.989 (0.000)	15.57 (< 0.01)
Land use*depth	0.03 (0.99)	6.46 (< 0.01)	0.08 (0.99)	2.10 (0.09)	0.68 (0.61)	21.77 (< 0.01)	10.19 (< 0.01)

Table 8.2 Pair-wise comparison of effects of selected land use types for selected parameters for physical and chemical properties of soil

	Different in effects (p-value)									
Land use type pairs	STN	STP	STK	SOC	EC	pH	Bulk density	Clay	Sand	Silt
Dense forest—Plantation	36.26 (0.01)	2.03 (0.10)	38.05 (0.17)	0.12 (0.03)	−0.004 (0.60)	0.04 (0.59)	0.04 (0.02)	0.50 (0.11)	−2.50 (< 0.01)	2.00 (< 0.01)
Dense—Degraded vegetation	41.46 (< 0.01)	3.44 (< 0.01)	164.80 (< 0.01)	0.13 (0.02)	0.003 (0.70)	−0.43 (< 0.01)	0.07 (< 0.01)	0.55 (0.08)	−3.40 (< 0.01)	3.00 (< 0.01)
Dense forest—Agriculture	56.12 (< 0.01)	3.80 (< 0.01)	160 (< 0.01)	0.21 (< 0.01)	−0.16 (< 0.01)	−1.00 (< 0.01)	0.24 (< 0.01)	−10.7 (< 0.01)	8.20 (< 0.01)	2.50 (< 0.01)
Dense forest—Agroforestry	1.26 (0.92)	0.70 (0.58)	19.00 (0.49)	0.12 (0.03)	−0.08 (< 0.01)	−1.00 (0.23)	0.11 (< 0.01)	−3.6 (< 0.01)	2.90 (< 0.01)	0.80 (0.07)
Plantation—Degraded vegetation	5.20 (0.70)	1.40 (0.26)	126.75 (< 0.01)	0.01 (0.82)	0.01 (0.33)	−0.49 (< 0.01)	0.03 (0.09)	0.05 (0.87)	−0.10 (0.03)	1.00 (0.03)
Plantation—Agriculture	19.9 (0.15)	1.78 (0.16)	121.75 (< 0.01)	0.09 (0.10)	−0.16 (< 0.01)	−1.00 (< 0.01)	0.20 (< 0.01)	−11 (< 0.01)	10.70 (< 0.01)	0.50 (0.25)
Plantation—Agroforestry	−35.00 (0.01)	−1.33 (0.29)	−19.05 (0.49)	−0.002 (0.97)	−0.08 (< 0.01)	−0.14 (0.08)	0.07 (< 0.01)	−4.1 (< 0.01)	5.40 (< 0.01)	−1.2 0 (< 0.01)
Degraded vegetation—Agriculture	14.70 (0.29)	0.37 (0.77)	−5.00 (0.86)	0.08 (0.15)	−0.17 (< 0.01)	−0.58 (< 0.01)	0.17 (< 0.01)	−11 (< 0.01)	11.70 (< 0.01)	−0.50 (0.25)

(continued)

Table 8.2 (continued)

Land use type pairs	Different in effects (p-value)									
	STN	STP	STK	SOC	EC	pH	Bulk density	Clay	Sand	Silt
Degraded vegetation—Agroforestry	−40.20 (< 0.01)	−2.73 (0.03)	−145.80 (< 0.01)	−0.01 (0.80)	−0.08 (< 0.01)	0.33 (< 0.01)	0.04 (0.04)	−4.2 (< 0.01)	6.40 (< 0.01)	−2.20 (< 0.01)
Agroforestry—Agriculture	55.00 (< 0.01)	3.11 (0.01)	140.80 (< 0.01)	0.09 (0.09)	−0.08 (< 0.01)	−0.90 (< 0.01)	0.13 (< 0.01)	−7 (0.31)	5.37 (< 0.01)	1.7 0 (< 0.01)

general converting or disturbing natural ecosystem may result in difference of carbon content with land used. As forest vegetation shows closed type of nutrient cycling, add nutrient on surface layer by pulling nutrient from deeper layer and at the same time add nutrient with leaf and litter material from tree canopy. The same findings were observed by Woldeamlak and Stroosnijder (2003) and Genxu et al. (2004). The effect of land used and soil depth with its interaction was found to be significant. Shift of land use changes from natural forest to managed agro-ecosystem or biological interference may be caused to decline available phosphorus content with land use and depth of soil. This result is an agreement with findings made by Saikh et al. (1998) and Woldeamlak and Stroosnijder (2003) but contrasts with that made by Sánchez et al. (2002). The lowest concentrations of these parameters were found in agriculture land use practices. Sole cropping or agriculture system have open type of nutrient cycling, most of nutrient exhausted by crop rather adding nutrient in field ecosystem.

8.3.2 Land Use Types and SOC

In case of carbon, the content of carbon between different pairs of land use is significant except P-DV, P-AF, DV-AF, P-AG, DV-AG, and AF-AG. The average SOC is estimated to be more by 0.12, 0.13, and 0.21 g/kg and 0.12 in DF when compared to P, DV, AG, and AF, respectively (Table 8.2).

8.3.3 Land Use Types and STP

The STP of different land use pairs was found to be significantly different in DF-DV, DF-AG, DV-AF, and AF-AG. The STP in DF is found to be more than that of DV and AG by 3.44 kg/ha and 3.80 kg/ha, respectively. Similarly, the STP in AF is found to be 3.11 kg/ha more than that in AG. However, it is 2.73 kg/ha less in DV when compared to AF (Table 8.2). The remaining land use pair shows no significant differences with respect to the STP.

8.3.4 Land Use Types and STK

The potassium content between the land use pairs, namely, DF and P, DF and AF, and DV and AG, is not found to differ significantly (Table 8.2). However, for the rest of the land use type pairs, the difference is found to be significant. The STK is found to be higher in DF when compared to DV and AG. Similarly, it is found to be higher in P when compared to DV and AG. DV is found to have a lower STK when compared to AF. Further the STK of AF is found to be higher than that of AG.

8.3.5 Land Use Types and the EC

The differences in the EC are not found to be significant between the land types, namely, DF and P, DF and DV, and P and DV. EC of DF is found to be lesser than that of AG and AF. Similarly, EC of P is found to be lesser than that of AG and AF (Table 8.2). In case of DV it is found to be lesser than that of AG and AF, whereas the EC of AF is found to be lesser than that of AG.

8.3.6 Land Use Types and the pH

The pH of the selected land use types differs significantly from each other excepting DF and P, DF and AF, and P and AF (Table 8.2). DF is found to have a lower pH value when compared to DV and AG. P is also found to be having a lesser pH when compared to that of DV and AG. DV is found to have a lower value of pH than AG but a higher value of pH when compared to AF. The pH of AF is also found to be lesser than that of AG.

8.3.7 Land Use Types and Bulk Density

The bulk density of DF is found to be greater than those of P, DV, AG, and AF. Although the bulk density of P and that of DV is not found to differ significantly, P is found to have greater bulk density when compared to AG and AF. Similarly, DV is found to have a greater bulk density when compared to AG and AF (Table 8.2). AF is also found to have a greater bulk density than AG.

8.3.8 Land Use Types and Soil Structure Content

The clay content of DF is not found to differ significantly from that of P or DV. However, it is found to have a lesser clay content than that of AG and AF. Similarly, P is found to have a lesser clay than that of AG and AF (Table 8.2). DV is also found to have a lesser clay content when compared to AG and AF. The sand contents in DF, P, DV, AG, and AF are found to be significantly different from each other. DF is found to have a lower sand content when compared to that in P and DV, whereas it has a higher sand content when compared to that in AG and AF. P is found to have a lower sand content than that in DV and a higher sand content than that in AG and AF. The sand content in AF is also found to be higher than that in AG (Table 8.2). DF is found to have relatively higher silt content when compared to that in P, DV, AG, and AF. The silt content in P is found to be higher than that in DV and AG, but its silt content is found to be lesser than that in AF (Table 8.2). DV is found to have a less silt content when compared to that in AG and AF. AF is found to have higher silt content when compared to that in AG.

8.3.9 Correlation Between STN and SOC

The correlation between STN and SOC of the soil is found be positive and high for DF, P, DV, AG, and AF for both the selected depths except in agroforestry for the depth 20–40 cm (Table 8.3). For a depth of 0–20 cm the highest correlation is observed in AG (0.99). It is followed by P (0.96), AF (0.93), DF (0.82), and DV (0.75) in the decreasing order of correlation (Table 8.3). For a depth of 20–40 cm the ordering of land use types in the decreasing order of correlations is AG (0.93), DF (0.91), DV (0.91), P (0.86), and AF (0.17). Storage of soil organic carbon (SOC) and nitrogen (N), availability of soil N and phosphorus (P) were found to be increased under agroforestry compared to crop monocultures (Thakur and Thakur 2014; Verma et al. 2017; Bijalwan et al. 2019). Agroforestry provides a significant pathway to sustainable agricultural systems and diversification of income and plays a critical role in preserving microclimate and by providing permanent cover for soil and water. It is considered economically feasible and sustainable practice with the ability to reduce emission and sequester carbon (Kumar et al. 2021; Thakur et al. 2021a, b).

8.3.10 Correlation Between Other Parameters for Selected Depths

In what follows the correlations between parameters of physical properties, chemical properties, and the nutrient content of the soil are discussed based on Table 8.4. The figures in the brackets denote the respective coefficient of correlation. For depths up to 0–20 cm, a significant and positive correlation is observed between the bulk density and STN (0.52), SOC (0.68), STK (0.37), and STP (0.65). On the other hand, a significant negative correlation is observed between pH and STN (−0.18), SOC (−0.39), STK (−0.44), and STP (−0.43). Similar to the findings on pH, the correlation between EC and STN (−0.16), SOC (−0.39), STK (−0.24), and STP (−0.32) is also found to be negative. STN is found to have a positive correlation with SOC (0.79), STK (0.27), and STP (0.67). STP is found to be positively correlated with STK (0.42) and SOC (0.67).

For depths beyond 20 cm, i.e., for 20–40 cm of depth the bulk density is found to be positively correlated with STN (0.33) and STK (0.30). STK (−0.50) and pH are

Table 8.3 Correlation between STN and SOC for different combinations of selected land use types and selected depths

Depth	Selected land use types				
	Dense forest	Plantation	Degraded vegetation	Agriculture	Agroforestry
0–20 cm	0.82 (< 0.01)	0.96 (< 0.01)	0.75 (0.01)	0.99 (< 0.01)	0.93 (< 0.01)
20–40 cm	0.91 (< 0.01)	0.86 (< 0.01)	0.91 (< 0.01)	0.93 (< 0.01)	0.17 (0.63)

Table 8.4 Correlation between selected parameters for physical and chemical properties of soil

Depth		BD	pH	EC	STN	STP	STK	SOC
0–20 cm	BD	1	−0.76*	−0.78*	0.52*	0.65*	0.37*	0.68*
	pH		1	0.82*	−0.18	−0.43*	−0.44*	−0.39*
	EC			1	−0.16	−0.32*	−0.24	−0.39*
	STN				1	0.67*	0.272	0.79*
	STP					1	0.42*	0.67*
	STK						1	0.29*
	SOC							1
20–40 cm	BD	1	−0.13	−0.66*	0.33*	−0.04	0.30*	0.23
	pH		1	0.21	−0.19	0.12	−0.50*	−0.08
	EC			1	−0.23	0.13	−0.25	−0.12
	STN				1	0.34*	0.26	0.65*
	STP					1	−0.11	0.46*
	STK						1	0.26
	SOC							1

* indicates the significance ($P < 0.05$)

found to be negatively correlated. STN is found to have a positive correlation with STP (0.34) and SOC (0.65). STP and SOC (0.46) also show a positive correlation.

8.3.11 Dependence of STN, STP, STK, SOC, EC, pH, Bulk Density, Silt, Sand, and Clay on the Land Use Types and Depth

The regression of nitrogen content on land use and depth (Table 8.5) shows that when compared to DF, the STN is lesser by 36.26, 41.47, 56.17, and 1.27 kg/ha for P, DV, AG, and AF. Further it is lower by 30.89 kg/ha in depth of 20–40 cm when compared to the depth 0–20 cm. The regression of STP on land use and depth shows that when compared to DF, the phosphorus content is less by 2.03, 3.44, 3.81, and 0.70 kg/ha for P, DV, AG, and AF. Further it is lower by 3.25 kg/ha for depth 20–40 cm when compared to depth 0–20 cm. In case of STK, it is higher in all land use types when compared to DF except for the AF (Table 8.5). Further it is higher by 37.88 kg/ha and significant in the depth of 20–40 cm when compared to the depth of 0–20 cm. The regression of SOC on land use and depth shows that when compared to DF, the carbon content is lesser by 0.12, 0.13, 0.21, and 0.12 g/kg for P, DV, AG, and AF. Further it is lower by 0.35 g/kg in the depth of 20–40 cm when compared to the depth of 0–20 cm. The regression of EC and pH shows the various trends when compared to DF (Table 8.5). The EC concentration is lower only in DV (not significant) and in the depth of 20–40 cm but significant. While pH is found to be lower by 0.05 in P, it is not significantly different from the reference category DF. Further pH conc. is higher by 0.38 in the depth of 20–40 cm when compared to the depth of 0–20 cm (Table 8.5).

Table 8.5 Regression of STN, STP, STK, SOC, EC, pH, bulk density, silt, sand, and clay on the land use types and depth

Variables	STN	STP	STK	SOC	EC	pH	Bulk density	Silt	Sand	Clay
Constant	315.26 (< 0.01)	17.00 (< 0.01)	423.09 (< 0.01)	0.83 (< 0.01)	0.12 (< 0.01)	5.81 (< 0.01)	1.46 (< 0.01)	34.00 (< 0.01)	47.25 (< 0.01)	18.75 (< 0.01)
Land use type										
Plantation	−36.26 (0.01)	−2.03 (0.15)	−38.05 (0.16)	−0.12 (0.03)	0.004 (0.56)	−0.05 (0.69)	−0.04 (0.04)	−2.00 (< 0.01)	2.5 (< 0.01)	−0.50 (1.12)
Degraded vegetation	−41.47 (< 0.01)	−3.44 (0.01)	−164.80 (< 0.01)	−0.13 (0.02)	−0.003 (0.70)	0.44 (< 0.01)	−0.07 (< 0.01)	−3.00 (< 0.01)	3.49 (< 0.01)	−0.55 (0.08)
Agriculture	−56.17 (< 0.01)	−3.81 (0.01)	−159.80 (< 0.01)	−0.21 (< 0.01)	0.17 (< 0.01)	1.01 (< 0.01)	−0.24 (< 0.01)	−2.50 (< 0.01)	−8.29 (0.00)	10.79 (< 0.01)
Agroforestry	−1.27 (0.92)	−0.70 (0.61)	−19.00 (0.49)	−0.12 (0.04)	0.09 (< 0.01)	0.10 (0.38)	−0.11 (< 0.01)	−0.80 (0.07)	−2.91 (< 0.01)	3.70 (< 0.01)
Dense forest (ref)										
Depth										
20–40 cm	−30.89 (< 0.01)	−3.25 (< 0.01)	−37.88 (0.03)	−0.35 (< 0.01)	−0.04 (< 0.01)	0.38 (< 0.01)	0.04 (< 0.01)	0.00 (1.00)	0.00 (1.00)	0.00 (1.00)
0–20 cm (ref)										

The regression on soil physical properties like bulk density and soil texture are carried out and compared with DF and depth (0–20 cm). The bulk density of P, AG, AF, and DV is found to be lower and significantly different from that of DF. However, it is found to be higher by 0.04 g/cc in the depth of 20–40 cm when compared to the depth of 0–20 cm. The regression on soil texture shows a different trend when compared to dense forest. The sand component of soil texture is lower in percentage in AG (−8.29) and AF (−2.91), while the clay content is lower in plantation and degraded vegetation. However, silt content of soil texture shows lower trend in all types of land use when compared to dense forest (Table 8.5).

8.3.12 SOC, STN, STP, and STK Concentration of the Soil

The concentration of these parameters (SOC, STN, STP, and STK) decreased with soil depth for all land use except in case of STP for DF and AG. Among all the selected land use types, the highest concentrations of nutrient were observed in the DF followed by AF in the depth of 0–20 cm. The concentration of SOC (6.59 Mg/ha), STN (2.28 Mg/ha), STP (0.018 Mg/ha), and STK (0.42 Mg/ha) was observed in DF, showing highest concentration among the all land uses at the top soil layer. However, the lowest concentration pattern of above-said parameters was found in AG land use practices (Table 8.6). Similar demonstration has been done by several workers (Thakur et al. 2014, 2018; Bijalwan et al. 2017; Kumar et al. 2021; Thakur et al. 2019b, 2020).

Table 8.6 Total SOC, STN, STP, STK

Land use	SOC(Mg/ha)	STN(Mg/ha)	STP (Mg/ha)	STK(Mg/ha)
Soil depth 0–20 cm				
DF	6.54	2.28	0.018	0.42
P	3.8	2.05	0.017	0.38
DV	5.03	1.92	0.011	0.26
AG	3.37	1.52	0.010	0.25
AF	4.60	2.17	0.017	0.40
Soil depth 20–40 m				
DF	3.16	2.17	0.011	0.38
P	2.45	1.76	0.009	0.34
DV	2.51	1.74	0.012	0.21
AG	2.20	1.50	0.0128	0.23
AF	2.92	1.94	0.0122	0.36

8.4 Conclusion

The conclusions of this study showed that transformation of natural ecosystems into accomplished agroecosystems bring about significant changes in the quality of soil resources. The physio-chemical properties of soils change by cultivation practices, biological interference, or anthropogenic factors. These manmade changes not only are limited to surface soil but also show remarkable changes under subsurface of soil. So it is concluded human mismanagement leads to deterioration of quality and productivity of soil. Therefore, in order to improve fertility and productivity of soil, the following measures have been suggested:

1. Incorporation of existing cultural practices with recent appropriate technology like integrated farming, agroforestry, and silvi-pasture.
2. Strengthening fertilizer management through INM (integrated nutrient management), like composting, green manure, etc.
3. Adequate use of natural resources at sustainable basis to stop further soil degradation.

Finally, surrounding areas of AABR should be restricted to anthropogenic approach or have certain degree of limitation to improve soil health.

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Vegetation Biomass and Carbon Stock Assessment Under Different Forest Types of Temperate and Alpine Forest Ecosystem of Western Himalayas

9

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Abstract

Sustainable Development Goals 13 (SDG-13) states all stakeholders need to strengthen and improve their efforts to reduce the impacts of climate change. Globally, forests play a vivacious role in changing climates, alleviation and adaptation. Forest is a storehouse of 350,000 Tg carbon (C) that is highest among any terrestrial ecosystems. Temperate forests contribute ~14% of total forest C storage and covers 767 million hectares worldwide. This article discusses the biomass and C stocks of vegetation in forest types of temperate and alpine forest ecosystems of the Himalaya. The total biomass of trees (aboveground + belowground) varied between forest types, ranging from 47.5 to 355.6 Mg ha^{-1}, with Himalayan temperate forest having the highest biomass. Similarly, the biomass C in different forest ecosystems varied from 2.8 to 242.8 Mg C ha^{-1}. The over-all vegetation biomass of different forest types fluctuated between 48.8 and 492.2 Mg ha^{-1} with highest in *Quercus leucotrichophora* forest. However, the biomass C varied between 24.4 and 246.1 Mg C ha^{-1} among diverse forest types. The whole soil C density, i.e., humus and soil (0–40 cm layer), varied significantly (37.7–133.1 Mg C ha^{-1}) among different forest types. Total detritus biomass and biomass C ranged from 0.11 to 8.06 and 0.05 to 4.03 Mg ha^{-1}, respectively, with maximum in the fir forest of Kashmir Himalaya. The Ecosystems C density varied from 38.4 to 324.2 Mg C ha^{-1} with highest in

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Q. leucotrichophora forest. Thus, the forest ecosystems of Himalayan region store a large quantity of C in biomass. Hence, there is an urgent need to conserve and strengthen these forest ecosystems for better mitigation and adaptation against climate change.

Keywords

Biomass · Carbon sequestration · Climate change · Forest types · Himalaya

9.1 Introduction

Forest ecosystems are considered as natural warehouses for biomass and carbon (C) storage. These ecosystems confiscate and hoard more carbon (contains over 350,000 Tg C) compared to any other land-dwelling ecosystem that are an imperative natural "brake" on changing climate. Specifically, in the preceding two decades, there has been swelling attention in the quantification of forest ecosystems biomass and its prospective concerning C fixation. Knowledge of biomass C density of diverse vegetative ecosystems is a key central constituent to assess the forestlands involvement to the universal C cycle. A functional association among floral multiplicity and C storage and confiscation could have an imperative inference for the C sink supervision for projects of emission reduction, reforestation, and afforestation that emphasize on management and conservation of forest ecosystems (Gairola et al. 2011). The badly behaved changing climate augments substantial strain to humanities and its surroundings, which is an ultimate menace to sustained development. From ever-changing patterns of weather leading to frequent cloud bursts, floods, to growing levels of sea risking of disastrous flooding, the influences of changing climate are universal in range and extraordinary in gage, disparities in ecology, reduction in biological diversity, and further ecological vicissitudes.

Soils encompass to fold of the atmosphere C and ~75% of the total organic C pool on the earth (Prentice et al. 2001). Any alteration in the profusion and configuration of soil C can considerably disturb the universal cycle of C and numerous other imperative procedures (Batjes 1996). Soil organic C is sensitive to a series of elements comprising weather, landscape, topsoil and flora organization, land management practices, and other anthropogenic situations (Tan et al. 2004). Even though 40% C of soil is institute underneath woodlands, woodlands soil C pools (particularly in hilly zones) are less sampled and less studied than C pools of aboveground (Lal 2005). Soils of cold-temperate hills have extraordinary high level of organic C, but with vast variations in relation to space for the reason of the multifaceted topography and capricious climate and vegetation groups, it is difficult to estimate. Tree-based systems are resilience to climate change and provide diversified outputs (Yadav et al. 2018a, b, c).

Forest ecosystem C stock can be largely classified as biotic C and pedologic C constituents. In earthly bionetworks, woodlands are the greatest fruitful amid their biotic constituents. As vegetation mature, they confiscate C in their tissues, and as plant biomass quantity rises, carbon dioxide from the atmospheric is alleviated (Yadav et al. 2015, 2016, 2017, 2019a, b). C account for about 43–50% of the dry biomass of trees (Malhi et al. 2002; Negi et al. 2003). Trees accumulate C in their above and belowground biomass until they reach maturity; ~1/2 of trees mean dry weight will be C (Anonymous 2004). Besides that, long-lived trees accumulate a huge biomass, by this means seizing huge quantities of C in several decades of their development cycle. Therefore, woodlands can sequester and hold great C quantities over extensive times. These creative physiognomies of woodlands brand them striking for climate change alleviation and mitigation (Nabuurs et al. 2000). Precise C stocks assessments in woodlands have been attaining universal consideration as countries pursue to fulfill with contracts under the UNFCCC (Brown 2002). Prevailing C pools assessments, deposited in numerous forest ecosystems, can be supportive in building conclusions about management of C and its conservation.

Globally, temperate forests span 767 million ha and contribute for ~14% of forest C stock (Pan et al. 2011). The highest prospective for C storage in these ecosystems is often found in the tree biomass (Son et al. 2001; Peichl and Arain 2006), although the litter, detritus wood, and understory biomass also contribute significantly (Whittaker and Woodwell 1986). Therefore, neglecting the biomass C and other constituents may lead to a noteworthy under-valuation of the whole storage of C. The role of temperate and alpine forests in India is significant because of their prospective to accrue a huge quantity of C in diverse pools. Thus, the objective of the current study is to assess the C stock and the soil physico-chemical characteristics of dry temperate as well as alpine forest ecosystem of Western Himalayan region in order to devise better management and conservation strategies.

9.2 Methodology

9.2.1 Estimation of Biomass

9.2.1.1 Tree Biomass

The whole number of trees falling within the plot (20 m × 20 m) was enumerated to assess the biomass. A meter tape was used to measure the diameter at breast height (DBH). The number of stem in different diameter class was used to determine the stem volume of trees, which was multiplied by the volume factor of respective species specified in working plan or by the volume equation given under IPCC guidelines. The existing literature was used to determine specific gravity (Rajput et al. 2017).

$$\text{Biomass of stem} = \text{Stem woods mean specific gravity} \times \text{Volume stem}$$

The biomass of stem was multiplied with biomass expansion factor of the specified species to obtain entire biomass of tree (Brown 2002). Trees below ground biomass were computed as per IPCC guidelines (1996) and Cairns et al. (1997)

methodology. Tree biomass was calculated by summing up aboveground tree biomass and belowground tree biomass.

9.2.1.2 Shrub Biomass

Shrubs are important constituent of the forest ecosystem and contribute significantly to the biomass of these ecosystems. Destructive sampling procedure was followed to measure biomass of shrubs. Shrub biomass was estimated using 5 m × 5 m quadrates. All the shrubs falling within the limits of the quadrates were itemized. The calliper was used to measure the diameter of the tillers at base using the technique described by Chaturvedi and Khanna (1982). The fresh weight of the shrubs was taken using spring balance. A sub sample of the shrubs was laboratory dried to obtain the dried weight of shrubs.

9.2.1.3 Herb Biomass

Destructive sampling was done to measure herbs biomass. Examination of community was carried out at the peak of plants growth during rainy season. Herb biomass was computed using 1 m × 1 m quadrates. The quadrates were selected by following principles of species area curve method. Herbaceous vegetation, present in each quadrate size 1 m × 1 m, was species wise separated and help of herbarium was taken to identify the specimen. The entire herb biomass befalling inside the quadrate’s boundaries was cut at ground level and weighed, sub sampled, and oven dried at 65 + 5 °C until consistent weight was obtained.

9.2.1.4 Surface Litter

The layer on the surface of the floor of the forest that includes dead debris (below certain diameter) comprises leaves, twigs, bark, flowers, fruits, and other vegetative material which were freshly fallen or partially decomposed. Both biomass and biomass C of surface litter were quantified in the forest types examined. Surface litter was collected using 1 m × 1 m quadrates. Weighed samples were sub-sampled and oven dried to a consistent weight at 65 + 5 °C and then grounded and ashes.

9.3 Carbon Estimation

The C pools of different components, i.e., vegetation (herb, shrub, and tree), soil, and ecosystem, were measured. The carbon content in the biomass of vegetation was considered 50% of the vegetative biomass. The vegetative biomass was multiplied with 0.50 fraction IPCC default value to arrive at C stock in different components of the ecosystem. The soil was analyzed in the laboratory to measure the C content of the soil.

9.3.1 Vegetation Carbon Density

Vegetative C density was obtained by adding biomass C of tree, shrubs, and herbs. To get biomass C, the biomass of tree, shrubs, and grass was multiplied by a factor of 0.5 (IPCC default value). Corrected dry ash of litter was presumed to contain 50% C.

$$\begin{aligned}\text{Vegetation C density}\left(\text{Mg ha}^{-1}\right) = {} & \text{Tree biomass C}\left(\text{Mg ha}^{-1}\right)\\ & + \text{Shrub biomass C}\left(\text{Mg ha}^{-1}\right)\\ & + \text{Herb biomass C}\left(\text{Mg ha}^{-1}\right)\end{aligned}$$

9.3.2 Soil Carbon

Soil C is an important indicator of its soil fertility status besides structural and biological properties. Carbon density in soil is determined by multiplication of the bulk density, depth, and soil C content (Nelson et al. 1996).

$$\text{Soil C}\left(\text{Mg ha}^{-1}\right) = \left[\text{Soil bulk density}\left(\text{ g cm}^{-3}\right) \times \text{Soil depth (cm)} \times \text{C}\right]$$

9.3.3 Ecosystem C Density

The C storage of vegetative (tree, shrub, and herb), detritus, and soil components, viz., vegetative C density, detritus C density, and soil C density, was combined to get ecosystem C density.

$$\begin{aligned}\text{Ecosystem C density}\left(Mg\ ha^{-1}\right) = {} & \text{Vegetation C density}\left(Mg\ ha^{-1}\right)\\ & + \text{Detritus C density}\left(Mg\ ha^{-1}\right)\\ & + \text{Soil C density}\left(Mg\ ha^{-1}\right)\end{aligned}$$

9.4 Results and Discussion

9.4.1 Biomass of Vegetation

The total biomass of trees (aboveground + belowground) among diverse forest types vacillated from 47.7 to 355.6 t ha^{-1} with the highest biomass in Himalayan temperate forest, whereas minimum tree biomass was found in Himalayan dry temperate and alpine forest types.

Biomass C density of these forest ecosystems varied between 23.8 and 242.8 Mg C ha^{-1}. Vegetative biomass is a central biological variable for understanding the progression and prospective forthcoming fluctuations in climatic structure. The biomass and biomass C in the upper west Himalayan forest varied from 279.3 (*Quercus semecarpifolia*) to 377.6 (*Abies pindrow*) and 128.4 (*Quercus semecarpifolia*) to 173.7 (*Abies pindrow*) Mg ha^{-1}, respectively (Sharma et al. 2010). Gairola et al. (2011) testified biomass and biomass C ranging from 296 to 298.6 and 148 to 149.3 Mg ha^{-1}, respectively, in Garhwal region of Indian Himalaya. In Kashmir region of Indian Himalaya Dar and Sundarapandian (2015) recorded forest biomass and biomass C in the range of 254.3–294.8 and 114.4–135.6 Mg ha^{-1}. Vegetative biomass is a greater universal accumulator of C compared to the atmosphere. Vicissitudes in vegetative biomass quantity are even now disturbing the universal atmosphere as a net C source and having the prospective either to confiscate C in upcoming or to turn into an even bigger source. Contingent on the biomass quantity, the coverage of vegetation has a straight impact on limited, provincial, and even universal climate, predominantly on humidity and air temperature. Hence, a universal biomass calculation and its delicacies are a crucial contribution to changing climate predicting prototypes and alleviation and adaptation strategies.

These differences in tree biomass in a forest ecosystem are an expression of tree's inherent growth characteristics, apart from the alterations in trees density. The lack of trees in alpine pasture and dry alpine scrub forest resulted in zero tree biomass in those vegetation-systems. Alterations in biomass of trees are the expression of integral growth physiognomies of component species, their distinct biological niches, climatic variability, and trees density. Additionally, biological mass is also associated to human or natural turbulences (Lugo and Brown 1992). A cross-section of aboveground, belowground, and total biomass values of trees for temperate and alpine forest ecosystems is given in Table 9.1. The table indicates that there is a huge variation in the tree biomass in temperate and alpine forests ecosystem as reported in Himalayan forest type ecosystems (Table 9.1). This can be attributed to the fact that different climatic zones have varying temperature and rainfall/precipitation, which limits the growth of trees.

The total vegetative biomass of different forest types vacillated between 48.8 and 492.2 Mg ha^{-1}, whereas the biomass C ranged from 24.4 to 246.1 Mg C ha^{-1} among different forest types (Table 9.2). Dar et al. investigated the biomass and biomass C of different forest types of Kashmir region in the Himalaya and found that they ranged from 101.1 to 296.4 and 50.5 to 148.2 Mg ha^{-1}, respectively. However, in temperate and dry alpine forest ecosystem, the biomass and biomass C fluctuated from 0.58 to 252.2 and 0.29 to 126.1 Mg ha^{-1}, respectively, in Indian Himalaya (Kumar 2018). Vipasha (2019) recorded that biomass in Himalayan temperate forest ecosystems varied between 308.7 and 492.2 mg ha^{-1} and biomass C varied between 154.3 and 246.1 Mg ha^{-1}. The variations in shrubs biomass in diverse forest ecosystems are associated to species configuration and intrinsic growth competence of species. According to Ross and Walstad (1986), shrub biomass may be ascribed to elements such as size, age, state, and native and species habit. In birch-rhododendron

Table 9.1 Comparison between estimates of tree aboveground biomass (AGB), belowground biomass (BGB), and total biomass (TB) under different forest ecosystems

Forest types/location	Tree AGB ($t\ ha^{-1}$)	Tree BGB ($t\ ha^{-1}$)	Tree TB ($t\ ha^{-1}$)	Total tree C density ($t\ C\ ha^{-1}$)	References
Upper west Himalayan *Abies pindrow* Spach.	305.3 ± 31.9	–	377.6± 38.6	173.7± 17.7	Sharma et al. (2010)
Upper west Himalayan *Quercus semecarpifolia* Sm.	224.2 ± 21.6	–	279.3± 26.3	128.4 ± 12.1	Sharma et al. (2010)
Abies pindrow forest, Chamoli Garhwal	237.9	–	296.0	148.0	Gairola et al. (2011)
Mixed broadleaved conifer forest, Chamoli Garhwal	240.1	–	298.6	149.3	Gairola et al. (2011)
Fir-spruce forest, Sirmour (HP)	–	–	334.70	164.07	Bhat (2012)
Populus deltoides forest Anantnag district (J&K)	204 ± 23	50.3 ± 4.9	254.3 ± 28	114.4 ± 12.6	Dar and Sundarapandian (2015)
Cedrus deodara forest Anantnag district (J&K)	228.3 ± 4.4	55.9 ± 3.1	284.2 ± 7.5	130.7 ± 8.1	Dar and Sundarapandian (2015)
Pinus wallichiana forest Anantnag district (J&K)	218.3 ± 9.3	53.8 ± 2	272.1 ± 1.3	125.2 ± 5.2	Dar and Sundarapandian (2015)
Mixed coniferous forests Anantnag district (J&K)	222.3 ± 3.2	54.6 ± 2.9	276.9 ± 6.1	127.4 ± 7.4	Dar and Sundarapandian (2015)
Abies pindrow forest Anantnag district (J&K)	237.0 ± 9.8	57.8 ± 2.2	294.8 ± 12	135.6 ± 5.5	Dar and Sundarapandian (2015)
Himalayan dry temperate and alpine forest ecosystem	39.5–207.1	8.25–43.5	47.7–250.5	23.8–125.2	Kumar (2018)
Himalayan temperate forest	87.3–355.6	18.3–130	105.6–485.7	52.8–242.8	Vipasha (2019)

Table 9.2 Vegetation biomass and vegetation carbon density under different forest types

Forest types	AGB (t ha^{-1})	BGB (t ha^{-1})	Tree biomass (t ha^{-1})	Shrub biomass (t ha^{-1})	Herb biomass (t ha^{-1})	Total vegetation biomass (t ha^{-1})	Vegetation C density (t C ha^{-1})	References
Deodar forest, Kashmir (J&K)	228.30	55.90	284.2	0.95	0.25	285.4	142.70	
Blue pine forest, Kashmir (J&K)	218.30	53.80	272.10	2.1	0.26	274.46	137.23	
Fir forest, Kashmir (J&K)	237.0	57.80	294.80	1.20	0.44	296.44	148.22	
Bhojpatra forest, Kashmir (J&K)	79.00	21.80	100.80	0.15	0.15	101.10	50.55	
Himalayan temperate forest	–	–	–	–	–	404.35	202.2	Rajput et al. (2017)
Dry broad-leaved and coniferous forests, Kinnaur (H.P.)	103.11	25.00	128.11	1.05	0.47	129.63	64.82	Kumar (2018)
Neoza pine forest, Kinnaur (H.P.)	79.83	16.75	96.58	0.94	0.40	97.92	48.96	Kumar (2018)
Dry deodar forest, Kinnaur (H.P.)	207.06	43.50	250.56	1.23	0.45	252.24	126.12	Kumar (2018)
Dry blue pine forest, Kinnaur (H.P.)	123.83	26.00	149.83	0.78	0.48	151.09	75.55	Kumar (2018)
Sub alpine birch forest, Kinnaur (H.P.)	39.50	8.25	47.75	0.58	0.53	48.86	24.43	Kumar (2018)
Sub alpine fir forest, Kinnaur (H.P.)	104.96	24.03	128.99	0.63	0.47	130.09	65.05	Kumar (2018)
Birch-rhododendron scrub forest, Kinnaur (H.P.)	49.00	10.31	59.31	19.24	0.42	78.97	39.49	Kumar (2018)
Alpine pasture, Kinnaur (H.P.)	–	–	–	–	0.58	0.58	0.29	Kumar (2018)
Dry alpine scrub, Kinnaur (H.P.)	–	–	–	0.94	0.36	1.30	0.65	Kumar (2018)
Ban oak forest, Kullu (H.P.)	355.63	130.08	485.71	4.62	1.88	492.21	246.10	Vipasha (2019)
Deodar forest, Kullu (H.P.)	246.36	53.26	299.26	6.80	2.70	308.76	154.38	Vipasha (2019)
Blue pine forest, Kullu (H.P.)	292.89	63.56	356.44	6.40	2.38	365.22	182.61	Vipasha (2019)
Fir/spruce forest, Kullu (H.P.)	328.01	68.90	396.91	7.15	3.20	407.26	203.63	Vipasha (2019)

scrub forest, dominant shrub is *Rhododendron campanulatum* resulting in higher biomass owing to its hefty habit. The greater herbaceous biomass in alpine pasture can be attributed to sufficient sunlight due to lack of an overstory canopy, also stated by Grelen and Whrey (1978), Singh and Singh (1980), Ramakrishna (1984), Hazra and Patil (1986), and Heinrichs and Schmidt (2010) (Table 9.2).

The amount of C storage in forest vegetation fluctuates according to topographical position, management system imposed, biotic and abiotic stresses, species type, and stand age. The maximum values of total vegetation C density in ban oak forest may be ascribed to forest's high biomass owing to presence of large tree population in the forest. The higher humus content in ban oak forests may be due to a dense cover produced by *Quercus leucotrichophora* thereby preventing sunlight to reach soil surface, thus hindering its decomposition. The foliage creating the uneven to even sphere-shaped crown has massive influence to augment the depth of humus sheet above the soil. However, the absence of humus in alpine pasture and dry alpine scrub may be a result of low litter production, high wind velocity, and overgrazing in these ecosystems.

9.4.2 Soil Carbon Density

The humus depth of different west Himalayan forest types is summarized in Table 9.3. Among various forest types in Kashmir hills of Himalaya, the soil C density ranged from 61.3 (fir forest) to 91.4 (Bhojpatra forest) Mg C ha^{-1}. Kumar (2018) in Himalayan temperate and alpine forests has reported that the soil c density ranged between 45.6 (Neoza pine forest) and 130.3 (birch-rhododendron scrub forest) Mg C ha^{-1}. Birch-rhododendron scrub forest exhibited the maximum of humus depth (4.41 cm) which was found considerably more than that of all other forest types. He ascribed the higher humus depth in birch-rhododendron scrub to dense cover provided by *Rhododendron campanulatum* thereby preventing sunlight to reach soil surface and thus impeding decomposition. The foliage that forms the irregular to even sphere-shaped crown exerts enormous influence on the level of humus deposit above the soil, whereas nil value of humus in alpine pasture and dry alpine scrub may be due to low leaf-litter production in these ecosystems along with the high wind velocity, formation of thick mat by alpine grasses, and overgrazing.

The total soil C density that includes humus + soil (0–40 cm), varied considerably among different forest types, ranged between 37.7 and 133.1 mg C ha^{-1} (Vipasha 2019). Ban oak forest (133.1 t C ha^{-1}) exhibited highest C density among the forest types of temperate and alpine forest. Universally, in temperate forest, soil carbon density (SOC) shares up to 1 m averages at 12.2 kg m^{-2} (Prentice et al. 2001; Lal 2005), 13.9 kg m^{-2} in cool-temperate-wet forest (Post et al. 1982), and 11.3 kg m^{-2} across all woodlands (Sombroek et al. 1993). Chhabra et al. (2003) reported soil C density of 161.9 t ha^{-1} for a one-meter-thick soil layer in montane temperate forest. The soil carbon stock (SOC) displays sizeable spatial inconsistency, both horizontally (as per land use) and vertically within soil profile. Regardless of type of vegetation, the SOC shrinks with soil depth (Trujilo et al. 1997).

Table 9.3 Soil carbon stock under different forest types

Forest types	Humus depth (cm)	Carbon density (t C ha^{-1})				References
		Humus	0–20 cm	21–40 cm	Total C density {humus + soil (0–40 cm)}	
Deodar forest, Kashmir (J&K)	–	–	–	–	62.30	
Blue pine forest, Kashmir (J&K)	–	–	–	–	67.20	
Fir forest, Kashmir (J&K)	–	–	–	–	61.3	
Bhojpatra forest, Kashmir (J&K)	–	–	–	–	91.4	
Dry broad-leaved and coniferous forests	1.28	4.79	59.37	47.02	111.18	Kumar (2018)
Neoza pine forest	0.27	0.36	28.42	16.84	45.62	Kumar (2018)
Dry deodar forest	0.61	0.54	52.52	31.74	84.81	Kumar (2018)
Dry blue pine forest	0.74	0.63	35.43	20.49	56.55	Kumar (2018)
Sub alpine birch forest	0.99	2.90	44.50	27.36	74.76	Kumar (2018)
Sub alpine fir forest	3.35	8.30	41.18	24.09	73.56	Kumar 2018
Birch-rhododendron scrub forest	4.41	11.30	71.55	47.54	130.39	Kumar (2018)
Alpine pasture	0.00^h	0.00	33.66	17.40	51.06	Kumar (2018)
Dry alpine scrub	0.00^h	0.00	23.70	14.02	37.73	Vipasha (2019)
Ban oak forest	4.00	8.83	64.71	59.58	133.12	Vipasha (2019)
Deodar forest	2.70	6.86	53.33	43.48	103.67	Vipasha (2019)
Blue pine forest	1.90	6.12	49.16	39.15	94.43	Vipasha (2019)
Fir/spruce forest	3.73	8.55	59.26	50.51	118.32	Vipasha (2019)

h = 0.05

Information accessible in Table 9.3 shows that the soil organic C density varied considerably influenced due to humus and in soil layers (0–20 cm and 21–40 cm soil) layer by the vegetation effect. In all types of forests, the C density declined with the increasing soil depth.

SOC is determined by a number of biotic and abiotic factors, such as microclimate, floral and faunal diversity, land use and management, etc. Litter input (leaf and root) contributes significantly to forest soil C. The upper layer of soil has active symmetry with biotic and anthropological actions and is normally better-off in C compared to the lower strata. Shreshtha et al. (2004) also reported comparable outcomes earlier in Nepal for watershed of mountainous region. The growth and functions of flora are controlled by the accessibility of soil nutrients to plants, whereas SOC dynamics rely on the inputs reported from the vegetation growth. Therefore, in an ecosystem, vegetation and soil C dynamics are inextricably linked. The contribution may be from aboveground litter (leaf) and or belowground, fine roots (Bloomfield et al. 1996), and microbial activity regulating their disintegration rate.

The C pools in soil from diverse types of forest in this study are lower than reported for Garhwal region Uttarakhand (Raina and Gupta 2013) but are comparable to those reported by other researchers (Wani et al. 2013) in Kashmir Himalayas (Panwar and Gupta 2013) and Himachal Pradesh. Additionally, the values in Table 9.3 clearly indicate that soil C density (humus, 0–20 cm and 21–40 cm) was highest in birch-rhododendron scrub forest. Hence, birch-rhododendron scrub forests have a greater capacity to accumulate C in soil layer, implying increased C mitigation prospective.

9.4.3 Detritus Carbon Density

A scrutiny of information in Table 9.4 discloses that litter biomass (Mg ha^{-1}), dead twig biomass (Mg ha^{-1}), total detritus biomass (Mg ha^{-1}), and total detritus carbon (Mg C ha^{-1}) varied significantly under different temperate and alpine forest types. Dar et al. recorded biomass and biomass C in the range of 2.89–8.06 and 1.44–-4.03 Mg ha^{-1}, respectively, in Kashmir region of Indian Himalaya, while in Kinnaur region of Indian Himalaya, Kumar (2018) reported the biomass and biomass C ranging from 0.11 to 5.99 and 0.06 to 3.0 mg ha^{-1}, respectively.

Significantly maximum biomass in surface leaf-litter was found in birch-rhododendron scrub forest (3.15 Mg ha^{-1}), which was followed by sub-alpine-fir-forest (2.83 Mg ha^{-1}), dry-broad-leaved and coniferous-forests (2.35 Mg ha^{-1}), sub-alpine-birch-forest (1.80 Mg ha^{-1}), dry-deodar-forest (1.39 Mg ha^{-1}), dry-blue-pine-forest (1.35 Mg ha^{-1}), neoza-pine-forest (1.35 Mg ha^{-1}), alpine-pasture (0.15 Mg C ha^{-1}), and least in dry-alpine-scrub (0.11 Mg ha^{-1}), respectively. Result pertaining to dead twig biomass varied significantly among different forest types (Table 9.4). It was found to be maximum in birch-rhododendron-scrub-forest (2.84 Mg ha^{-1}) that was expressively higher than all other and followed the order: sub-alpine-fir -forest (2.40 Mg ha^{-1}), dry-broad-leaved and coniferous-forests (1.70 Mg ha^{-1}), sub-alpine-birch-forest (1.27 Mg ha^{-1}), dry-deodar-forest (1.18 Mg ha^{-1}), dry-blue-pine-forest (1.04 Mg ha^{-1}), neoza-pine-forest (0.85 Mg ha^{-1}), and nil on both alpine pasture as well as dry alpine scrub.

Data in Table 9.4 demonstrates that total detritus biomass varied (0.11–-8.06 Mg ha^{-1}) significantly across different forest types. Detritus biomass was found to be maximum in fir forest (8.06 t ha^{-1}) of Kashmir Himalaya and followed the order: Birch-rhododendron-scrub-forest (5.99 Mg ha^{-1}) > sub-alpine-fir-forest (5.23 Mg ha^{-1}) > dry-broad-leaved and coniferous-forests (4.05 Mg ha^{-1}) > sub-alpine-birch-forest (3.07 Mg ha^{-1}) > dry-deodar-forest (2.57 Mg ha^{-1}) > dry-blue-pine-forest (2.39 Mg ha^{-1}) > neoza-pine-forest (1.64 Mg ha^{-1}) and least in alpine-pasture (0.15 Mg ha^{-1}). Vipasha (2019) in Himalayan temperate forest reported that biomass and biomass C varied from 3.63–4.60 and 1.82–2.21 Mg ha^{-1}, respectively.

Furthermore, the total detritus C density also ranged considerably among diverse forest types. The highest detritus C was recorded in fir forest (4.03 t ha^{-1}) in

Table 9.4 Litter, dead branches biomass, total detritus biomass, and total detritus carbon density under different forest types

Forest types	Litter biomass (t ha^{-1})	Dead twig biomass (t ha^{-1})	Total detritus biomass (t ha^{-1})	Total detritus C (t C ha^{-1})	References
Deodar forest, Kashmir (J&K)	–	–	3.28	1.64	
Blue pine forest, Kashmir (J&K)	–	–	4.60	2.30	
Fir forest, Kashmir (J&K)	–	–	8.06	4.03	
Bhojpatra forest, Kashmir (J&K)	–	–	2.89	1.44	
Dry broad-leaved and coniferous forests, Kinnaur (H.P.)	2.35^{c}	1.70^{c}	4.05^{c}	2.03^{c}	Kumar (2018)
Neoza pine forest, Kinnaur (H.P.)	0.79^{f}	0.85^{g}	1.64^{f}	0.82^{g}	Kumar (2018)
Dry deodar forest, Kinnaur (H.P.)	1.39^{e}	1.18^{e}	2.57^{e}	1.29^{e}	Kumar (2018)
Dry blue pine forest, Kinnaur (H.P.)	1.35^{e}	1.04^{f}	2.39^{e}	1.20^{f}	Kumar (2018)
Sub alpine birch forest, Kinnaur (H.P.)	1.80^{d}	1.27^{d}	3.07^{d}	1.54^{d}	Kumar (2018)
Sub alpine fir forest, Kinnaur (H.P.)	2.83^{b}	2.40^{b}	5.23^{b}	2.62^{b}	Kumar (2018)
Birch-rhododendron scrub forest, Kinnaur (H.P.)	3.15^{a}	2.84^{a}	5.99^{a}	3.00^{a}	Kumar (2018)
Alpine pasture, Kinnaur (H.P.)	0.15^{f}	0.00^{h}	0.15^{g}	0.08^{h}	Kumar (2018)
Dry alpine scrub, Kinnaur (H.P.)	0.11^{g}	0.00^{h}	0.11^{g}	0.06^{h}	Kumar (2018)
Ban oak forest, Kinnaur (H.P.)	2.63	1.00	3.63	1.82	Vipasha (2019)
Deodar forest, Kullu (H.P.)	2.32	2.09	4.41	2.21	Vipasha (2019)
Blue pine forest, Kullu (H.P.)	2.01	1.65	3.66	1.83	Vipasha (2019)
Fir/spruce forest, Kullu (H.P.)	2.48	2.11	4.60	2.30	Vipasha (2019)

a–h = 0.05

Kashmir Himalaya followed by birch-rhododendron-scrub-forest (3.0 Mg C ha^{-1}), which is significantly different from other forest type and lowest in dry-alpine-scrub (0.06 t C ha^{-1}). The distinction in detritus C stored among the types of forest may be due to biotic and abiotic factors and disparities in stand age and its structure, litter contribution and its disintegration rate, and altitude (Pregitzer and Euskirchen 2004; Peichl and Arain 2006; Taylor et al. 2007). The alteration perhaps can be owed to the outcome of ecologically organized disintegration rates and organization past, besides of variances prompted by debris contributions linked with status of vegetation.

9.4.4 Ecosystem Carbon Density

Records obtainable in Table 9.5 disclose that the ecosystem C density (38.4–324.2 Mg C ha^{-1}) under different forest types of temperate and alpine forest varied significantly. The ecosystem C stock differed from 139.8 to 205.7 Mg ha^{-1} in

Table 9.5 Vegetation, soil, detritus, and ecosystem C density under different forest types

Forest types	Vegetation (t C ha^{-1})	Soil (t C ha^{-1})	Detritus (t C ha^{-1})	Ecosystem (t C ha^{-1})	References
Deodar forest, Kashmir (J&K)	130.70	62.30	3.28	196.90	
Blue pine forest, Kashmir (J&K)	125.20	67.20	4.60	198.20	
Fir forest, Kashmir (J&K)	135.6	61.30	8.06	205.70	
Bhojpatra forest, Kashmir (J&K)	45.4	91.4	2.89	139.80	
Dry broad-leaved and coniferous forests, Kinnaur (H.P.)	64.82	111.18	2.03	178.02	Kumar (2018)
Neoza pine forest, Kinnaur (H.P.)	48.96	45.62	0.82	95.40	Kumar (2018)
Dry deodar forest, Kinnaur (H.P.)	126.12	84.81	1.29	212.21	Kumar (2018)
Dry blue pine forest, Kinnaur (H.P.)	75.55	56.55	1.20	133.29	Kumar (2018)
Sub alpine birch forest, Kinnaur (H.P.)	24.43	74.76	1.54	100.72	Kumar (2018)
Sub alpine fir forest, Kinnaur (H.P.)	65.05	73.56	2.62	141.22	Kumar (2018)
Birch-rhododendron scrub forest, Kinnaur (H.P.)	39.49	130.39	3.00	172.87	Kumar (2018)
Alpine pasture, Kinnaur (H.P.)	0.29	51.06	0.08	51.42	Kumar (2018)
Dry alpine scrub, Kinnaur (H.P.)	0.65	37.73	0.06	38.43	Kumar (2018)
Ban oak forest, Kullu (H.P.)	246.09	133.12	1.82	381.04	Vipasha (2019)
Deodar forest, Kullu (H.P.)	154.38	103.67	2.21	260.25	Vipasha (2019)
Blue pine forest, Kullu (H.P.)	182.61	94.43	1.83	278.87	Vipasha (2019)
Fir/spruce forest Kullu (H.P.)	203.63	118.32	2.30	324.25	Vipasha (2019)

Kashmir region of Indian Himalaya. In temperate and dry alpine forest ecosystem, the C stock varied between 51.4 and 212.2 Mg ha^{-1} in Kinnaur region of Indian Himalaya (Kumar 2018). In Himalayan, temperate forest ecosystem the C storage fluctuated from 38.4 to 381.0 Mg ha^{-1} in Indian Himalaya.

The results pertaining to total vegetative C density varied considerably among diverse forest types. The highest value was displayed in ban oak forest (246.09 Mg C ha^{-1}), which is a climatic climax forest ecosystem in north-western Himalaya. The total soil C density which includes humus and soil (0–40 cm) differed considerably among forest types. Ban oak forest (133.12 Mg C ha^{-1}) (Table 9.5) also showed the maximum value of soil carbon density while dry-alpine-scrub (37.73 Mg C ha^{-1}) showed the lowest value among all forest types. Additionally, total detritus carbon differed considerably across different forest types. The maximum detritus C was observed in birch-rhododendron-scrub-forest (3.0 Mg C ha^{-1}) while lowest in dry-alpine-scrub (0.06 Mg C ha^{-1}) forest. Figures demonstrated in Table 9.5 illustrate total ecosystem C density (vegetation + soil + detritus) of different forest types. The highest ecosystem C density was found in ban-oak-forest (324.25 Mg C ha^{-1}), while minimum in dry-alpine-scrub-forest (38.43 Mg C ha^{-1}).

Forest (vegetation + soil) comprises ~1240 Pg of C (Dixon et al. 1994), and the total C stockpile fluctuates extensively across the latitudes. Of 37% of earthly C stockpile in forest biomass is found in lower latitude while 14 and 49% in mid-latitude and high latitudes, respectively. From tundra to tropical rainforest, the vegetation C density rises with declining latitudes (Fisher 1995). In boreal forest, the characteristic vegetation C density has a range from 40 to 60 Mg C ha^{-1}, 60 to 130, and 120 to 194 Mg C ha^{-1} in temperate forest and in tropical forest, respectively, with the C of an undisturbed TRF (tropical rain forest) reaching as high as 250 Mg C ha^{-1}. On the other hand, soils contain approximately two-third of the earth's C in forest ecosystem (Dixon et al. 1994). Information obtainable in Table 9.5 discloses that C density varied significantly in all the components of all the ecosystems, viz., vegetation, soil, detritus, and ecosystem as a whole, with different forest types. Uppermost ecosystem C density was recorded in dry-deodar-forest. The relative high values of vegetation carbon density as well as soil carbon density in this forest types resulted in the high ecosystem carbon density. A high value of carbon densities in soil as well as in the biomass of temperate Himalayan forest ecosystems indicate the importance of these forest types in climate change alleviation and mitigation, and necessitate the urgent need for their management and conservation on priority basis.

9.5 Conclusion

The present article provides relevant information regarding living tree biomass, C stocks, and entire ecosystem C density storage of a temperate and alpine-forest ecosystem. The outcomes of the current study will be supportive to understand the C storage in numerous species/forest types of temperate and alpine ecosystems in different parts of the world having alike kinds of species configuration. This kind of biological information is essential for preservation and workable application, and could deliver imperative evidence to the strategy creators at both nationwide and worldwide level and also to find operative explanations to complications that are menacing the comparable ecologically delicate areas. Hence, we can see the biomass and biomass C varied frequently in different forest ecosystems and their different components. However, it is very much apparent that forest ecosystems in the Himalayan region store a significant amount of C in soil and biomass. Considering the importance of the forests in carbon storage, these need to strengthen and conserve to effectively fight against climate change. Thus, C sequestration in soil and biomass of these terrestrial forest ecosystems in Himalayan region contribute substantially to global carbon sequestration.

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Part IV

Advance Approaches for Agrobiodiversity Conservation and Restoration

Molecular Approaches in Conservation and Restoration of Agrobiodiversity

10

Ashok Kumar Dhakad, Prashant Mohanapuria, Rumesh Ranjan, Vivek Vaishnav, and Santosh Kumar Yadav

Abstract

Agrobiodiversity is the variety and variability of animals, plants and microorganisms that are used directly or indirectly for food and agriculture, including crops, livestock, forestry and fisheries. It also includes the diversity of non-harvested species that support production (soil microorganisms, predators, pollinators) and those in the wider environment that support agroecosystems. Now, the agrobiodiversity is threatened by changing patterns of land use (urbanization, deforestation), agricultural modernization (monocultures and abandoning of traditional, biodiversity-based practices), westernization of diets and their supply chains. After analysing the target species, strategies adopted to conserve and promote agrobiodiversity are in situ and ex situ conservation along with habitat conservation, management and promotion of agrobiodiversity through sustainable uses. Recently, molecular techniques are facilitating the identification and evaluation of interspecific diversity and evolutionary history, restoration of

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potential species which may be vulnerable in the near future and conservation of closely related species for the possibility of exploring useful bioactive molecules present in them. These molecular approaches include both non-PCR- and PCR-based techniques. PCR-based techniques have been widely applied in conservation and restoration of agrobiodiversity through molecular characterization, assessing genetic diversity, DNA barcoding, phylogenetics, QTL mapping, MAS, genome sequencing, pangenome construction, etc. Besides these, target genes were discovered for quantitative traits using association mapping and genome-wide prediction studies. Different biotechnological tools have also been employed for genomic manipulation through important gene cloning and genetic modification and genome editing tools in important crop germplasm to conserve, manage and restore from wild population to avoid its depletion. These DNA technologies can be a viable option to develop genetically modified crops with enhanced resistance and improved yields to fight against climate change, droughts and chronic food shortages. National Plant Germplasm System (NPGS) and GenBank repositories are developed to maintain agricultural biodiversity and ensure the preservation of the genetic resources and reduce the genetic vulnerability. Thus, a wide array of DNA approaches available may be used to exploit and harness the diversity in wild crop resource of agriculture for achieving higher genetic gains for food and nutritional security.

Keywords

Agrobiodiversity · Conservation · Restoration · Molecular approach · Quantitative traits · Genome manipulation

10.1 Agrobiodiversity

Agrobiodiversity comprises the diversity of genetic and natural resources related to agriculture and its allied fields. The variety and variability of animals, plants and microorganisms that are used directly or indirectly for food and agriculture, including crops, livestock, forestry and fisheries are defined as agrobiodiversity (FAO 1999a). It is the result of interaction between the environment, genetic resources and management systems/practices. Agrobiodiversity consists of variety and variability in organism that basically starts with the genetic level followed by species level, community level and lastly at ecosystem level as presented in Fig. 10.1. A most common section of biodiversity is agricultural biodiversity, which is made up of all the biodiversity, managed and unmanaged, domesticated and wild, harvested or non-harvested species that is necessary for existence of animal kingdom, directly or indirectly used in food and feed. Agriculture plays a significant role in protecting and enhancing biodiversity. The Asia Pacific region is an important centre of origin of several crops, animals and livestock. The region consists of about 45 countries having more than 50% world population. Obviously, the area shows a huge variability in physical geography, topographic and agroecological conditions with

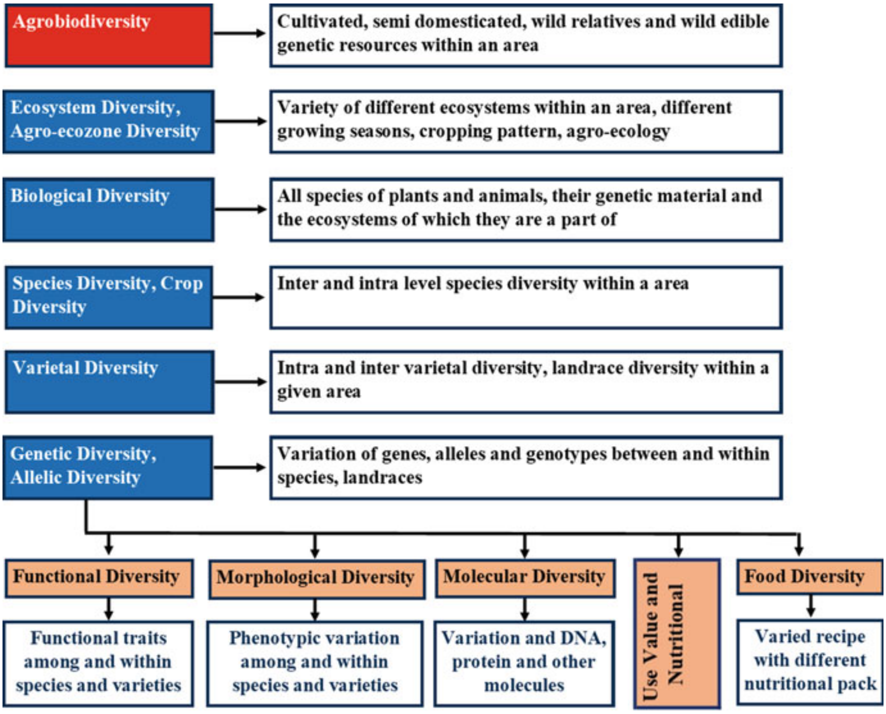

Fig. 10.1 Agrobiodiversity and its classification (Joshi et al. 2020)

a relating richness in biodiversity in fauna and flora. These conditions produced rich genetic diversity in agricultural crops. Besides this, various traditional cultures and societies occurred in this region, every one of whom has been choosing and utilizing genetic resources as per their need and requirements. These plant genetic resources consist of domesticated and wild plants/crops, of which, domesticated resources include agronomic plants, forest and fruit trees, grasses and vegetables exhibiting the relationship among them that is presented in Fig. 10.2. Thus, poor and marginal inhabitants in this region are massively relying on the agriculture and its diversified crops including wild relatives, minor crops and underutilized traditional crops for food security and livelihood.

10.1.1 Present Status

Agrobiodiversity is the basic foundation of agriculture and its allied science from domestication to its current improvement form. Genetic resources constitute microbes, plants and animals likely to have gene of economic importance. Globally, food and nutritional security largely depend on sustainable agricultural genetic resources; thus its conservation and utilization are mainly focused. Genetic resources

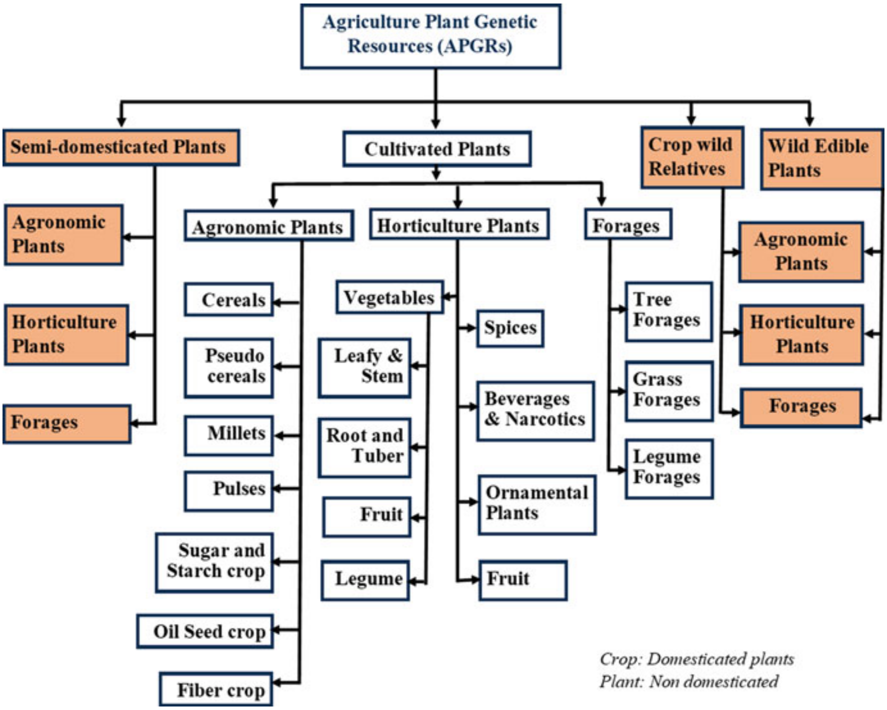

Fig. 10.2 Classification of agricultural plant genetic resources (Joshi and Shrestha 2017)

have in fact been the mainstay of the food chain since the beginning of agriculture. According to Groombridge (1992) and Heywood (1995), there are reportedly an estimated 400,000 and 300,000 plant species.

According to Wilson's (1992) report, nature has given us 30,000 species of edible plants, but farmers today grow only 170 crops and their 325 relatives, of which out of the 170 species of edible plants, only 30 are feed on the earth, three major crops being rice, wheat and maize (FAO 1996). About 25 species of plants were raised in India. Today 12 plant species provide 80% of the world's food (Johnson 2008). Examination of the diversity of plant resources in the global food supply system reveals the size of only two crops, namely, rice (26%) and wheat (23%) show predominance. About 1500 edible plant species are widely exploited by indigenous peoples. These include 521 species of leafy vegetables/vegetables, 145 tuber and root crops, 647 fruits, 101 buds and flowers and 118 seeds and nuts. Apart from this, approximately 9500 plant species are of ethnical uses either in medicinal purpose (7500) or multipurpose (3900) (NAAS 1998).

Today, 75% of the world's food production depends on 12 plants and five animal species. Thirty percent of human requirements for food are fulfilled by animal, out of which ruminants support 12% of the world's population (Sivaraj et al. 2018). The diversity in wild flowers and their related taxa is estimated approximately

320 species, of which, 60 species are extinct. According to the categories, the number of agri-horticultural value is as follows: vegetables, 54; cereals and millets, 51; oilseeds, 12; legumes, 31; fruits, 109; fibre plants, 24; condiments and spices, 27; and others, 26. The number of wildlife species occurring in the various phytogeographical areas varies, being higher in Western Ghats, 145 spp.; North-Eastern Region, 132 spp.; and Western Himalayas, 125 spp., compared to other regions, viz. Eastern Ghats, 91; Eastern Himalayas, 82; the Gangetic plains, 66; and the Indus plains, 45 (Arora and Nayar 1984). Approximately 51,000 insect species have been traced in India that make up 6% of the world's insect species. Food production system of Indian agriculture is directly or indirectly affected by forest resources. Among the 1250 species of grasses, about 600 of which are considered promising wild forages (Arora et al. 1975). India is also rich in animal genetic resources comprising ten buffalo breeds, 30 breeds of cattle, 20 breeds of goats, 39 breeds of sheep, six horses, eight camels, 15 species of poultry and a few breeds of pigs.

10.1.2 Importance with Respect to Common People

The complete depletion of biodiversity in modern ecosystems is causing great concern among agricultural researchers. The existing production system increases productivity but is not stable enough as it involves huge nutrient losses (through leaching, volatilization) that results in high energy costs (Ranjan and Yadav 2019) and also emergence of new weed species along with diseases and pests that results to the use of costly chemicals. As a result, it has a significant impact on the environment (soil erosion, air and water pollution, loss of biodiversity) and social services (Tilman 1999). People are now realizing that agriculture not only provides food but also protects biodiversity of life, landscapes, land and water, prevents disasters, improves rural livelihoods (supports employment, strengthens the farm-related economy and maintains cultural landscapes), reduces poverty and provides opportunities for recreation opportunities for public (Negri 2005). This reduction of agrobiodiversity can be managed carefully by educating farmers, students and researchers about its practical importance.

Biodiversity can be helpful in many ways to mankind like boosting of nutrition value, productivity potential and financial gain. It may be helpful in diversifying the goods and income opportunities by avoiding monocropping and overdependence on 'cash crops'. Agrobiodiversity can preserve soil and boost up the soil fertility naturally and contribute to long-term intensification, while reducing reliance on external inputs. It is also used to assist the safe control of pests and disease management. Agrobiodiversity reduces the negative influence of agriculture on vulnerable habitats, such as forests and endangered species. The huge biodiversity in agriculture and its allied fields is directly supportive in preserving or restoring the native species, particularly medicinal plants and herbs, as well as other flora and fauna. It improves the resiliency and sustainability of farming systems.

Agrobiodiversity is very helpful in protecting the environment and resources by practising resource management techniques to mitigate the effects of climate change.

10.1.3 Causes of Depletion of Agrobiodiversity

The plant genetic erosion has already started during the twentieth century in 154 countries, of which, the main responsible factors are deforestation (~60 countries), substitution of local varieties (~80 countries), population explosion and industrialization (~45 countries) and overexploitation (~55 countries) as per FAO report released at Leipzig in 1996. Other factors apart from those were shifting cultivation, overgrazing, climate changes, agricultural reform, law and policy, disease and pests. Agrobiodiversity loss leads to genetic erosion, the loss of genetic diversity, including the loss of individual genes and the loss of particular combinations of genes (Qualset et al. 1997). The replacement of local varieties by improved one is the major factor responsible for genetic erosion in most of the countries. The gene or combination of gene complex found in old varieties is unique in them and is not found in new one. This often, the cultivation of old varieties reduced drastically when mega commercial varieties are introduced into traditional area of farmers. Since the 1900s, some 75% of plant genetic diversity has been lost as farmers worldwide have left their multiple local varieties and landraces for genetically uniform, high-yielding varieties (FAO 1999b). About 30% of livestock breeds are at risk of extinction; six breeds are lost each month. The MNCs largely financed for intense modernized agricultural practices (Schmidhuber and Tubiello 2007), and also the international-aided projects have been reduced in the area that are largely growing primitive cultivars; as a result old varieties are replaced by genetically homogeneous high-yielding hybrids/varieties since 1950 (Negri 2005). Besides, these very poor extension service and market organizations in developing countries (Poulton et al. 2010) and overexploitation of fragile lands (Jacobsen 2012) increase the genetic erosion. Growing culinary demand reduces biodiversity by promoting industrial agricultural production that encourages large-scale, monocrop systems rather than promoting community-based seed production (Jones and Rakotoarisaona 2007).

10.1.4 Remedial Measures

Most of the developing nations had developed certain laws for the conservation managements and uses of their plant genetic resources and are poised with developed nation for the institutional support. One of the measures, i.e. sui generis systems, is for protecting agrobiodiversity which is innovative in dealing with legal and political issues. For the survival of mankind, the crop diversity for food and agriculture, as well as ecosystem diversity, needs to be well protected and sustainably used at local, regional and international levels. There are certain international agreements, i.e. the Convention on Biological Diversity (CBD), the

International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), the Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS) of the WTO and the convention of the International Union for the Protection of New Varieties of Plants (UPOV), that deal with agrobiodiversity issues. The Biological Diversity Act, 2002, was born out of India's attempt to realize the objectives enshrined in the United Nations 1992 which recognizes the sovereign rights of states to use their own biological resources. The act was enacted in 2002; it aims at the conservation of biological resources, managing its sustainable use and enabling fair and equitable sharing benefits arising out of the use and knowledge of biological resources with the local communities. The following are some of the recommendations for conservation, management and use of agrobiodiversity as cited in Policy Paper 4 by the National Academy of Agricultural Sciences, India (1998), for the effective management of agrobiodiversity in India.

Areas having an association with agrobiodiversity should have an implementation of comprehensive mission mode programme. Well documentation of agrobiodiversity and available indigenous techniques should be carried out. Collection, characterization and safe preservation of all flora should be available at different institutions, educational organizations and communities, by establishment of the National Gene Bank. Development and deployment of alternative plant conservation techniques like in vitro conservation and cryopreservation for non-orthodox, vegetative propagated and other high value crops, for example, medicinal and aromatic plants, by establishment of standard protocols under the collaborative association with respective institutions may play a vital role in the conservation of agroforestry. By understanding the proper culture practices and type of agro-systems, species and growth areas, traditional cultivars/landraces should be conserved within their respective natural habitats. Keeping in view the importance of ethnic communities especially women has played a role in conservation of traditional varieties, so they must be motivated through rewards and recognitions.

On-farm conservation by finding the favourable conservation model(s) through pilot-scale experiments should be employed and assess the agroecosystem's health using indicator species. Along with plants and animals, aquatic life and microscopic organisms should be in the priority for conservation. A decentralized approach while recognizing the important contributions made by ICAR for respective animal and fish resource should be carried out by including all the related stakeholders. Easy, safe and secure access may be provided at national information network and database to strengthen the knowledge hub. Availability of effective instruments/technologies by establishment of national legislation on agrobiodiversity/genetic resources with an aim for conservation, management and proper employment of those resources should also be initiated. Awareness regarding PGR policies like plant variety protection, farmers' and breeders' rights acts, sui generis system and so on will be initiated at national level. Knowledge dissemination on conservation and efficient management of agrobiodiversity should be initiated at the very bottom grassroots level, including students, and gram sabha/panchayat levels.

10.2 Conservation of Agrobiodiversity

The proper conservation and use of agrobiodiversity are fundamental to sustainable development and food security. Plant genetic resources (a major component of agrobiodiversity) are the fundamental to fulfilment of basic needs of a human community like food, feed, fuel, fibre, fertilizer, etc., and huge loss in economic and social development has been experienced. Hence, agri-genetics and its allied resources have to be conserved and managed for sustainable use. Thus the importance of germplasm is realized; its collection and conservation are carried out worldwide for all the crops (Pilliai et al. 2002). Germplasm is conserved either by in situ or ex situ method as graphically presented in Fig. 10.3. These are complementary systems rather than independent.

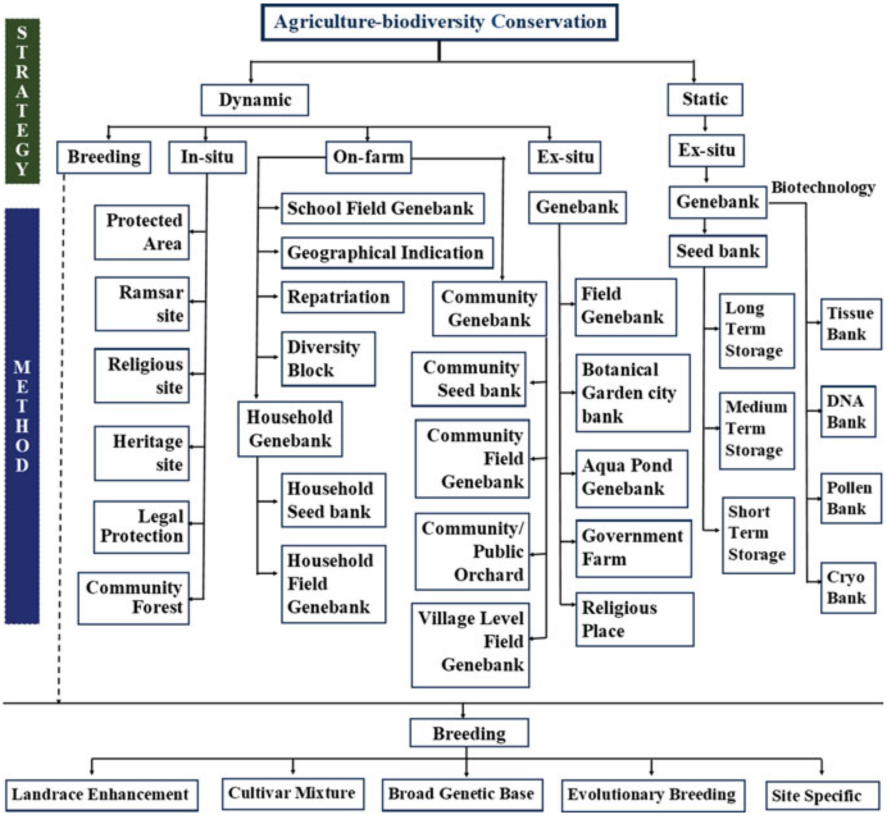

Fig. 10.3 Agrobiodiversity conservation approaches (Joshi et al. 2017)

10.2.1 In Situ Methods

In situ conservation is mainly achieved by two ways, viz. on-farm conservation and creating protected areas for crop wild resources (CWRs), of which on-farm conservation is considered at the local level for overall conservation and utilization of agrobiodiversity. In situ conservation of agrobiodiversity includes habitat protection of wild populations and maintenance of native species and varieties in traditional agroecosystems. It includes conservation of species at their niche like biosphere reserve, national parks, wildlife sanctuaries, biodiversity hotspots, community reserves and sacred groves. Hill agriculture and terrace farming are the best examples of conservation of native of wild agrobiodiversity. Landraces will be genetically conserved through participatory rural appraisal, agricultural extension services, joint forest management, etc. The Convention on Biological Diversity has given utmost importance to this method of conservation especially for the wild species and landraces that are adapted to their local climate and satisfy the palatability of localities (Convention on Biological Diversity 1992). An international project on ‘Strengthening the Scientific Basis of In Situ Conservation of Agricultural Biodiversity’ had been stated in the 1990s in line with the Convention on Biological Diversity programme especially on agrobiodiversity conservation globally. It was started initially in eight countries focusing on 27 agricultural crops for maintaining their genetic diversity on farm giving more focus on wild germplasm and landraces (Jarvis and Hodgkin 2008). The effort was given to conserving available diversity in home garden (Eyzaguirre and Linares 2004), on-farm conservation of neglected and underutilized crops.

Nowadays, several modern tools and techniques are being available to assess their genetic vulnerability to changing climate and degrading soil fertility status; farmers are more aware to conserve traditional crops and their cultivation practices at own farms (Lipper et al. 2010). On-farm conservation of agrobiodiversity is helpful in safeguarding the traditional knowledge associated to biodiversity which is an integral part of peoples social and cultural identity. The in situ or on-farm conservation strategies can strengthen farmer seed systems and promote climate resilient integrated home garden production systems, especially underutilized crop species and carbon-rich farming. Besides, the concept of CWR management programmes was started in the three decades back at their respective habitats by creating the protected areas. Nowadays, several countries have started the on-farm conservation programmes, for example, Armenia on wheat; Australia on *Melaleuca*, *Vitis* CWRs, *Potamophila parviflora* and rice; Azerbaijan on *Beta lomatogona*; Bolivia on potato; Bulgaria on *Trifolium*, *Medicago*, *Vicia*, *Onobrychis*, *Lolium*, *Dactylis*, *Bromus*, *Festuca*, *Poa* and *Agrostis*; China on 115 CWRs; Costa Rica on *Phaseolus lunatus*; Ecuador on *Caryodaphnopsis*; Ethiopia on coffee CWRs; Guatemala on teosinte CWRs; Hungary on *Populus nigra*; India on *Myristica*, rice, corn, wheat, citrus, banana, sugarcane, maize, millet, oilseeds, spices, legumes and mango CWRs; Iran on *B. lomatogona*; Iraq on *Vicia* CWRs; Ireland on *Brassica* CWRs; Israel on cereal, pulse CWRs; Japan on *V. angularis*; Lithuania on *Corylus*, *Fragaria*, *Origanum*, *Thymus*, *Vaccinium*, *Mentha* and *Trifolium* CWRs; Mauritius on *Coffea* spp.;

Mexico on teosinte and *Phaseolus coccineus*; Nepal on *Oryza rufipogon* and *Fagopyrum* CWRs; Nicaragua on teosinte; Paraguay on CWRs of 22 crop genera; Slovak Republic on *Trifolium*, *Poa*, *Phaseolus* and *Festuca Dactylis* CWRs; Former Soviet Union on wheat, fodder grasses, wild apples, peaches, pistachios, walnuts, apples, pears, prunes, pistachio, apricot and almond CWRs; Sri Lanka on *Oryza*, *Solanum* and *Hibiscus* spp.; Syria on wheat and *Vicia*; Turkey on wheat, barley, chickpea, lentil, chestnut, plum and tree CWRs; and the United States on *Vitis rupestris*, *Allium columbianum*, *A. geyeri*, *Solanum fendleri*, *S. jamesii*, *Carya*, *Capsicum* and 23 other CWRs (Meilleur and Hodgkin 2004).

10.2.2 Ex Situ Methods

It refers to the conservation of germplasm outside their niche area or natural habitat that supports either storage or perpetuation facilities that maintain their genetic constitution and viability. There are different approaches, viz. seed conservation (i.e. cryopreservation storage for recalcitrant seeds and seed gene bank for orthodox seed), plant conservation (i.e. clonal repositories, herbal garden, botanical garden, arboreta and field gene bank), in vitro conservation, cryopreservation and DNA conservation (i.e. DNA library, gene banks, etc.).

The NBPGR, New Delhi, has approximately 440,991 accessions and has been conferred with the second-largest gene bank in the world consisting 1947 crop species and their wild relatives. This figure includes 164,401 accessions of cereals, 59,270 accessions of millets, 7088 accessions of forage, 7590 accessions of pseudo-cereals, 66,634 accessions of legumes, 659 accessions of ornamentals plants, 1646 accessions of agroforestry plants, 59,170 accessions of oilseeds, 15,704 accessions of fibre crops, 26,327 accessions of vegetables, 276 accessions of fruits and nuts, 8068 accessions of medicinal plants and narcotics, 3152 accessions of spices and condiments, 10,235 accessions of duplicate safety samples (lentil, pigeon pea) and 10,771 accessions of wheat and barley. This data includes ~5034 recommended varieties and ~4316 genetic stocks, of which 1762 species are conserved (http://www.nbpgr.ernet.in/Research_Projects/Base_Collection_in_NGB.aspx). The modern cultivars develop from the uses of landrace and have been used tremendously in CIMMYT and IRRI for wheat, maize and rice breeding programme (Witcombe et al. 1996). To safeguard from, natural and artificial disaster, long-lasting facilities were built up at Svalbard Global Seed Vault, Norway, to store the seed material. The main objective of this vault is for backup having duplicate seed sample from the core collection of world crops. Till 2019, the vault holds 992,032 samples and has storage capacity of 4.5 million of seed samples.

10.3 Role of Molecular Approaches

Plant genetic resources can be handled at the intersection of food security, agriculture, trade and environment. Crop diversity is at great risk due to genetic erosion and genetic vulnerability. Such risk can be managed with proper cooperation, good science, adequate resources and political will. Among them DNA-based scientific approaches for the conservation of genetic resources are important ones as listed in Table 10.1.

10.3.1 Conservation

Proper documentation regarding the prospective application and benefits through characterizing and evaluating the crop genetic diversity is a must along with the conservation of them. For effective utilization, different techniques like morphometric, physiological, anatomical, biochemical, etc. are previously used. But, nowadays molecular tools are often used to assess the genetic identity, evolutionary history and many more areas. Besides, molecular tools also help to determine the individual reproductive success, breeding behaviour of species and the existence of gene flow along with their consequences. Gene flow is the introduction of genetic materials from one population to others of same or related species changing the composition of gene pool preference (Papa and Gepts 2003). Information obtained from the molecular markers or DNA sequences helps us in better understanding taxonomy, domestication and evolution, which provide a good basis for effective conservation in crop biodiversity (Nwakanma et al. 2003).

Table 10.1 Biotechnology tools used in crop genetic resources (FAO 2006)

Objective	Activity	Technology
Conservation	Gene bank	In vitro conservation
		Cryopreservation
Management	Identification	Genetic fingerprinting
	Characterization	Protein analysis—isozymes
		DNA analysis—RAPD, RFLP, SNPs microsatellites, gene array, sequencing
		DNA barcoding
	Plant health	ELISA diagnostics
		Virus treatment
	Evaluation	QTL mapping, genetic maps
Restoration	Molecular breeding	Marker-assisted selection
	Wide crossing	Embryo rescue
	Genetic modification	Transgenesis, cisgenesis
	Genome-wide editing	CRISPR/Cas9 system

10.3.2 Management

Different practices have to be carried out for the proper management of germplasm that has been established in a collection, which is usually a field, seed or in vitro gene bank. The main motto behind such practices is to safeguard the genetic diversity and integrity along with maintaining the identity of the sample stored and material available for distribution to users. At the same time, these technologies also help in the detection of unnecessary materials (McGregor et al. 2002), presence of contaminants as well as contamination with introgressed genes from commercial varieties or other accessions. Any kind of changes that occurred in the genetic structure of the accession which may be due to nature itself or due to human intervention can be detected and monitored effectively using the molecular data (Chwedorzewska et al. 2002).

Molecular markers play an important role in carrying out the different activities for the management of gene bank once it got established. For instance, in a gene bank, regeneration of seeds or other reproductive plant material in storage is a critical duty, for which different parameters like species concerned, the quality of the individual accessions and conditions of their storage are required (FAO 1997). Any changes that took place in alleles or in allele frequencies due to adopted conservation strategies like gene banks can be detected using markers (de Vicente et al. 2005). Second, markers prevent the unnecessary wastage of resources by detecting any kind of unintentional duplication or over duplication of accessions during the duplication of rare accession for their preservation (de Vicente et al. 2005). Third, core collections have been established to minimize expenses and/or stimulate greater and more efficient usage by farmers and breeders.

10.3.3 Restoration

Exploitation of gene pool present in the wild species helps in improving the genetics of related crop species. Conservation of such wild relatives is of utmost importance to maintain the agricultural biodiversity (FAO 1997). As per FAO (2002), crossing domesticated population with the wild relatives is the mostly followed practised to get the desired gene. Gene flows in between perennial rice and rice, between sugar beet and wild beet, maize and teosinte are some of the examples which have been reported. Sustainable restoration and use of genetic resources available in the wild crop species are only possible in the presence of molecular markers (Ferreira 2005). Such genetic resources can be transferred successfully in the cultivated cultivars using molecular markers only, while gene flow may lead to change in genetic diversity and extinction of wild population. Incorporation of gene in wild species from the domesticated population gives path to disappearance of such wild population in its original genetic state (Papa 2005). In such case molecular markers help in the restoration of wild species by identifying them among the mixed population of hybrid and non-hybrid wild relatives.

10.4 A Brief Review of the Basic Molecular Techniques

With advent of biotechnology, there have been different techniques to detect the variation and polymorphism at DNA level among the organism from same or different taxa. One of the initial technologies to detect DNA-level genetic variation is the use of cellular enzymes involved in the nucleic acid metabolism. Discovery of the restriction enzymes and restriction endonucleases has been termed as the most significant, because of their ability to cut the DNA strands or nucleic acid chain on desirable site, which is called as ‘recognition or restriction site’ for the particular enzyme. Every restriction endonuclease enzyme has specific recognition site to cut the DNA strand. The DNA fragments generated from restriction enzyme share a common sequence at the end of restriction site but will have a different sequence composition on the other end. The electrophoresis technique helps to separate the DNA fragments of different length based on their different molecular weight. With the advent of thermal cycler machines, a different enzymatic reaction, known as the polymerase chain reaction (PCR), has been applied widely to amplify a specific region or fragment of DNA molecule in the organisms using known sequence of very small fragments of nucleotides termed as ‘primers’. There are techniques that use PCR-based approach along with using arbitrary/semi-arbitrary primer. Based upon these approaches, the basic techniques can be categorized as category 1, non-PCR-based methods; category 2, arbitrary (or semi-arbitrary) primed techniques, and category 3, site-targeted PCR techniques.

10.4.1 Non-PCR-Based Techniques

There are different blotting techniques, which are used to detect the sequences of polypeptides (proteins) and nucleic acid (DNA and RNA). Electrophoretic separation of polypeptides and nucleic acids is a major component of all three, Southern blotting, Northern blotting and Western blotting techniques. After the electrophoresis, the separated products are transferred to a membrane made up of nitrocellulose, or polyvinylidene difluoride (PVDF), etc. for immobilization. The molecule of interest is visualized through radio-labelling or enzymatic labelling or DNA probe binding, etc. Based on the choice of targeting molecule (DNA, RNA or protein), the blotting technique is preferred. Western blot hybridization technique is used for detection of specific proteins with help of antibodies based on their binding specificity. Southern blot technique is used to detect specific DNA sequences using labelled probes. Similar to Western blot technique, Northern blotting is used to analyse mRNA to study its gene expression. Southwestern blotting combines features of both Southern and Western blotting techniques and is useful for fast characterization of both DNA binding proteins and their specific genomic sites.

Variable number tandem repeats (VNTR) are non-coding regions in the genome in the form of short nucleotide sequences organized as a tandem repeat. Tandem repeats are common in chromosomes of all organism with varied length. Some of the repeats have been found heritable also. Hence the detection of VNTR helps for genetic differentiation of organism at intra- and interspecific level. Another, the restriction fragment length polymorphism (RFLP) technique is a non-PCR-based technique, in which genomic DNA is fragmented with the help of restriction enzymes, followed by gel electrophoresis. The restricted DNA fragments are then transferred to a filter through Southern blotting. Before wide application of PCR-based molecular technique, the RFLP had been applied in genome mapping, localization of genetic disease genes, determination of risk for a disease, genetic fingerprinting and paternity testing. The information of VNTR is considered important for linkage mapping through RFLP technique (Arens et al. 1995).

10.4.2 Arbitrary (or Semi-Arbitrary) Primed Techniques

Advent of PCR technique facilitated use of a single 'arbitrary' primers in the polymerization chain reaction for the amplification of multiple copies of discrete DNA. These multiplied DNA fragments (also known as 'amplicon') have similar nucleotide sequences at one end and represent both of the complimentary strands of the DNA. In the follow-up of this reaction, several secondary techniques, such as multiple arbitrary amplicon profiling (MAAP) (Caetano-Anollis 1994), APPCR (arbitrary primed PCR) (Welsh and McClelland 1990) and DAF (DNA amplification fingerprinting) (Caetano-Anollis et al. 1991), similar to RAPD had been developed. But lack of heterozygous information and detection of only dominant alleles from the genome limited their application.

Amplified fragment length polymorphism (AFLP) technique, which combines both RFLP (restriction digestion) and PCR methods, has been found highly reproducible to detect the genetic variation among the organism (Vos et al. 1995). It is also considered as dominant marker technique, but using specific gel scanners, heterozygote alleles can also be detected, hence called as semi-dominant technique. The semi-arbitrary PCR methods, such as M13, are used as primers in PCR reactions to amplify the minisatellite region and VNTR cores (Heath et al. 1993). Single primer amplification reaction (SPARs) is also similar to the earlier technique but differs on using the core motifs of microsatellites (Gupta et al. 1994) and creates high polymorphic banding pattern. Inter-simple sequence repeat (ISSR), another technique similar to SPAR, involves the regions between to SSRs in the genome; hence at the same time, it is highly specific though highly polymorphic (Kantety et al. 1995). SAMPL technique has also been applied for genetic differentiation. It integrates AFLP and SSR techniques using enzyme assay with microsatellite primer-based amplification of digested nucleic acid product (Morgante and Vogel 1994). RAPD is a type of PCR which amplifies random fragments of DNA in a large template by using short primers. Williams et al. (1990) developed random amplified polymorphic DNA (RAPD) a technique using very short ten base primers to generate random fragments from template DNAs. RAPD fragments can be separated and used as genetic markers or a kind of DNA fingerprint. The above-mentioned approaches and techniques have been applied for DNA fingerprinting, species identification, population genetic characterization, gene diversity assessment and genome mapping of the species (Lu et al. 1996).

10.4.3 Site-Targeted PCR Techniques

In contrary to arbitrary primer techniques, site-targeted primers can be used to amplify the conserved region or specific region of the targeted genome in site-targeted PCR techniques. In such techniques, the variation in the amplicon among different organism may be less polymorphic due to high specificity. These techniques can be used with very small sample size of the DNA material. It requires high-resolution electrophoresis techniques due to the comparatively small size of the amplicons from the specific regions of the genome. Some of the high-detection gel electrophoresis techniques are thermal gradient gel electrophoresis (Riesner et al. 1992), denaturing gradient gel electrophoresis, single-strand conformational polymorphism (Hayashi 1992) and heteroduplex formation (White et al. 1992). In the cleaved amplified polymorphic sequence (CAPS) procedures, in the initial, the amplified segment of DNA (through PCR) is digested with a specific restriction enzyme followed by its staining in ethidium bromide and separation through gel electrophoresis. Later, the bands are visualized through gel documentation system (Ghareyazie et al. 1995). CAPS technique is applied to target the restriction sites within a desirable locus in the genome. Microsatellites or simple sequence repeats (SSRs) are those regions of the genome which are more likely to face mutation. Therefore, the SSR regions help to detect variation at specific level. The SSRs of flanking regions are utilized to design sequence-tagged microsatellite (STMS) (Beckman and Soller 1990), making them highly specific to a taxa. These markers are capable to amplify the co-dominant information from the DNA strands, hence helping to determine the heterozygosity as well (Saghai-Maroof et al. 1994).

10.5 Application of the Biotechnological Innovations

10.5.1 Germplasm Identification and Diversity Assessment

Identification of plant germplasm and genetic diversity assessment of a germplasm collection are widely applied implication of molecular marker technique throughout the world for more than four decades. Over the last two decades, with integration of sequencing techniques, DNA fingerprinting has been widely applied in germplasm identification and characterization (Korir et al. 2012). The above-discussed molecular marker techniques covering both non-PCR-based or PCR-based and dominant or co-dominant information-based (e.g. restriction fragment length polymorphism (Williams et al. 1991), RAPD (Williams et al. 1990), SSR (Powell et al. 1996), ISSRs (Zietkiewicz et al. 1994), AFLP (Vos et al. 1995), SAMPL (Morgante and Vogel 1994), M-AFLP (Albertini et al. 2003), sequence-related amplified polymorphism (Li and Quiros 2001), CAPS (Williams et al. 1991), SCoT (Collard and

Mackill 2009), DNA sequencing and DNA microarray analysis (Biswas et al. 2011) and SNPs) all have been applied for DNA fingerprinting for the last three decades.

Integration of next-generation sequencing methods have established SNPs as widely preferred technique for intraspecific germplasm identification (Dong et al. 2010; Jiang et al. 2010) and diversity analysis (Ravel et al. 2006). The AFLP technique has been found robust to detect relatedness among cultivars (Guo et al. 2005) like cotton (Murtaza 2006), agave offsets and bulbils (Juarez et al. 2009). Modified AFLP has been found more efficient than AFLP to detect intra-varietal genetic differences in *Lupinus angustifolius*, *Poa pratensis*, *Cynara cardunculus* grapevine and cassava (Yang et al. 2001; Albertini et al. 2003; Acquadro et al. 2005; Cretazzo et al. 2010; Whankaew et al. 2011). Estimation of genetic relationships could be revealed with the help of RAPD technique in broccoli (Lu et al. 2009), radish (Liu et al. 2008a), cherry (Demirsoy et al. 2008), cucurbits (Verma et al. 2007), strawberry (Gidoni et al. 2006), etc. RFLP markers have been found effective for the identification of creeping bentgrass (*Agrostis stolonifera* L.) cultivars (Caceres et al. 2000) and tall fescue (*Festuca arundinacea*; Busti et al. 2004).

Microsatellites have been found highly robust and specific to estimate the heterozygosity and hence genetic differentiation of the cultivars, due to its reproducibility (Jannati et al. 2009). Microsatellites were utilized to reveal the genetic differentiation in wheat (Bryan et al. 1997), tomato (Bredemeijer et al. 1998), potato (Ashkenazi et al. 2001) and pelargonium (Becher et al. 2000). The most polymorphic co-dominant markers of SSR have been applied not only for identification of the cultivars but for the genomic mapping as well in several crops like tomato (Caramante et al. 2011), wheat (Roder et al. 2002), rice (Anand et al. 2012), potato (Karaagac et al. 2014), Chinese bayberry (Xie et al. 2011), mango (Tsai et al. 2013), perennial ryegrass (Jones et al. 2001), diploid ryegrass (Wang et al. 2009), annual ryegrass (Nie et al. 2019), alfalfa (Herrmann et al. 2010), white clover (Kolliker et al. 2001), orchard grass (Jiang 2013) and maize (Dubreuil et al. 2006). ISSR markers are more reproducible than RAPD markers due to its specificity and use in rice (Joshi et al. 2000), *Oryza granulata* (Qian et al. 2001), wheat (Pradeep et al. 2002), barley (Sanchez de la Hoz et al. 1996), maize inbred lines (Kantety et al. 1995), sorghum (Yang et al. 1996), finger millet (Salimath et al. 1995), *Vigna* (Ajibade et al. 2000), pea (Lu et al. 1996), soybean (Wang et al. 1998), white lupin germplasm (Gilbert et al. 1999), oilseed rape cultivars (Charters et al. 1996), potato cultivars (McGregor et al. 2000), *Diplotaxis* species (Martin and Sanchez-Yelamo 2000), cucurbits (Dje et al. 2006), lotus (Tian et al. 2008), radish (Liu et al. 2008a), citrus (Amar et al. 2011), sweet potato (Li et al. 2008a), Chinese rhubarb (Hu et al. 2010), watermelon (Dje et al. 2010), cocoa germplasm (Charters and Wilkinson 2000), potato cultivars (Prevost and Wilkinson 1999) and chrysanthemum cultivars (Wolff et al. 1995) to study the genetic differentiation and genetic relatedness among their genotypes.

SRAP technique has been found very effective to estimate the genetic diversity and phylogenetic relationship (Budak et al. 2004; Zaefizadeh and Goliev 2009). SRAP markers were used to investigate the genetic diversity in sesame (Zhang et al. 2011); citrus (Amar et al. 2011); radish (Liu et al. 2008a); potato, rice, lettuce and celery (Li and Quiros 2001); cotton (Lin et al. 2003); buffalo grass (Budak et al.

2004); and rapeseed mustard (Li et al. 2007). SAMPL technique was applied to assess genetic diversity in lettuce (Witsenboer et al. 1997) and sweet potato (Tseng et al. 2002). SAMPL has been found more robust and with higher polymorphism in comparison to AFLP markers in *Withania somnifera* (Negi et al. 2006). CAPS markers had been successfully employed on vegetative propagated polyploid plants like strawberry (Kunihisa et al. 2005), sweet potato (Tanaka et al. 2010) and citrus (Amar et al. 2011) for discrimination of their cultivars. Collard and Mackill (2009) found the start codon targeted (SCoT) polymorphism-based marker technique of potential application in plant identification. This technique has been successfully applied in mango, rice and peanut for identification of cultivars and varieties (Collard and Mackill 2009; Xiong et al. 2009). In comparison to dominant markers, viz. RAPD and ISSR, SRAP markers have been found with higher polymorphism to study the genetic diversity in buffalo grass (Budak et al. 2004).

Retrotransposon-based markers have also been applied to reveal genotype description and identification in plants (Kumar and Hirochika 2001). For identification of varieties, trait mapping, population diversity analysis in cereals and potatoes, inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon microsatellite-amplified polymorphism (REMAP) markers have also been used (Spooner et al. 2007). Highly specific to desired genomic region, the retrotransposon-based insertion polymorphism (RBIP) approach has been successfully applied for genetic characterization of *Pisum* genotypes (Flavell et al. 1998). PCR-IRAP technique has been successfully applied in a set of 20 most commonly grown potato by Novakova et al. (2009). Several other studies have been conducted in plants with retrotransposon-based techniques to estimate their genetic diversity (Kalendar et al. 1999; Vitte et al. 2004).

10.5.2 DNA Barcoding and Phylogenetic Studies

Application of DNA markers through development of species-specific DNA barcodes is not widely implicated due to high mutation rate and evolutionary complexity of the genome. DNA barcodes are developed from the cytoplasmic inherited genetic information such as chloroplast genomic regions like *psbA-trnH*, *rbcL*, *atpH-atpl*, *petA-psbJ*, *ndhA-ndhA*, *trnK-trnK*, *petB-petD*, *ndhC-trnV*, *trnS1-trmG1*, *trnW-psaJ*, *clpPclpP*, *trnT-psbD*, *rbcL-accD*, *accD-psal*, *ndhF*, *petN-psbM*, *psbM-trnD*, *psbE-petL*, *Rpl32-trnL*, *rpoB-trnC*, *rps16-trnQ*, *trnHpsbA*, *trnS2-trnG2* and *matK* (Dong et al. 2012). In rice, DNA barcodes were developed for 21 species, namely, *O. glaberrima* and *O. barthii*, *O. glumipatula* and *O. longistaminata*, *O. grandiglumis* and *O. alta*, *O. meyeriana* and *O. granulata*, *O. minuta* and *O. malampuzhaensis*, *O. nivara* and *O. sativa* subsp. *indica* and *O. sativa* subsp. *japonica* and *O. rufipogon* (Zhang et al. 2021). These markers could help to reveal the mislabelled species at the gene bank of IRRI, Philippines, centres. Chloroplast genome phylogenetic analysis revealed that the *O. nivara* is close to *O. sativa* L. ssp. *indica* and the *O. sativa* L. ssp. *japonica* is close to *O. rufipogon* in Asian cultivated and wild rice (Brozynska et al. 2014), and the African rice (*O. glaberrima* and

O. barthii) were clustered together but in separate group with the Asian rice (Wambugu et al. 2015). A 24 candidate loci from plastid genome were used to validate and develop DNA barcodes for 231 diverse rice genotypes, for selection of suitable barcoding loci for DNA barcoding in rice (Singh et al. 2017). The 18 Egyptian *Triticum* accessions were discriminated using the *matK* and *rbcl* barcode primers by Awad et al. (2017). The phylogenetic analysis is carried out by Osman and Ramadan (2019) based on nucleotide and amino acid sequences on 20 *Triticum* species. The *matK* gene classified into diploid, tetraploid and hexaploid *Triticum* species based on cluster analysis. DNA barcoding is a powerful tool and can have a significant impact on basic agricultural research (Mi et al. 2012) as well as conservation monitoring and priority assessments in threatened species (Shapcott et al. 2015) and medicinal plant (Chen et al. 2010) with their habitats, within local communities and across large biogeographic area.

DNA is a suitable molecular technique used for authentic identification and its correct placement in taxonomic classification based on the phylogenetic analysis. Yao et al. (2010) used ribosomal *ITS* for DNA barcoding and implemented it in several plant species, i.e. 322 species of *Astragalus* (Fabaceae), 234 species of *Indigofera* (Fabaceae), 223 species of *Trifolium* (Fabaceae), 206 species of *Miconia* (Melastomataceae), 199 species of *Draba* (Brassicaceae), 185 species of *Centaurea* (Asteraceae), 178 species of *Veronica* (Plantaginaceae), 176 species of *Oxalis* (Oxalidaceae), 174 species of *Ficus* (Moraceae), 162 species of *Solanum* (Solanaceae), 161 species *Senecio* (Asteraceae), 138 of species of *Aspalathus* (Fabaceae), 127 species of *Acacia* (Fabaceae), 124 species of *Rubus* (Rosaceae), 124 species of *Begonia* (Begoniaceae), 123 species of *Polygala* (Polygalaceae), 118 species of *Artemisia* (Asteraceae), 118 species of *Cliffortia* (Rosaceae), 117 species of *Ruellia* (Acanthaceae), 117 species of *Euphorbia* (Euphorbiaceae), 117 species of *Impatiens* (Balsaminaceae), 113 species of *Eryngium* (Apiaceae), 106 species of *Eucalyptus* (Myrtaceae), 104 species of *Croton* (Euphorbiaceae), 99 species of *Calceolaria* (Calceolariaceae), 98 species of *Cuscuta* (Convolvulaceae), 97 species of *Dianthus* (Caryophyllaceae), 96 species of *Salvia* (Lamiaceae), 94 species of *Berberis* (Berberidaceae), 86 species of *Rhododendron* (Ericaceae), 84 species of *Macaranga* (Euphorbiaceae), 83 species of *Acer* (Sapindaceae), 82 species of *Prunus* (Rosaceae), 81 species of *Pilea* (Urticaceae), 81 species of *Coffea* (Rubiaceae), 273 species of *Allium* (Alliaceae), 43 species of *Cyrtanthus* (Amaryllidaceae), 34 species of *Crinum* (Amaryllidaceae), 49 species of *Pinanga* (Arecaceae), 52 species of *Kniphofia* (Asphodelaceae), 50 species of *Costus* (Costaceae), 318 species of *Carex* (Cyperaceae), 52 species of *Eleocharis* (Cyperaceae), 31 species of *Lachenalia* (Hyacinthaceae), 45 species of *Luzula* (Juncaceae), 42 species of *Juncus* (Juncaceae), 79 species of *Gagea* (Liliaceae), 78 species of *Lilium* (Liliaceae), 49 species of *Fritillaria* (Liliaceae), 37 species of *Musa* (Musaceae), 227 species of *Maxillaria* (Orchidaceae), 139 species of *Oncidium* (Orchidaceae), 121 species of *Dendrobium* (Orchidaceae), 120 species of *Disa* (Orchidaceae), 100 species of *Ophrys* (Orchidaceae), 85 species of *Paphiopedilum* (Orchidaceae), 56 species of *Phalaenopsis* (Orchidaceae), 48 species of *Masdevallia* (Orchidaceae), 46 species of *Gomesa* (Orchidaceae), 42 species of *Satyrium*

(Orchidaceae), 42 species of *Dendrochilum* (Orchidaceae), 41 species of *Cyrtochilum* (Orchidaceae), 38 species of *Telipogon* (Orchidaceae), 36 species of *Dichaea* (Orchidaceae), 33 species of *Diuris* (Orchidaceae), 33 species of *Scaphyglottis* (Orchidaceae), 30 species of *Cymbidium* (Orchidaceae), 115 species of *Poa* (Poaceae), 46 species of *Alpinia* (Zingiberaceae) and 37 species of *Amomum* (Zingiberaceae).

10.5.3 QTL Mapping and Marker-Assisted Selection

A quantitative trait locus (QTL) is a region of DNA which is associated with a particular phenotypic trait. The genomic location of any QTL is unknown as similar to any marker, and it should be inferred based on association analysis of phenotype and marker (Mulualem and Bekero 2016). In QTL mapping a structured population is developed from bi-parental crosses such as inbred lines, to discover the marker-trait association, while in association mapping, historical patterns of genetic recombination help to identify the marker/loci in genetic linkage for generations, in high resolution. Genetic association mapping (AM) or linkage disequilibrium (LD) mapping is a method that relies on LD to study the relationship between phenotypic variations and genetic polymorphism (Breseghello and Sorrells 2006). The DNA markers linked to agronomically important genes may be used as a molecular tool for marker-assisted selection (MAS) in breeding. QTL mapping has been undertaken in some of the crops like maize (Li et al. 2008b), tomato (Stevens et al. 2007) and wheat (Naz et al. 2008). In maize, the loci linked to downy mildews were identified and transferred to downy mildew-susceptible inbred line for development of resistance (George et al. 2003). Advanced backcross (AB-QTL) was also performed to develop inbred lines for discovery of QTL analysis (Tanksley and Nelson 1996). AB-QTL technique was applied for detection of QTL in crops like tomato (Chaib et al. 2006), wheat (Kunert et al. 2007), barley (Li et al. 2006) and rice (Cheema et al. 2008). QTL mapping studies were carried out in rice for grain quality (Lou et al. 2009); milling quality, protein content and colour characteristics (Tan et al. 2001); leaf width and grain number (Tian et al. 2015); drought resistance (Gomez et al. 2010); blast resistance (Fukuoka and Okuno 2001); submergence tolerance (Nandi et al. 1997); and basal root thickness (Liu et al. 2008b); in wheat for grain yield under multi-environment (Bonneau et al. 2013), terminal heat tolerance (Paliwal et al. 2012), preharvest sprouting tolerance (Kulwal et al. 2005), stripe rust resistance (Santra et al. 2008), powdery mildew resistance (Asad et al. 2014), senescence-related traits under high temperature (Vijayalakshmi et al. 2010) and root penetration ability (Botwright Acuña et al. 2014); and in maize for yield and agronomic traits (Park et al. 2014), stay green traits (Wang et al. 2012), early plant vigour in chilly environments (Presterl et al. 2007), drought tolerance (Agrama and Moussa 1996), downy mildew resistance in maize (Nair et al. 2005), head smut resistance (Li et al. 2008c) and root architectural traits (Burton et al. 2014). Advance backcross QTL analysis approach was effectively used rice, wheat, maize, barley, soybean, cotton and tomato (Jiang 2013).

There are different molecular approaches used under the umbrella of MAS, such as marker-assisted backcrossing (MABC), marker-assisted gene pyramiding (MAGP), marker-assisted recurrent selection (MARS) and genomic selection (GS). The MABC technique has been used in different crops such as rice (Hasan et al. 2015), wheat (Yadawad et al. 2017), barley (Xu et al. 2018), soybean (Rawal et al. 2020), cotton (Wu et al. 2017), tomato (Osei et al. 2018), pea (Mannur et al. 2019), etc. Marker-assisted convergent crossing (MACC) was used to pyramid multiple genes/QTLs used in wheat (Gupta et al. 2010) and rice (Luo et al. 2012). The various researchers have successfully applied marker-assisted selection using different genes/markers like SSR for yield in rice (Liang et al. 2004); RFLP for bacterial blight in rice (Chen et al. 2002); SSR for brown plant hopper in rice (Shabanimofrad et al. 2015); PCR-based markers for rice blast (Tian et al. 2019); SSR for drought tolerance in wheat (Malik et al. 2015); SNP for yield in maize (Cerrudo et al. 2018); RFLP for maize earliness and yield in maize (Bouchez et al. 2002); SCAR and CAPS for sugarcane mosaic virus in maize (Dussle et al. 2002); SSR for maize rough dwarf disease in maize (Xu et al. 2020); SNP for corn borer in maize (Badji et al. 2018); SSR for quality protein maize (Hossain et al. 2018); PCR-based marker for yield in barley (Schmierer et al. 2004); SSR for drought tolerance in barley (Merchuk-Ovnat et al. 2016); SSR and DArT markers for *Fusarium* head blight (FHB) along with agronomic traits in barley (Lv et al. 2014); STS, RAPD, SCAR and AFLP for bacterial blight resistance in common bean (Tar'An et al. 2001); SSR for resistance to *Fusarium* wilt in chickpea (Cobos et al. 2009); RAPD, CAP and AFLP for powdery mildew resistance in mung bean (Chen et al. 2007); SNP for drought resistance in common bean (Mukeshimana et al. 2014); SSR and SNP for salinity resistance in chickpea (Pushpavalli et al. 2015); SSR for drought resistance in chickpea (Hamwieh et al. 2013); SSR for salinity resistance in cowpea (Chankaew et al. 2014); RFLP and SSR Al tolerance in soybean (Abdel-Haleem et al. 2014); SSR and SNP for salt tolerance in soybean (Ha et al. 2013); SSR for drought tolerance in soybean (Abdel-Haleem et al. 2012); SSR and SNP for frost resistance in pea (Klein et al. 2014); SSR for drought resistance in pea (Iglesias-Garcia et al. 2015); etc. Different varieties like Pusa Basmati 1 (IPB1) variety using QTL (xa13)-chromosome 8 and QTL (xa21)-chromosome 11 for bacterial leaf blight resistance from IRBB55; improved Sambha Mahsuri (improved BPT 5204) using xa5, xa13 and xa21 for bacterial leaf blight resistance; Vivek QPM9 using opaque-2 from Vivek Hybrid maize for high tryptophan, lysine and iron content; and improved Pusa RH10 using xa13, xa21, pi54 and piz5 for bacterial leaf blight resistance and blast resistance were also developed based on MAS (Singh and Singh 2015).

10.6 Exploiting Natural Variation Through Molecular Approaches

10.6.1 Sequencing and Resequencing Techniques

Arabidopsis thaliana is a model species for whole genome sequencing in other plants due to its small genome size and hence provides a baseline to study the genetic architecture in other plants. Today, the whole genome of few other plant species from cereals, millets, legumes, oilseeds, vegetables, fruits and trees has been sequenced. Based on the economic value of a crop and its genome size and ploidy level, the whole genome projects are initiated. Some other genomic features such as polyploidy, repetitive sequences, transposable elements, noncoding RNAs, heterozygosity, etc. enable the researchers to select small genome crop plants (Saini et al. 2020). *Oryza sativa* (420 Mb split in 12 chromosomes) has smaller genome size compared to *Triticum aestivum* (17 Gbp split in 21 chromosomes). Sanger's sequencing technology was very costly, time-consuming and very complex. The advent of NGS technology has facilitated quick and fast sequencing of large genome size crops as well. A whole genome sequence is useful to determine the gene regulation of desired traits for their improvement in the crops. The whole genome sequences also help to determine the evolutionary history of the species development, hybridization, selection and adaptation of particular species. It also paves a base for comparative structural and functional genomics to understand the biological process in non-model plant species. Most importantly, it supports DNA marker-based investigation in small-scale assessment for development of specific markers. With help of transcriptome sequencing, gene regulations in the crops have also been investigated for traits related to stress physiology. Altogether, the techniques of genotyping by sequencing (GBS), whole genome sequencing (WGS) and resequencing of crop genome have been used to develop the highly specific marker technology for exploration of genetic relationship and genetic differentiation among breeding products and genetic mapping of desired genes (Vlk and Repkova 2017). These techniques have also facilitated easy resequencing of the whole genome. A '3000 Rice Genome Project' conducted resequencing with resolution of 14× sequencing depth; ~18.9 million SNPs in rice were discovered by Illumina-based next-generation sequencing with average genome coverages (94%), and mapping rates (92.5%) (The 3000 Rice Genomes Project 2014), which provide the baseline for large-scale discovery of novel alleles for important rice phenotypes exploring the genomic diversity within *O. sativa*.

A number of crop species have been sequenced now at genomic level, of which the major sequenced crop genomes mainly for tropical countries are *Oryza sativa* ssp. *indica* (430 Mb; Yu et al. 2002), *Oryza sativa* ssp. *japonica* (420 Mb; Goff et al. 2002), *Triticum aestivum* (17,000 Mb; Bennetzen et al. 2012), *Zea mays* (2300 Mb; Schnable et al. 2009), sorghum (~730 Mb; Paterson et al. 2009), foxtail millet (490 Mb; Bennetzen et al. 2012), tomato (900 Mb; The Tomato Genome Consortium 2012), potato (844 Mb; The Potato Genome Sequencing Consortium 2011), eggplant (1126 Mb; Hirakawa et al. 2014), soybean (1115 Mb; Schmutz et al. 2010), mung bean (579 Mb; Kang et al. 2014), chickpea (~738 Mb; Varshney et al. 2013), pigeon pea (833.07 Mb; Varshney et al. 2011), common bean (587 Mb; Schmutz et al. 2014), cabbage (630 Mb; Liu et al. 2014a), Chinese cabbage (529 Mb; The Brassica rapa Genome Sequencing Project Consortium 2011), cucumber (367 Mb; Huang et al. 2009a), rapeseed (1130 Mb; Chalhoub et al. 2014), sugar beet (714–758 Mb; Dohm et al. 2014), strawberry (240 Mb; Shulaev et al. 2011), cranberry (470 Mb; Polashock et al. 2014), watermelon (~425 Mb; Guo et al. 2013a), melon (450 Mb; Gonzalez et al. 2010), tobacco (4500 Mb; Sierro et al. 2014), marijuana (~820 Mb; Van Bakel et al. 2011), hot pepper (3480 Mb; Kim et al. 2014), caster bean (320 Mb; Chan et al. 2010), camelina (785 Mb; Kagalem et al. 2014), robusta coffee (710 Mb; Denoeud et al. 2014), coca (430 Mb; Argout et al. 2011) and *Eragrostis tef* (772 Mb; Cannarozzi et al. 2014). Besides these agricultural crops, several other important crop genomes like papaya (372 Mb; Ming et al. 2008), banana (D'Hont et al. 2012), grape (475 Mb; The French-Italian Public Consortium for Grapevine Genome Characterization 2007), sweet orange (367 Mb; Xu et al. 2013a), clementine mandarin (367 Mb; Wu et al. 2014), peach (265 Mb; The International Peach Genome Initiative 2013), pear (527 Mb; Wu et al. 2013), Chinese plum (280 Mb; Zhang et al. 2012), date palm (671 Mb; Al-Dous et al. 2011), jujube (444 Mb; Liu et al. 2014b), oil palm (1800 Mb; Singh et al. 2013), eucalyptus (640 Mb; Myburg et al. 2011), poplar (485 Mb; Tuskan et al. 2006), moso bamboo (2075 Mb; Peng et al. 2013) and neem (364 Mb; Krishnan et al. 2012) were also sequences for further crop improvement and subsequent germplasm conservation.

10.6.2 Pangenome Construction

Pangenome construction is an approach to cover all the structural and functional genomic variants of a species or a crop unique to them. The pangenome of a species or crop represents its entire gene pool exhibiting all the useful genes, viz. core genes (present in all individuals) and dispensable genes (present in few individuals only). In plants, a pangenome of a species contains all useful genes related to plant architecture, root architecture, quality and nutritional enhancement, biotic and abiotic stress tolerance, etc. (Tettelin et al. 2005). Pangenome of few crops like soybean (Concibido et al. 2003), wheat (Huang et al. 2003), rice (Thalapati et al. 2012) and sorghum (Tao et al. 2017) has been constructed. Several strategies like comparative de novo, iterative assembly, map to pan, comparative reconstructed genomes, metagenome-like and pan-transcriptomic are available for the development of pangenome (Tao et al. 2019), but comparative de novo approach (Gordon et al. 2017), iterative assembly approach (Hurgobin et al. 2018) and the map-to-pan approach (Wang et al. 2018a) were declared the most promising approaches. Recently, it has been used in *Oryza sativa* (Schatz et al. 2014), *O. rufipogon* (Zhao et al. 2018), *Triticum aestivum* (Montenegro et al. 2017), *Zea mays* (Hirsch et al. 2014), *Glycine soja* (Li et al. 2014), *Brassica oleracea* (Golicz et al. 2016), *Brassica* *napus* (Hurgobin and Edwards 2017), *Brassica rapa* (Lin et al. 2014) and *Brachypodium distachyon* (Gordon et al. 2017).

10.7 Discovery of Genes Underlying Quantitative Traits

The important agronomic traits are genetically governed by few or many genes and hence are polygenic in terms of mode of inheritance. Since the last two decades, this goal has extensively been accomplished using linkage mapping of quantitative trait loci (QTLs) or QTL mapping developing inbreed lines of the desired crops. However, with advancement of DNA marker technology, next-generation genome sequencing techniques and strong computational support for statistical analysis, the focus is now turning towards the use of association mapping (Mackay and Powell 2007) as well. The genome-wide prediction models provide support to the association mapping to identify the genes with small effect on the desired traits in a representative training population that can be later identified for all meta-population of the crop (Desta and Ortiz 2014). In the crop or its germplasm resource with narrow genetic base, variation is induced through mutagenesis followed by the next-generation sequencing technology to find out the novel genetic variation associated with the superior trait (Jankowicz-Cieslak et al. 2017). The advanced technique of microbial biotechnology aided with DNA recombination, gene editing and gene coning tools supports insertion of desired gene sequence in specific plants, which can further lead to the development of genetically modified plants.

10.7.1 Association Mapping (AM)

QTL mapping and association mapping (AM) are dependent on the strength of statistical association between a genetic/DNA marker and trait of interest. Association mapping is a concept based on the principle that markers tightly linked to the trait of interest will remain stable over multiple generations of recombination. The presence of linkage disequilibrium (LD) is a prerequisite for AM (Stich et al. 2006). And, unlike QTL mapping, LD-based AM can be applied to a set of genotypes, ex situ conserved germplasm assemblage, elite germplasm bank and raised plantations. Genome-wide association study (GWAS) and candidate gene-based association study (CGAS) are mainly two approaches to finding out the gene associated (Gupta et al. 2014). The basic requirement for AM is confined to a population of the species of interest with known genetic structure and state of LD, a robust phenotyping of the desirable traits, high-resolution genotyping and model-based statistical analysis (Oraguzie et al. 2007). The first association mapping studies for quantitative traits in plants were carried out by Bar-Hen et al. (1995) using RAPD analysis, Virk et al. (1996) using isozymes markers and followed by 13 QTL identified with RFLP loci in 64 oat varieties including landraces by Beer et al. (1997). The first attempt was made for genome-wide association study (GWAS) in *Arabidopsis thaliana* by Aranzana et al. (2005). The association studies on the major crop species, i.e. maize, wheat, rice, soybean, sorghum, barley and cotton along with the model plant species *Arabidopsis*, helped to find out the genetic variation associated with many agronomic, physiological and reproductive traits (Ersoz et al. 2007; Sukumaran and Yu 2014; Ibrahim et al. 2020).

The association studies have now been carried out successfully in many crops like rice for agronomic traits (Huang et al. 2010), yield and its components (Agrama et al. 2007), starch quality (Bao et al. 2006), salinity tolerance (Patishtan et al. 2018), biofortification traits (Descalsota et al. 2018), gelatinization temperature, gel consistency and pericarp colour (Yang et al. 2018); wheat for flowering time (Rousset et al. 2011), kernel size and milling quality (Breseghello and Sorrells 2006), stem rust resistance (Yu et al. 2011) and seedling heat tolerance (Maulana et al. 2018); maize for drought tolerance (Lu et al. 2010), grain yield and flowering time (Zhang and Yuan 2019), seed set (Gao et al. 2019), kernel composition and starch pasting properties (Wilson et al. 2004), sweet taste (Tracy et al. 2006), carotenoid content (Harjes et al. 2008) and leaf blight (Kump et al. 2011); teosinte (*Zea mays* ssp. *parviglumis*) for multiple traits (Weber et al. 2008); sorghum for agronomic traits (Morris et al. 2012), biomass traits (Spindel et al. 2018) and drought tolerance (Spindel et al. 2018); barley for agronomic traits (Pasam et al. 2012), growth habit (Rostoks et al. 2006), flowering time (Stracke et al. 2009), salinity tolerance (Saade et al. 2016), days to heading, leaf rust, yellow dwarf virus, rachilla hair length and lodicule size (Kraakman et al. 2006) and winter hardiness (Von Zitzewitz et al. 2011); oat for agronomic and kernel quality traits (Achleitner et al. 2008); foxtail millet for agronomic traits (Jia et al. 2013); pearl millet for flowering time (Saıdou et al. 2009); common bean for plant architecture, lodging and productivity (Resende et al. 2018); soybean for Fe deficiency and chlorosis (Wang et al. 2008); rapeseed for branch number (He et al. 2017) and seed oil quality (Zou et al. 2010); peanut for seed quality traits (Wang et al. 2011); cotton for plant architecture (Su et al. 2018), yield components (Liu et al. 2018), fibre quality (Abdurakhmonov et al. 2008), drought tolerance (Hou et al. 2018), salinity tolerance (Sun et al. 2018), protein, oil and fatty acids (Du et al. 2018); canola for leaf traits, flowering time and phytate content (Zhao et al. 2007) and oil content (Zou et al. 2010); sugarcane for disease resistance (Wei et al. 2006); potato for late blight resistance (Malosetti et al. 2007); sugar beet for agronomic traits (Wurschum et al. 2011), sugar content and yield (Stich et al. 2008); alfalfa for biomass yield and stem composition (Li et al. 2011); perennial ryegrass for flowing time and water-soluble carbohydrate (Skot et al. 2007); and switch grass for heading and anthesis (Taylor et al. 2018).

10.7.2 Genome-Wide Prediction (GWP)

Advanced to the QTL mapping and association mapping, genome-wide prediction (GWP) or genome-wide selection (GWS) which is based on the simultaneous selection for a large number of markers covering the entire genome helps to estimate the genomic estimated breeding values of the selected parents for the desired trait (Saini et al. 2020). To estimate the breeding value based on genomic characterization only, a training population is assessed with high-resolution genome sequencing and robust phenotyping. With the help of GWP, genomic selection can be performed in a testing population without phenotyping for few cycles of the generations (Crossa et al. 2017). Using this technique efficiently reduces the cycle length with enhanced genetic gain and the selection response per unit time without phenotyping. A number of studies for dissection of complex traits, viz. grain yield, quality, biotic and abiotic stresses, etc., through genomic selection have been carried out for several crops like rice (Grenier et al. 2015; Spindel et al. 2015), wheat (Poland et al. 2012; Rutkoski et al. 2014; Pierre et al. 2016), maize (Bernardo and Yu 2007; Guo et al. 2013b) and cassava (Oliveira et al. 2012). In oat (*Avena sativa*), the genomic selection was found to be more efficient than phenotypic selection through best linear unbiased prediction (BLUP) of β-glucan content (Asoro et al. 2013). Massman et al. (2013) performed genomic selection on *Zea mays* for yield and stover quality traits. This work was the first report on crops comparing genome-wide selection with marker-assisted recurrent selection of superior genotype. Onogi et al. (2015) applied genome-wide markers on Asian rice (*Oryza sativa*) and found the genomic-BLUP (GBLUP) most accurate among eight other models for prediction of breeding value analysing a dataset of 110 cultivars. For accurate prediction of breeding value and acceleration of genetic gain in breeding using genomic data, few genomic selection models have been applied in crops. Spindel et al. (2016) described a genomic selection model in which, they could be able to predict the breeding value for growth- and yield-related traits in a breeding population of tropical rice, through de novo genome-wide association study, with the help of SNPs.

10.8 Genome Manipulation Through Biotechnological Approaches

10.8.1 QTL/Gene Cloning and Genetic Modification

QTL is a central theme for genetic improvement of targeted trait and restoration of wild germplasm into the domesticated one. QTL genes are identified after fine mapping and cloning of candidate genes. The QTL regions are normally extended to several centimorgans on genetic map and might contain a large number of genes (Varshney et al. 2014). Therefore, it is difficult to identify the specific locus responsible for the traits, and QTL should be refined known as fine mapping (Jaganathan et al. 2020). The major works on crop related to gene/QTL cloning cover gene addition/insertion and gene subtraction through genetic engineering techniques. With the advent of NGS technique, the mutation mapping techniques like *MutMap*, *MutMap-Gap* and *MutChromSeq* are used to identify genomic regions governing important agronomic traits (Kumawat et al. 2019). Target gene/QTL cloning and even fine mapping have been attempted in several crops, for example, rice for plant height (Huang et al. 2009b), tillering and panicle branching (Yu et al. 2017), grain weight, grain length and grain width (Bhatia et al. 2018), grain number and heading date (Ashikari et al. 2005), rooting depth (Uga et al. 2013), leaf width and aluminium tolerance (Spindel et al. 2013); wheat for dormancy (Barrero et al. 2015), grain weight (Roder et al. 2008), grain protein content (Trick et al. 2012) and powdery mildew resistance (Xie et al. 2017); maize for flowering date (Salvi et al. 2007), glume architecture (Wang et al. 2005), leaf angle (Zhang et al. 2014), root initiation (Taramino et al. 2007), streak virus resistance (Nair et al. 2015), tassel and ear architecture (Chen et al. 2014); barley for awn length (Liller et al. 2017), frost resistance (Francia et al. 2007), grain threshability (Schmalenbach et al. 2011) and boron tolerance (Sutton et al. 2007); sorghum for grain weight (Han et al. 2015) and seed dormancy (Li et al. 2016); soybean for seed number and leaflet shape (Jeong et al. 2012), phytophthora resistance (Li et al. 2016) and root knot nematode resistance (Xu et al. 2013b); common bean for angular leaf spot resistance (Keller et al. 2015); chickpea for ascochyta blight (Deokar et al. 2019); tomato for fruit weight (Frary et al. 2000) and shape (Sun et al. 2015), locule number (Munos et al. 2011) and yellow leaf curl virus resistance (Yang et al. 2014).

Genetic transformation using transgenic techniques can directly improve the productivity in terms of quantity and quality of a crops than traditional one through managing stress created in crops (including disease-resistant, insect-resistant, cold-resistant and herbicide-resistant) (Fang et al. 2016). The first genetically modified crop was tobacco and commercially cultivated genetically modified whole food crop was tomato (Martineau 2001). Then after, various transgenic crops were genetically engineered, which have the characteristics of herbicide tolerance, drought and salinity tolerance, enhancing photosynthesis, nitrogen and water use efficiency, phytoremediation, biofortification and resistance against insect-pest and pathogens, for example, rice for trait stacking (Cantos et al. 2014) and high amylose content (Sun et al. 2017); maize for phytate reduction (Shukla et al. 2009) and male sterility (Djukanovic et al. 2013); alfalfa for low lignin content (Weeks et al. 2008); potato for low acrylamide content (Rommens et al. 2008) and late blight resistance (Haverkort et al. 2009); wheat for baking quality (Gadaleta et al. 2008) and resistance to powdery mildew (Qiu 2014); soybean for improved oil quality (Haun et al. 2014); and sugarcane for enhanced cell wall composition (Hyeong et al. 2012). Out of these target traits, genetic modification for herbicide resistance was the important one developed in maize, soybean, sugar beet, cotton, rice, oilseed rape and coffee (Nalluri and Karri 2020).

10.8.2 Genome Editing (GE)

With the advent of genome editing tools, a revolution of the field of crop science has been seen by manipulating the targeted QTLs or genes in plant genome. It is emerging and a potential editing tool for both plant gene functional analyses and crop improvement (Bharat et al. 2020). Through the advanced next-generation sequencing techniques, millions of mutations can be detected in a very short period of time and introduced beneficial mutation at genomic level identifying key regulatory genes of superior traits (Jankowicz-Cieslak et al. 2017). Initially, zinc finger nuclease (ZFN) and transcription activator like effect or nuclease (TALEN) have appeared as engineered nucleases (Osakabe and Osakabe 2015). Recently, the clustered regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated protein 9 nuclease (Cas9) has been developed as a more simple, flexible engineered nuclease and the most widely applied genome editing tool (Wada et al. 2020). After proof-of-concept demonstrations in agricultural crops involving the primary CRISPR/Cas9 module, several modified Cas9 cassettes like *Nmcas9*, *Sacas9* and *Stcas9* have been used for improving target specificity and reducing off-target cleavage (Jaganathan et al. 2018). The CRISPR/Cas9 technique has been used to perform site-specific mutations in several plant species (Chaudhary et al. 2019). The CRISPR/Cas9 technique has successfully been applied for abiotic and biotic stress management and for improving productivity of various crops like rice (Zhou et al. 2015; Li et al. 2017a; Wang et al. 2020), wheat (Kim et al. 2018; Wang et al. 2018b; Zhang et al. 2019), maize (Li et al. 2017b), tomato (Ron et al. 2014; Ito et al. 2015; Pan et al. 2016; Klap et al. 2017), soybean (Haun et al. 2014; Tang et al. 2016), citrus (Jia and Wang 2014; Zhang et al. 2017), soybean (Cai et al. 2018), potato (Andersson et al. 2017), watermelon (Tian et al. 2017), grapes (Nakajima et al. 2017), rapeseed (Li et al. 2018), cotton (Chen et al. 2017; Janga et al. 2017), alfalfa (Meng et al. 2017; Gao et al. 2018), barley (Kapusi et al. 2017), cassava (Odipio et al. 2017), ipomoea (Watanabe et al. 2018), legumes (Wang et al. 2017), banana (Kaur et al. 2018), carrot (Klimek-Chodacka et al. 2018), cacao (Fister et al. 2018), improving oil quality of soybean (Haun et al. 2014), salvia (Zhou et al. 2018), lettuce (Bertier et al. 2018) and many more crops yet to be reported by upcoming years. Using GE technique, the desired mutants in various crops have been reported so far, and out of these, several may be utilized as pre-breeding germplasm material after confirming characterization for further breeding pipeline of crop varietal improvement.

DNA base editing is the newest evolution of CRISPR-based technologies, which can directly install single base change (point mutations) in cellular DNA without inducing a double-stranded DNA break (Kantor et al. 2020). It has emerged now as an alternative tool to homology-directed repair (HDR)-mediated replacement, facilitating precise editing of plant genome by converting one single base to another in a programmable manner without a double-stranded break and a donor repair template (Bharat et al. 2020). Given that achievement of precise gene editing through CRISPR/Cas-mediated HDR in plants remains neither routine nor feasible in many laboratories, base editing is becoming an efficient technology for converting one target nucleotide into another without DSBs and DRT (Hess et al. 2017). The widely used methods of base editing in plants are cytidine base editor (CBE) and adenine base editor (ABE), and these are frequently used to edit various traits in staple agriculture, viz. rice for higher yield (Hua et al. 2019), improved nitrogen use efficiency (Zong et al. 2017) and blast resistance (Ren et al. 2018), tomato for herbicide resistance (Shimatani et al. 2017), potato for herbicide resistance (Veillet et al. 2019) and rapeseed for herbicide resistance (Kang et al. 2018). Anzalone et al. (2019) recently developed a new and more precise genome editing technique, called prime editing. More recently, prime editing was applied to two plant species, rice (Tang et al. 2020) and wheat (Yan et al. 2020), indicating that this technology holds tremendous potential for genome editing applications in plants just to treat the several problems of creating resistance against insect-pest and diseases.

10.9 Conclusions and Future Perspectives

At present, agricultural production has relied on extensive use of chemical fertilizers and pesticides for increasing dosage with residual effects, while soil and water pollution are becoming much severer and, thus, the quality of agricultural products continues to decline with loss of crop genetic diversity. The nutritious food provides the first defence mechanism to combat against such diseases, and agrobiodiversity is the prime source that has desirable genes conferring to high nutrition content and other biotic and abiotic stress resistance. With the advancement of science especially in the field of plant breeding and biotechnology, traditional plant breeding to mutation breeding to recombinant DNA technology to molecular breeding and finally to precise genome editing made the process easier and efficient for the crop improvement followed by germplasm conservation and restoration of wild genes into cultivated one. There are many promising examples where a plant genetic resource along with modern-era technology results in increases in crop quality and yields not only in major cereals but also in neglected and underutilized agricultural and allied crops.

In order to respond to the rapid loss of agricultural biodiversity, climate change and the growing demands for food, fuel, fodder and employment from agricultural sector, the following activities need immediate attention: (a) strengthen network collaboration between national and international research institutions, such as the CGIAR centres in the region; jointly identify and undertake PGR-related priorities and activities; (b) implement biotechnological tools for underutilized and neglected crops in the region such as minor millets and legumes to enhance their productivity followed by germplasm conservation; (c) promote the use of new methodologies and techniques for conservation and utilization of indigenous large gene pools in view of better gene bank management; (d) develop and test methodologies for promoting and developing pre-breeding germplasm enhancement for broadening the genetic base of breeding materials through utilization and manipulation of wild and rare alleles; (e) encourage capacity development and establishment of facilities for undertaking molecular and biochemical characterization of promising germplasm resources (e.g. DNA fingerprinting, association and fine mapping, genetic modification, genome editing, etc.); and (f) empower traditional maintainers in the region for in situ conservation on farm to enhance conservation of landraces and wild relatives of cultivated crops. Different biotechnologies tools employed today can be very useful for conservation, management and restoration of crop genetic resources. At last, the natural genetic variation present in existing crop germplasm should be explored through molecular approaches like sequencing techniques and pangenome construction for their efficient use for agro-diversity utilization.

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Adapting Land Degradation and Enhancing Ethnic Livelihood Security Through Fruit Production: Evidence from Hilly Areas of Bangladesh

11

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Abstract

The unique agro-climatic condition of Chittagong Hill Tract (CHT) in Bangladesh allows a wide range of fruit production that plays a vital role in reducing land degradation caused by shifting cultivation and improving the socio-economic sphere of the hilly people. Therefore, the study was conducted to explore the fruit production in the Rangamati district of CHT and its contribution to the earnings of the local ethnic people. The study was descriptive survey research, carried out through data collection from randomly selected 120 respondents utilizing the in-person interview technique. Findings revealed that jackfruit, pineapple, banana, and mango were the prominent major fruits while pomelo, lemon, honeydew melon, and watermelon were the most popular minor fruits of the study area that contribute a significant production of fruits every year. Additional earnings, nutrition supply, and controlling of land degradation were the key attracting reasons behind fruit cultivation, but impediments like lack of good planting material and poor communication network mainly hampered fruit production and marketing. However, fruit production was the

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second largest (16%) agricultural income source of the respondents; a substantial portion (90%) of it came from major fruits. Most of the respondents (56.7%) benefitted up to 15% of their family income from fruits, contributing largely to their sound family income (BDT 217,000). The study findings showed that respondents with larger farm sizes and more favorable attitudes towards fruit cultivation earned better than others. Overall, the study outcomes offer new empirical evidence on the economic importance of fruit production in hilly areas that the policymakers may use to develop plans on promoting its cultivation not only for the economic outcome but also for meeting the nutrition demand of the country.

Keywords

Land degradation · Adaptation · Major fruits · Minor fruits · Ethnic livelihood security · Bangladesh

11.1 Introduction

Bangladesh is blessed with a diverse range of tropical and sub-tropical fruits. Around 70 different kinds of fruits grow in different parts of Bangladesh (Islam et al. 2013; BBS 2013). Fruit generates 10% of income for the national economy and covers 1–2% of total cultivable land in Bangladesh (Sampa et al. 2019). Fruits are vital for people in this country for income, supplemental food, nutritionally balanced diets, and protection from diseases. Some of the species have medicinal values, while others are used for fuelwood, timber, and livestock feedstuff (Rahman et al. 2017; Sajib et al. 2014; Haque et al. 2009). Though the country is nearly self-sufficient in food grain production, it still lags behind in meeting the nutritional requirements of its people (Rahman and Rahman 2014). According to an FAO report, Bangladesh's per capita daily fruit intake was 75.68 g in 2017, compared to the WHO-recommended minimum requirement of 200 g/capita (FAO 2017). To ensure mass nutrition, researchers are working to enhance yield by developing improved varieties, quality planting materials, and appropriate cultural management of fruit crops (Rahman and Rahman 2014).

The Chittagong Hill Tract (CHT) is one of the major fruit-producing regions of Bangladesh (BBS 2015). The suitable climatic conditions of CHT allow for a wide variety and diversity of fruit production in this region. High-value fruits like bananas, mango, jackfruit, pineapple, papaya, litchi, lemons, and guava abundantly grow on the hill slopes of the area (Dewan et al. 2015). Generally, major fruits are commercially cultivated on a wide scale, while most of the minor fruits are occasionally eaten throughout the fruiting season, which have less market demand and are grown on a limited scale (Rahman and Rahman 2014; Pasha and Uddin 2019). Among all fruits, the banana is dominant in the region, mainly cultivated in shifting cultivation with other crops. More than one-fourth of households cultivate bananas in their farming plots and homestead gardens (Khan et al. 2012) because of their higher yield and cash income. However, jackfruit, pineapple, and papaya also contribute significantly to the hill people's household economy (Ahammad and Stacey 2016).

Traditional land-use systems (like shifting cultivation) were once a source of varied foods for local people in CHT. But these systems hardly meet the food demands of growing populations. Furthermore, they have a negative impact on hill ecosystems, causing forest destruction, decreased productivity, and soil erosion. Thus, establishing fruit species in place of traditional shifting cultivation may lessen land degradation (i.e., soil erosion) in the long term. Over the last several decades, CHT has seen a boom in the expansion of fruit production areas. At least 30% of the total land mass of this region is currently covered with different fruit plantations (Bala et al. 2013; Ahammad and Stacey 2016). Besides nutritional advantages, suitable agro-climatic features, proper land utilization, and a good source of income are the competing motives for why fruit production is expanding in hilly areas (Hossain et al. 2017).

The primary livelihood of the ethnic people of the CHT is agriculture-dependent. More than half of the annual net income of all CHT families comes from different agricultural sources. They are reliant on at least one agricultural activity for food and cash income. Among the ethnic groups, the Marma, Khumi, Bawm, and Mro people secure more than 67% of their net annual family earnings from agriculture-related activities, including fruit cultivation. As such, fruits offer both subsistence needs and profits for both ethnic and Bengali communities and play a unique role in the socioeconomic sphere of the hill people by improving their income status (Hossain et al. 2020, 2017; UNDP 2009; Rasul and Tripura 2016).

In recent years, the Rangamati district of CHT has seen a silent revolution in fruit production. Commercial fruit cultivation on the hill slopes makes people economically empowered and protects them from soil degradation. This area can supply fruits to meet a significant amount of the nationwide fruit demand and contribute to the domestic economy. But there is a dearth of research work about fruit production in the CHT, especially in Rangamati. Though several studies by Hossain et al. (2017), Rahman et al. (2017), Abdullah et al. (2020a), and Abdullah et al. (2020b) investigated fruit production activities in CHTs, they did not explore their contribution to the income of the tribes. In the light of the above situations, a study was performed in Rangamati to (1) explore the comparative performance of major and minor fruit in the study area, (2) assess the perceived reason of fruit production, (3) measure the contribution of fruit production to the livelihood of local ethnic communities, and (4) identify the major obstacles of fruit production. The analytical view of the study would help to promote the future establishment of fruit in the CHT region and its contribution to the national economy.

11.2 Methodology

11.2.1 Description of the Study Area

The study was accomplished in Rangamati district of Bangladesh. Rangamati is located between the latitudes of 22°27′ and 23°44′ north and the longitudes of 91°56′ and 92°33′ east (Fig. 11.1). It is bordered by India on the north and east, Bandarban district on the south, and Khagrachari and Chittagong districts on the west. The Rangamati district is the country's largest in terms of area, with 6116.19 km^2 (Rangamati Hill District Council 2011). The district has a total of 508,182 populations, with males accounting for 54% and females for 46%. The average literacy rate is 43.60%, with males accounting for 51.47% and females for 34.21% of the population. Agriculture accounts for 59.08% of total income, followed by non-agricultural 6.06%, industry 0.46%, commerce 10.70%, transportation and communication 1.06%, service 13.48%, construction 0.83%, religious service 0.19%, rent and remittance 0.73%, and others 7.41% (Bangladesh Bureau of Statistics 2012). The study area is highly susceptible to land degradation causes by landslides as the region is dominated by tertiary and quaternary sediments that have been folded, faulted, and elevated before being deeply dissected by rivers and streams. The area has Dhihing, Dupitila, Girujan clay, Bhuban, Bokabil, and Tipam sandstone formations. Because of the modification of sandstone and shale in their geology, the Bhuban and Bokabil formations have the most sensitivity to landslides (Haque et al. 2018). Because the bedrock and soil structure of these

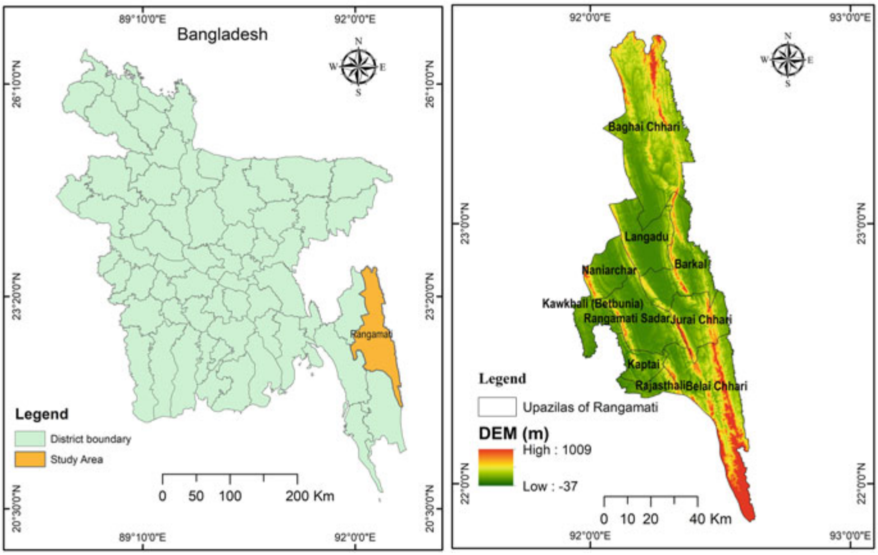

Fig. 11.1 Study area map

hills are unstable, the areas are prone to landslides (Islam et al. 2017a, b). Bangladesh is located in the tropical monsoon area, and its climate is characterized by high temperatures, frequent rainfall, often severe humidity, and seasonal changes (Banglapedia 2014). Rangamati is one of the country's attractive tourist places because of harboring Kaptai Lake, Sajek Valley, Chakma Rajbari, Buddhist Vihara at Rajban, Hanging Bridge, Shuvolong Water Fall, Furaman Hill, Tribal Cultural Institute and Museum, etc. Rangamati has a tropical monsoon climate, with yearly average temperatures ranging from 36.5 to 12.5 °C, and annual rainfall of 2673 mm with a humidity level of 71.6% (Bangladesh Bureau of Statistics 2012).

11.2.2 Framework of the Study

The ethnic people of the greater CHT were practicing shifting cultivation for a long time. However, age-old traditional shifting cultivation was degrading the lands and failed to supply required foods for the people, and leads to a livelihood vulnerability. The Department of Agricultural Extension and other relevant organizations identified the drawbacks of traditional shifting cultivation and found that this sort of practice is not sustainable in terms of environmental development, and food and livelihood security. In the last decade, there have been tremendous efforts to motivate the ethnic people and develop their knowledge and skill on fruit production as an alternate land use practice. This explored the perceived reasons (environmental, economic, and socio-cultural) that motivated the hill people to move from shifting cultivation to multipurpose fruit production practices. Besides, sustainability of the fruit production system was measured by asking the pattern of practices, i.e., selection of planting material, planting system, watering and weeding system, and nutrient and disease-pest management system among other practices, they followed and benefit, i.e., income, family consumption, nutritious and secured food supply, among other benefits, they received (Fig. 11.2).

11.2.3 Population and Sampling

An in-person interview was performed with the respondents through a semi-structured interview schedule to obtain relevant data. All the ethnic people involved in fruit cultivation of the selected areas were the study's target population. From the target population, 120 ethnic household heads were selected randomly.

11.2.4 Assessing Reasons of Fruit Production

Eight reasons behind fruit production were identified and ranked. Based on their extent of importance, a Reason Index (RI) was calculated using the following formula (Saha et al. 2021):

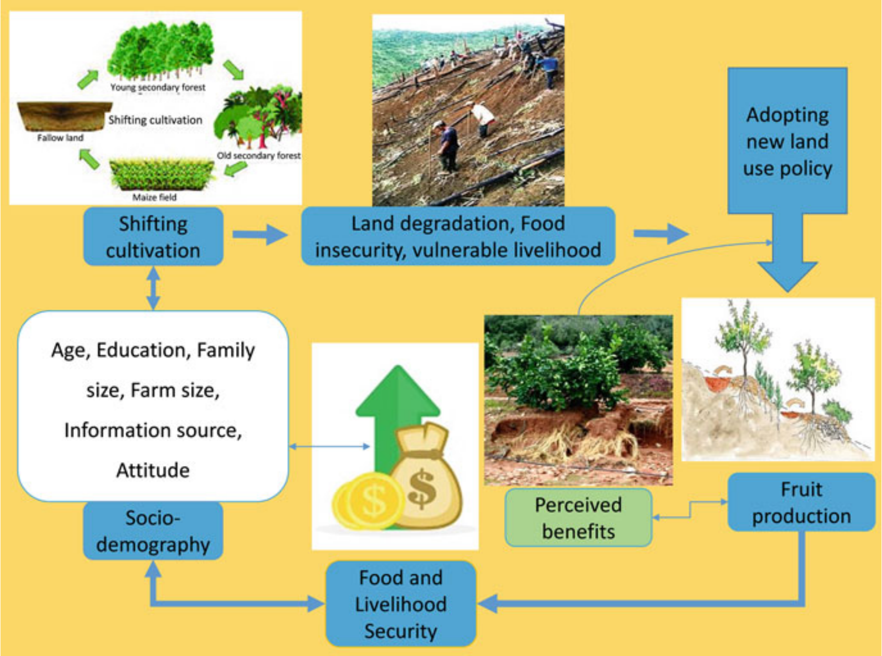

Fig. 11.2 Conceptual framework of the study

$$\text{Reason index(RI)} = \text{SDA} \times 1 + \text{DA} \times 2 + \text{UND} \times 3 + \text{AG} \times 4 + \text{SAG} \times 5 \tag{11.1}$$

where:

SDA = Strongly Disagree, DA = Disagree, UND = Undecided, AG = Agree, SAG = Strongly Agree

11.2.5 Estimation of the Relative Contribution of Fruits to Family Income

The percent contribution of fruits was calculated in the following way (Hoque et al. 2018),

$$A = (B/C)100 \tag{11.2}$$

where:

A = Percent contribution of fruits to family income
B = Income from fruits
C = Total family income

11.2.6 Problem Confrontation Index

Thirteen problems were selected through focus group discussion (FGD) and arranged to investigate the difficulties faced by the fruit growers. Based on their extent of problem facing, a Problem Confrontation Index (PCI) was calculated using the following formula (Hoque and Haque 2011):

$$\text{Problem Confrontation Index(PCI)} = \text{LP} \times 1 + \text{MP} \times 2 + \text{HP} \times 3 \qquad (11.3)$$

where:

LP = Low Problem
MP = Moderate Problem
HP = High Problem

Statistical Package for Social Science (SPSS) was used to analyze data, and simple statistics like percent, frequency count, mean, and standard deviations were employed. Coefficients of correlations (r) were computed to explore the relationships between selected characteristics of the respondents and their income from fruit production, and a 0.01% level of probability was used as a basis for exploring the association between the dependent and independent variables.

11.2.7 Data Collection and Statistical Analysis

Systematic fieldwork is an important aspect of socio-economic survey research. In this context, an in-depth survey and necessary efforts were given to make the fieldwork successful and realistic. Data were collected by the researchers through interviewing techniques using an interview schedule. Initially, a draft interview schedule was created and pre-tested with a few participants. To meet the study's objectives, the draft interview schedule was amended based on the results of the pre-test by adding or removing specific elements. The researcher took the utmost care to establish rapport with the respondents so that they did not feel hesitant or hostile to furnish proper responses to the questions of the interview schedule. The questions were explained and clarified whenever any respondent feel difficulty in understanding them properly. The fact that ethnic groups in some locations cannot understand Bengali or English was particularly concerning. As a result, we sought the assistance of local extension experts to ensure that respondents comprehended the questions and responded appropriately.

Collected data were coded, complied with, and tabulated for processing and analysis in accordance with the objectives of the study. The SPSS/PC+ computer program was used to perform the data analysis. For clarity of understanding, tables and graphs were used for the presentation of results. Excel, statistical software was also used for the graphical presentation of data. Various statistical measures such as range, mean, percentage, and standard deviation were used in categorizing and describing the selected personal characteristics of the respondents. Coefficients of correlations (*r*) were computed to explore the relationships between selected characteristics of the respondents and their income from fruits production.

11.3 Results and Discussions

11.3.1 Sociodemographic Characteristics of the Respondents

All of the respondents in the study were ethnic people. Data presented in Table 11.1 show that most percentage (68.4%) of the respondents were middle-aged with an average of 37.30 years old which indicated the good working capability of the respondents. Hasan et al. (2021) observed almost analogous findings in their study where respondents were on average 40 years old, and Hasan et al. (2017) noticed that younger respondents maintained high social contact and possessed a broader viewpoint than older people. The highest portion (41.7%) of the respondents received

Table 11.1 Sociodemographic characteristics of the respondents

Characteristics	Categories	Respondents (%)
Age (years)	Young (≤28)	20.8
	Middle (29–54)	68.4
	Old (>54)	10.8
Education (years)	Primary (1–5)	30.0
	Secondary (5–10)	41.7
	Higher secondary (>10)	28.3
Family size (number)	Small (≤4)	33.3
	Medium (5–6)	55.9
	Large (>6)	10.8
Farm size (Ha)	Small (0.02–1)	5.0
	Medium (1.01–3.03)	89.2
	Large (>3.03)	5.8
Frequency of contact with information sources	Low (≤18)	18.4
	Moderate (19–29)	74.1
	High (>29)	7.5
Attitude towards fruit production	Unfavorable (≤30)	14.2
	Moderately favorable (31–37)	77.5
	Highly favorable (>37)	8.3

secondary level education. The number of family members ranged from 3 to 7 with an average of 4.98, which was higher than the national average (4.2) (BBS 2018). According to Adane et al. (2019) fruit farming is labor-intensive activities requiring more labor, so the family with more members can fill the labor shortage and increase the income from fruit. The majority of the respondents (95%) owned medium to large farm size. Most percentage of them moderately contacted with information sources (74.1%) and exhibited moderate to highly favorable attitudes towards fruit cultivation (85.8%).

11.3.2 Status of Fruit Cultivation

11.3.2.1 Major Fruits

The high market demand of major fruits encouraged most of the respondents to engage in major fruits production on a large scale. In Fig. 11.3, the major fruits have been arranged according to percent respondents cultivated where jackfruit was the most popular (65%) major fruit that ranked first followed by pineapple (second), banana (third), and mango (fourth). According to the study of Hossain et al. (2017), banana, pineapple, jackfruit, and mango possessed the most area of fruit cultivation and highly produced fruits in hilly areas of Bangladesh. In another study, Rahman et al. (2017) identified mango and litchi as the dominant fruit species in Khagrachari district of CHT.

Low production cost and water requirement made jackfruit as the most cultivated fruit. Following jackfruit, pineapple was the second most popular crop. The brown acidic hilly soil of Rangamati was very suitable for pineapple cultivation, and it was small in size and very sweet to taste. Banana was another popular crop in the study

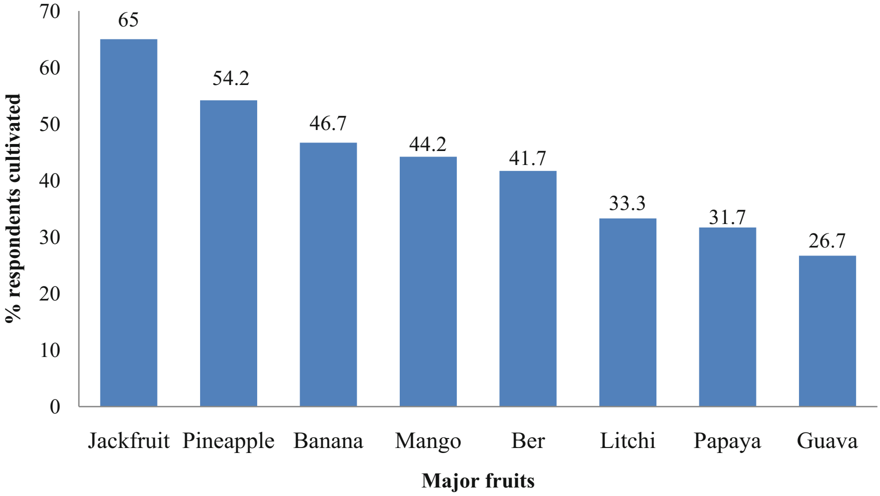

Fig. 11.3 Distribution of major fruits according to percent respondents cultivated

areas which was not only important for fruit but also for mocha (young banana inflorescence) and kolagach (the inner part of banana tree). Mango was a widely grown fruit crop, and the Amrapali variety of mango gained popularity among the growers for its countrywide demand.

Shifting cultivation is widely practiced in hilly areas but considered harmful to the environment in the long run. So, the thought of modified shifting agriculture with intensive major fruit cultivation is emerging which can prevent soil erosion, sustain production, and ensure food security. Different govt. agencies and NGOs have already started horticulture-based (especially fruits) land use in the CHT for soil conservation and forest restoration (Ahammad and Stacey 2016).

11.3.2.2 Minor Fruits

Minor fruits are generally less demandable than major fruits and grown on a small scale. Figure 11.4 shows the distribution of minor fruits according to percent respondents cultivated. Among all, pomelo was cultivated by the majority (45.8%) of the respondents that ranked first followed by lemon (second), honeydew melon (third), and water melon (fourth).

Acidic soil of hilly areas was very congenial to citrus fruit production like pomelo and lemon. Thus, these fruits were grown on a large scale in comparison to other minor fruits of Rangamati. Honeydew melon is also known as honey melon, which is a cultivar group of the muskmelon. It is like bangi (one type of muskmelon) but doesn’t crack after maturation. It is an integral part of the local ethnic carnival Baisabi or Biju (prime traditional festival of ethnic people of CHT). Among these fruits, the orange orchard was only found in *Sajek* of Baghaichari Upazilla.

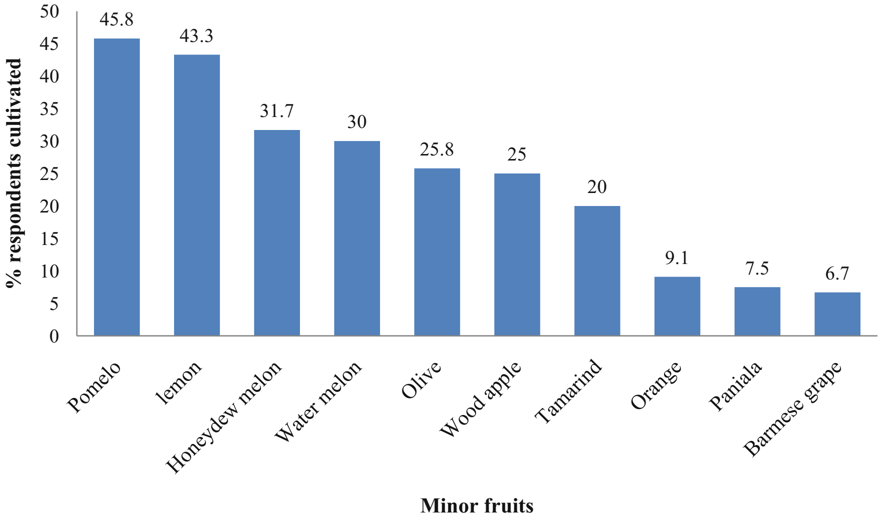

Fig. 11.4 Distribution of minor fruits according to percent respondents cultivated

Minor fruits are appreciated for their high nutritional status and medicinal value. They are rich in bioactive compounds, fiber, and phyto-chemicals. They are considered healthy foods and effective against diseases associated with aging, caused by toxic oxygen radicals. Despite these advantages, their export status is not satisfactory. But there is enough scope for increasing export of minor fruits that will not only offer more income to the ethnic people but also provide health benefits to the world consumers (Rahman and Rahman 2014).

11.3.2.3 Locally Produced Underutilized Minor Fruits

Rahim et al. (2011) identified 46 underutilized minor fruits from different parts of Bangladesh. These fruits are wildly grown and not commercially cultivated due to less demand and market price. Being wild, they are pest resistant and grow without management practices. These fruits are a potential source of nutrients and can help to meet the nutritional demand of the people. Though these fruits are part of ethnic peoples' culture, lack of planting material restricts their expansion. As a result, most of the species are on the verge of extinction. Abdullah et al. (2020a) opined forest destruction, mono-cropping, and unsustainable land-use changes accelerate the disappearing trend of these species from natural habitats. Saha and Sundriyal (2012) suggested sustainable extraction of these kinds of fruits or other forest products for forest conservation and biodiversity protection. A list of identified underutilized minor fruits has been presented in Table 11.2.

A total of 11 underutilized minor fruit species were identified where Moraceae was the dominant family. The scientific details of the three fruits have not been found. In the study sites, identified underutilized minor fruits were mainly wildly grown. The locals were not concerned about conserving these diminishing fruit species, as they collected those without following a scientific manner. As these were less known and not so popular in the local market, these hardly contributed to their income. But different findings were reported by Mahapatra and Panda (2012), where wild fruits had a significant contribution towards the livelihood of indigenous tribal of eastern India.

11.3.3 Perceived Reasons for Fruit Production

The rank order of reasons for fruit production has been shown in Table 11.3. This table shows that additional income from fruit cultivation was the top reason (ranked first) for fruit cultivation followed by the supply of nutrition (second), proper land utilization and control of land degradation (third), and ensuring food security (fourth).

Most of the respondents were involved in agricultural practices. They hardly had any other options to engage in business and services as they lived in a remote area. So, apart from cereal crop production in jhum, fruit cultivation added additional income to their family. It ultimately helped to improve their livelihood status by eliminating poverty. Furthermore, fruit is a good food and source of nutrients. Hence, fruit helped to ensure food security in the hilly areas and prevented suffering

Table 11.2 List of some locally produced underutilized minor fruits

Local name	Bangla name	English name	Scientific name	Family	Features
Gutgutte	Gutgutia	–	–	–	Fruit is light green and very sour
Roktogulo or Roskogulo	–	–	–	–	Fruit is deep red
Sorbekgulo	Dumur	Fig	*Ficus* sp.	Moraceae	Fruit contains numerous seed, becomes yellow to red when it ripens
Jogonagulo	Dumur	Fig	*Ficus* sp.	Moraceae	Fruit contains numerous seed, becomes yellow to red when it ripens
Prejam	–	–	–	–	Fruit is small in shape, very sour, becomes red when it ripens
Ho gulo	Kau	Cowa	*Garcinia cowa*	Clusiaceae	The fruit becomes yellow when ripens
Dembol	Daophal	False mangosteen	*Garcinia xanthochymus*	Clusiaceae	Yellow-colored fruit and very sour
Bottagulo	Dewoa	Monkey jack	*Artocarpus lacucha*	Moraceae	Yellow-colored fruit, jackfruit like inner part
O fol	Tut fol	Mulberry	*Morus indica*	Moraceae	Multiple fruit, 2–3 cm long, becomes red to black when ripens, sweet in taste
Surjomukhi hola	Surjomukhi kola	Sunflower banana	*Musa* sp.	Musaceae	Fruit becomes vermillion red when ripens
Badamphogona	Cashew apel	Cashew apple	*Anacardium occidentale*	Anacardiaceae	Light reddish to yellow fruit

Table 11.3 Rank order of reasons of fruit production

Reasons	Reason index	Rank
Earn more income	567	First
Supply nutrition for good health	556	Second
Proper utilization of land and control land degradation	518	Third
Ensure food security	503	Fourth
Increases employment opportunity	491	Fifth
Poverty reduction	482	Sixth
Protection of biodiversity	472	Seventh
Medicinal values	406	Eighth

Table 11.4 Distribution of respondents according to their annual income

	Respondents		
Categories	Number	Percent	Mean
Up to BDT 100,000	3	2.5	217,000
BDT 100,001–200,000	68	56.7	
More than BDT 200,000	49	40.8	
Total	120	100	

from malnutrition. According to Shaheb et al. (2014), farmers in Bangladesh prioritize additional income generation and nutrient supply for homestead fruits and vegetable production. It permits farmers with direct access to necessary nutrients that may not be readily accessible or within their financial reach. They added that this additional earning is mainly utilized to procure supplementary food items and leads to diversification of the family diet.

11.3.4 Contribution of Fruit Production to Family Income

11.3.4.1 Annual Family Income

Fruits contribute significantly to the economy of Bangladesh. The respondents in the study area cultivated fruit for household consumption, direct cash income, and land utilization. The annual family income of the respondents ranged from BDT 86,340 to BDT 562,000 with an average of BDT 217,000. Findings presented in Table 11.4 shows that the highest proportion (56.7%) of the respondents belonged to BDT 100,001–200,000 income category followed by more than BDT 200,000 income category (40.8%).

It is well known that the higher is the income of a family, the greater the control over the society by that family. The average income of the respondents (BDT 217,000) of the study areas was much higher than the national average (BDT 159,035) (BBS 2016). Fruit cultivation was one of the key reasons behind this economic solvency. Moreover, ethnic people were no longer solely dependent on agriculture for their livelihood. With time, they were changing their traditional agriculture-based lifestyle, shifting to urban areas and engaging in non-farm activities for sufficient wages. Consequently, a significant portion of them engaged in different services and business activities. And these non-farm earnings contributed significantly to the average income of the respondents. The higher annual income allowed them to invest more in farming operations.

11.3.4.2 Sector-Wise Annual Family Income

Though agriculture was once the primary occupation of most of the respondents, they were shifting towards non-farm activities over the recent years. So, they earned their livelihood from different sectors as presented in Fig. 11.5. This figure exhibits that a substantial portion (41%) of the respondents' income came from grain, pulse, and oil crop production followed by nonagricultural activities (23%) and fruit production (16%). The findings of this figure reveal that farm activities were the primary income source of the respondents (77%), which is analogous with Adane et al. (2019), where most of the respondents depended on farming for livelihood.

Jhum or shifting cultivation is a popular practice in the hilly areas and is extensively practiced in the Rangamati of CHT (GoB and FAO 2013). So, most of the respondents cultivated cereal, pulse, oil, and spices in jhumon a large scale which ultimately made it a significant source of income. Among agricultural sources, fruit cultivation was the second-highest contributor to family income, because fruit trees provided the locals with some additional benefits. Apart from fruits, they were the source of timber and fuelwoods. Moreover, in the study areas, intercropping was practiced in fruit orchards with aroids, zinger, and turmeric which ultimately helped to utilize the land and ensured additional revenue from fruit cultivation. Ahammad and Stacey (2016) found that shifting agriculture now also includes fruit cultivation (e.g., pineapple, banana, jackfruit, and mango).

11.3.4.3 Contribution of Fruit Production to Family Income

Fruit production was an important source of income of the respondents and significantly contributed to their income, presented in Table 11.5. Findings of this table indicate that the highest portion (56.7%) of the respondents made up to 15% of their family income from fruit cultivation, and it was 15.01–30% of their family income for the next 35% of the respondents. So, a majority (91.7%) of the respondents benefitted up to 30% of their family income through fruit cultivation. As reported by Mahapatra and Panda (2012), indigenous fruits contributed 15% of income of tribal households in eastern India.

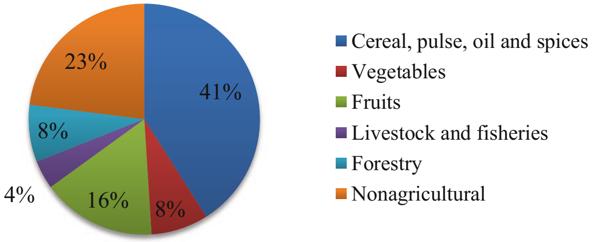

Fig. 11.5 Sector-wise family income

Table 11.5 Distribution of respondents according to their fruit production contribution towards family income

Categories	Respondents	
	Number	Percent
Contribution (up to 15%)	68	56.7
Contribution (15.01–30%)	42	35
Contribution (more than 30%)	10	8.3
Total	120	100

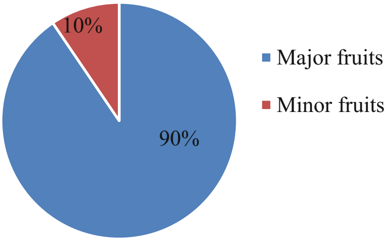

Fig. 11.6 Comparative contribution of major and minor fruits

Fruit cultivation was a source of additional revenue for the respondents. So, their average annual income was much higher than the national average. It indicated that the majority of the fruit growers of the study area had better livelihood status than others. Economic solvency allowed them to put more emphasis on their children's education and spent a good amount of money on it. That's why the educational attainment of the respondents was quite satisfactory. These findings are in line with Sarker et al. (2017), where lemon production improved the living condition of the people by reducing poverty. Schreckenberg et al. (2006) also observed the contribution of indigenous fruit production towards poverty reduction in Cameroon and Nigeria. Another study by Jamnadass et al. (2011) showed that indigenous and exotic fruits cultivation improved the livelihood and nutritional status of locals in sub-Saharan Africa. Reta et al. (2020) showed in their study that wild forest fruits ensured food security and were a good source of income for people in eastern Ethiopia. According to a study conducted by Adane et al. (2019), fruit production played an important role in making additional money and contributed to the livelihood of small farmers in Southern Ethiopia. In India, Mahapatra et al. (2005) observed that sales of non-timber forest products like fruits allowed locals to stay in their villages rather than shifting to cities for jobs that were a chief source of income during down periods in the agricultural cycle.

Results displayed in Fig. 11.6 show that major fruits had a 90% contribution to the total income from fruits. These findings led to the conclusion that the respondents of the study area were mainly associated with major fruits cultivation. It was due to major fruits had high market demand and high price in the local market. Moreover, planting materials were also readily available for major fruits. So, the fruit growers found major fruit production more profitable than minor fruits. According to Srivastava et al. (2017), minor fruits are comparatively less appetizing than other popular fruits, which have lesser market demand and are grown to a limited scale only. Nevertheless, the potential of the minor fruits is significant. They play a prominent role in their diversified supply, even if individual contributions are limited in quantity and time. Many under-utilized minor fruits are important in socio-economic, biodiversity, and conservation aspects on a local and regional basis. They are also the source of nutrition for wild animals and birds (Pasha and Uddin 2019).

11.3.5 Relationship Between the Selected Characteristics of the Respondents and Their Income from Fruits

This section deals with the relationship of selected characteristics of the farmers with their income from fruits cultivation. Results presented in Table 11.6 indicate that two out of six characteristics showed a positive and significant relationship with income. Those were: (a) Farm size and (b) Attitude towards fruit cultivation. That means respondents with higher abovementioned characteristics earned better than others from fruit cultivation.

Farmers with large farms in CHT are generally affluent, and it is the tangible determinant of wealth (Langford 2017). They are capable of taking risk of cultivating fruits to a large extent. Extensive fruit cultivation needs high investment and ultimately ensures high return. The findings of Rahman et al. (2017) exhibited that fruit production is higher in the large farm than smaller and medium ones. This is due to several factors like high tree density in the large farms, large farm owners use quality input materials (seed, seedling, fertilizers, pesticides), and regularly follow proper management techniques that facilitate fruit production. In another study, Adane et al. (2019) reported that there is more diversification of components when there is a large farm, which improves the earnings from the system. So, the higher the farm size the higher the return from fruit cultivation.

Attitude towards fruits production had a significant influence on respondents' income from fruits production. Favorable attitudes towards fruit cultivation motivated farmers to put intensive effort into fruit orchard management and invest on a large scale, ultimately resulting in a high profit from fruit cultivation. Hasan et al. (2010) also noticed a significant relationship between attitude and increased income from fruit cultivation.

Table 11.6 Relationship between selected characteristics and their income from fruits production of the respondents

Independent variable	Coefficient of correlation value "*r*"
Age	0.075^{NS}
Education	0.054^{NS}
Family size	0.103^{NS}
Farm size	0.286^{a}
Source of information	0.072^{NS}
Attitude	0.622^{a}

[a] Correlation is significant at 1% level (2 tailed); *NS* Non significant

11.3.6 Problems Faced by the Respondents in Fruit Production and Marketing

The respondents were confronted with different problems during fruits production. A total of 13 problems were identified and ranked as presented in Table 11.7. According to this table, the most severe problem the respondents faced was the unavailability of planting material (ranked first) followed by lack of suitable transport and communication system (second), the high price of input materials (third), and low fertility of the soil (fourth).

The absence of smooth communication facilities in the hilly areas impeded agricultural activities. To collect quality planting materials, respondents needed to contact local DAE office, research stations, and nurseries. But due to a troublesome communication system, they hardly managed the materials, and local nurseries' capacity was limited to meet the growing demand. Besides, many nurseries were unable to supply quality planting materials. If quality materials were available, farmers had to pay a high price. These findings were also true for the fruit growers of Khagrachari reflected in the study of Rahman et al. (2017). Furthermore, poor communication and storage systems led to a huge post-harvest loss of fruits which was in line with the findings of Hossain and Islam (2017). Hasan (2013) and Dewan et al. (2015) reported that lack of cold chain management is one of the major obstacles in the fruit and vegetable sector of Bangladesh. Along with these, the growing price of necessary crop inputs like fertilizers, fungicides, insecticides, etc. made fruit cultivation spendy. Over the recent years, loss of soil fertility was a growing concern in the study area. Exhaustive practice like jhum/shifting cultivation was mainly responsible for this. Besides, soil erosion became severe in the hill soil due to steep topography and high intensity of rainfall that washed away topsoil with

Table 11.7 Rank order of the problems faced by the respondents in production and marketing of fruits

Problem statements	PCI[a]	Rank
Unavailability of good planting material	234	First
Lack of transportation and communication	232	Second
High price of the input materials	222	Third
Low fertility of soil	220	Fourth
Disease and insect infestation	210	Fifth
Lack of storage facility	175	Sixth
Lack of marketing facility	160	Seventh
Post-harvest losses of fruits	159	Eighth
Wild animal damage (monkey, bat, etc.)	158	Ninth
Non-availability of extension personnel in time	154	Tenth
Lower income from minor fruits	150	11th
Lack of fruit processing industry	144	12th
Lack of knowledge of improved agricultural practices	140	13th

[a] PCI = Problem Confrontation Index

nutrients. Langford (2017) also blamed these reasons for soil fertility problem in the hill soil. Moreover, the acidic nature of hill soil caused an imbalance in the availability of micro and macronutrients.

11.3.7 Suggestions to Increase Fruit Production

The respondents provided suggestions on increasing fruit production, presented in Table 11.8. According to this table, most of the respondents (63.3%) suggested that "supply of good planting material at lower price" could improve the fruit production situation in hilly areas followed by "Development of communication and transport facility" (second), "Providing credit facility" (third), and "Arrangement of storage facility" (fourth).

The respondents in the study area had been facing problems in collecting quality planting material due to a poor communication system. Easy availability of planting material at a lower price would boost their fruit farming activities. As initial investment in the fruit orchard was high due to costly planting and input materials, land preparation, labor, etc., it was challenging for a general farmer to bear the expense. Credit facilities from GOs and NGOs could solve the problem. In his study, Langford (2017) found that these people have less access to credit due to a reluctance of microfinance institutions to distribute loans and collect weekly repayments in remote areas. Furthermore, the high-interest rate discourages farmers from taking loans (Rahman et al. 2017). Generally, most of the fruits are perishable. Weak communication and transport facilities made it difficult for farmers to ship their products to the market without degrading quality. So, storage facilities in the hilly areas could prevent this post-harvest loss of fruits and encourage farmers in fruit cultivation to a greater extent. Hossain et al. (2017) also agreed on improving road infrastructure and storage facilities for increasing fruit production in the CHT. In the

Table 11.8 Rank order of suggestions to increase fruit production

Suggestions	Percent	Rank
Supply of good planting material at lower price	63.3	First
Development of communication and transport facility	56.7	Second
Credit facility	51.7	Third
Arrangement of storage facility	46.7	Fourth
Establishment of fruit processing industry	41.7	Fifth
Proper market price for the produce	40	Sixth
Arrangement of training facility	37.5	Seventh
Amendment of existing supply chain	35.8	Eighth
Coordination between fruit growers and extension workers	34.2	Ninth
Practice of integrated pest management	30.8	Tenth
Increasing awareness to produce indigenous minor fruit plants	29.2	11th
Provide irrigation facility	23.3	12th

opinion of Langford (2017) and Rahman et al. (2017), poor connectivity results in high transport costs and ultimately influences the market prices of products.

11.4 Conclusions

This study investigated ethnic hilly peoples' extent of practices of major and minor fruits and their contribution to family income for sustaining livelihoods. Findings revealed that among the different major fruit species, jackfruit was most abundant followed by pineapple and banana. Due to less popularity, minor fruits were grown on a limited scale where pomelo, lemon, honeydew, and watermelon were prominent species. Among underutilized minor fruits, the majority belonged to the Moraceae family. Making additional income, nutrition supply, controlling land degradation, and ensuring food security were the main reasons behind respondents' fruit cultivation initiatives. Fruits had a significant contribution towards the livelihood of the respondents which was reflected in their sound annual income status. Fruit production was the second-largest agricultural income source, and more than half of them (56.7%) benefitted up to 15% of their income from fruit cultivation. Respondents' farm size and attitude towards fruit cultivation were the key factors that influenced their income from fruits. Thus, it may be decided that any attempt to increase these two characteristics would be helpful for the income improvement of the respondents from fruit cultivation. The key problems they faced during the production and marketing of fruits were less availability of good planting material, poor communication network of the area, expensive input materials, and low soil fertility. According to their suggestions, provision of good planting material with lower price, good communication facilities, provision of credit, infrastructure development for fruit storage, and processing could mitigate their problems to a large extent. The research results will be suitable for planning and implementing the fruit-based agriculture system in the hilly areas of Bangladesh for the economic empowerment of the ethnic communities.

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Restoration and Conservation of Plant Genetic Resources via Molecular Techniques: An Important Measure for Sustainable Agriculture

12

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Ayushi Tripathi, and Shiv Kant Shukla

Abstract

The importance of biodiversity for our planet and mankind has arisen strongly over the past years which gave birth to the field of conservation and restoration biology. Agrobiodiversity is focused on food and nutritional security by implementation of novel approaches to achieve sustainable ecosystem. All current tools and techniques of biotechnological interventions aid in exploring and developing conservation strategies, rescue methods and its restoration. Some of the conservation techniques are in situ, ex situ and on-farm along with genome study of cultivars with full characterization and identification of molecular markers. The molecular marker technology for the development of gene banks of the threatened and rare species is imperative to restore the genetic erosion. The molecular method for characterization confers the identification of genotype and thus detecting variation at genetic or DNA level and thereby barring any environmental factors. The systematic approach for identification of agrobiodiversity hotspots is essential for in situ conservation. The study emphasizing the ecological dynamics to mitigate the loss of biodiversity in the protected areas is required to be strengthened. The amendments of policies for regulation of the food availability and security through sustainable agricultural practices can play a pivotal role in management of the agrobiodiversity. Human race evolved where domestication of any plant species led in such a way that can satisfy human necessity in the form of food (fat, protein macro-/micronutrients), animal feed and

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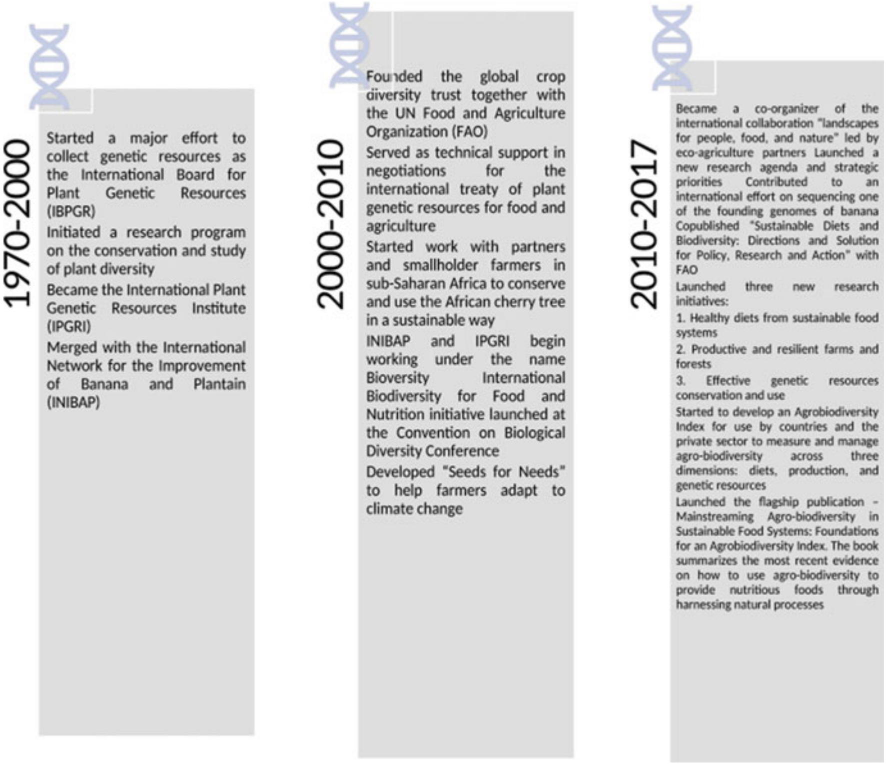
medicinal requirements, and hence propagation of horticultural, aromatic and medicinal plants was disseminated by farmers. Therefore, biotechnological tools such as micropropagation, protoplast culture, development of DNA bank facility, DNA-based marker identification and cryopreservation should be applied for the conservation and improvement of the plant species. There are some molecular approaches like molecular marker identification along with sequencing and molecular library formation which are big innovations for present species preservation techniques. This can prompt the acknowledgement of new units for protection, regardless of whether they be raised to the situation with recently isolated species or characterized as exceptional subsets of more boundless species. These techniques are explained in this chapter with their advantages in species preservations. Overexploitation can lead to extinction of species. It's our duty to conserve agrobiodiversity for future generations. Molecular approaches in conservation of various plants species will be discussed in this chapter with an objective of restoration of plant genetic resources for sustainable agriculture.

Keywords

Conservation · Agrobiodiversity · Molecular · Sustainable · Markers

12.1 Introduction

Agrobiodiversity renders revamping of diet, nourishment and nutritional status of the nation. The major chunk of population suffers from micronutrient deficiencies and inadequate energy requisite (Kahane et al. 2013). Further developing availability to a scope of yields would offer wholesome advantages to the provincial and metropolitan poor. Cultivating frameworks that keep up with and use agrobiodiversity have solid potential for improving food security and subsequently developing sustenance (Priyanka et al. 2021). Agrobiodiversity is a component of biological diversity of relevance to food and agriculture and also includes the assortment of creatures, plants and miniature organic entities, at the hereditary species and environments. The agrobiodiversity at hereditary level incorporates the variety among assortments and landraces of similar harvest and their wild family members. Plant hereditary assets for food and farming are prime wellspring of worldwide food security (Maxted 2013). The food production and utilization of plant diversity are major mainstay for manifesting secure food future and are dependent on the crop production influenced by climatic and global changes, geographical distributions and human response to health and diseases. The conservation of food and plant biodiversity is imperative in establishing sustainable agriculture systems and alleviating the climatic changes (Hammer et al. 2003). The regions of Eastern Himalayas and Western and Eastern Ghats are threatened zones for both agrobiodiversity and wild biodiversity hotspots (Nautiyal et al. 2008). There are approximately 7000 species of plants used by farmers out of which only



1970-2000

Started a major effort to collect genetic resources as the International Board for Plant Genetic Resources (IBPGR)

Initiated a research program on the conservation and study of plant diversity

Became the International Plant Genetic Resources Institute (IPGRI)

Merged with the International Network for the Improvement of Banana and Plantain (INIBAP)

2000-2010

Founded the global crop diversity trust together with the UN Food and Agriculture Organization (FAO)

Served as technical support in negotiations for the international treaty of plant genetic resources for food and agriculture

Started work with partners and smallholder farmers in sub-Saharan Africa to conserve and use the African cherry tree in a sustainable way

INIBAP and IPGRI begin working under the name Bioversity International Biodiversity for Food and Nutrition initiative launched at the Convention on Biological Diversity Conference

Developed "Seeds for Needs" to help farmers adapt to climate change

2010-2017

Became a co-organizer of the international collaboration "landscapes for people, food, and nature" led by eco-agriculture partners Launched a new research agenda and strategic priorities Contributed to an international effort on sequencing one of the founding genomes of banana Copublished "Sustainable Diets and Biodiversity: Directions and Solution for Policy, Research and Action" with FAO

Launched three new research initiatives:

1. Healthy diets from sustainable food systems

2. Productive and resilient farms and forests

3. Effective genetic resources conservation and use

Started to develop an Agrobiodiversity Index for use by countries and the private sector to measure and manage agro-biodiversity across three dimensions: diets, production, and genetic resources

Launched the flagship publication - Mainstreaming Agro-biodiversity in Sustainable Food Systems: Foundations for an Agrobiodiversity Index. The book summarizes the most recent evidence on how to use agro-biodiversity to provide nutritious foods through harnessing natural processes

Fig. 12.1 Milestones in biodiversity conservation over the years (https://www.bioversityinternational.org/about-us/who-we-are/history/)

30 species deliver 90% of caloric or nutritional intake. Conventional breeding has narrowed down the genomic pool (Gruber 2017). The biotechnological tools could improvise on widening of genetic diversity and could aid in raising disease and pest-resistant varieties thus enhancing its yield. The strategies of conservation of agrobiodiversity involve ex situ (outside it's natural habitat), on-farm and in situ (on its natural habitat) methods (Love and Spaner 2007). In Fig. 12.1, the milestones of historical biodiversity conservation work are given. The plant genetic resources have been conserved by in situ methods and is often termed as on-farm conservation. Since the crops exhibited resistance against pests and diseases and conferred high market value, therefore, on-farm conservation technique is an approach to maintain locally developed crops for sustainable agricultural practices (Maxted et al. 1997a, b). Some approaches for crops and forage species conservation incorporate seed bank, gene bank, tissue bank and community field gene bank.

The agrobiodiversity preservation implies the techniques for saving life assortments on Earth in the entirety of its structures and keeping regular biological systems working and sound. Molecular markers are explicitly DNA-based markers which can give a decent assessment of hereditary variety and biodiversity preservation (Polegri and Negri 2010). The advancement of molecular markers depends on

Fig. 12.2 Impact of climatic factors on agri-diversity

polymorphisms found in DNA, and the data taken in natural variety can be utilized to quantify the connections between organic entities and, furthermore, other genetic variety concentrates. Therefore, molecular markers have crucial significance in biodiversity preservation. To take care of the roughly ten billion total populaces by 2050, it is important to expand the yield of staple harvests up to 70—every available ounce of effort. The seed vault is an endeavour to guarantee against the deficiency of seeds in other quality banks during huge scope local or worldwide emergencies. A few endeavours are being made by the analyst local area all throughout the planet to expand the current hereditary base by using the accessible germplasm in various crops. Impact of different climatic factors on agrobiodiversity is shown in Fig. 12.2. This chapter discusses about impact of agrobiodiversity on food, nutrition and health, conservation strategies and its global drivers with policy implementation to strengthen conservation approaches.

12.2 Impact of Agrobiodiversity on Food, Nutrition and Health

The new United Nation's 2030 Agenda for Sustainable Development attempts at alleviating hunger and achieving food security which is very much required for the utilization of the biodiversity by purchaser open food market and dietary assortment. The logical discoveries feature the diminished levels at the overall scale worldwide even in most of the industrialized economies (Aguilar et al. 2015). The standard of propelling agrobiodiversity in burning-through good dieting routine is the tendency for biodiversity-related attributes in various cultivating rehearses. Food biodiversity at the ranch level can maintain the enhancement of healthy living being and neighbourhood of dietary varieties, especially when taken together with educated food choices and specialization, engaging a task for market-based purchasing power. Integrative methodologies such as practical gathering, geographic whole diet and food framework approaches in agrobiodiversity for food, nourishment and healthy lifestyle demand an extended attention and hard work to address the declining agrobiodiversity production and to focus on quality yield enhancement via advanced agriculture technologies (Johns et al. 2013). The purpose of agrobiodiversity conservation is when producers in neighbourhood areas of the concentrated agrarian

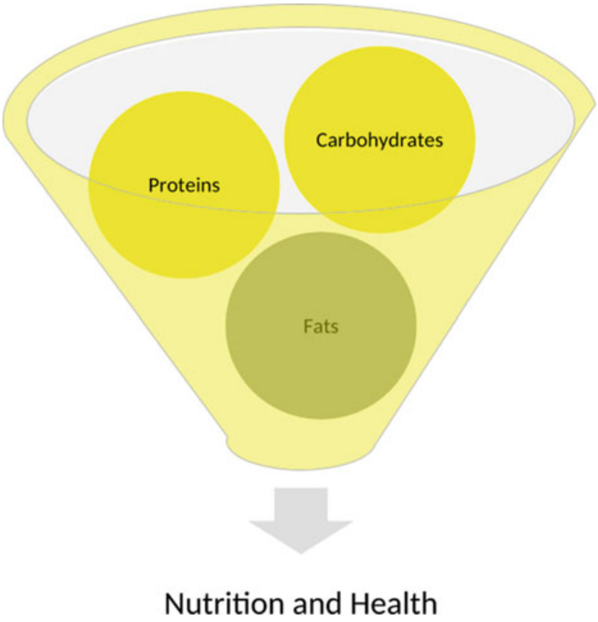


Fig. 12.3 Influence of food on nutrition and health

biodiversity can't get access to various crop varieties in light of inadequate resources and related dietary changes (Davis et al. 2012; Sibhatu et al. 2015). Majorly affected cultivators are smallholders and local people. Still many individuals in the planet don't get sufficient food to eat. With the increasing population, there is huge demand of food and its alternatives. The characterization of different food components on human health is given in Fig. 12.3. Plant sciences facilitated with normal, social and health sciences are required for strategic planning and policy-relevant research by working on agrobiodiversity for sustainable food security (Jones et al. 2014).

The world's farm technologies giving food to the developing living populace demonstrated as one of the incredible achievements resulted in human progress. Regardless of the dramatic expansion in population beyond 150 years, agrarian biodiversity has given gigantic nourishment and medical advantages. Agrarian biodiversity can be grouped at three significant levels—environmental, organismal and genetic (Heywood 1999), every level of which falls in a hierarchal way (Table 12.1). These are subset of biodiversity as well as address an expansion of it like cultivars, unadulterated lines, breeds and strains and territories (ranchers' fields and fisheries) that are nearly sabotaged by protection researcher as a feature of natural variety. It includes all species and the harvest assortments (counting wild family members), animal varieties and races and microorganism strains that are both straightforwardly or in a roundabout way associated with agribusiness, both as sustenance and feed for animals, and the geographical locales of cultivating. A large number of individuals on the planet do not have sufficient eating regimens and have ailing health. Agrobiodiversity in cultivating frameworks has solid potential for working on this openness and subsequently further developing nourishment, in light of the fact that there is the gigantic chance of investigation of native,

Table 12.1 The elements of agricultural biodiversity (modified from Heywood 1999)

Agroecological diversity	Organismal diversity	Genetic diversity
Biomes	Kingdoms	Gene pools
Agroecosystems	Phyla	Populations
Agroforestry systems	Families	Individual genotypes
Agrosilvicultural	Genera	Genes
Home gardens	Species	Nucleotides
Forest ecosystems	Subspecies	Breeds
Fisheries (fresh water systems/marine systems)	Varieties/cultivar/ landraces	Strains
Fields/plots		Pure lines

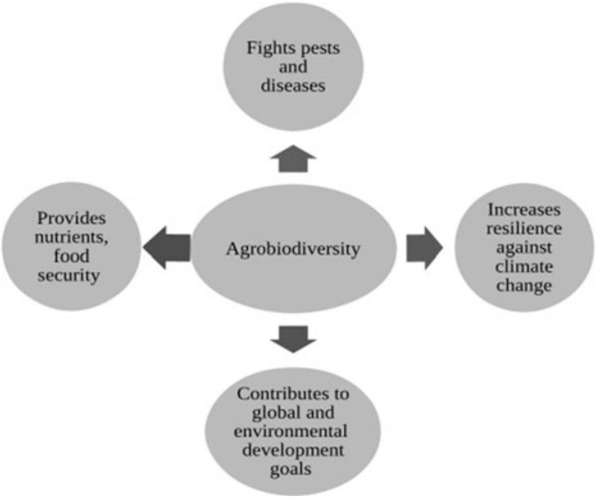


Fig. 12.4 Global impact of agrobiodiversity

disregarded and underutilized food crops that are rich in macro or miniature supplement. Transformation in agricultural practices and adaptation of advance farming techniques can play an effective role in the production of food crops to nourish the human population worldwide. Various difficulties are faced related to over- and undernourishment as in some country people are not receiving sufficient food and in other part of the world people are over-nourished due to lack of healthy sustenance and unhealthy lifestyle. These are the adverse consequences on diverse availability of dietary supplements, nourishment and strength of society (Nakhauka 2009). The adverse impact is needed to be analysed, examined and aimed towards sustainable agriculture utilizing advanced techniques and understanding the importance of econutrition (Ebi K 2009). Figure 12.4 comprises the global impact of agrobiodiversity. There is urgent need to coordinate ecological and human well-being, unifying the entire association between farming, environment and human sustenance (Blasbalg et al. 2011).

Strategic planning for agrobiodiversity for sustainable nutrition has been proposed by Frison et al. (2011): it contains a proof-based way to deal with nutrition, health and sustainable agribusiness for the small-scale growers.

The assessment and exploitation of nearby food sources and their types, traditional cooking styles, cultural strategies, nutrition schooling and research on novel and further developed techniques for food stock and processes need high attention for enhanced showcasing.

The parts of agrobiodiversity that sway most straightforwardly on nourishment and health are the variety of wild plant and cultivars and domesticated animals utilized in agribusiness, wild species, the environments wherein they develop, hereditary assets, crop wild family members (CWR) and the landraces, cultivars and breeds created from these wild species.

12.3 Conservation Strategies and Molecular Methods

The area of conservation biology is introduced by the scientific community in the mid-twentieth century to address the marked decline in global diversity. This issue gained attention at international platform and recognizes it as a global concern, and actions are planned for the manageable utilization of regular assets (Engels and Ebert 2021). The field of atomic hereditary qualities was developing quick and presenting new modern methods giving huge new freedoms to traditionalists. Preservation science worked around essential plans with time to ensure territorial biodiversity with explicit issues and worldwide sizes of networks and societies in the later time (Margules and Pressey 2000). Activity plans were shaped in such a manner where supported improvement of human prosperity includes regular environment, local area framework and business benefits; however lately expanding hereditary disintegration has fostered a genuine danger to the prosperity of humankind (Corlett and Primack 2008). Keeping up with environments, its cycles and normal flow of progressions, hereditary variety and wild genera of any species should be secured and moderated (Ashmore 1997).

For attaining sustainable ecosystem, it is needed to foster methodologies for the protection of biodiversity, especially for the crops utilized for food and feed. According to Article 12 of CBD (1992), research program proposition is at present shaped in such a manner by which researchers are empowered to arrange, moderate, oversee and accomplish most extreme hereditary variety protection for the two plants and creatures.

There are two essential methodologies, each framed of different parts of preservation that can help protectionist to keep up with hereditary variety. These two are ex situ and in situ preservation. As per CBD (1992) states that safeguarding of environments and normally existing natural surroundings is characterized under in situ technique with the effective administration and recuperation of feasible number of species as it was in its unique structure, while ex situ protection is characterized as the preservation of organic variety that is a long way from its unique geological area in a misleadingly settled office. In short in situ protection is displayed in characteristic natural surroundings or ex situ in some misleadingly established climate relying upon the particular need.

There is a central contrast of perspectives between both the procedures, for example, in situ contains area, character, upkeep and monitoring objective taxa in its unique area, though ex situ includes the area, inspecting, transport and capacity of target taxa in controlled condition. Because of this slight cooperation between the two methodologies, these two can't be considered as option in contrast to each other; they are more similar to correlative and should be utilized in a consecutive way to accomplish required variety (Fig. 12.5).

These two classifications further partitioned into the accompanying explicit apparatuses, ex situ as seed/undeveloped organism stockpiling, in vitro capacity, innate material like DNA stockpiling/quality bank and botanic nurseries and in situ as natural save conservation and ranch-based protection (Maxted 2013).

In general, most parts of the genetic procedures in conservation of biodiversity have proven to be invaluable tools with the following applications: (1) the monitoring and portrayal of population elements and gene flow (2) assessment of current and verifiable population size (3) assessment of parentage, relatedness, regenerative capacity, mating frameworks and social association (4) detection of connections among various germplasm in seed banks (5) identification of copies in seed banks and (6) assessment of the degree of hereditary variation present in germplasm pools and its transition over the long run.

Population genetics comprises various co-dominant markers such as minisatellite, microsatellite (multiple tandem repeats) and SSRs (simple sequence repeats). Maternally inherited components mtDNA and cpDNA are used for species identification, developing phylogenies and understanding evolutionary lineages. Mitochondrial and chloroplast genomes are forms of maternal lineages and so provides a strong potential for phylogenetic studies. Sequencing, single copy (sequence) data open an entirely new gateway with data automation in making this basic information accessible for the stream of conservation biology which until recently has paid much less attention and was kept financially limited in resources. This is the fact that we for sure never will be able to know all existing species on our planet; without recognizing the particular genotype, it is impossible to safeguard it; hence it is most important to identify and characterize the particular genotype. In this context, the ESA (Endangered Species Act) in the United States is only allowing those species which are well identified and characterized for protection.

12.3.1 Ex Situ Techniques

The methodologies applied for ex situ strategy include the engendering of plant species, genotype either by ordinary strategy using seeds (breeding technique), vegetative plant parts or utilizing applied biotechnological techniques such as plant tissue culture, micropropagation strategies, cryopreservation, germplasm assortments, quality banking alongside different cutting-edge methods presenting novel hereditary alteration in the current genetic supply, support of existing populace

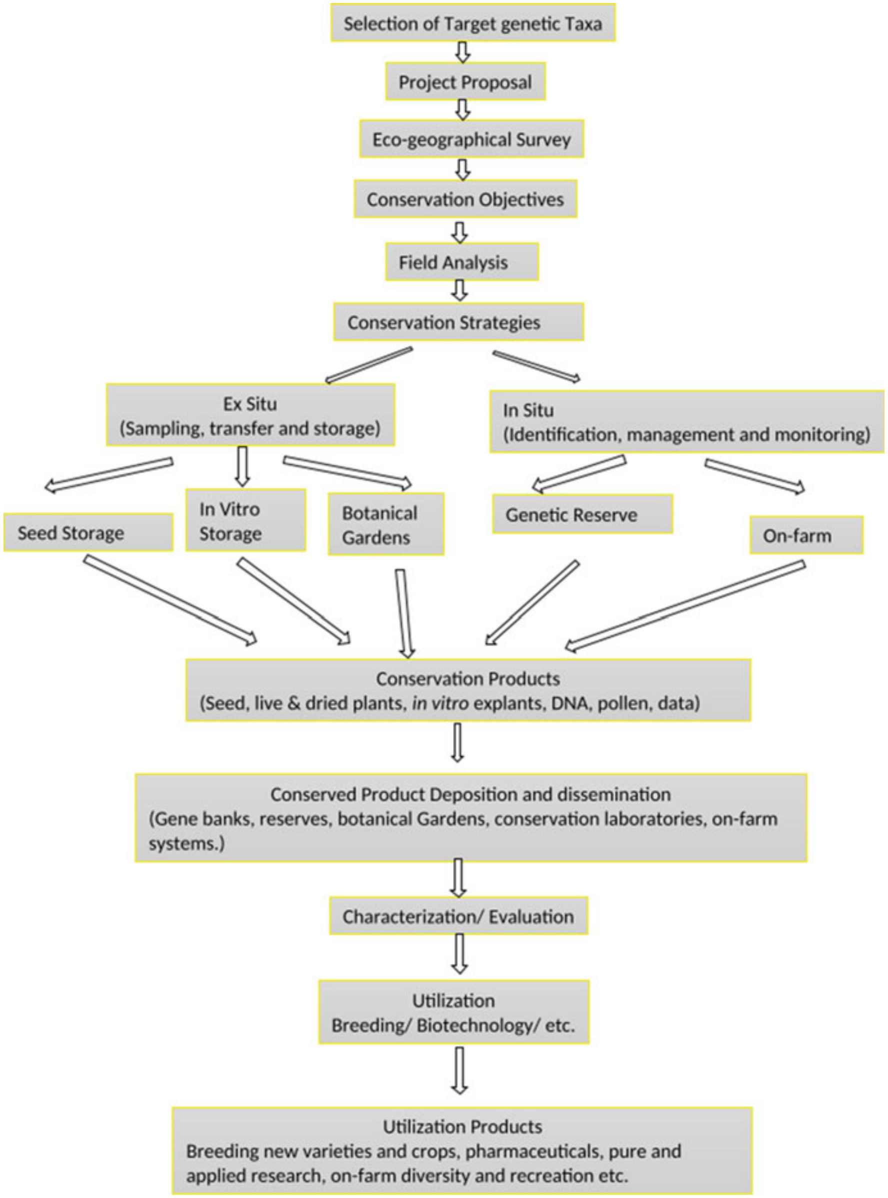


Fig. 12.5 Conservation strategies and molecular methods

and renewed introduction of the qualities of wild genera (Schemske et al. 1994). In this class hereditary variety is protected by gathering and keeping up with species/

subspecies or assortment of plants in quality banks, greenhouses or as seed, tubers, tissue explants and DNA under controlled conditions.

12.3.1.1 Seed/Embryo Storage

Collection and storage of seeds/embryos is a very simple and widely accepted way to save diversity. Seeds and embryos are the natural source of dispersal, easily stored and regenerative form of major plant entities. This process involves collection of samples, transfer to the facility and storage at ultra-low temperatures (−20/−80 °C). Only those species are likely stored by this method, those that can withstand in low temperature without losing viability and dried up to moisture content (~5–6%) by desiccating its seeds or embryos before freezing them. The advantages of this technique are that it is reproducible and efficient for storage in long term. By this robust technique, wild taxa of any species can be easily stored and accessed whenever needed; however, this method is disadvantageous for storing recalcitrant species.

12.3.1.2 Botanical Gardens

By and large, professional flowerbeds were frequently connected with fancy and restorative gardens yet clearly not to exhibit the species explicit hereditary variety. These days these nurseries safeguard living examples of species that were initially gathered from its unique area and moved to it. The incredible benefit of this methodology is that nurseries have no restriction on picking which species to save; rather they safeguard any wild species that may not be provided adequate need to moderate. There are two issues with this strategy: first being the restricted space as they for the most part arranged in the middle of metropolitan calm nations, yet the majority of the plant variety existed in heat and humidity; thus this becomes costly while keeping up with offices of nurseries or other control zones, which are additionally restricted by space accessibility. The subsequent one is that not many members of any species can be ensured, and this significantly limits the variety found in nature. In any case, if the objective species is nearly annihilated and not many of them are left, then at that point this might be the most suitable choice accessible.

12.3.1.3 In Vitro Conservation

In vitro protection infers the support of explants in a purified microorganism-free climate; it is a vegetative engendering of unmanageable species. This technique offers a substitute to handle quality banks. It includes the advancement of tissue societies of explants on supplement agar and their stockpiling under surrounding state of temperature and mugginess for either lethargic or suspended development. The interaction is beneficial over others as it offers an answer for stubborn animal varieties and effectively accomplished clonal spread independent of the period (Pathak and Mohammad 2014). Somaclonal variety is the fundamental issue related with this strategy; for keeping away from this, an all-around effective convention should be produced for most species, utilizing atomic innovation with minimal expense necessity. Cryopreservation is one of the important in vitro conservation technique (Hoyt 1988) where in vitro cultures are frozen at very low temperature in liquid nitrogen (196 °C) and which can be conserved for longer period (Chen et al. 2011). Different plant species can be cryo-safeguarded by utilizing techniques accessible like confirmation, embodiment drying out and furthermore joining these two strategies together (Kami et al. 2009).

12.3.1.4 In Vitro Gene Bank/Germplasm Protection

The fundamental motivation behind germplasm preservation is to safeguard hereditary parts for a consistent period on the grounds that the seed frequently neglects to develop because of basic and fragmented arrangement and ill-advised undeveloped organism development and here and there normal pressure (Ellis 1991). There are numerous assortments developed, which produce stubborn seeds that can't be dried at a moistness sufficiently low to take into account stockpiling at low temperatures (Roberts 1973). These sorts of hereditary banks are regularly utilized for assortments like potatoes, rubber, coconut, mango, coffee, bananas, cassava, cocoa and pulse crops. The upsides of quality banks are that wild taxa of any genotype are effectively open for use and accessible for assessment. Numerous super foundations, for example, the International Plant Genetic Resources Institute (IPGRI), the Consultative Group on International Agricultural Research (CGIAR) centres and the International Centre for Agricultural Research in Dry Areas (ICARDA), have effectively partaken in the protection of uncommon plant species and those that are in danger of termination (Reed et al. 2004). The drawback of this is that examples are helpless to nuisances, illnesses and harm; subsequently it needs further developed offices to guarantee protection.

12.3.1.5 Pollen/DNA Conservation

The protection of dust grains is endeavoured under appropriate conditions that permit their resulting use for future intersection with plant material in regular fields. It might convey to foster haploid plants from dust societies; however till now summed up conventions have not been grown at this point. The capacity of DNA is the most acknowledged and modest strategy for safeguarding genotype with the assistance of suitable innovation, yet the recovery of whole living beings or any cell/tissue from DNA can't be conceived at this point; however single or gathering of qualities could be used. The data set of DNA bank is key and gives multidimensional data for the productive use of the germplasm. The upside of dust stockpiling is that it is practical and straightforward, yet the drawback is that material that comes from fatherly beginning would just be preserved, and with DNA protection, there are plenty of resulting subatomic procedures that are needed to be convenient.

12.3.2 In Situ Techniques

The conservation of hereditary variety at the local land where it initially existed either in the wild living space or in agribusiness frameworks falls under in situ mode. In situ preservation is the maintenance of normal assets for supported degree of variety in species, environments, cycle of advancement, human networks and culture (Soulé 1985).

A large portion of the current nature holds and stops are set up to save significant widely varied vegetation or to ensure lovely scene in its regular condition, yet in the current setting, the primary point has become to secure basically the individuals who are at risk of termination. In situ conservation is a significant device for ecological manageability, as it is totally normal in jam plants for their biodiversity and follows the transformative cycle (Ashmore et al. 2011). In situ conservation includes a few obstacles, for example, division of natural surroundings, environmental change and irrational utilization of plant assets, pathogenic living beings and intruder species in climate, where ex situ preservation hampers developmental cycle by adjusting hereditary variety of specific plant/animal types, while in situ strategy is harmless to the ecosystem and additionally secures variety right at home making this a superior other option.

12.3.2.1 Natural Reserve Conservation

The protection of natural life in the recreation centre incorporates area, personality, the executives and checking in a specific geo area. This interaction is most appropriate to countless wild species, as the administration region is generally economical. Conservation of wild species in a reserve involves the location, identity, management, and monitoring of genetic diversity in a particular geo location. This technique is the most appropriate for the huge number of wild species, because the management facility is relatively inexpensive. Whether considering plants or animals, the objective is to sustain the minimum number of individuals that can contribute to genetic diversity within the species. If very few individuals are protected, genetic diversity will decline over time, and if large numbers are protected, resources are wasted in managing the large population. To manage such efforts, conservationists will need to estimate the effective population size (Ne), that is, the number of conserved individuals that would undergo the same amount of random genetic drift as the actual population. The disadvantage is that the conserved material cannot be immediately utilized for human necessities and, if the management regime is minimal, little characterization or evaluation of data may be available.

12.3.2.2 Farm-Based Conservation

This technique includes the support of development of conventional harvests and frameworks by ranchers inside routine agrarian practice. Customary cultivars are planted and gathered in a cycle, and each season, the ranchers save a portion of the reaped seed for re-planting. Consequently, this technique is profoundly acknowledged for the nearby climate and is probably going to contain locale explicit alleles that might demonstrate value for future reproducing programs. The home nursery is a firmly related variation of on-ranch preservation of landraces yet for a small scope. It includes the development of more enhanced material in patio or kitchen gardens. The home nurseries centre around the requirement for therapeutic, flavour and vegetable (e.g. tomatoes, peppers, brinjal, mint, thyme and beans). The benefit of the on-ranch method is that it guarantees the upkeep of exceptionally adjusted flavours alongside those wild species that customary farming frequently relies upon. Be that as it may, these landraces might have lesser efficiency than their advanced partners, so customary ranchers ought to be given some help and maybe alert to guarantee ceaseless cultivating. It ought to be noticed that the financial force of today would in general demonstrate in opposition to the continuous development of the world's native people groups who are presently encountering quick hereditary disintegration and could confront a significant elimination.

12.3.3 Biotechnological Conservation Approaches

Biotechnology plays a fundamental part in the plant protection programs at the public and worldwide level (Bajaj 1995; Benson 1999; Rao and Riley 1994) which has driven a few boundaries fundamental for setting up manageable biological system. The advancement in biotechnological approaches, for example, cutting-edge sequencing, hereditary change, underlying science and in vitro culture strategies, has contributed fundamentally in translational research and furthermore gives the infection-free planting material. A few methodologies have prompted the protection and rebuilding of the seeds, other planting materials and explicitly jeopardized and undermined plant species as a method of ex situ preservation.

12.3.3.1 Gene Banks

The protection of hereditary assets which are nearly terminated is upheld by the quality banks where such species are preserved in transient span until another strategy could be produced (Dulloo et al. 2006). The put away germplasm can be kept up with at −20 and −70 °C for up to 2 years and long-haul length individually. There are a couple of fundamental DNA banks, for example, the Royal Botanic Garden, the US Missouri Botanical Garden, the Australian Plant DNA Bank of Southern Cross University and Leslie Hill Molecular Systematics Laboratory of the National Botanical Institute.

12.3.3.2 Cryopreservation

Cryopreservation alludes to the capacity and preservation of organic tissue tests at −196 °C by fluid nitrogen where at this outrageous temperature it restrains every one of the cell and metabolic exercises of the tissues put away and consequently can be put away for longer length. The most favoured tissue for capacity are shoot apices or meristematic cells to guarantee the sickness-free plantlet is recovered when resuscitated again on culture media after extended time frame (Scowcroft 1984). The review has revealed about this procedure for not changing the quality, force and hereditary cosmetics of the preserved material (Ogbu et al. 2010). The extracted zygotic undeveloped organisms of species delivering obstinate species like coconut, pecan and jackfruit can be cryopreserved (Engelmann and Assy Bah 1992; De Boucaud et al. 1991; Chandel et al. 1995).

Biotechnology opens an entryway to hereditary markers in plant and creature rearing done by regular and sexual means. By atomic composing of not many cells

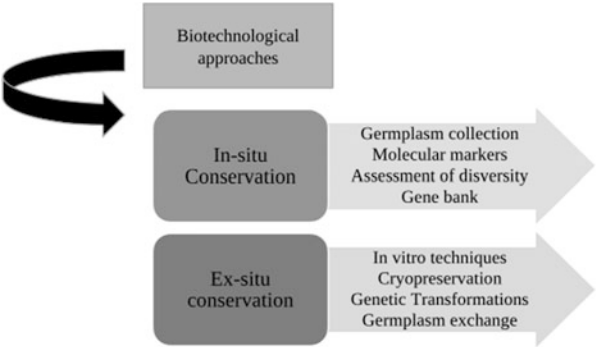


Fig. 12.6 Approaches for conservation of plant genetic resources and agrobiodiversity

for the presence or nonappearance of specific qualities, the destiny of descendants can be anticipated. Subatomic hereditary procedures are instruments for concentrating on the appropriation and degree of hereditary variety inside and among species and in the portrayal of increases, and creating innovation, different kinds of subatomic investigation are being set up (Ayad et al. 1997). Some methods for conservation of plant genetic resources and agrobiodiversity are given in Fig. 12.6. For instance, subatomic markers have been effectively applied in concentrating on the hereditary variety of rattan species, a significant asset in Southeast Asia that is at significant danger of elimination through uncontrolled backwoods abuse (Changtragoon et al. 1997).

The replacement of standard agrarian structures by current modern methods and the consolidation of high-yielding assortments have been considered to reduce crop assortment similar with landrace or wild species precursors. The Green Revolution relied upon introgression of qualities for irritation and infection obstruction and plant stature decrease on account of wheat and rice. This trial achievement cleared way for get-together hereditary assets in gene bank assortments for the present and future use. In the 1970s the hereditary markers, biochemical and afterwards atomic were used to assess the hereditary variety. DNA markers chipped away at the advancement of the hereditary linkage maps, the distinctive confirmation of single-quality attributes, quantitative property loci and utilization of nuclear raising techniques through “marker-helped” introgression and assurance.

12.4 Worldwide Plan of Action, Implementation and Gaps

The overall changes are driven by natural change, demography, land-utilization elevation and the gigantic extension joining of food systems and overall business areas, similarly as urbanization, peri-metropolitan turn of events and public masterminding. On the record of natural change, the displaying of harvest yield features that the arrangement and species-level transformations will depend upon the fundamental incorporation of biodiversity (Parry et al. 2014). The natural change difficulties associate with the rancher’s information frameworks just as agrobiodiversity frameworks. The blend of ware markets has incited a public-level decline of developing masses, regardless of the biodiversity of overall food frameworks. The overall reconciliation of work market is correspondingly a driver (Khoury et al. 2014). Adjusting designs happen at the close by sizes of individuals, families and organization. Such counter-inclinations recommend that great conditions, for instance, farm-level resource availability and adaptable social inclinations, can suitably propel agrobiodiversity use and safeguarding in these one-of-a-kind circumstances. The interrelatedness of numerous drivers is determinant of agrobiodiversity preservation and correspondingly how advancement is organized. Planning the plant hereditary assets with natural and human sciences is the desperate need to perceive the locales and buyer populaces that are at the danger of misfortune and conceivable termination of the food plant biodiversity and food instability (Garnett et al. 2013). Then again, local conditions empower the similarity of agrobiodiversity use with potential supportable policy-relevant pertinent logical analysis. In the geographic areas that have maintained huge utilization of agrobiodiversity, non-static practices of cultural identity and indigenous groups tend to exert positive feedback.

12.5 Conclusion

A wide approach of agrobiodiversity is proposed with the significance of biotechnological tools and technology in agriculture. Conservation strategies for agrobiodiversity need to be broadly based and complementary, paralleling similar developments in the conservation of wild biodiversity. Attention is focused to the dynamics of biodiversity and agrobiodiversity and the need to take this into account while planning management regimes. A broadly based approach to genetic conservation of agrobiodiversity is also proposed and attention drawn to the large range of species, wild, semidomesticated and cultivated used in traditional farm systems and contribute to household economies. Although there is considerable potential for biotechnology to contribute to improved yields and reduced risks for agricultural losses, as well as more plentiful, affordable and nutritious food for poor consumers, it is also reported unlikely that biotechnological techniques will be applied to the majority of the areas involved, so that dependence on traditional methods of selection and breeding will continue to be needed to enhance productivity. It is to be critically analysed that biotechnology need to be considered as one part of a comprehensive sustainable alleviation strategy and technological quick fix for world's hunger. Biodiversity is viewed as the reason for sustaining life in the world, assuming a significant part as bioeconomic. It has been anticipated that the twenty-first century would be a period of bioeconomy driven by progresses in bioscience and biotechnology. Bioeconomy might turn into the fourth economy after agrarian, mechanical, and data innovation, affecting manageable improvement in agribusiness, ranger service, natural insurance, light industry, food supply and medical care and other miniature economy perspectives. Other than these endeavours, it would be better for the association of nearby networks in biodiversity protection programs to make it beneficial.

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Molecular Approaches in Restoration of Agro-Biodiversity

13

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Abstract

Agro-biodiversity is a prerequisite for the sustainability of any agroecosystem. Loss of agro-biodiversity is a serious global threat today. Numerous rare and endangered plants grown naturally may also contribute a lot in sustaining the farm ecosystem. Understanding the nature of existing genetic diversity in landraces, wild species, and agroecosystems is the foremost important requirement of restoration and conservation of important, rare, and endangered crop species under ongoing anthropogenic changes. Recent advances in molecular tools and techniques have enabled researchers to identify and understand the nature and composition of agro-biodiversity at the molecular level. Marker-assisted selection (MAS) has elevated the precision of identifying actual conservation units and phylogenetic relationships and, thus, aided in formulating different restoration and conservation strategies. Integration of analytical tools such as population genomics, phylogenomics, metagenomics, etc. addresses conservation concerns, whereas whole-genome sequencing has opened a new dimension for elucidating the genome architecture and its interaction with other species. Organelle genomes have allowed us to excavate a more detailed evolutionary history of any species of our interest. Overall, molecular technologies have unlocked the avenues of research focusing on genetic rescue and restoration and thus saving the agro-biodiversity from extinction.

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Keywords

Agro-biodiversity · Marker-assisted selection · Genomics · Metagenomics · Phylogenetic relationships · Genetic rescue and restoration

13.1 Introduction

Biodiversity indicates the variety of living organisms that inhabit the earth. It is measured at three levels, viz. gene, species, and ecosystems. Agricultural biodiversity is the foremost important resource for food security and ecological sustainability. Numerous rare and endangered wild plant species from farming and non-farming habitats might also contribute significantly towards sustainability of various ecosystems, but they now are also at the risk of extinction. Rapid growing population, destruction of wild habitats, and changing climate in the twenty-first century have led to a significant and irreversible damage to the plant biodiversity. The degradation of agro-biodiversity particularly in recent few decades has been a serious global threat to different ecosystems and associated inhabitants. Loss of diversity could be due to the abiotic factors (high and low temperature, soil and water pollution, drought, salinity and alkalinity, altitudes) and biotic factors (habitat fragmentation, diseases, and insect pests). Another possible dominating reason could be the adoption of new high-yielding crop varieties and other modern agricultural production technologies at a very large scale without conserving traditional varieties. This has triggered the imbalance in the food pattern of inhabitants, as well as in regular ecosystem functioning. Currently, over one billion human beings are hungry, and two billion are malnourished with one or more nutritional deficiencies (FAO 2017; Fanzo et al. 2018). Further, climate change has proliferated the hunger and undernourished populations in this century. To accomplish the demand of all the 9.2 billion people worldwide by 2050, the overall food production has to be augmented by 60–70%, i.e. cereal with above 1 billion tonnes and meat with 200 million tonnes production, by assuming the dynamics of current and future population growth rate, income, and dietary pattern (Tilman et al. 2011; Alexandratos and Bruinsma 2012).

India displays a significant amount of biodiversity, and much of its population particularly in rural areas still depends for their livelihood on nearby existing biodiversity. The genetic agro-biodiversity may provide breakthroughs to make the crops of the future more sustainable and more productive, capable of growing better today and including adaptions to combat effects of climate change tomorrow. Thus, by visualizing the significance of plant diversity in sustainable food production and overall ecological balance under the ongoing scenario of climate change, the conservation as well as utilization of existing biological diversity in most sustainable way is the prime necessity today. Advances in biotechnological tools and techniques have generated unique opportunities for efficient conservation and utilization of agro-biodiversity. Molecular tools have opened a new niche for efficient understanding of nature and distribution of existing landrace diversity, wild species, and agroecosystem diversity as well as for formulating different restoration and conservation strategies against ongoing anthropogenic changes. MAS and various genomic tools have enabled us to elucidate the actual diversity at DNA level, phylogenetic relationships among different species, which could be highly relevant for germplasm restoration and conservation programs. Metagenomics and next-generation sequencing (NGS) tools on the other hand have emerged as potential weapon for understanding structural and functional aspects of genome as well as physiological, biochemical, and molecular mechanisms involved in plants, while interacting with various environmental factors. Adaptive genomics can address various conservation concerns more efficiently in relatively shorter period of time. The right application of molecular approaches can provide the great avenues of research for genetic rescue and restoration and, thus, can contribute towards conservation of agro-biodiversity.

13.2 Current Scenario of Agro-Biodiversity

Globally, out of 2.5 lakh plant species, only 150 species dominate the world's agriculture landscape, and 12 species contribute up to 80% of the world's food chain (Motley et al. 2006). More interestingly, less than 30 crops form the foundation of agriculture today, and particularly rice, wheat, and maize alone contribute to more than 50% of the world's daily calorie requirement. High-yielding varieties and hybrids form the basis of modern-day agriculture which has completely replaced high adaptive, broad genetic-based landraces and wild relatives of almost all the species. Every population maintains its level of diversity through natural mating that allows a proper gene flow. Narrow genetic diversity is generally associated with poor fitness, higher mortality, reduced growth, and immunity and ultimately poses the increased risk of extinction; thus species diversity is always considered in conservational programs (Frankham 2005). Environmental factors of a particular habitat determine the nature of the allelic expression of any genome. On the contrary, mating among closely related individuals leads to increased homozygosity, inbreeding depression, and subsequent loss of fitness.

Landraces are important repositories of gene pools that enrich agro-biodiversity and stabilize agroecosystems for sustainable functioning. They are less productive but are crucial for crop breeding due to their broad genetic base and high adaptive potential to specific environmental conditions (Brush 1999). Farm ecosystems alone contain a huge proportion of agro-biodiversity which has been traditionally monitored and managed by farmers for ages. Monocropping and modern-day commercial agriculture have led to the extinction of many useful landraces and wild relatives (Wouw et al. 2010) which is referred to as genetic erosion. To meet changing environmental conditions and human requirements, it is necessary to conserve the diversity including wild relatives and obsolete types of domesticated crops. Understanding the nature of available landrace, wild species, and agroecosystem diversity is the foremost important requirement of conservation biology of endangered species under anthropogenic changes. Therefore, conserving the diversity through in situ, ex situ, on-farm, and home gardening is essential to cater the environmental issues and fulfil the human needs. However, much proportion of available crop diversity has been conserved as in situ and ex situ either as gene banks or breeders' materials (da Silva Dias 2015). As per FAO (2010), more than 7.4 million accessions of different crops are stored and being maintained in above 1750 gene banks globally. The in vitro tissue culture and cryopreservation techniques have also contributed towards a better and more efficient ex situ management of the available genetic resources.

13.3 Molecular Approaches for Restoration and Conservation of Agro-Biodiversity

Genetic diversity indicates the variations in genetic architecture or genes or alleles and is the most important among the three levels of biodiversity as it influences the long-term existence and performance of any population. The knowledge of the genetics of any species, its habitat, and phylogeny is a fundamental requirement to efficiently deal with the conservational issues of that species (Commander et al. 2018). Genetic diversity is a crucial aspect that decides the survivability of a species (Hoban et al. 2020). Therefore, understanding the structural and functional characteristics of genetic variability of any species is the utmost important aspect for prioritizing different conservational efforts. Plenty of molecular methodologies have been evolved recently for the genetic improvement and conservation of different plant species; however, each of them may have few merits and demerits. Protein, DNA, and RNA markers are being exploited globally for understanding the level of genetic variability in various agricultural crops. MAS has elevated the precision of identifying actual conservation units and phylogenetic relationships and formulating different strategies in conservation and restoration programs. Further, molecular marker-based genetic diversity analysis in in situ and ex situ preserved crop plants along with their wild relatives will reduce the redundancy and duplicacy that will ultimately save time, space, and money. Population genetics assists in having an idea of existing gene and genotypic frequency in any population which can be well utilized in both theoretical as well as realistic agro-biodiversity conservational efforts (Bobo-Pinilla et al. 2021).

Understanding phylogeny through molecular approaches enlightens the role of evolutionary and ecological mechanisms and their interaction for manipulating the diversity (Webb et al. 2002). Integration of analytical tools such as population genomics, phylogenomics, metagenomics, etc. addresses various conservation concerns, whereas whole-genome sequencing has opened a new dimension for elucidating the genome architecture and its interaction with other species. Organelle genomes have allowed excavating a more detailed evolutionary history of any species of our interest. Major quantitative trait loci (QTLs) governing the expression of important traits from landraces and wild relatives could be identified and transferred to the cultivated elite lines of crops with the help of available molecular tools. This technique is being exploited worldwide in a number of crops. This will not only save the diversity of genes from extinction but also help in genetic improvement programs of agricultural crops.

13.3.1 Gene or DNA Banks

The concept of plant gene or DNA banks has emerged with a huge potential of conservation, characterization, and utilization of plant biological diversity existing throughout the world. The gene or DNA collections either as live plants or seeds for on-site and off-site conservations have become an important resource and have the great potential to address the biodiversity crisis globally. On-site or in situ conserved plant-population maintains itself within its natural ecosystem habitat and keeps evolving with time and climatic situations. On the contrary, off-site or ex situ conserved plants are stored in the form of seeds, cells, tissues, or genomic DNA under controlled conditions of low temperature. In situ conservation includes natural habitats, whereas ex situ conservation includes genetic reserve, on-farm, as well as home gardens. Through ex situ conservation, a huge amount of genetic diversity can be preserved in the least possible space (Bobo-Pinilla et al. 2021). Such banks not only guarantee the conservation of agro-biodiversity against diseases, insect pests, and climate change but also provides researchers an opportunity to identify novel genes and their products.

International Crops Research Institute Semi-Arid Tropics (ICRISAT) maintains one of the worlds' oldest and biggest gene banks of chickpea, groundnut, and millets with a total of 122,522 accessions. Further, it is a reservoir of 4278 accessions of five small millets as well as 744,177 samples from across 148 countries. This acts as a safety backup for several plants which have now disappeared from their natural habitats in African and Asian countries. Likewise, field gene banks can save crop varieties from impending catastrophes and climate change (Table 13.1). Duplication of material is a biggest practical issue in gene bank management that enhances the space, costing, and workload of the managers. In this context, the molecular characterization through DNA markers and other genomic approaches are the potential tools that enable us in the characterization and refinement of core collections. The molecular and phenotypic passport data would help us to train prediction models and screen almost all the accessions for beneficial traits like tolerance to adaptation against extreme climates and major diseases which can subsequently enhance the efficiency of germplasm restoration and conservation (Khan et al. 2012).

13.3.2 Molecular Marker Technology

The magnitude of genetic diversity decides the adaptability and survival of a plant under varying habitats. Markers like biochemical markers or isozymes, phytochemical markers, and DNA-based markers are frequently used to understand the genetic variability and the relationship within and between populations of a plant species. More particularly DNA markers are more preferred for genetic diversity studies.

Table 13.1 Important global gene banks or hubs maintaining crop genetic resources for agro-biodiversity conservation and genetic improvement

Gene bank/hub/institute	Country	No. of accessions	Focused area/crops
International Maize and Wheat Improvement Center (CIMMYT)	Mexico	153,000 (wheat), 28,000 (maize)	Wheat, beans, maize, cacao, potato, and cassava
International Institute of Tropical Agriculture (IITA)	Nigeria	23,000 (African crops)	Tef, finger millet, roots and tubers, banana, cassava, yam, maize, soybean, Bambara groundnut, cowpea, bean
Biosciences Eastern and Central Africa (BECA)	Kenya	–	Genomic characterization of African orphan crops
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	India	125,000	Genetic improvement of chickpea, groundnut, various millets, sorghum, and pigeon pea
International Center for Tropical Agriculture (CIAT)	Colombia	38,000 (beans), 23,000 (forages), 6600 (cassava)	Beans, forages, cassava
International Potato Center (CIP)	Peru	–	Potato, sweet potato, Andean root and tuber
International Center for Agricultural Research in the Dry Areas (ICARDA)	Syria	145,000	Barley, chickpea, grass pea, lentil, wheat, wild relatives of cereals and legumes
International Rice Research Institute (IRRI)	Philippines	128,000	Rice
International Livestock Research Institute	Ethiopia	19,000	1723 tropical forage species
AfricaRice	Côte d'Ivoire	20,000	Rice
Spanish Plant Genetic Resources National Center (CRF)	Spain	42,586	All crops, legumes, cereals
Fundació Miquel Agustí (FMA)		1774	Tomato, common bean

Source: https://www.genebanks.org/genebanks/, Díez et al. (2018)

Randomly amplified polymorphic DNAs (RAPDs) are quick and easy to perform arbitrary markers which are usually exploited in plant species for diversity analysis; however, they have the problem of reproducibility. Simple sequence repeats (SSRs) are short and tandemly repeated nucleotide sequences available throughout the eukaryotic genome. It's a co-dominant marker with a frequency of one in every 6–7 kb in the plant genome and henceforth exhibits a high degree of allelic diversity. Other markers used for diversity studies in the plants are inter simple sequence repeats (ISSRs) which exist all over the plant genome and are utilized when the information on DNA sequence is limited. On the other hand, sequence characterized amplified regions (SCARs) are more reproducible markers and are developed from sequencing of RAPDs. Other co-dominant markers are restriction fragment length polymorphisms (RFLPs) that detect variations based on differences in the restriction sites of the enzyme. Performing RFLPs is a bit tedious and expensive as they require more amount of purified DNA and radioactive substances. Other markers used for genetic diversity studies in plants are amplified fragment length polymorphisms (AFLPs) in case when the preceding genetic information is lacking. Single nucleotide polymorphisms (SNPs) are among the modern-day markers that are found most abundantly in the genome and, thus, are the powerful tool for varietal identification, characterization, genetic diversity, linkage mapping studies, etc. Expressed sequence tags (ESTs) are frequently used markers for identifying active genes of beneficial agronomic traits, gene cloning, and genetic diversity studies. These powerful molecular markers are being well utilized for germplasm characterization, DNA fingerprinting, understanding the magnitude of actual genetic diversity, and establishment of DNA banks.

In addition, chloroplast DNA in plants is also often used as genetic markers as compared to the mitochondrial genome due to its lower rates of structural mutations. Studying the historic DNA gives better understanding of the ancestral relationships and predicting the evolution pattern in similar species as well in the future. These markers have a great potential in determining genetic variation and evolutionary history in agriculture crops including rare and endangered species and help in developing conservation strategies and conducting restoration practices. Also, identification of conservation units such as excluding the influence of cryptic species and hybridization has become far easier with these markers. Molecular marker-assisted phylogenetic relationships can efficiently distinguish conservation priorities for biodiversity hotspots and discerning species. Molecular markers can contribute to dynamic monitoring and assessment of conservation activities, and instructing the strategies in ex situ conservation programs could be precisely achieved with molecular marker tools (Li et al. 2020).

13.3.3 DNA Microarray

DNA microarray is a modern-day robust and high-throughput technique used to detect the expression patterns of hundreds or thousands of loci simultaneously. Ready-made chips printed with thousands of small and defined dot or spot containing a known DNA sequence (probe) are used to detect gene expression of a large number of unknown samples at a time. This technique eliminates the requirement of either agarose or polyacrylamide gels. The microarray technique can be easily applied for the identification of useful genes, their expression patterns, and useful mutations from samples at a time (Galbraith and Edwards 2010; Govindarajan et al. 2012). The useful genetic resources conserved at various gene banks could be analysed without wasting much time. This will generate important information about useful gene sequences which could be directly utilized in restoration and conservation programs of agro-biodiversity already stored or to be stored for a long term.

Further, harmful genes can be identified from poorly surviving plant types and can be eliminated through various biotechnological tools for improved survival.

13.3.4 Plant DNA Barcoding

DNA barcoding is a novel approach for taxonomic categorization and species identification in plants that involves sequencing DNA in a specific gene (Mosa et al. 2019). This offers hope for finding unidentified specimens that cannot be identified solely on the basis of morphological characteristics. The ambiguous behaviour among closely related species or varieties can be easily detected through DNA barcoding. Nowadays, barcoding the extrachromosomal DNA such as chloroplast DNA is being efficiently used in discriminating the plant species (Kress and Erickson 2007).

13.3.5 Tissue Culture and In Vitro Conservation

Modern plant biotechnology uses a hydroponic-oriented approach, where plants are grown on the soil-less media containing essential nutrients under suitable light conditions. Long-term conservation of crops has been a challenge for years particularly in the case of recalcitrant seeds and vegetative propagating crops. Plant species that do not produce seeds can be efficiently stored for years through various in vitro techniques, and new plants can be generated through micropropagation by growing suitable explants on suitable artificial nutrient media supplemented with growth hormones under controlled light and temperature. In this backdrop, in vitro conservation constitutes as an effective approach for conserving such species without much requirement of space and management. Numerous gene banks have conserved important PGRs in vitro under controlled aseptic conditions (Sánchez-Chiang and Jiménez 2010; Ramírez-Mosqueda et al. 2019). Novel genetic variations can be created in plants through tissue culture techniques involving protoplasts, anthers, microspores, ovules, and embryos (Zhang et al. 2014; Kaeppler et al. 1998). Protoplasts of two non-compatible plant species can be fused to generate variability or transfer the desirable genes, which is not possible through traditional breeding methods. The pathogens are one of the reasons for the loss of plant species, which can be eradicated through tissue culture techniques (Wang et al. 2018). The living cells or tissues of important and rare species can be well preserved at ultra-low temperatures (−190 °C) through cryopreservation (Roque-Borda et al. 2021). Immature and weak embryos of important and rare plants can be rescued and cultured in vitro to generate a healthy plant through embryo rescue technique (Shen et al. 2011). These in vitro techniques act as a safeguard for agro-biodiversity against extinction. This in association with modern-day molecular tools could be highly efficient for agro-biodiversity analysis and preservation.

13.3.6 Genomics

A thorough understanding of the nature, magnitude, and functional implications of existing genetic variation in a population is the prerequisite for utilizing the genomic tools and techniques to address the biodiversity conservational issues. Genomic approaches provide an increased resolution of population structure, various functional, and evolutionary aspects by deploying rapid and low-cost sequencing of either part of the genome or entire genome and advanced bio-informatics tools (Escalante et al. 2014). Further, metagenomics approaches also give the in-depth understanding of an individual and its interaction with the surrounding ecosystems. The abrupt change in the climate has exacerbated the loss of agro-biodiversity. Adaptive genetic variation plays an important role in responding against varying climates and thus improves the chances of plant survival in adverse situations. Genomic approaches enable us for detecting such adaptive genetic variations pertaining to major traits like biotic and abiotic stress tolerance which are useful for climate change mitigation perspectives. The eroded genetic resources have created a major bottleneck for plant improvement programs. Genomics bridges the gap between preserving agro-biodiversity and plant breeding (Mascher et al. 2019). Detection of potentially harmful genetic mutations or alterations at early stages also enables us to preserve or manage before substantial or irreversible changes occur.

Genomic approaches particularly GWAS, i.e. genome-wide association studies, and whole-genome sequencing potentially uncover the thousands of available genetic variations related to adaptability and diseases (Rao et al. 2021). The Sanger method of sequencing (Sanger et al. 1977) is a predominantly used approach for decades for carrying out the routine molecular studies. Accurate genotype to phenotype map for plants in a gene bank gives more precise estimates of genetic value that can offer a great plant breeding potential. Genomics-assisted pre-breeding is another approach for identifying the valuable genetic variations that could be directly exploited in plant breeding programs. Traditional markers and quantitative PCR-based SNP chips including hybridizing array and genotyping by qrtPCR such as Fluidigm dynamic arrays, Illumina GoldenGate, and Applied Biosystems OpenArray are commonly used modern-day tools in the field of genomics. Other techniques include high-density SNP chips like high-density oligonucleotide hybridizing array (i.e. Affymetrix GeneChip and Illumina BeadChip), target DNA or gene sequencing (i.e. fragment capture with oligonucleotide array), genotyping by next-generation sequencing (i.e. exon capture technique), and random DNA sequencing like high-throughput sequencing of representative genomic DNA through restriction-site-associated DNA sequencing. Resequencing the whole genome from more than one individual in the population sample using next-generation sequencing technology like whole-genome sequencing not only detects the nucleotide variations but also formulates the basis for various conservational applications (Hodges et al. 2007; Baird et al. 2008; Perkel 2008; Decker et al. 2009). Conservation genomics and metagenomics are the growing fields where genomic principles are applied to preserve the viability of populations and the biodiversity of living organisms (Supple and Shapiro 2018). Population genomics deals with a large-scale comparison of genomic sequences of populations for scanning genetic similarity and dissimilarity among populations. Comparative genomics is a newly emerged science for the identification of new genes and phylogenetic relationships which could be efficiently utilized for better management of restoration and conservation of important crop species (Alföldi and Lindblad-Toh 2013).

13.3.7 Transcriptomics

Transcriptomics involves the whole transcriptome or a whole set of RNA formed by a genome under a definite condition. Transcriptomes are generally smaller than genomes as junk DNA does not transcribe into RNA transcripts. Gene expression studies directly help in understanding the actual response of plants under varying degrees of adverse climatic conditions. This enabled us to predict the useful phenotypes with higher accuracy and easier identification of genes directly involved in acclimatization and adaptive responses against environmental stresses which can help in solving biodiversity restoration and conservation issues (He et al. 2016). High-throughput techniques like DNA microarray and RNA sequencing could enable us in isolating transcripts and genes pertaining to tolerance against various adverse climates (Mosa et al. 2017). RNA sequences can be plotted against a known reference genome for detecting useful genetic variations or regions which could be straightaway utilized in breeding for better adaptation (De Wit et al. 2012; Bryant et al. 2017). Transcriptomic data enable us to reveal the phylogenomic studies to infer ancient evolutionary histories (Tekle and Wood 2018) and taxonomic status of any plant that will assist in formulating conservation strategies of agro-biodiversity.

13.3.8 Proteomics

The science of proteomics deals with the high-throughput study of all the proteins formed by an individual under a definite circumstance. A variety of proteins having significant roles in various physio-chemical mechanisms under climatic conditions could be identified that can have potential contributions in stress-adaptive phenomena (Ramalingam et al. 2015). Proteomic fingerprinting facilitates the assessment of biodiversity that exists in different populations. Modern techniques like mass spectrometry and different quantitative and bioinformatics approaches have empowered the efficient identification and characterization of key proteins from different plant parts exhibiting various physiological mechanisms (Glinski and Weckwerth 2006). The worthy information like type and concentration of proteins involved in stress tolerance is essential for conservation of risky germplasm and breeding for tolerant genotypes. This could be well applied in crops that are at the risk of getting lost due to unfavourable environmental factors.

13.3.9 Metabolomics

Metabolomics is another important aspect in which different metabolites involved in cellular metabolism and biochemical activities are identified and quantified under different circumstances. As metabolite directly yields a particular phenotype, hence it is a better and more precise indicator of gene expressions. Usually, the metabolomics tools are important in elucidating the plant phenotypes under varied degrees of stresses that cause poor adaptation of plants under changing climates. Thus, plants undergo metabolic reprogramming by themselves to adapt better to predominating stress by generating more quantities of anti-stress molecules like antioxidants, compatible solutes, and several stress-responsive proteins (Doerfler et al. 2014). Metabolomics approaches such as metabolic fingerprinting, profiling, and targeted analysis have emerged as cutting-edge functional biology disciplines for a better and in-depth elucidation of plant-adaptive mechanisms at cellular and subcellular stages under biotic and abiotic stresses. Further, these approaches along with genomic tools enable us for more accurate discovery of potential candidate genes and dissecting pathways involved in key adaptive mechanisms. Applying this knowledge in different important plant genetic resources can help in their better restoration and conservation practices.

13.3.10 Next-Generation Sequencing (NGS)

Recent development in the field of genome sequencing has enabled us for accurate and low-cost sequencing of part of a genome or entire genome of any individual. Such technologies can be used for sequencing non-model organisms also which was not easier through traditional techniques due to the availability of limited genetic information. NGS techniques like whole-genome sequencing and genome sampling (SNPs, target capture sequencing) provide unprecedented power to understand high-resolution patterns of genetic variation present in the natural plant populations (Funk et al. 2012; Leache and Oaks 2017). Furthermore, due to the presence of reference genomes in major crops, the sequencing-based genotyping has overcome the bottleneck of molecular marker technologies. NGS-based gene expression and gene interaction studies have provided a better understanding of the actual genetic background of any phenotype and its complex interactions with the surrounding environment through $G \times E$ interaction studies (Mardis 2008; Neale and Kremer 2011). Further, the massive sequencing potential of NGS has made the metagenomics and phylogenetic studies easier (Thomas et al. 2012) which would definitely contribute towards the restoration and conservation of agro-biodiversity.

13.3.11 Genetic Engineering and Genome Editing

Genetic engineering manipulates the genetic make-up of an individual by directly inserting and expressing the desired gene from one organism. Previously, target sequence modifications were well utilized for transferring favourable genes from exotic sources into elite plant materials. But now the genetic engineering has changed the entire scenario. It has a great potential to change and actually increases the agro-biodiversity of the planet through various gene and genome editing tools (Johnson et al. 2016; Supple and Shapiro 2018). It can insert desirable traits, knockout undesirable traits, and manipulate the DNA for up- or downregulating the expression depending on the requirement of plant species. This has been successfully demonstrated in many commercial crops like *Gossypium* species, *Zea mays*, *Solanum melongena*, etc. and marketed globally with high socio-environmental critics. However, GE technologies provide opportunities for more precise and targeted changes in the DNA of any individual. Recently popularized and accepted highly precise molecular tools like CRISPR, i.e. clustered regularly interspaced short palindromic repeats, have opened a new niche for gene or genome editing in agriculture and biodiversity conservation by saving lot of time (El-Mounadi et al. 2020; Jaganathan et al. 2018). These technologies can actually transmit the changes across breeding population, even in the wild relatives through gene drives. Advanced tool-like synthetic gene drives open up a way for creating additional diversity and better conservation of diverse PGRs.

13.4 Major Challenges in Conservation and Restoration of Agro-Biodiversity

Recent development and advancement in molecular science have opened new niches for efficient identification, understanding, and preservation of existing agro-biodiversity. However, there are still numerous challenges among environmental researchers and conservators. Understanding the actual distribution pattern and the nature of genetic diversity among a very large number of PGRs preserved in or off-site locations is a big challenge today. Further, elucidating the role of various ecological factors involved in the distribution of diversity in all major crops and their wild relatives is a growing thrust area. Most useful combination of agro-morphological, biochemical, and molecular characters needs to be defined to understand the patterns of diversity. Both on-site and off-site conservations face practical challenges like tracking the identity of an accession, maintaining the genetic integrity of accessions, and handling the needless duplications in or across gene banks (Mascher et al. 2019). Duplications and redundancy of PGRs not only increase space and cost but also make its management difficult. Though plenty of molecular tools are available, screening all of them is a major practical issue. Phylogenetic studies have been restricted to few major species so far, which have to extend to explore other rare and endangered species as well. Identifying the ecological factors, their influence, and responses of plants to such factors at the molecular level has been initiated in major crops only which needs to be done in other crops also for a better understanding of adaptive responses. Though biotechnology has enormous potential for understanding and preserving genetic diversity, high investment requirement is the biggest challenge today.

13.5 Conclusion and Way Forward

The availability of biodiversity is definitely an essential requirement for the short- and long-term existence of any plant species, balancing ecosystems and achieving global food security on sustainable basis. The ever-growing human population and subsequent change in climate have led to the loss of a significant amount of agro-biodiversity. Restoration and conservation of available biodiversity of crop species have become the utmost important global objective for environment sustainability. Advances in molecular and genomic techniques have indispensably assisted in detecting actual genetic diversity at the DNA level, phylogenetic relationships, and identification of important genes pertaining to tolerance against various abiotic and biotic stresses for developing efficient restoration and conservation strategies. Molecular markers like RAPD, microsatellites, AFLP, RFLP, ISSR, SCAR, SNP, and ESTs have undoubtedly been proven to be promising approaches in detecting the nature and the extent of actual genetic diversity within and between species from diverse habitats. Genomics and metagenomics approaches have a greater potential to efficiently elucidate the genetic composition, structure, and functional aspects of available PGRs as well as rare and endangered species and develop successful preservation strategies. In situ and ex situ conservations have taken care of agro-biodiversity to an extent; however, duplication and other issues are major challenges in their management. Molecular tools could help in the effective screening of a large number of PGRs, detecting the duplications and useful genes and formulating long-term conservation programs. However, the pressing need for further exploring the genetic diversity available at nature habitats and various gene banks, understanding their composition and usefulness, and conserving them could be easily efficiently achieved through modern-day molecular approaches.

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Genomics Approaches for Restoration and Conservation of Agro-Biodiversity

14

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Abstract

Agro-biodiversity provides foods for living biota along with several things for easy living and survival on the planet. It is in various forms and goods like firewood; approximately two billion population globally utilize firewood as a source of energy for cooking and heating; fiber, like cotton, wool, silk, and flax; drugs, approximately 25% of drugs utilized come from plants; and for construction of household and utilization of timber wood as furniture, sports goods, and many. Nowadays it is an alarming threat because of the reduction in free space, smaller and fragmented habitats, and overexploitation by human for urbanization and fulfillment of their needs. This degradation and destruction have caused imbalance in the nature which has resulted in several calamities and disasters in the recent past. So it is important to protect and conserve the agro-biodiversity to

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save the nature by bringing stable management practices to maintain at optimal level and extract sustainable benefits in the present as well as in the future. However, the process of conservation of biodiversity is being done by many conservators, economists, and social workers. But with the advent of new advanced tools and techniques and scientifically proven procedures, it will be easy and effective in short period as compared to traditional methods. The restoration and conservation of genetic diversity among wild species and landraces are the foremost important requirements. The use of molecular approaches like DNA barcoding, molecular markers techniques, genomics, transcriptomics, metabolomics, and genetic engineering will help detect the variation and similarity at genetic level among the species. This chapter provides an overview of the different molecular techniques and approaches used in restoration and conservation of agro-biodiversity.

Keywords

Agro-biodiversity · DNA barcoding · Molecular marker techniques · Genomics · Germplasm restoration

14.1 Introduction

The biodiversity is classified on the basis of scientific facts, genomic constitution, uses, and significance. The biodiversity which is most useful for human race is agriculture-related diversity known as agro-biodiversity. This diversity of agriculture and its related commodities either introduced or present in the ecosystem are highly stable until and unless some external forces or unnatural events disturb (Hagmann and Muller 2001). For as long as 10,000 years, efficiency of crop has been upgraded by means of the procedures of rearing. Carrying out breeding includes the choice of certain hereditary variations of a couple of picked plant species as per their appropriateness for use, regardless of whether it is palatable or cannot be consumed. The two key essentials to both rearing and development are variety and determination. New hereditary varieties are developed using wild populations which emerge from a moderate procedure of blending the genomes with sexual multiplication.

However, the modern agriculture practices mainly deal with the conservation and utilization of valuable genetic resources. These genetic resources are widely used by plant breeders to utilize and make favorable combinations and develop new varieties. The conservation and restoration of these resources play a vital role in breeding programs. In addition, the absence or losing the wide germplasm resource and stock will pave way to limitations in future classical breeding approaches. This advanced technology acts as a strong technique in the determination of genetic similarity and phylogenesis based on dissimilarity in different cultivars and germplasm lines for their genetic traits. The appropriate use of molecular technique could be used not only for identifications of variation within and between the species but also for restoration and conservation of genetic resources.

14.2 Status of Agro-Biodiversity in India

There are about 250,000 worldwide known species of the plant; approximately 7000 of them have historically been utilized in the diets of human. At present, only about 30 species of the crops play a major role in world out of which only three species, namely, rice, maize, and wheat, provide more than half of the calories consumed in the world on daily basis. Hence, it is important to conserve the variability of plant, animals, and microorganisms at species, genetic, and ecosystem level to endure the key purpose of agroecosystem (Table 14.1).

The conservation and restoration of biodiversity at present is important to be used safely and wisely to preserve for the future. However, the initial approach of classifying biodiversity based on morphological and physiological traits was supported by taxonomic and phylogenetic studies. The idea of hereditary markers is certainly not a new one; Gregor Mendel utilized hereditary markers based on phenotype in his studies in the nineteenth century. Afterward, hereditary markers based on phenotype for *Drosophila* prompted the foundation of the hypothesis of hereditary linkage.

The conventional plant breeding is a time-consuming and laborious method. More accurate and fast approach to identify and select the desired trait is marker-assisted selection (MAS) (Tester and Langridge 2010). The molecular markers are used in mapping and tagging of genes/quantitative trait loci (QTLs), positional cloning, identification of hybrids, selection of parents, heterosis prediction, evaluation of somaclonal variations, phylogenetic analysis, purity testing, and DNA fingerprinting. The application of a genetic marker depends on its position in genome, cost, and its simple use. Previously genetic markers were not used for diversity and evolutionary analysis, and their physical location was mostly unknown. The genome sequencing technologies accurately define the genomic location of genetic markers. The molecular markers are differentiated based on prior sequence information, mode of transmission (biparental or uniparental; nuclear

Table 14.1 Status of cryopreserved germplasm as on December 31, 2019 (ICAR-NBPGR 2020)

Crop/crop group	Present status (number)
Recalcitrant and intermediate seeds	
Fruits and Nuts plants (incl. orchid)	3583
Spices and condiments	164
Plantation crops	121
Agroforestry and forestry	1645
Industrial crops	1341
Medicinal and aromatic	37
Subtotal	**6891**
Orthodox seeds	3911
Dormant buds	389
Pollen grains	591
Genomic resources	2114
Total	**13,896**

Table 14.2 DNA barcoding markers and application

DNA barcode markers used	Application	References
Two-loci combination of rbcL and matK	The Consortium for the Barcode of Life (CBOL) Plant Working Group recommended chloroplast DNA barcode for land plants	CBOL Plant Working Group et al. (2009)
ITS2 region	Identification of medicinal plants and their closely related species	Chen et al. (2010)
DNA barcode markers	Identification of mahogany family (*Meliaceae*) tree species	Muellner et al. (2011)
Standard plant DNA barcode markers	Identification of wood samples collected at timber-processing units in Andhra Pradesh and Tamil Nadu	Nithaniyal et al. (2014)
Standard plant DNA barcode markers	Identification of timber found in *Araucaria* rain forests of the southern Atlantic coast of Brazil	Bolson et al. (2015)

or organellar inheritance), number of loci per marker (single or multiple), and method of analysis (i.e., hybridization-based and PCR-based). In the early 1980s, the unknown nucleotide sequence in the form of primer showed variation in the germplasm based on restriction enzyme site of action. The first DNA marker technology was restriction fragment length polymorphism (RFLP) used for plant genotyping (Botstein et al. 1980). Later, different types of molecular markers were developed, i.e., simple sequence repeats (SSRs) (Litt and Luty 1989), random amplification of polymorphic DNAs (RAPDs) (Williams et al. 1990), cleaved amplified polymorphic sequences (CAPS) (Konieczny and Ausubel 1993), sequence characterized amplified regions (SCARs) (Paran and Michelmore 1993), inter-simple sequence repeats (ISSRs) (Salimath et al. 1995), amplified fragment length polymorphisms (AFLPs) (Vos et al. 1995), and many more. These methods were good for a small number of samples and were found to be more expensive, laborious, and time-consuming for large-scale analysis. The single nucleotide polymorphisms (SNPs) are the most popular and abundant marker (Rafalski 2002; Zhu et al. 2003). Initially, the expressed sequence tags (ESTs) were used for single base-pair resolution and variation identification (Deschamps et al. 2012). Nowadays, whole genome sequencing technologies dealing with SNPs (single nucleotide polymorphisms) which have comparatively low operation costs are more popular. Moreover, these sequence-based markers are inherently able to capture vast amount of variation at single-base resolution, making them particularly useful for the detection of perfect markers (DNA polymorphisms causally linked to traits of interest) and discovery and analysis of the alleles involved.

DNA barcoding helps in estimating the species richness and diversity. The main reason for inflated biodiversity is misinformation of species identities (Sloan et al. 2009; Kunin et al. 2010). The robust bioinformatics algorithms along with these advanced techniques will give precise and accurate information of these species (Table 14.2).

Genotyping by sequencing approach is being used successfully for rapid discovery of sequence-based molecular markers to construct a genetic map without a reference genome (He et al. 2016). An extremely large number of markers being used for high-density genetic maps and GBS can serve as a reference genome for making physical maps and correcting unordered sequence contigs (Poland and Rife 2012; Chung et al. 2017). If a reference genome is available, markers can be ordered along with the physical map, and no need to calculate recombination frequencies for linkage map construction. If the coverage is low, markers can be used to narrow points of recombination from 100 to 200 kb intervals (Deschamps et al. 2012; Huang et al. 2009; Xie et al. 2010; Chung et al. 2017). A genetic map of pearl millet using the GBS approach has been reported by Moumouni et al. (2015). They generated high-quality SNPs to construct a genetic map with an average interval of 2.1 (±0.6) cM between the SNP markers. Their study demonstrated that GBS can produce a denser and more uniform genetic map than previously published genetic map methods. The high resolution of SNP markers was identified in barley, and the GBS mapping data were used to confirm that the semi-dwarf gene (arise) is located on barley chromosome 5H (Liu et al. 2014). Construction of a GBS linkage map using the sequence-based markers leads to the RAD technique (Baird et al. 2008), which has been used in barley QTL analysis (Chutimanitsakun et al. 2011). Spindel et al. (2013) used a 384 plex GBS protocol and added 30,984 SNP markers to 176 recombinant inbred lines mapping population of rice indica × japonica and mapped quantitative trait loci (QTLs) for leaf width and aluminum tolerance. Thomson et al. (2012) demonstrated that 384 plex SNP genotyping on the BeadXpress platform is a robust and efficient method for marker genotyping and mapping in rice (Heffner et al. 2009; Huang et al. 2009; Jannink et al. 2010). GBS was applied to bread wheat, resulting in the incorporation of thousands of markers in the bread wheat linkage map (Poland et al. 2012). There are few studies reporting the utilization of molecular markers (Table 14.3) for conserving plant or agro-biodiversity analysis.

Among the main causes of native plant extinction is the introduction of invasive species (Barbier et al. 2013). Biological invasions are recognized as one of the most important causes of ecosystem degradation as well as community structure, local species, and biodiversity losses worldwide (Pyšek et al. 2012). The conservation and restoration of ecosystem lead to protection of the whole ecosystem. In a similar manner, plant species protection and conservation are carried out through in situ (on site) conservation (Table 14.4).

14.3 Omics Approaches to Strengthen Agro-Biodiversity

The complete genetic characterization of organism is only possible through advanced genomic tools and techniques. The history, origin, and evolution can be determined with the use of these genomic approaches. It can also lead to restoration and conservation of the agro-biodiversity by providing an insight into structural and functional processes. The disturbance in nature due to change in climatic conditions

Table 14.3 Diverse molecular markers and application in species identification

Molecular markers used	Application	References
Amplified fragment length polymorphisms (AFLP)	Screened 36 downy mildew-resistant alfalfa plants and 36 susceptible plants for DNA polymorphisms using 14 AFLP primer combinations	Obert et al. (2000)
Sequence characterized amplified regions (SCARs)	Identified population-specific SCAR markers in *Jatropha curcas*. Characterized radiation-induced and tissue culture-derived dwarf banana plants by using a SCAR marker	Basha and Sujatha (2007), Suprasanna et al. (2008)
Randomly amplified polymorphic DNA (RAPD) markers	Two RAPD markers (OPF04700 and OPA091375) were found to be linked to the plant height gene	Dhanasekar et al. (2010)
Diversity arrays technology (DArT)	Appropriate for genotyping large genome size polyploid species, such as wheat	Zhang et al. (2011)
Simple sequence repeats (SSRs)	Confirmed the purity of hybrids between salt-resistant and susceptible genotypes of mung bean	Nirmala et al. (2016)
Expressed sequence tags (ESTs)	Genetic diversity among 27 castor accessions	Thatikunta et al. (2016)
Single nucleotide polymorphism (SNP)	Identify Korean specific ecotypes of *C. tricuspidata* via amplification refractory mutation system (ARMS)-PCR and high-resolution melting (HRM) curve analyses	Lee et al. (2017)
Amplified fragment length polymorphisms (AFLP)	Evaluated the variation and relationships of 25 French pea accessions using fatty acid profiling	El-Esawi et al. (2018)

is the main reason for loss in habit and habitat of organisms. With this climate change and adverse conditions, individuals survive with adaptive genetic variation. This genetic technique helps to elucidate changes in the individuals and their behavior with the surrounding based on environment or climatic conditions. The mitigation strategies followed with respect to change in climatic conditions can be well studied using these genomic approaches. The change or alteration at genetic level in early growth stages can be monitored using these approaches. Thus, genomics links agro-biodiversity with plant breeding (Mascher et al. 2019). This branch of science is known as conservation genomics. It helps in conserving the biodiversity of living organisms (Supple and Shapiro 2018). The genetic similarity and differences among large populations can be scanned using a new branch of science, comparative genomics. The phylogenetic relationships can be detected which can be used for restoration and conservation of diverse crop species (Alföldi and Lindblad-Toh 2013).

Another omics approach that involves the study of RNA composition of an individual genome under a particular condition is known as transcriptomics. The genetic expression of individual varies with the change in environmental condition. It provides broad perspective of the genetic changes, response, and behavior caused

Table 14.4 In vitro conservation of different plant species

Plant species	In vitro Conditions	Storage period	Storage temperature	Reference
Solanum tuberosum L. (potato germplasm)	Microtubers produced on media devoid of ABA and containing high sucrose concentrations and N6-benzyladenine (44.38 mM)	12 months	6 ± 1 °C	Gopal et al. (2004)
Spiranthes brevilabris (Orchidaceae)	It maintains a high degree of mycobiont specificity under in vitro symbiotic seed germination conditions	12 months	SCC	Stewart and Kane (2007)
Drosophyllum lusitanicum (L.) Link	Double-node cuttings were maintained on Murashige and Skoog's medium supplemented with 60 g dm^{-3} sucrose, 20 g dm^{-3} mannitol, and 0.91 PM zeatin	4, 8, and 12 months	25 °C	Gonçalves and Romano (2007)
Elettaria cardamomum Maton. (cardamom)	In vitro conservation by slow growth method was achieved on 1/2 MS (major salts) + 5 μM BAP + 0.7% agar (conservation medium); about 70% of the cultures survived	18 months	25 ± 2 °C	Tyagi et al. (2009)
Medusagyne oppositifolia (jellyfish tree)	Long-term in vitro cultures of M. oppositifolia were slow growing and eventually lost the ability to multiply and root	6 months	22 ± 2 °C	Marriott and Sarasan (2010)
Castanea sativa (chestnut)	Slow growth storage has been achieved for *Castanea sativa* (cv. Montemarano) shoot cultures where 82% of explants survived	48 months	8 and 23 °C	Capuana and Di Lonardo (2013)

due to changes in environmental conditions leading to restoration and conservation of biodiversity (He et al. 2016). The evolutionary and phylogenetic studies can also be evaluated using transcriptomic approach (Tekle and Wood 2018). Ramalingam et al. (2015) stated that proteins have a significant role in adaptive mechanism under different stress conditions. The branch of science which deals with study of proteins is known as proteomics. The protein concentration and level vary with the change in available conditions. It can be detected using various techniques like mass spectrometry to determine proteins and their amount; array-based proteomics based on functions, regulation level, and interacting partners within the cell; and bioinformatics approaches to exhibit different physiological mechanisms (Glinski and Weckwerth 2006). The detection of such changes in the species at protein level will help in the conservation and preservation of biodiversity by avoiding unfavorable and stress conditions.

Another branch of science is called metabolomics which deals with metabolites at cellular level and their biochemical activities. The generation of anti-stress molecules and proteins like antioxidants and compatible solutes under the influence of stress condition is observed in the metabolomics study (Doerfler et al. 2014). It can help in dissemination of various metabolic pathways and find adaptive mechanisms to control any change. In this way metabolomics in association with other approaches play a significant role in the restoration and conservation of species. The genetic engineering approach is used to manipulate the genetic makeup using insertion of desired gene. Favorable gene insertion from wild and exotic germplasm into elite material results in desired end product. It is precise with high-accuracy rate which uses various genome editing tools (Johnson et al. 2016; Supple and Shapiro 2018). Also it can knockout undesirable and unwanted traits, i.e., manipulate the DNA as per plant species. It has been successfully proven in various commercial crops like *Gossypium* species, *Zea mays*, *Solanum melongena*, etc. The studies suggest that various pathways used through transcriptomics, proteomics, and metabolomics approaches will accelerate the conventional and molecular breeding in characterization of germplasm and eventually restoration and conservation of biodiversity.

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Part V

Technological Intervention for Agricultural Development

15

Polyhydroxyalkanoate Production in Transgenic Plants: Green Plastics for Better Future and Environmental Sustainability

Manoj K. Sharma, Shashank Singh, Neelesh Kapoor, and R. S. Tomar

Abstract

In the present time, polyhydroxyalkanoates have established itself as the alternatives of petroleum-based synthetic polymers due to their biodegradability and eco-friendly nature. Several efforts have been done toward this direction by using microorganisms. Since the last two decades, several scientists have engaged in search of cost-effective alternatives of producing polyhydroxyalkanoates at larger scales. Therefore, many plant species have been genetically engineered for this purpose. The major obstacles in producing PHA polymers in transgenic plants are the regulation of the appropriate monomer's composition and ratio synthesized in their cells. Efforts are on the way to encounter these difficulties as soon as possible. Among the targeted cell organelles, plastids have been considered as the best sites for higher production of polyhydroxyalkanoates because of its maternal inheritance and it is unaffected by gene silencing. The research is also going on for enhancing the production and accumulation of these biopolymers in transgenic plants. Polyhydroxyalkanoate production technologies are still costly, but these could be cost-effective in the near future. The present chapter describes about the current status of transgenic plants developed for the production of polyhydroxyalkanoates at cheaper costs.

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Keywords

Bacteria · Bioreactors · Environmental pollutants · PHA · Transgenic plants

15.1 Introduction

Over the past 60 years, the development of synthetic polymers has reduced the men's dependence upon the utilization of plant product-based polymers such as rubber, cotton, wood, etc. But the excessive and ever-growing demands of utilizing synthetic polymers raise the global environmental concerns. Therefore, the scientific community has engaged to discover alternatives of synthetic polymers. As an alternative of synthetic polymers, polyhydroxyalkanoates (PHAs) came into existence. These are the natural products of certain bacterial cells. Therefore, scientists decided to produce biological polymers by using bacterial cells as bioreactors. This was first time exploited in 1980 by Imperial Chemical Industries (Anderson and Dawes 1990). This industry generated a large setup for the bulk production of polyhydroxyalkanoates using polymer-accumulating bacterial strains such as *Ralstonia eutropha*. But the cost of producing PHAs through this way was very high. So again there were also the requirements of cost-effective alternatives for producing biopolymers. The development of advanced biotechnological tools attracted the concern of global scientists toward the utilization of plant bioreactors for producing renewable biological polymers. Therefore, the scientific community moved toward the utilization of plant bioreactors for generating polyhydroxyalkanoates (PHAs) in a cost-effective and eco-friendly manner. For this purpose, a variety of transgenic plant species including *Arabidopsis*, tobacco, rapeseed, cotton, alfalfa, flax, sugarcane, *Camelina*, and oil palm were tested at larger scales and generated new dimensions of producing biopolymers.

Polyhydroxyalkanoates (PHAs) are biopolyesters that are synthesized naturally in a broad range of bacterial cells such as *Alcaligenes eutrophus* and many other species as an inert carbon and energy reserve accumulated in the cytoplasm up to about 80% of the total dry weight in the form of round-shaped granules with a diameter of 0.2–1.0 μm (Sabbagh and Muhamad 2017). These polymers are made up of about 600–35,000 identical monomer units. Polyhydroxyalkanoates act as water-insoluble storage compounds which are synthesized under environmental stress conditions in the excess of carbon and the limiting quantities of important growth nutrients such as nitrogen, phosphorus, iron, magnesium, potassium, sulfur, zinc, or oxygen (Masood et al. 2014). These biopolymers are depolymerized during the exhausted carbon source conditions. Thus, the degraded products could be used by microbes as an energy and carbon source (Anderson and Dawes 1990).

Polyhydroxyalkanoates (PHAs) are considered similar to the conventional plastics in reference of its properties such as thermoplastic and polypropylene nature (Anjum et al. 2016). Instead of petrochemical plastics, PHAs are natural, nontoxic, biodegradable, and renewable (Sharma et al. 2016). These properties make PHA an attractive alternative of petrochemical plastic. In the near future, it is hopefully projected that the production of synthetic plastic polymers could possibly reached up to about eight hundred ten million tons (810 million tons) by the end of 2050 (Gumel et al. 2013). As it is well known that plastic pollution has been an unbeatable burning issue across the globe, it has been an urgent necessity to find out the eco-friendly alternatives of synthetic plastics. That's why, the scientific community and industries are engaging to produce synthetic polymers through natural means. Generally microbial bioreactors are utilized in producing PHAs at larger scales, but the whole process of bioplastic polymer production is still highly expensive than the process of producing petrochemical-based synthetic polymers due to the cost of the nutrition for microbial cultures (Baikar et al. 2017). So the scientific community has engaged in optimizing transgenic plants as novel bioreactors for production of PHAs at cheaper costs. The present chapter summarizes the information about PHA, its structure, biosynthesis, and the current status of transgenic plants which were engineered for producing PHAs at cheaper costs.

15.2 PHA Structure and Biosynthesis

Polyhydroxyalkanoates are generally linear polyesters consisting of several 3-(*R*)-hydroxy fatty acid monomers (HA) linked together by ester bonds. These ester bonds are produced by the linkage of carboxylic group of one monomer unit to the hydroxyl group of another monomer unit (Sudesh et al. 2000; Lenz and Marchessault 2005). On the basis of the presence of carbon atoms in the monomers, polyhydroxyalkanoates are generally categorized into two major groups. The first group is called short chain length polyhydroxyalkanoates (scl-PHAs), and the second group is medium chain length polyhydroxyalkanoates (mcl-PHAs). Short chain length polyhydroxyalkanoates (scl-PHAs) generally consist of 3–5 carbon atoms, whereas the medium chain length polyhydroxyalkanoates (scl-PHAs) have 6–14 carbons. Under natural conditions, the short chain length polyhydroxyalkanoates (scl-PHAs) are synthesized in *Cupriavidus necator*, while the medium chain length polyhydroxyalkanoates (scl-PHAs) are accumulated in *Pseudomonas* species. The examples of short chain length PHAs are P(3HB) [poly-3-hydroxybutyrate], P(4HB) [poly-4-hydroxybutyrate], and P(3HV) [Poly (3-hydroxyvalerate)] or the copolymer P(3HB-co-3HV), whereas the P(3HHx) [poly-3-hydroxyhexanoate], P(3HO) [poly-3-hydroxyoctanoate], and copolymer P (3HHx-co-3HO) are considered as medium chain length PHAs (Kim and Lenz 2001). Each polyhydroxyalkanoate (PHA) polymer generally consists of about 1000–10,000 monomers, but most of them are synthesized by short chain length (SCL) monomer units (Van der walle et al. 2001). The chemical structure of polyhydroxyalkanoates (PHAs) is depicted in Fig. 15.1.

Most of our knowledge about biosynthesis of polyhydroxyalkanoate is mainly based upon the studies on the production of polyhydroxybutyrate (PHB) in cytoplasm of a gram-negative soil bacterium *Ralstonia eutrophus* or *Alcaligenes eutrophus* bacteria. This bacterium has the capability of producing polyhydroxyalkanoate in a natural way and could accumulate the polymer up to

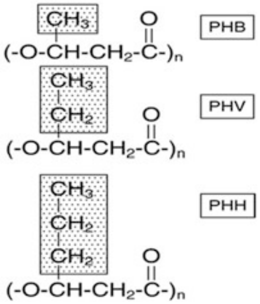

Fig. 15.1 The chemical structure of polyhydroxyalkanoates (PHAs). The pendant *R* groups (shaded boxes) vary in chain length from 1 carbon (C1) to over 14 carbons (C14). Structures shown here are poly-3-hydroxybutyrate (PHB) [*R* = methyl], poly-3-hydroxyvalerate (PHV) [*R* = ethyl], and poly-3-hydroxyhexanoate (PHH) or poly-4-hydroxybutyrate (P4HB) [*R* = propyl]. (Adapted from Suriyamongkol et al. 2007)

85% of its total dry body weight when grown on culture media with excess of glucose. In this way, it acts as an energy source, but the production of this polymer is limited when there is growth-limiting conditions such as lack of macroelements such as nitrogen, phosphorus, and trace elements or the lack of oxygen in culture media (De Koning 1995). Previous studies reported that the polyhydroxybutyrate (PHB) could be depolymerized into acetoacetate and further into acetyl coenzyme A (CoA) by applying growth-limiting conditions (Steinbuchel and Valentin 1995). Therefore, it is clearly demonstrated that the acetyl coenzyme A acts as a precursor of polyhydroxybutyrate biosynthesis in bacterial cell. Polyhydroxybutyrate (PHB) decomposes into 3-hydrobutyrate (3-HB) monomers that can be used by fungi and bacteria as carbon sources. The biosynthesis of PHB was first time described in 1973 in a bacterium *Ralstonia eutrophus* by Gottingen and Hull (Senior and Dawes 1973). There are three key enzymes, namely, acetoacetyl-CoA reductase, 3-ketothiolase, and PHA synthase which leads to the production of polyhydroxybutyrate by using acetyl-CoA. PHA synthase uses CoA thioester of (*R*)-hydroxy fatty acids as substrate. The enzyme popularly known as 3-ketothiolase encoded by gene phaA or phbA is mainly responsible for catalyzing the reversible condensation of two molecules of acetyl-CoA into acetoacetyl-CoA molecule. The acetoacetyl-CoA reductase encoded by *phaB or phbB* gene reduces acetoacetyl-CoA into *R*-(−)-3-hydroxybutyryl-CoA. After that the *R*-(−)-3-hydroxybutyryl-CoA finally polymerizes into polyhydroxybutyrate (PHB) by the action of PHA synthase enzyme encoded by a gene called *phaC or phbC* (Yunus et al. 2008; Kosseva and Rusbandi 2018). The polyhydroxyalkanoates (PHAs) biosynthesis pathway is schematically depicted in Fig. 15.2. Polyhydroxyalkanoates are generally biosynthesized through two possible routes. The first route is based upon β-oxidation pathway intermediates and also on alkanoic acids. In this process, the levorotatory *S*-3-hydroxyacyl-CoA is converted into *R*-3-hydroxyacyl-CoA, a dextrorotatory enantiomer by the action of an enzyme epimerase. In the second route, the fatty acid biosynthesis intermediates such as *R*-3-hydroxyacyl-ACP are used. In this process, the acyl carrier protein

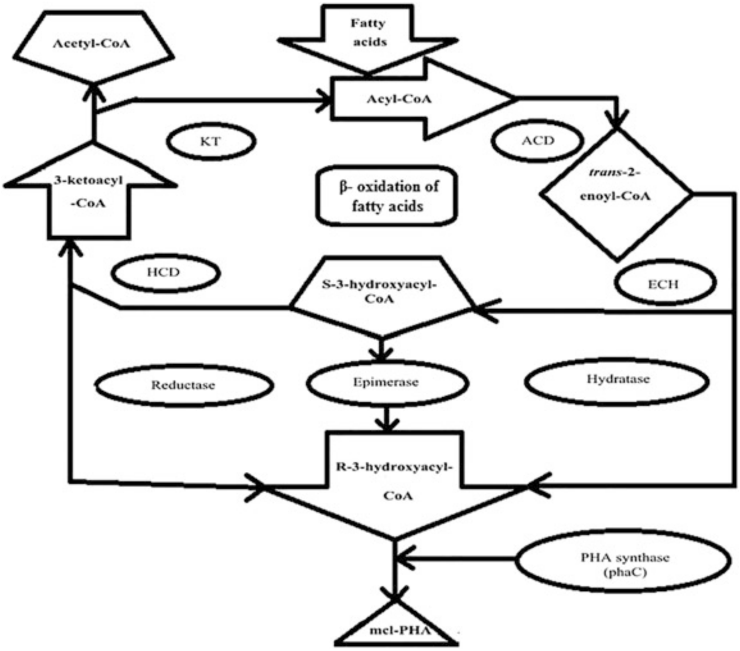

Fig. 15.2 The medium chain length polyhydroxyalkanoates (mcl-PHA) biosynthesis pathways occur in the peroxisomes of transgenic plants. Here, enzyme ACD = acyl-CoA dehydrogenase; ECH = enoyl-CoA hydratase; HCD = L-3-hydroxyacyl-CoA dehydrogenase; and KT = -β-ketothiolase. (Reproduced from Dobrogojski et al. 2018)

(ACP) is replaced by coenzyme A using an important enzyme 3-hydroxyacyl-CoA-ACP transacylase. Both these processes are completed by a gene called phaC [Kosseva and Rusbandi 2018].

15.3 PHA Production in Transgenic Plants

The production of PHAs by using microorganisms is costly because of various factors such as variety and amount of nutrition supplied for microbes, optimized growth environment, and sterilized conditions (Din et al. 2012; Mozejko-Ciesielska and Kiewisz 2016). Therefore in comparison to microbes, transgenic plants are considered as cheaper eco-friendly alternatives. The biosynthesis of PHAs in transgenic plants mainly depends upon mineral salts, water, light, and carbon dioxide (CO_2). The PHA production in transgenic plants is generally based upon the availability of acetyl-CoA, a primary substrate for PHA biosynthesis, because the plant cells do not have the abilities to degrade PHA as the microbes do. Acetyl-CoA is the main metabolite of plant's catabolic and anabolic processes. The plant cellular compartments such as cytoplasm, mitochondria, peroxisomes, and plastids are rich in acetyl-CoA. Therefore, the scientists targeted these compartments as the major sites for producing and accumulating various PHAs in transgenic plants. The literature showed that the first experimental research attempt for producing PHA was successfully achieved in the cytoplasm of transgenic *Arabidopsis thaliana*. After this work several another research experiments were also conducted using various plant species. But the deficiency of acetyl-CoA and acetoacetyl-CoA because of their utilization in plant hormone and steroid biosynthesis pathways limited the production of PHAs inside plant cell cytoplasm. Like cytoplasm, mitochondria also have the limitations of the deficiency of acetyl-CoA because of its utilization during cellular respiration. Plastids appear to the best site for PHA biosynthesis in plants because there acetyl-CoA is present in higher concentrations and mainly utilized for the biosynthesis of fatty acids. The plastids are the organelles which work properly despite the structural changes and have the ability to store larger starch granules. But the plastids do not have the stocks of beta ketothiolases. The beta ketothiolases are located in the cell's cytoplasm. This problem could be overcome by applying specific DNA-encoding plastid-targeted sequences inserting in the vectors. The peroxisomes are also considered as high potential sites for the production of PHAs in transgenic plant cells because of having high reductive strength of NADH and their beta oxidation of fatty acids. Peroxisomes are important cell organelles because of synthesizing medium chain length polyhydroxyalkanoates (mcl-PHAs). Since the last two decades, several scientists are doing research on producing PHAs in transgenic plants. The detailed information regarding the current status of transgenic plants developed for producing polyhydroxyalkanoates are given in Table 15.1.

15.4 Conclusion and Future Prospects

The environmental pollution generated through petroleum-based synthetic polymers has become a very big global challenge. The production of synthetic polymers is increasing day by day, and now it has appeared in an unbeatable form of pollutants. The management of the plastic and its products is not an easy task; it takes several hundreds of years to be decomposed. Therefore, it is a need of present time to find out eco-friendly biodegradable alternatives. Polyhydroxyalkanoates (PHAs) have appeared as a smart choice of scientific community as well as industry in the form of plastic alternatives. PHAs are the major class of biodegradable biopolymers which are biosynthesized by microorganisms in a natural way. The production of PHAs by using microorganisms is costly because of various factors such as variety and amount of nutrition supplied for microbes, optimized growth environment, and sterilized conditions. Therefore in comparison to microbes, transgenic plants are considered as cheaper eco-friendly alternatives. The biosynthesis of PHAs in transgenic plants mainly depends upon mineral salts, water, light, and carbon dioxide (CO_2). Some cellular compartments such as cytoplasm, mitochondria, peroxisomes, and plastids have been targeted as important sites for producing and accumulating PHAs in transgenic plants. Since the last two decades, several scientists have engaged in research for optimizing transgenic plants as bioreactors for producing PHAs. Several plant species including *Arabidopsis thaliana*, *Camelina*, tobacco,

Table 15.1 The current status of transgenic plants engineered for production of polyhydroxyalkanoates (PHAs)

Plant species	Genes	Targeted cell organelle	PHA type	References
Arabidopsis thaliana	*phaA*, *phaB*, *phaC*	Cytoplasm, nucleus, vacuole	P3HB	Poirier et al. (1992)
Arabidopsis thaliana	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Nawrath et al. (1994)
Arabidopsis thaliana	*phbB*, *phbC*	Cytoplasm	P3HB	Poirier et al. (1995)
Arabidopsis thaliana	*phaC1*	Peroxisomes	mclPHA	Mittendorf et al. (1998)
Arabidopsis thaliana	*phbA*, *phbB*, *phaC*	Plastids	P3HB-3HV	Slater et al. (1999)
Arabidopsis thaliana	*phbA*, *phbB*, *phaC*	Plastids	P3HB-3HV	Valentin et al. (1999)
Arabidopsis thaliana	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Bohmert et al. (2000)
Arabidopsis thaliana	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Bohmert et al. (2002)
Arabidopsis thaliana	*phaC*$_{Ac}$	Peroxisomes	scl-mclPHA	Arai et al. (2002)
Arabidopsis thaliana	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Kourtz et al. (2005)
Arabidopsis thaliana	*phbA*, *phbB*, *phaC*	Cytoplasm	P3HB-co-3HV	Matsumoto et al. (2005)
Arabidopsis thaliana	*phbA*, *phbB*, *phaC*	Peroxisomes	scl-mclPHA	Matsumoto et al. (2006)
Arabidopsis thaliana	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Kourtz et al. (2007)
Arabidopsis thaliana	*phaA*, *phaB*, *phaC1*	Plastids	scl-mclPHA	Matsumoto et al. (2009)
Arabidopsis thaliana	*phaA*, *phaB*, *phaC*	Peroxisomes	scl-PHA	Tilbrook et al. (2011)
Arabidopsis thaliana	*phaA*, *phaB*, *phaC*	Peroxisomes	P3HB	Tilbrook et al. (2014)
Beta vulgaris	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Menzel et al. (2003)
Brassica napus	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Houmiel et al. (1999)
Brassica napus	*phbB*, *phaC*	Plastids	P3HB-co-3HV	Slater et al. (1999)
Brassica napus	*phaA*, *phaB*, *phaC*	Plastids	P3HB, P3HB-co-3HV	Valentin et al. (1999)
Brassica napus	*phbA*, *phbB*, *phaC*	Cytoplasm	P3HB	Poirier and Gruys (2001)

(continued)

Table 15.1 (continued)

Plant species	Genes	Targeted cell organelle	PHA type	References
Camelina sativa	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Patterson et al. (2011)
Camelina sativa	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Malik et al. (2015)
Elaeis guineensis	*phaA*, *phaB*, *phaC*	Plastids	P3HB, P3HB-co-3HV	Omar et al. (2008)
Elaeis guineensis	*phaA*, *phaB*, *phaC*	Mesocarp	P3HB	Omidvar et al. (2008)
Elaeis guineensis	*phaA*, *phaB*, *phaC*, *tdcB*	Plastids	P3HB, P3HB-co-3HV	Parveez et al. (2008)
Elaeis guineensis	*phaA*, *phaB*, *phaC*, *tdcB*	Immature embryos	P3HB, P3HB-co-3HV	Fuad et al. (2008)
Elaeis guineensis	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Ismail et al. (2010)
Elaeis guineensis	*phaA*, *phaB*, *phaC*, *tdcB*	Plastids	P3HB-co-3HV	Ariffin et al. (2011)
Elaeis guineensis	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Parveez et al. (2015)
Glycine max	*phbA*, *phbB*, *phaC*	Vacuoles	P3HB	Schnell et al. (2012)
Gossypium hirsutum	*phaB*, *phaC*	Cytoplasm, plastids	P3HB	John and Keller (1996)
Linum usitatissimum	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Wrobel-Kwiatkowska et al. (2004)
Linum usitatissimum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Wrobel-Kwiatkowska et al. (2007)
Linum usitatissimum	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Wrobel-Kwiatkowska et al. (2009)
Linum usitatissimum	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Szopa et al. (2009)
Linum usitatissimum	*phbA*, *phbB*, *phbC*	Fibers	P3HB	Kulma et al. (2015)
Linum usitatissimum	*phaC1*	Peroxisomes	mclPHA	Wrobel-Kwiatkowska et al. (2019)
Medicago sativa	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Saruul et al. (2002)
Nicotiana tabacum	*phbB*, *phaC*	Cytoplasm	P3HB	Nakashita et al. (1999)

(continued)

Table 15.1 (continued)

Plant species	Genes	Targeted cell organelle	PHA type	References
Nicotiana tabacum	*phbA*, *phbB*, *phbC*	Cytoplasm	P3HB	Nakashita et al. (2001a)
Nicotiana tabacum	*phbA*, *phbB*, *phbC*	Plastids	sclPHA	Nakashita et al. (2001b)
Nicotiana tabacum	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Arai et al. (2001)
Nicotiana tabacum	*phbA*, *phbB*, *phaC*	Chloroplast	P3HB	Zhang et al. (2002)
Nicotiana tabacum	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Bohmert et al. (2002)
Nicotiana tabacum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Suzuki et al. (2002)
Nicotiana tabacum	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Lossl et al. (2003)
Nicotiana tabacum	*phbA*, *phbB*, *phbC*	Plastids	P3HB	Lossl et al. (2005)
Nicotiana tabacum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Arai et al. (2004)
Nicotiana tabacum	*phaC2*, *aadA*	Plastids	mclPHA	Wang et al. (2005)
Nicotiana tabacum	*phaB*, *phaC*	Cytoplasm	P3HB	Matsumoto et al. (2011)
Nicotiana tabacum	*phaA*, *phaB*	Plastids	P3HB	Bohmert-Tatarev et al. (2011)
Nicotiana tabacum	*phaB*, *phaC*	BY-2 cells	P3HB	Yokoo et al. (2015)
Oryza sativa	*phbB*, *phbC*	Cytoplasm	P3HB	Endo et al. (2006)
Panicum virgatum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Somleva et al. (2008)
Panicum virgatum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Somleva and Ali (2010)
Panicum virgatum	*phaA*, *phaB*, *phaC*, *FBPase*, *SBPase*	Plastids	P3HB	Somleva et al. (2012)
Populus tremula × alba	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Dalton et al. (2011)
Saccharum officinarum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Brumbley et al. (2003)
Saccharum officinarum	*cTP-CPL*, *HCHL*	Plastids	pHBA	McQualter et al. (2005)
Saccharum officinarum	*phaA*, *phaB*, *phaC*	Cytoplasm, plastids	P3HB	Petrasovits et al. (2007)
Saccharum officinarum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Purnell et al. (2007)
Saccharum officinarum	*phaA*, *phaB*, *phaC2*, *phaJ2*, *FatB2*, *KasA1*	Peroxisomes	scl-mclPHA	Anderson et al. (2011)

(continued)

Table 15.1 (continued)

Plant species	Genes	Targeted cell organelle	PHA type	References
Saccharum officinarum	*phaA*, *phaB*, *phaC*	Peroxisomes, vacuoles	sclPHA	Tilbrook et al. (2011)
Saccharum officinarum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Petrasovits et al. (2012)
Saccharum officinarum	*phaA*, *phaB*, *phaC*	Plastids	P3HB	Petrasovits et al. (2013)
Saccharum officinarum	*NphT7*, *phaA*, *phaB*, *phaC*	Plastids	mclPHA	McQualter et al. (2015)
Solanum tuberosum	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Bohmert et al. (2002)
Solanum tuberosum	*phaC1*	Cytoplasm	mclPHA	Romano et al. (2003)
Solanum tuberosum	*phaC1*, *phaG*	Plastids	mclPHA	Romano et al. (2005)
Solanum lycopersicum	*phaCAB Operon*	Chloroplast	P3HB	Mozes-Koch et al. (2017)
Tamarix aphylla	*phbB*, *phbC*	Cytoplasm	P3HB	Endo et al. (2006)
Zea mays	*phaA*, *phaB*, *phaC*	Peroxisomes	P3HB	Hahn et al. (1999)
Zea mays	*phbA*, *phbB*, *phaC*	Plastids	P3HB	Poirier and Gruys (2001)
Zea mays	*IlvA*, *phaA*, *phbB*, *phbC*	Plastids	P3HB	Mitsky et al. (2003)
Zea mays	*phbA*, *phbB*, *phaC*	Chloroplast	P3HB	Zhong et al. (2003)

PHA = polyhydroxyalkanoate, P(3HB) = poly-3-hydroxybutyrate, P(3HB-co-HV) = poly (3-hydroxybutyrate-co-3-hydroxyvalerate), Scl-mclPHA = short chain length to medium chain length PHA, mclPHA = medium chain length PHA

sugarcane, maize, rapeseed, flax, cotton, and oil palm have been genetically engineered for producing PHAs. But till date, no one plant species is released for commercial production of biopolymers. The research is on the way, things are optimizing, and we hopefully expect that the transgenic plants would be available in the near future for producing PHAs at commercial scales.

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Applications of Artificial Intelligence for the Development of Sustainable Agriculture

16

Sangeeta Singh and Priyanka Jain

Abstract

The principle behind artificial intelligence (AI) is utilization of human intelligence in such an easy way that a machine can easily understand and execute from the simplest to toughest tasks. The main aim of AI includes learning, reasoning and perception. AI is having a huge application in all sectors of the society, starting from industry, healthcare, finance to agriculture. Machine learning (ML) is a part of artificial intelligence (AI) that can be applied to phenome, genome, genotype, transcriptome and proteome data to generate predictive models. Deep learning is a subset of machine learning in which artificial neural networks, algorithms inspired by the human brain, learn from a huge amount of data. Deep learning also allows the machines to solve the problems which are complex and leveraged with very diverse, unstructured and interconnected data. The more deep learning algorithms learn, the better is the performance. Agriculture is the oldest and most important profession in the world that is done to meet hunger and economic needs of the country. With an estimated population rise of nine billion by 2050, an increase in agricultural production by more than 70% is necessary to feed the population. Traditional methods of farming face several challenges like flood, drought, crop diseases, storage, etc. So, we need a smarter approach like AI to become more efficient and productive in agriculture. Artificial intelligence technologies help in yielding healthier crops; control pests; monitor soil and its growing conditions; organize data for farmers; help with the workload; help in irrigation, weeding and spraying with the help of sensors; and improve a wide range of agriculture-related tasks in the entire food supply chain. By the use of artificial intelligence, various products have been developed like drones, robots and automated machines which can revolutionize agriculture

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in the near future by providing more useful applications to this sector. Artificial intelligence will help the world deal with food production issues for the growing population.

Keywords

Artificial intelligence · Sustainable agriculture · Machine learning · Population · Food production

16.1 Introduction

The agriculture sector will face serious challenges to feed billions due to continous increasing population of the world, which is targeted to touch nearly ten billion by the end of 2050 (FAO 2017). The agriculture sector is very important in the sense of food production, a basic source of livelihood, maintenance of environment, generating employment, providing raw material to industries and the generation of national income. Agriculture plays an important role in significantly increasing per-capita income of the rural community, which earns its livelihood through agriculture. India is an agriculture-based country where 50% of employment is generated because of this and agriculture sector accounts for 18% of GDP. The traditional method of agriculture will not help in boosting agriculture. We need advanced tools and methods, which can increase the rural development and rural transformation and will eventually lead to economic growth of country (Shah et al. 2019).

Artificial intelligence (AI) has been recently introduced in agriculture. The term “artificial intelligence” was given by an American scientist John McCarthy in the year 1956. McCarthy along with Alan Turing, Allen Newell, Herbert A. Simon, Marvin Minsky and Arthur Samuel are known as the founding fathers of AI. Nowadays we are using AI in our daily life and activities like computer science, Facebook, Netflix, Alexa, Siri and many other important fields. The term artificial intelligence is composed of two words, “artificial” and “intelligence”. Intelligence is the ability to think, calculate, reason and learn from experience, to solve problems and to adapt to new situations. Intelligence can also perceive relationships, learn from past experience, store and retrieve information from memory, solve problems, evaluate complex ideas, use natural language and categorize, simplify and adjust new situations. Intelligence is based on the following parameters:

- Learning from experience
- Identifying problems
- Problem solving
- Ability to make accurate decisions
- Ability to prove the outcomes
- Ability to think logically
- Ability to learn and improve

The dictionary defines “intelligence” as the ability to sense, act, solve and understand, while the word “artificial” means unnatural and developed by human. So, AI is defined by John McCarthy as “the science and engineering of making intelligent machines”. It is “an approach to make a computer, a robot or a product to think how smart humans think, learn, decide and work when it tries to solve problems”. AI can also be defined as development of computer systems that are capable of performing tasks which require human intelligence such as decision-making, object detection, solving complex problems and so on. AI is the most discussed, popular and researched area in the current era as it was introduced with the aim to develop a technology which functions like a human brain (Parekh et al. 2020). In this technology, first softwares are fed with training datasets in which they get trained and provide desired outputs. Many artificial intelligence systems are powered by machine learning (ML), and some are powered by deep learning (DL). Machine learning is a subset of AI while deep learning is a subset of ML. Artificial intelligence is the wide area which includes several tools with the help of the following subfields like machine learning, deep learning, artificial neural network, natural language processing, cognitive processing, computer vision, Internet of things (IoT), graphical processing unit, etc. AI has wide applications in fields like medicines, health, academics, computers, industry, home, offices, etc. It is also widely used these days in the field of agriculture to increase its production. It helps in real-time monitoring, harvesting, marketing and processing of crops (Yang et al. 2007). Agricultural equipment and machines, drones, robots, etc. have boosted agricultural produce. AI is also applied to achieve breeding targets through genomic selection which decreases the time and money required for better yield of crop. This chapter summarizes importance of AI, its types and its wide applications in agriculture.

16.2 Types of Artificial Intelligence

It is divided into two types:

Type 1—It is based on an embedded level of intelligence. This includes narrow AI, general AI and strong AI.

Type 2—It is based on functionalities. This includes reactive, self-awareness and limited type AI (Fig. 16.1).

16.2.1 Weak or Narrow AI

It is a type of AI, where machine is involved to perform only a narrowly defined set of specific tasks with no thinking ability. The machine just performs a set of pre-defined functions. It is the most common and currently widely used AI form.

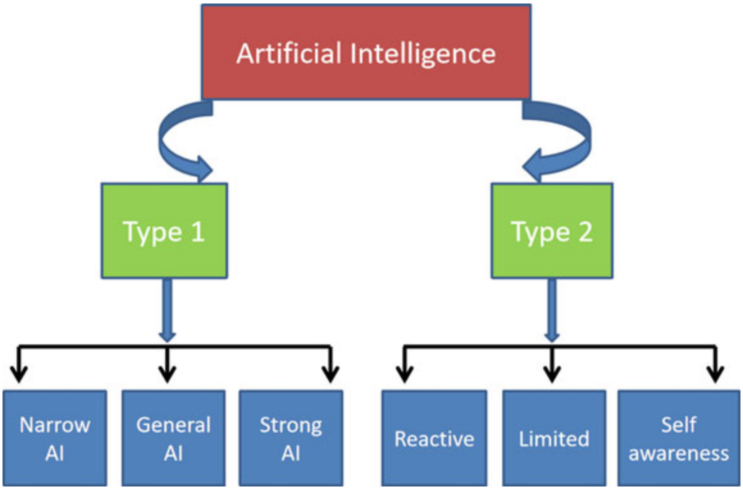

Fig. 16.1 Types of artificial intelligence

Examples of weak AI include Siri, Alexa, self-driving cars, AlphaGo and so on. Almost all the AI-based systems built till this date fall under the category of weak AI.

16.2.2 General AI

General AI is a type of intelligence which could perform any intelligent task with efficiency like a human. The concept behind the general AI is to make such devices or systems which can act and think smartly like a human on its own. Till now we have no such systems which can actually be called an example of general AI and can act or behave like a human. The systems with general AI are still undergoing research, and it will take lots of efforts and time to develop such systems as this would be a major step towards AI.

16.2.3 Strong AI

Strong AI is such type of AI, where machines will possess the ability to think and make decisions just like the humans. As of now, no examples of strong AI exist, but it is expected to create machines that are as smart as humans.

Artificial super intelligence (ASI) is a term referring to the time when the capability of computers will surpass human beings.

16.2.4 Reactive Machine AI

Reactive machine AI is such type of AI which operates solely based on the present data. It cannot create conclusions for future actions. It takes into account only the current situation. They are the oldest form of AI with extremely limited capabilities, have no storage capacity and, therefore, are unable to learn from the past. They can only react in a limited means. Purely reactive machines are the most basic types of artificial intelligence. IBM's Deep Blue system and Google's AlphaGo are examples of reactive machines.

16.2.5 Limited Memory AI

Limited memory AI is such type of AI which uses the past data from its memory to make conclusions of the future. Such an AI has a short-lived or a temporary memory. For example, self-driving cars use sensors to identify civilians crossing the road, steep roads, traffic signals and so on to make better driving decisions. This helps to prevent any future accidents.

16.2.6 Self-Awareness AI

The self-aware AI includes machines that have their own consciousness and become self-aware. This type of AI does not exist yet.

16.2.7 Theory of Mind AI

The Theory of Mind AI is a more advanced type of artificial intelligence which focuses mainly on emotional intelligence so that human beliefs and thoughts can be better comprehended. The Theory of Mind AI has not yet been fully developed, but continuous and rigorous research is going on in this area.

Artificial intelligence (AI) requires big data and machine learning (ML) approaches to scale. So, machine learning is a subset of AI, while deep learning is a subset of ML and is inspired by the architecture and function of the brain. Geoffrey Hinton et al. showed the training of a deep neural network that can recognize handwritten digits with >98% precision and branded this method as "deep learning". Deep learning has mind-blowing achievements with large amounts of data and high computational power that is much higher than other machine learning methods (Table 16.1). Machine learning is a way of reaching artificial intelligence. Aurthur Samuel defined machine learning as is the area that has given computers ability to learn without programmed explicitly. Types of machine learning systems are classified based on how they are trained. There are four types of ML systems (Fig. 16.2):

Table 16.1 Different deep learning algorithm and their applications

DL application	DL algorithm	Plant	Platform	Stress type	Stress name	References
Identification	LeNet architecture	Banana	Manual	Biotic stress	Early scorch, cottony mould, ashen mould, late scorch, tiny whiteness	Amara et al. (2017)
Identification	AlexNet, GoogLeNet, VGGNet-16, ResNet-20	Apple	Manual	Biotic stress	*Alternaria* leaf spot, mosaic, rust, brown spot	Liu et al. (2018)
Identification	Inception-v3, ImageNet	Cassava	Manual	Biotic stress	Cassava brown streak disease, cassava mosaic disease, brown leaf spot, cassava green mite damage, cassava red mite damage	Ramcharan et al. (2017)
Identification	AlexNet, ALexNetOWTBn, GoogLeNet, Overfeat, VGG	Apple, banana, blueberry, cabbage, cantaloupe, cassava, celery, cherry, corn, cucumber, eggplant, gourd, grape, onion, orange	Manual	Biotic stress	Bacterial spot, apple scab, cedar apple rust, black rot, banana sigatoka, banana speckle, brown leaf spot, cassava green spider mite, *Cercospora* leaf spot, common rust, northern leaf blight, esca (black measles), late and early blight, cucumber mosaic, downy mildew, powdery mildew, frogeye leaf spot, leaf scorch, *Septoria* leaf spot, *Septoria* leaf blight, spider mites, tomato mosaic virus, leaf mould, target spot, TYLCV, huanglongbing	Ferentinos (2018)
Identification	AlexNet, GoogLeNet	Apple, blueberry, cherry, corn, grape, peach, bell pepper,	Manual	Biotic stress	Apple scab, apple black rot, apple cedar rust, cherry	Mohanty et al. (2016)

		potato, raspberry, soybean, squash, strawberry, tomato			powdery mildew, corn grey leaf spot, corn common rust, corn northern leaf blight, grape black rot, grape black measles, grape leaf blight, orange huanglongbing (citrus greening), peach bacterial spot, bell pepper bacterial spot, potato early blight, potato late blight, squash powdery mildew, strawberry leaf scorch, tomato bacterial spot, tomato early blight, tomato late blight, tomato leaf mould, tomato *Septoria* leaf spot, tomato two-spotted spider mite, tomato target spot, tomato mosaic virus, tomato yellow leaf curl virus	
Identification	Modified LeNet	Olive	Manual	Biotic stress	Olive quick decline syndrome	Cruz et al. (2017)
Identification	CNN	Cucumber	Manual	Biotic stress	Melon yellow spot virus, zucchini yellow mosaic virus, cucurbit chlorotic yellows virus, cucumber mosaic virus, papaya ring spot virus, watermelon mosaic virus, green mottle mosaic virus	Fujita et al. (2016)
Identification	CaffeNet, ImageNet	Pear, cherry peach, apple, grapevine	Manual	Biotic stress	Porosity (pear, cherry, peach), powdery mildew (peach), peach leaf curl, fire blight	Sladojevic et al. (2016)

(continued)

Table 16.1 (continued)

DL application	DL algorithm	Plant	Platform	Stress type	Stress name	References
					(apple, pear), apple scab, powdery mildew (apple), rust (apple, pear), grey leaf spot (pear), wilt (grapevine), mites (grapevine), downy mildew (grapevine), powdery mildew (grapevine)	
Identification	AlexNet, ZFNet, VGG-16, GoogLeNet, ResNet-50, ResNet-101, ResNetXt-101, Faster RCNN, R-FCN, SSD	Tomato	Manual	Biotic and abiotic stress	Grey mould, canker, leaf mould, plague, leaf miner, whitefly, low temperature, nutritional excess or deficiency, powdery mildew	Fuentes et al. (2017)
Identification	CNN	Maize	UAV	Biotic stress	Northern corn leaf blight	DeChant et al. (2017)
Identification	VGG-FCN, VGG-CNN	Wheat	Manual	Biotic stress	Powdery mildew, smut, black chaff, stripe rust, leaf blotch, leaf rust	Lu et al. (2017)
Identification	VGG-A, CNN	Radish	UAV	Biotic stress	*Fusarium* wilt	Ha et al. (2017)
Identification	SCRNN	Tomato	Manual	Biotic stress	Bacterial leaf spot, early blight tomato, late blight, *Septoria* leaf spot, two-spotted spider mite, tomato mosaic virus, tomato leaf mould, target spot of tomato and tomato yellow leaf curl virus	Yamamoto et al. (2017)

Classification	AlexNet, GoogLeNet	Tomato	Manual	Biotic stress	Tomato yellow leaf curl virus, tomato mosaic virus, target spot, spider mites, *Septoria* spot, leaf mould, late blight, early blight, bacterial spot	Brahimi et al. (2017)
Identification, classification, quantification	AlexNet	Soybean	Manual	Biotic and abiotic stress	Bacterial blight, bacterial pustule, frogeye leaf spot, *Septoria* brown spot, sudden death syndrome, iron deficiency chlorosis, potassium deficiency, herbicide injury	Ghosal et al. (2018)
Quantification	VGG-16, VGG-19, Inception-v3, ResNet50	Apple	Manual	Biotic stress	Black rot	Wang et al. (2017)
Prediction	DNN	Tomato	Manual	Abiotic stress	Water stress	Kaneda et al. (2017)

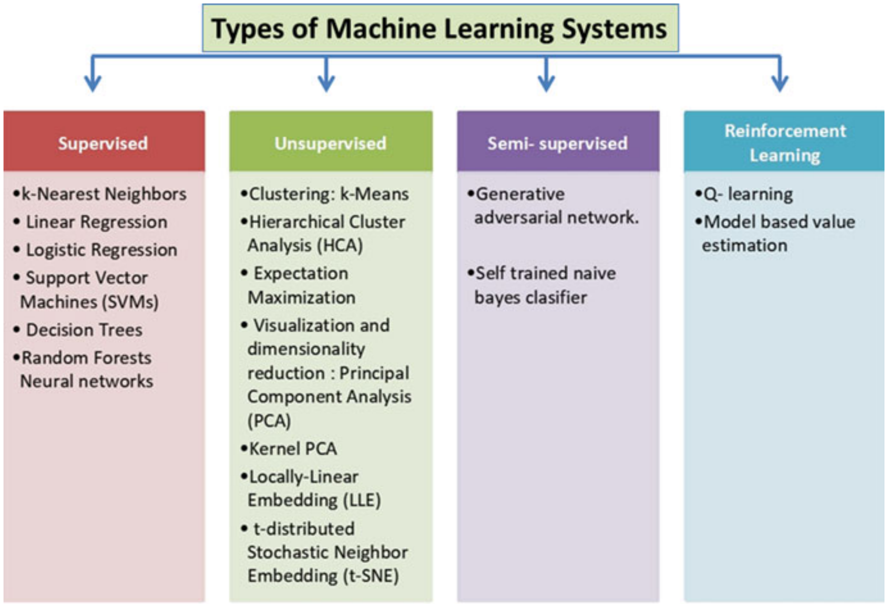

Fig. 16.2 Types of machine learning systems

1. Supervised
2. Unsupervised
3. Semi-supervised
4. Reinforcement learning

In supervised learning, training data is given to different algorithm that includes the expected solutions, termed as labels. For example, in our email box, spam filter is a labelled training set for supervised learning as it learns how to categorize new emails. Another example is prediction of target values, for example, car price, based of several features like age, mileage and brand; these all are predictors. This type of task is called regression. Another example is logistic regression that is used mainly for classification. The supervised learning algorithms are mainly as follows: *k*-nearest neighbours, linear regression, logistic regression, support vector machines (SVMs), decision trees and random forests neural networks.

During unsupervised learning, training data is not labelled, and the algorithm tries to learn without a trainer. Major unsupervised learning algorithms covering dimensionality reduction are as follows: hierarchical cluster analysis (HCA), clustering *k*-means, expectation maximization, principal component analysis (PCA), kernel PCA, locally linear embedding (LLE) and t-distributed stochastic neighbour embedding (t-SNE).

In semi-supervised learning, labelled training data, with less amount of labelled data and lot of unlabelled data is used.

Reinforcement learning is a like an agent that can observe environment, accordingly choose and perform actions and then get rewarded. It should learn on its own which is the most suitable strategy, known a policy, in order to get most reward over time.

16.3 Open Data Repositories for Machine Learning

- UC Irvine Machine Learning Repository
- Kaggle datasets
- The Amazon's AWS datasets
- Meta portals https://dataportals.org
- https://opendatamonitor.eu
- https://quandl.com
- Wikipedia's list of machine learning datasets
- https://www.quora.com

16.4 Steps for Machine Learning or Life Cycle of AI

There are various steps in the life cycle of AI, which must progress in a specific order to attain the final result. The major phases in AI can also be referred to as the planning phase, data phase, development phase and deployment phase.

1. **Planning phase:** The first step of the life cycle is to plan your project and make an outline of input, processing and output.
2. **Data phase:** In this phase raw data is selected. The selection of data is very crucial for the success of experiment. So, this step of life cycle is very important. The selected data must be of good quality and bigger in size (for more reliable prediction), and it should be kept in right formats like .csv, .txt, etc.
3. **Development phase:** After data collection it should be processed properly. We should check the characteristics, format, correlations, general trends, outliers and quality of data for effective output. Filter the data, if data has missing values, noise, duplicate values and invalid data. Feature selection and extraction are performed; the model is selected. The model is trained on the training data. Over- and under-training is an important parameter during training of the model. The model should neither be under-trained nor over-trained. Then we do a test; we check for the accuracy of our model by providing a test dataset parallel to it. Testing the model determines the percentage accuracy of the model as per the requirement of the project.
4. **Deployment phase:** The model is applied to make predictions on new cases. Interpretation of the outcome in machine learning projects is the most difficult part for those without any data science background. The final step is to implement, document and maintain the data science project so that the stakeholder can continue to leverage and improve upon its models.

16.5 Application of AI in Agriculture

Artificial intelligence has a wide role in agriculture starting from soil health to its production (Fig. 16.3). ML is an important part of agriculture as it increases crop yields and reduces losses in agriculture by timely predicting rains, droughts and similar cases. Below listed are few applications of AI in agriculture.

16.5.1 Soil Health Monitoring

Soil is an important component of agriculture. A healthy soil is essential for healthy growth of plant. Knowledge of agricultural soil properties, such as the estimation of soil drying, condition, temperature, moisture content, etc., will enhance crop yield. This information of soil is fed to an ML model that produces a reliable solution for providing valuable insights. Liakos et al. in the year 2018 discussed about the use of processed data captured by drone for monitoring crop and soil health by different companies. These companies apply deep learning algorithms to fetch out best result. Few examples are Trace Genomics and Plantix app (Plantix 2020), which uses machine learning for diagnosing soil defects. Plantix was developed by a Berlin-based agricultural tech start-up PEAT, which can identify defects and nutrient deficiencies in soil. Analysis is conducted by correlating particular foliage patterns

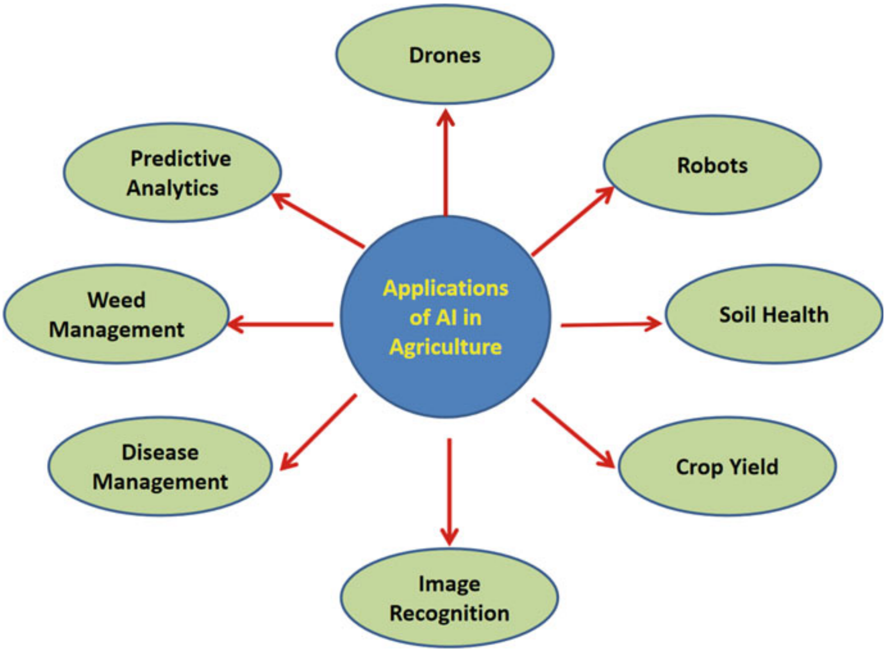

Fig. 16.3 Applications of AI in agriculture

with predefined software algorithms. The user can capture photos by smartphone camera, which can be identified by image recognition app to identify possible defects through images captured. Users are then provided with solutions and tips for soil restoration. According to the company, the accuracy of software for pattern detection is up to 95%. Trace Genomics, a Californian company, provides soil analysis services to farmers. Users can submit soil sample to the company, and the company will provide them with an in-depth summary of their soil contents (Trace Genomics 2020). The companies contribute towards healthy crop production. An important soil management technique known as management-oriented modelling (MOM) minimizes nitrate leaching and maximizes production (Li and Yost 2000). The technique fuzzy logic SRC-DSS classifies soil according to associated risks, but the limitation is that it needs big data (Lopez et al. 2008). An artificial neural network (ANN) can predict mean soil temperature, soil texture and soil moisture and predict and classify soil structure. This is cost-effective, saves time and has 92% accuracy but requires big data (Tajik et al. 2012; Levine et al. 1996; Bilgili 2011; Zhao et al. 2009; Elshorbagy 2008; Chang and Islam 2000). Moisture analysers and Mettler Toledo are used for soil moisture detection.

16.5.2 Crop Sowing and Monitoring

Using AI, not only the time of sowing can be predicted, but also the sowing can be done using AI-aided machinery. The use of AI and ML in agriculture has enhanced the crop monitoring and production. It is very necessary to select the proper crop for better yield, and selection of various parameters like the topography of region, climate, soil type, composition of the soil, market trends, etc. should be taken care of. Using algorithms of AI and ML, it is easy to predict the most appropriate crop that can maximize the yield. Commonly used tools for this purpose are ANN, *k*-NN, decision trees, etc. (Okori and Obua 2011; Dahikar and Rode 2014; Ghosh and Koley 2014; Kumar et al. 2015). AI is used in the pilot project to provide knowledge on the date of sowing, preparation of land, soil test-based fertilization, seed treatment, etc. resulting into 30% increase in average crop yield per hectare. Accurate prediction of disease has been a breakthrough in smart precision agriculture. AI and ML techniques have better ability to analyse heterogeneous and noisy data with high accuracy in comparison to the traditional statistical approaches (Gutierrez 2015; Mehra et al. 2016; Kim et al. 2014). The SVM technique was initially used for disease detection and classification (Rumpf et al. 2010). Raj et al. in 2015 discussed about the use of ML algorithms for pattern recognition in detecting diseases by using images of the crop leaves. AI and ML are helping agriculture by finding new ways to improve crop quality. AI-aided machines are an advantage over human limitations in analysing the data and improving crop quality.

16.5.3 Predictive Analytics

Predictions for water management, crop rotation, timely harvesting, type of crop to be grown, optimum planting, pest attacks and nutrition management are required by farmers to have good crop yield. Such type of predictions done by AI-based applications and tools in agriculture has helped farmers in accurate and controlled farming by providing them proper guidance. Predictions for crop prices can be very helpful as farmers are emotionally attached to their crops. For example, the prices of areca nut in Kerala were predicted using machine learning modals like SARIMA and LSTM. The images captured using satellites and drones can be used by AI to predict weather conditions, analyse crop sustainability and evaluate farms for the presence of diseases or pests and poor plant nutrition on farms. An example of such type of activity is aWhere, a Colorado-based company which uses machine learning algorithms to predict weather, analyse crop sustainability and evaluate farms for the presence of diseases and pests. They provide customized services to their clients who can be a farmer, researcher or a consultant based on their needs. This company is specialized to give high quality of result.

16.6 Drones

They have wide applications in the agricultural sector. With AI implementation in drones, it has become the future of agriculture. It has become easier for farmers to monitor crop health, weed identification, etc. A drone is capable to fly under any weather condition and can take pictures, but the image captured in rainy season may be a little blurred. They can monitor any geographical area. Drones help in various operations like data collection, field monitoring, disease detection and many machine learning (ML)-driven agriculture practices such as spraying inputs, surveillance, etc. An example is Sky Squirrel Technologies company that has introduced drones for high vineyard crop yield and reduced overall cost. Algorithms integrate and analyse the captured images to provide a health report of the crops (Vine View 2020). Gamaya, which is a Switzerland-based company, provides remote sensing and machine learning through high imaging camera. This is based on the pattern of light reflection by different plants having different physiologies and characteristics. This pattern changes as the plant grows and is affected by stressors. Using Gamaya's technology we can measure different types of plant stresses and chemical inputs in the soil and can also distinguish weeds from plants.

A deep learning application known as Neurala Brain was developed by the Neurala company which requires less training, less data storage and less computing resources.

senseFly drone works in collaboration with the eMotion Ag software. This drone captures 360 views of fields and helps in monitoring crops at different stages of growth and assesses the condition of the soil. senseFly was founded in 2009 and is the commercial drone subsidiary of Parrot Group.

There are various other types of drones like multirotor drone, fixed-wing drone, single-rotor helicopter, fixed-wing hybrid VTOL (vertical take-off and landing) type of drones, etc. which can be used in agriculture. Multirotor drone is the simplest form of drones used in agriculture. Fixed-wing drones use wings like planes and are used in agriculture. Single-rotor helicopter is more efficient as compared to other drones due to its long rotor blades. Fixed-wing hybrid VTOL is a hybrid type of drone. It is capable to take off from one place and have ability to sustain over some area vertically. Using the data captured by AI-equipped drones and analysed by collaborative software, farm owners are able to monitor crop growth and crop health and evaluate the condition of the soil. In turn, this information enables them to make decisions about managing weeds, diseases and pests, as well as the amount of fertilizer and pesticides to apply to crops. Drones are used for crop spraying, pesticide spraying, crop monitoring, remote sensing, precision agriculture monitoring, spraying fertilizers, etc. Drones are also known as unnamed aerial vehicles (UAV).

16.7 Robots

The robots developed for agricultural purposes are also known as agribot. Robots in agriculture are mainly used for harvesting, driverless tractors, fruit picking, etc. They are also used for pruning, weeding, spraying and monitoring, automatic milking, washing, etc. Using robots, we can increase agricultural produce and reduce human labour.

Companies are using AI techniques to develop robots to handle essential agricultural tasks such as harvesting crops at a higher capacity with less human power. The aim of AI has always been to minimize human efforts by using disruptive technology. The agriculture realm is one of the important fields of the world that needs automation and smart devices that can perform functions that traditionally needed human intervention. Blue River Technology (John Deere) has developed a robot called “See & Spray” which uses ML to monitor and precisely spray herbicide only where needed. Another example is “RIPPA” which exterminates pests and weeds (Blue River Technology 2020). There are different types of robots like Demeter, a robot for weed control, harvester robot, forester robot, horticultural robot, fruit-picking robot, etc. Demeter is a robot which works like normal harvester to cut crops but it is humanless.

The weeds are a major threat to crops. In order to eradicate weeds from fields, a four-wheeler robot named “weed controller” was developed which can easily remove and destroy the weeds from fields. Forester robots are used to cut woods and to harvest pulp and hard wood in the forests. Robo, a robot in horticulture, is used to cut grass in the lawns. The fruit-picking robot picks the ripe fruit without damaging leaves and branches of the tree. Agricultural robots can collect crop and soil samples and can do spraying, find diseases, perform mechanical weeding and identify different stresses using cameras and sensors. The robot developed by

Harvest CROO Robotics has helped strawberry farmers of California and Arizona to pick and pack their crops in very less cost.

16.7.1 Image Recognition

Image recognition is a technique of taking proper images with the help of AI. The features of these images are further compared with a database to find a match. In order to have smart agriculture, disease image recognition is required. Machine learning-based methods like deep learning and transfer learning have been used for disease recognition in crops. In the past few years, the UAV and their application, recognition, human body detection, forest fire detection, etc. have gained interest (Lee et al. 2017). The practical application of these methods requires actual disease image from crop field. There are databases of various disease image of very high pixels from fields like IDADP. These can be used for training and modelling of data. Lightweight models are handy and highly required. The existing datasets, such as ImageNet and PlantVillage, are not totally dedicated to agricultural disease images, so additional evaluation will be required. Because of diversity of imaging technologies from capturing the picture to delivery, it is piloted through remote controller to reach greater heights and perform several applications.

16.8 Weed Management

Weed is a major threat or hindrance for crop yield. Sometimes the crop loss may be 40–50% as a result of these weeds. A study on soybean targeting the yield loss due to weeds claimed that the there was 8–55% reduction in yield of soybean (Datta et al. 2017). The exposure time of crops with weeds decides their loss due to weed. These weeds may have a positive and negative effect on ecosystems. Some weeds are poisonous and cause allergies. So, these weeds must be eradicated for healthy growth of the crop. There are various weedicides available in the market, but they are not sufficient to eradicate the weeds. Also, these weedicides reduce soil quality and productivity of crops. Hence a smart system of weed management is required. These are various techniques used in AI for management of weeds. The weed identification using ANN and GA has high performance and reduces trial and error, but the major limitation is that it requires big data (Tobal and Mokhtar 2014). The weeds can also be removed and identified through robotics and sensors. The mechanical control of weeds is expensive, and continuous use of heavy machines will reduce soil productivity (Brazeau 2018). Support vector machine (SVM) and ANN were used in machines to detect stress in crops to enhance target-specific remedies timely, but this can detect only low nitrogen (Karimi et al. 2006). Digital image analysis (DIA) has above 60% accuracy and success rate, but this consumes time of years (Gerhards and Christensen 2003). Site-specific weed management can be done using technique, unmanned aerial vehicle (UAV), which has a high rate of weed detection within a short period of time, but this is expensive and requires vast human expertise (Granados 2011).

16.9 Disease Management

Disease is a major threat to crops. In order to have a better yield of crops, management of disease is necessary. There are various factors which attack plants and animals like soil type, rain, dry weather, wind, temperature, humidity, etc. Also, there are various diseases caused due to bacteria, virus, fungus, nematodes, etc. which affect plant health. Due to the unstable nature of biotic and abiotic factors, management of diseases becomes difficult, especially in case of large farming. For controlling diseases and losses that occurred due to diseases, farmers should adopt best practice for crop disease management. But these practices may require more time and money (Fang et al. 2007). Hence, there is requirement of faster methods for disease management. There are various AI applications for disease management. The application developed by using techniques like computer vision system (CVS), genetic algorithm (GA) and ANN works at high speed and can do multiple tasks (Balleda et al. 2014). In order to draw inferences for crop disease management, an approach based on fuzzy logic is used (Jesus et al. 2008). A system has been developed using rule-based engine which helps in disease detection and provides suitable treatment suggestions (Munirah et al. 2013). Using FL and TSS converted technique, system has been developed which resolves plant pathological problems quickly. But its limitation is that it requires high-speed Internet and uses voice service as multimedia interface (Kolhe et al. 2011).

16.10 Conclusion

The Indian agriculture faces serious challenges in terms of irrigation systems, weed issues, plant monitoring issues as a result of plant height, etc. Farming can be improved only on adoption of advanced solutions. Research is still going on to solve real challenges of farmers. In order to explore the enormous scope of AI in agriculture, applications need to be more robust, less time-consuming, user-friendly and cost-effective; only then will it be able to handle frequent changes in external conditions, facilitate real-time decision-making and make use of an appropriate platform for collecting contextual data in an efficient manner. The modern technology becomes more affordable when adopted by a huge number of farmers. AI-driven technologies are emerging to help improve efficiency and to address challenges facing the industry including crop yield, soil health and herbicide resistance. Agricultural robots and drones are highly valued application of AI in this sector. Crop and soil monitoring technologies will also be important applications going forwards as climate is continuously changing. The amount of data that can potentially be captured by technologies such as drones and satellites on a daily basis will give agricultural business a new ability to predict changes and identify opportunities. It is very necessary to be trained with these modern tools and equipment so that they can prove to be of value for a long time. Additionally, there should be extensive testing and validation of emerging AI applications as this sector is critically impacted by environmental factors that cannot be controlled unlike other industries where risk is easier to model and predict. So, we conclude that the agricultural sector will continuously be benefitted by adoption of AI.

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Information and Advanced Technology Applied at Agriculture and Livestock Development

17

Aswini Rangayasami and Karthik Kannan

Abstract

A larger part of the populace in India is occupying horticulture. With regard to horticulture improvement, data and innovations have assumed a significant part in agricultural nations like communication technology, fuzzy logic, pesticides, etc. And also the livestock sector is one of the important sectors in agriculture. It contributes significantly to the economy. In any case, animal creation frameworks in India depend intensely on customary practices. The absence of information with respect to logical practices is a significant limitation to work on the efficiency of livestock. However, various communication technologies like the Internet, mobile phones, radio, and television are most important tools for communication providing knowledge and information to farmers about agriculture. Mobile phones can reduce the distance between the farmer and buyers. Now farmers directly communicate with buyers. Television is contributing much to circulating data around cultivation in emerging kingdoms. Internet is also playing the main role to communicate with people all over the world. The use of chemical pesticides both occupationally and ecologically causes a range of human health problems. Many pesticides are not degradable; they persist in soil and leach to groundwater. In India pesticide from proper utilization of livestock waste is a good pesticide for crop without any side effects. Economic sectors are carried act by public sector agencies; centralized extension services have rarely made transmission of information on livestock production. By that time, various information

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and technologies are associated with the development of agriculture and livestock.

Keywords

Communication technology · Mobile phones · Television · Internet · Pesticides · Fuzzy logic

17.1 Introduction

Due to an increment in population and urbanization, it is assessed that in 20 years to come the interest for food including domesticated animal products will double. This suggests a conversation starter on how the farming and animal area will satisfy the normal need. At present, the cremation rate isn't identical to the normal interest because of different tests looked at by agriculture and domesticated animal fields including sicknesses, environmental change, poor management systems, hereditary qualities, farmer capacity and abilities, advertising, and lack of data for legitimate dynamic (Bamaiyi 2013). More developments are coming to foster domesticated animals and farming. Data and innovation are prerequisites that have been viewed as the head for the present. Especially in the field of governance to improve the quality of work processes and provide efficient and effective services in order to attract investment to the community to promote the potential of the village thus placing a village in the position of the village advanced in developing the potential empowerment of the village. E-government in government is relied upon to work on the nature of work and administration to the local area (Kurniasih et al. 2018). In the twenty-first century, agribusiness is one of the diverse industries which is expanding provincial pay just as long-term dependability of its normal assets. This can make various exercises that will influence farmers, partners, clients, and government industries. Data and advancements have moved the most significant data about farming in agricultural nations. These non-industrial nations presently are associated with created countries and getting the most recent data and innovations in regard to climate, regular assets, and other related data (Rao 2007). A large portion of the non-industrial nations is utilizing various advances and different hotspots for the improvement of agribusiness and financial turn of events. In these settings, non-industrial nations, for example, African and Asian nations, are utilizing data and correspondence innovations for the development of the agribusiness. The data and advances are helpful to forestry for effectively speaking with vendors and incrementing the information about the improvement of agriculture (Chhanchhar et al. 2014).

17.2 Importance of Information and Technology in Agriculture and Livestock Development

Information and communications technology (ICT) gives new methodologies and methods of communicating, transferring, and upgrading the information and data among various networks. ICT could be used to work with, fortify, and supplant existing data systems and organizations. The term ICT is used to incorporate a radio, TV, cell phone, web, phone, iPad, video-voice data system fax, and PC (Warren 2002). ICT spread formation of knowledge societies in rural areas of the developing countries, which can realize when knowledge and information are effectively improved agricultural and rural development (Gregg and Irani 2004). ICT is being utilized in the country from numerous points of view for animal health management, infection prevention, taking care of domesticated animals, herd management, and for marketing of milk (Fig. 17.1). Information was additionally recognized as a significant factor that will direct farmers in keeping up with productive utilization of farm resources (Adhiguru et al. 2009). In the recent 20 years, data and correspondence advancements in farming and provincial improvement have spread extremely quickly in all areas of the general public and also assumed a vital role in rural advancement; recently ICT has given huge outcomes in practically all spaces of rural life (Fawole and Olajide 2012). It has been presented in farming assignments which have given productive outcomes with country and agricultural improvement. For instance information and communication technologies can be used for distance learning programs and help the farmer for learning new approaches and technologies for the use of agriculture development in developing countries. Such kinds of advancements can give data, and communication advances in agribusiness have expanded their creation of data and information. Essentially, the people who have utilized the e-administrations and online business applications likewise expanded their pay (Sideridis et al. 2010). ICT has over and again exhibited this one probability for improving shortage in agricultural nations. In several occurrences, needy individuals have expert profits as expanded pay, better medical care, further developed schooling and training, admittance to job positions, commitment to government services, contacts with loved friends, undertaking improvement opportunities, expanded farming efficiency, etc. (Tiwari et al. 2010).

17.3 Status of Use of Information and Technology in India

In India today farmers were firmly connected with television, and they get market data from various sources like cell phones, radio, and TV. Farmers presently work with different data sources to tap markets and provide consumers with great quality products (Kashem 2009; Adhiguru et al. 2009). The Indian poultry industry has made considerable progress, from a backyard activity to an organized scientific and dynamic industry. Today India positions second in egg creation and tenth in chicken breeding the world and is giving direct and indirect work to about 1.6 million individuals in the country. However, the per capita utilization stayed low, for

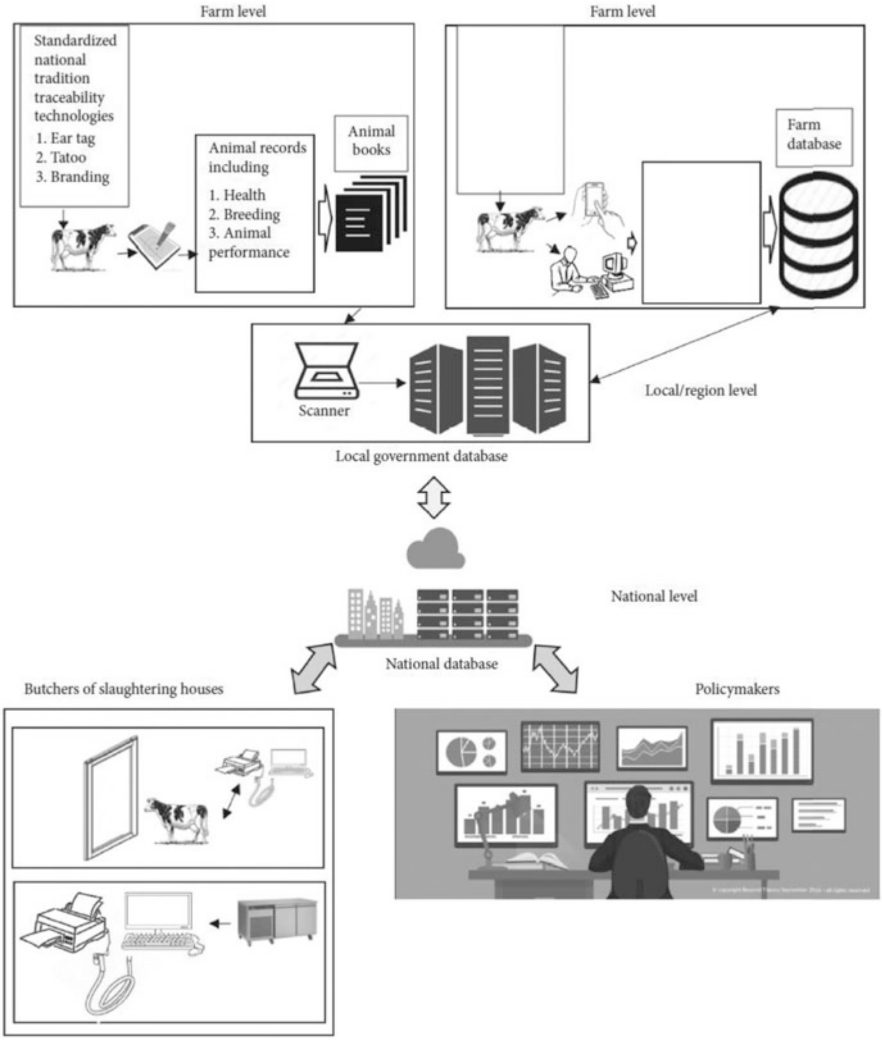

Fig. 17.1 Framework of different tools and technologies

example, 42 eggs/head/year, which is likewise far below the suggested level of 180 eggs/head/year. Also, ICT has brought huge changes to the help conveyance in numerous areas saving resources, time, and cash. Through central computerization of little and medium organizations, online purchasing has effectively started in the bigger urban areas, with remarkable additions in productivity. The E-learning has been prepared to share the information to the nation through instructive satellite-like EDUSAT. Also, telemedicine is an arising area where ICT has given the urban clinical offices to the rural country in cost-effective manner. The benefit of this kind of sensor is a continuous perception of dairy cows. Particularly the class of current

MEMS-based accelerometers is a promising possibility for an effective advertisement system, probably in the mix with extra portable sensors (Helwatkar et al. 2014). It is being said that ‘digital extension’ would be the significant type of innovation dispersal sooner rather than later. Fundamentally, data accessibility is request-driven rather than supply-driven. The challenge isn’t just to work on the availability of communication innovation to the rural population but also to work on its significance to local development. Central Institute for Research on Goats (CIRG) has developed e-mail conference system for goat outreach on its goat-nic.in server using free software called ‘majordoma’ which is available on www.greatcircle.com on a free Linux operating system (Singh and Radhika 2002). The utilization of ICT among farmers of Madhya Pradesh, Uttar Pradesh, and Tamil Nadu of India detailed that data obtaining and working with exchanges in information and yield showcases by ICT-based drives have likewise helped farmers in diminishing exchange cost (Adhiguru and Devi 2012). The utilization of cell phones is establishing an extraordinary pace despite the inadequately evolved rural areas. Portable innovation has given multidimensional advantages to the country’s individuals. For example, farmers likewise answered to utilize ICTs to know the market days, to know where items could be sold, and to recognize distinctive market areas for effective advertising of produce. Nonetheless, farmers are getting more information from radio and TV regarding agricultural information. For example, calls and short messaging services have been observed to be utilized frequently by farmers (Syiem and Raj 2015). Current correspondence advances can apply to conditions in provincial regions, which will assist with further developing correspondence, increment investment, spread data, and offer information and abilities.

17.4 Use of IT for Livestock Development

17.4.1 Animal Health Management or Disease Controlling IT

The utilization of biosensors and wearable advances is turning out to be progressively significant for animal well-being, the executives. These devices, whenever assembled exactly and utilized accurately, can give useful finding of infections in animals, ultimately diminishing the financial losses. Because of the superior exhibition of wearable advances and sensors, they can make a forward leap in animal improvement and promise to become one of the most effective and practicable innovations in the animal health market (Harrop 2016). One more significant utilization of biosensors is anti-infection detection. These are unrestricted and regular utilization of antimicrobial in many fields; it has turned into a significant danger for farmers. Biological insecurity is affected by the uninhibited utilization of sub-restorative anti-infection agents in concentrated animal feeding operations (CAFOs), which thus causes antitoxin obstruction in animals (Mungaro and Neethirajan 2014). Sounds analysers can also be used to monitor pig’s health and body conditions. Their sounds assist the farmer with assessing if the animal is under pressure. The obstruction of natural and foundation noise can impede the

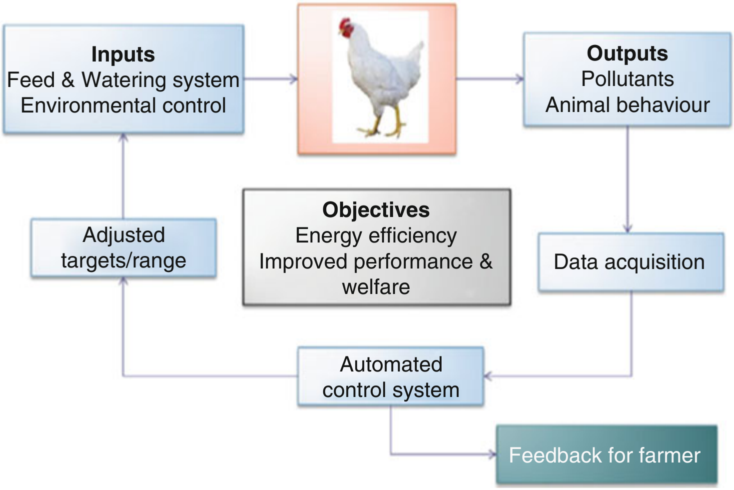

Fig. 17.2 Diagram of a strength indicating parameters and biomarkers measured by biosensor in a poultry farm (Neethirajan 2017)

identification of pig screams. A programmed shout identification strategy has been conceived as of late which recognizes the shouts of pigs from different sounds based on solid design, power, recurrence, span, and fluctuation. By utilizing various calculations and separating between the spectrograms, this classifier is a major forward leap in individual well-being, the board (Vandermeulen et al. 2015). Bird vocalizations can be utilized to assess warm solace for chicks during the warming stage (Fig. 17.2). Gathering standards of conduct and their vocalizations were observed to be related with the commotion abundance yet in addition of the clamour recurrence range. Such commotion sensors might be imperative to decide the impact of climate on chick well-being. Examining and corresponding the sound frequencies of various vocalizations during the existence of birds can fill in as an exceptionally helpful device for the recognition of the development of chickens (Moura et al. 2008; Fontana et al. 2015). Santos (2002) detailed that the National FMD Task Force of the Philippines utilizes a data framework in overseeing information in regard to infection circumstance, inoculation, and creature development, which gives precise data on the creature sickness circumstance of space at the fastest time. Reconnaissance information is unexpectedly shown to the client: reports, tables, and intelligent guides (Conte et al. 2005).

17.4.2 Animal Feeding Management

An imaginative automated brushing framework utilizes electronic leg bunches that work together with sensors mounted on the animal to record data on its dealing with and draining conduct and example (Lely 2016). Incorporating remote sensors for online well-being observing frameworks has been planned and been examined as checking frameworks (Busse et al. 2015). Relating vital subordinate control technique has additionally been applied to diminish work and return higher advantages in poultry taking care of the executives (Olaniyi et al. 2015). One more significant utilization of biosensors is antitoxin identification. Antitoxin opposition has turned into a significant danger for farmers. Natural unsteadiness is brought about by the uninhibited utilization of sub-remedial antitoxins in determined creature animal feeding operations (CAFOs), which thus causes antibiotic conflict in animals (Neethirajan 2017). The inappropriate administration of accessible grain, both dry and green grub, has been one of the serious issues being developed in creature farming and milk production field. The three significant sources of fodder supply are crop residues (paddy straw, wheat straw), developed feed, and feed from normal property assets like wilds, long-lasting fields, and grazing land. 'MakeFeed' the cow's proprietors can formulate adjusted feed from grill chickens, quails, guinea fowls, and dairy animals as per their physiological condition with the accessible resources. 'MakeFeed' is a Windows-based programming created by the researcher of Central Avian Research Institute for detailing of adjusted feed for most extreme production performance. It gives data on nutritive qualities to a wide scope of feed fixings alongside the greatest consideration level for every ingredient. It is easy to use and people having little PC information can use it adequately (Nath et al. 2002).

17.4.3 Breeding

The interest for creature source food varieties is quickly expanding in agricultural countries; for instance, in low pay nations, the interest in 2030 for meat (124%), milk (136%), poultry (301%), and eggs (208%) is anticipated to increment over that in 2000, separately. Reasonable accomplishment is relied upon to be trying, with a critical part of this perceived to be developing animal's efficiency. The capability of hereditary improvement to build animal's efficiency is, however, progressively being perceived by leaders, with numerous African nations currently expressly including hereditary improvement inside their national animal's development plans. The sorts of coordinated genetic improvement programs being done in Africa vary by framework. These incorporate variety supplanting with other African assortment, breeds from other tropical countries like India and Brazil, and similarly as breeds from elsewhere; cross reproducing is most routinely where a profoundly adjusted however humble useful native variety is crossed with an inadequately adjusted yet exceptionally useful exotic variety and less ordinarily inside breed improvement (Table 17.1). While there is an overall agreement that utilizing dairy advances, for example, further developing types of dairy cows can significantly expand ranch usefulness and pay, reception of such advances has been by and large low in non-industrial nations. In preservation hereditary qualities, support of both inside breed and across breed hereditary variety is essential point (Olliver and Foulley 2005), as they assume diverse yet basic parts in supporting animal creation. Choice can adversely influence both these parts, and rearing projects ought to warily

Table 17.1 Genotype of livestock used in different systems in various countries

Country	Production	Genotype	Breed	Reference
India	Mixed crop livestock system	Purebred cross/ buffaloes	Buffalo: Morrah, Nili-Ravi	Rao et al. (2014)
	Smallholder low input	Purebred and crossbred; indigenous cattle and buffalo	Local breeds and their crosses	Kumaresan et al. (2009)
Tanzania	Mixed crop livestock system	Crossbred, purebred exotic, purebred indigenous, synthetic	50–75% Holstein crosses, unspecified exotics, zebu	Msanga et al. (2000)
	Intensive urban/ peri-urban dairy production system	Purebred/crossbred	Friesian, Ayrshire, Jersey	Gillah et al. (2013)
Kenya	Large-scale commercial	Purebred	Holstein jersey brown Swiss	Muasya (2013)
Nicaragua	Extensive grass/ rangeland-based dual-purpose system	Crossbreed	Crosses between *B. taurus* and *B. indicus*	Corrales (2011), Galetto and Berra (2011)

screen hereditary variety. Inside a variety, the equality and pace of inbreeding, which are adversely associated with successful populace size, are by and large utilized as a boundary of inside breed variety. File choice dependent on data from family members prompts the decrease of compelling populace size and increments the likelihood of co-choosing direct relations (Wray and Thompson 1990). The hereditary variety of animals is usually addressed by the protection an adequate amount of varieties. In any case, species-wide variety should likewise be considered during determination inside a variety. As a rule, the FAO (2013) proposes that choice should moderate varieties as hereditarily and socially particular hereditary assets. The choice for expanded yield, while ignoring attributes associated with characteristics of protection interest like transformation, explicit hereditary variation, and nature of items, can diminish breed uniqueness between breed variety. Recognizable proof of determination attributes in nearby breeds ought to be exact and based upon information on the quality science. Advances in genomics and bioinformatics having permitted the ID of genomic marks may add to clarify the phenotypic uniqueness of breeds (Huson et al. 2014) and work with prioritization and the utilization of genomic breeding tools to save these significant characteristics. Genomic determination, in which characteristic estimation is restricted to the reference populace, added to put accentuation on the assortment of novel phenotypes. For example, milk quality characteristics presently incorporate absolute protein and fat substances as well as subcomponents like lactoferrin and unsaturated fats. Mid- and close to infrared spectroscopy permit quantitative assessment of the organization of natural examples and have discovered wide application in dairy cattle reproduction. Well-being-related characteristics address one more field of phenotypic examination and incorporate direct veterinary records, aberrant proportions of mastitis (e.g. milk electrical conductivity, milk mineral substance), female richness (e.g. milk chemical tests, active work), and qualities related. To lameness or metabolic syndromes. Growing interest is being placed on behavioural traits like cow temperament (Egger-Danner et al., 2014).

17.4.4 Marketing of Livestock Product

A portion of the young people broadly utilized ICTs on their residences. For elimination, in Western Kenya, 90% of the juvenile acknowledged ICTs in their development (IICD 2013). The most by and large used contraptions were MS Office for getting word ready and spreadsheets for developing and trading record-keeping. The frontline phone SMS and voice messages were consistently used to get ideal market costs, show up at clients, share exact creation information, and trade money. Models included item arrangements and agribusiness associations. Their essential thing M-Farm is a straightforward gadget for Kenyan ranchers where they just SMS the number 2025 to get information about the retail cost of their things, buy their property inputs straight forwardly from products at positive expenses, and find buyers for their produce. They accumulate markdown expenses of the items from the five huge business areas in Kenya and post them on their worth page. The iCow, the winning application in the apps for Africa competition 2010, allows small-scale dairy farmers to manage and trade livestock (Oafrica.com 2012). The stage has allowed customers to fabricate milk creation by the greater part and pay by 42%. iCow, in one of its things, helps hamburger ranchers track their cow's hatching periods to build animal numbers. Ranchers use an SMS code to enrol their cows and their insemination date. A huge piece of the adolescent got their information from the web, so the reality of the situation is that the web would be maybe the best stage to market and propel agribusiness expecting you wanted to actually look at the young. Web and online media were used to get ranch creation developments, market data, and information sharing. Farming advancements, for instance, further fostered an assortment of dairy cows, and further developed scavenges can chip away at the positions of smallholders through more significant returns, better house load pay, and further created sustenance. In the past 60 years, current advancements in creature rearing, taking care of, and creature medical services have been raised to change implies dairy creation into the market-masterminded dairy adventures in non-industrial nations (Duncan et al. 2013).

17.5 Dissemination of Agriculture and Livestock Information

In non-industrial nation's information communities, innovation plays a vital influence in the creation of schooling, well-being, and provincial improvement just as in agriculture development. This innovation has gotten huge change agribusiness advancement in underdeveloped nations where farmers are directly associated with market, purchasers, clients, and metrological division to get data in regard to climate and cost. The term ICT is used to incorporate a radio, TV, mobile phone, telephone, iPad, video-voice data framework fax, and computer (Warren 2002).

17.5.1 Mobile

ICT instruments, for example, cell phones have given new ways to deal with farmers to settle on speculative choices substantially more effectively than previously. Utilization of cell phone prompts to greater social union and worked on friendly connections. However, short message administration SMS and voice records have given upgrades in friendly relations. Cell phone-based social organizing in the agricultural nations goes to show the developing significance of this angle (Kyem et al. 2006; Oladele 2011). Cell phone innovation could give farmers the most recent and speedy information in a variety of ways. Education had been displayed to upgrade farmer's mindfulness and information on various impending advances and consequently improve the probability of utilizing cell phones for agricultural marketing. The utilization of cell phones for horticultural promotion may turn into a perfected cost-effective and opportune choice to smallholder farmers rather than traveling which might require utilizing more cash as well as investing more energy to get to advertise data (Katengeza et al. 2011). The cell phone has discounted the hole among merchants and farmers, and at the same time, farmers directly speak with purchasers and clients to track down the great cost of their item. Farmers before going to advertise get in touch with perhaps the best purchaser who buys products at a great cost. In the rustic spaces of non-industrial nations, cell phones are spreading step by step, and various associations have dispatched many undertakings for agribusiness advancement and increment the creation by utilizing various innovations in farming. Cell phones have set out other businesses to open doors for helpless farmers and have given the admittance to data about market, health, and climate administrations in distant regions. The uses of cell phones among farmers have played a positive effect on their pay and usefulness because before movement speak with purchasers and sell their item in great value (Grameen Bank 2007). Perhaps the main role of cell phones in the non-industrial nation showed that farmers utilize the cell phones for getting the data from various business sectors and climate data while other speak with agribusiness specialists to acquire data about the utilization of pesticides in their farm. For example, Bangladesh farmers directly contact purchasers and get the data about rice cost and vegetables, while some of them ask about the cost of coffee from global agent's nations. Two decades before, it was extremely challenging for farmers to take data about their creation from the market inside the space of minutes from their towns (Kefela 2011). Quality, timeliness, and dependability of data rule to address the issues and assumptions for the farmers as the entrance of portable administrations keeps on expanding across the cultivating networks with a possibility to further develop ranch efficiency and increment country pay (Mittal et al. 2010). Expanded public and private speculations can connect the infrastructural holes. An assortment of administrations is accessible through cell phones for taking data to the animal's proprietors. KrishiDarshan application on cell phones permits clients to associate with 'KrishiDarshan' program on Doordarshan. The possession of cell phones especially has turned into a need in the contemporary society independent of age, status, calling, pay gatherings, or spot of home (Chhanchhar et al. 2014).

17.5.2 Internet

Farmers generally were utilizing the web and their messages for speaking with their loved ones in different spots of the country. This web was renowned among the farmers in India. These day's farmers are utilizing various sites for getting the data about legitimate utilization of pesticides in their farms. The Korean agriculture forestry fisheries information service (AFFIS) additionally assumed a vital part in giving data to fishermen and farmers. The education executive's framework was set up in 2002 in which the principal capacity of this division was to provide on the web disconnected learning programs and instructive data administrations to the fisherman and farmers. The fisherman and farmers were given not many freedoms to learn through network access. It oversees instructive substance and has a lot of data about farming and fisheries. By utilizing the web, farmers worked on their abilities and accomplished a lot of data and utilized new advances in the agribusiness area. The organization was associated by phone landline in their spaces. In projects around 85–92% of the forestry was uninformed, and they have no information on PC. Besides, to give web information, forestry coaches were selected to give training to farmers. In these conditions, farmers were not feeling any dithering to get data about users to web and getting the data about pesticides just as market (ITU 2009; Meera et al. 2004). The web is perhaps the main wellsprings of discovering data about agribusiness just as another related issue (Burke and Sewake 2013). Looking for online data about banking is one of the most significant agribusiness action among farmers. In Malaysia, a current measurement shows that 94% of the Malaysian farmers utilized the web to look for agriculture data, while 85% of the farmers get data by utilizing instant messages. In India, the project has been started for the farmers about the application; Internet and mail serve as their middlemen and give the most recent data in regard to agriculture to farmers. The web was utilized to get to creation pamphlets, magazines, and papers. Looking for data from these and different stages was a difficult errand for the farmers as it involved crashing through numerous distributions or riding countless pages. Furthermore, for the illiterate farmer it becomes that the internet infrastructure in Kenya is still very sparse. By and by, these are extremely valuable assets, and everything necessary is to give a simple way to the farmers to explore those (Irungu et al. 2015).

17.5.3 Television

TV has given a lot of data to all partners of the general public. TV has made mindfulness and information among farmers about the utilization of innovations in cultivating TV products such sort of projects which make interest among masses, and generally the majority rely upon media for getting the data with respect to instruction, well-being, and farming (Age et al. 2012). The productive outcomes about agriculture improvement rely upon the utilization access, and the assembly of the local area depends on the TV. The specialists of agriculture augmentation accept that broad communications can bring positive changes and development of farming in non-industrial nations by utilizing the correspondence advances in their nations. DoordarshanJallandhar has a broadcast program called 'KhetiKhabranAtteMandian De Bhaa' devoted to the scattering of data with respect to farming and animal cultivation. DD Kisan, a 24 h TV station, was dispatched in May 2015 committed to agribusiness and associated areas. The PJTS rural college of Telangana has dispatched a broadcast program called Rythumitra/Ritumytra in relationship with the State Department of Agriculture and Teja station comprising of projects on agribusiness, cultivation, and animal sciences (Ali 2011). Electronic media have been observed to be exceptionally successful in ideally scattering data required by the farmers. The review recommended that most extreme respondents have concurred that portable web can be a valuable wellspring of agrarian data and a huge extent was uncertain that 'rural helpline can be a valuable wellspring of rural data'. However, 65.6% of the respondents were uncertain with regard to whether TV broadcast and projects gave adequate farming data and positively affect agrarian creation (Aldosari et al. 2019).

17.5.4 Radio

Radio is one of the most outstanding mechanisms of correspondence which has assumed an extremely indispensable part in society, monetary culture, and farming data. It is amazing specialized apparatus in rustic regions which gives agrarian and marketing data. Notwithstanding, it was shown that in creating countries there is an issue of selectivity in provincial regions; therefore farmers and different networks for the most part depend on radio to address their issues of data with respect to schooling, well-being, horticultural news, and climate data. The accomplishment of farming advancement programs in agricultural nations fundamentally relies upon the nature and level of utilization of broad communications diverts in the preparation of individuals for improvement overall. Radio is one of the best wellsprings of diffusing agrarian, specialized, and scientific data to the farmers (Murty and Albino 2012). The radio is a very advantageous apparatus of correspondence particularly for unskilled farmers to assemble data of different kinds on agriculture and different components to keep up to date with their insight and administrations. The credibility regarding radio information is one of the most important elements of communication process and its successful willgrowth proportionally if the receivers of the information perceive the sources to be trust worthy and competent. Food and Agriculture organization FAO working in Mali to provide information among rural farmers about marketing, weather, environmental, disease, water management an pest monitoring to increase the productivity of agriculture in their country. This sort of data was communicated by radio in distant regions. Radio innovation has assumed a significant part of the data about horticulture, climate, and utilization of pesticides among farmers (Weiss et al. 2000). AIR is communicating 'Kisanvani' program structure in more than 90 nearby radio stations focussing on different issues in regard to agribusiness, animal cultivation, poultry cultivating, and fisheries. The program additionally covers data with respect to work plans, preparing, and advancing offices. The Kisanvani program is communicated in every one of the significant dialects in the space of its inclusion (Ali 2011).

17.5.5 Newspaper

The motivation behind rural newscasting is to convey significant data to the farmers and simultaneously look for criticism (Hanumanaikar et al. 2011). Farmers can get to data on paper media by perusing or through practically educating their relatives when the farmers are proficient. Papers are thought of as significant for transferring ranch data to a large number of farmers disseminated the nation over. Before, papers have played a significant part in the improvement of agribusiness; what's more, in the wake of expanding level of education, the paper holds incredible possibility as a basis for dispersal of ranch data (Lahiri and Mikhopadhyay 2011). Paper courses give common material on creatures developing as news, ads, showcasing, measure guides, perspectives, reports, instances of conquering misfortune, featured articles, distributions, etc.

17.6 Conclusion

The government additionally should take drives for the advancement of agriculture and give training and most recent data by utilizing the correspondence advancement tools in their nations. The vast majority of agricultural nations' forestry schooling level is likewise low; subsequently legislature of these nations should have specialized and instructive projects for farmers in their nations and upgrade the limited work of farmers by utilizing data correspondence innovations so that farmers can likewise get great advantage from these advances and increment their pay and work on their norm of life. Besides, there is a deficiency of power in far-off regions that have likewise diminished the farming creation consequently making elective hotspots for increment the agriculture creation in these nations, for example, sunlight energy-based framework for agribusiness improvement. Creature cultivation in India is overwhelmed by conventional information and practices. Data dispersal is a significant mediation to work on the efficiency in farming and united areas. Just a little part of animal farmers access data in regard to animal farming practice in India.

The government and public and state level in India need to reorient rural approaches with the goal that a completely fledged system is shaped to tackle IT potential for helping generally agrarian and animal advancement.

17.7 Future Development Aspects of IT in Agriculture and Livestock

Throughout the long term, as farmers have embraced more innovation in their quest for more prominent yields, the conviction that ‘greater is better’ has come to rule cultivation, rendering limited scope operations unfeasible. However, progresses in advanced mechanics and detecting advances are threatening to disrupt the present agribusiness model. There is the potential for shrewd robots to change the monetary model of cultivating so that it becomes practical to be a small maker again says mechanical technology engineer George Kantor. Twenty-first-century mechanical technology and detecting advances have the potential to take care of issues as old as cultivating itself. I accept by moving to a mechanical farming framework; we can make crop creation fundamentally more proficient and more reasonable, says Simon Blackmore and architect. For domesticated animal farmers, detecting advancements can assist with dealing with the well-being and government assistance of their animals. Also, work is in progress to further develop observing and upkeep of soil quality and to gauge nuisance and sickness without falling back on aimless utilization of agrichemicals.

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Use of Wild Edible Plants Can Meet the Needs of Future Generation

18

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Abstract

Despite actual knowledge of measuring ecosystem services, the importance of biodiversity in sustaining such services in diverse landscapes and how indigenous cultures exploit, consume, and conserve plant resources in a biocultural regime received little attention. Malnutrition, food insecurity, a lack of sources of food, and famines are all problems that the world is facing due to poor crop yields, shortages, and increased rates of healthy food consumption. Reports of a potential from wild edible plants (WEPs) are primarily anecdotal, with minor and frequently incoherent science to back them up. Still, nowadays, day by day, many reports are published encouraged by findings in scientific journals that continually emphasize the wild edible plants' great nutritional value. It is suggested that limited resources strengthen these priority WEPs, as they have the best chance of success. Currently, production is limited because of a lack of intensification of WEP farming, a lack of genetic tools for trait development, and the need to optimize storage and supply linkages. These ideas will aid in the fight against

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hunger and malnutrition, while also benefiting farmers and other stakeholders involved in the agriculture process financially. This chapter discusses the conservation of WEPs utilized by local indigenous communities for sustainable utilization and forest management because it can encourage multifunctional forestry.

Keywords

Wild edible plants · Ecosystem services · Food composition · Food security · Biodiversity

18.1 Introduction

Food and nutrition security is a critical problem that our society is now dealing with (FAO 2012). Micronutrient deficiencies are expected to affect about two billion individuals, rendering people more susceptible to sickness, substantially impeding economic progress. Food security is a serious concern, particularly in import-dependent countries (Bongaarts 2007). On the other hand, the continent has highly biodiverse ecosystems with important, wild food plants usually overlooked (Toledo and Burlingame 2006).

The ancient tradition of humans' capabilities to acclimatize to native habitat and interact with the environment and human situations is implemented to consumable wild plants and animals. Plants have had a significant impact on human cultures since the initial hunter-gatherers and during many adaption periods. Many people around the world are dependent on several wild species, notably for food, medicine, and nutritional supplements (Bharucha and Pretty 2010). Plants with edible components growing spontaneously on farmland, croplands, or undisturbed natural areas are considered wild edible plants (Addis 2009). Several edible wild plants have contributed a significant role in various geographical locations of the world (Ruffo et al. 2002).

In many rural regions worldwide, wild plants contribute to people's food and nutrition security and health (Teketay et al. 2010; Sekeroglu et al. 2006). Requirements of local people in remote areas are fulfilled by wild edible plants (Sundriyal and Sundriyal 2001). Wild edible plants are the species of plants which are not cultivated but are available as food from various habitats (Beluhan and Ranogajec 2011). These plants are assessed from all over the world from different habitats, viz., forests, zones like west lands and roadsides, and cultivable lands. Wild edible plants are used by local people on a daily basis in different forms such as roots, tubers, leaves, flowers, fruits, seeds, etc. (Beluhan and Ranogajec 2011). They could have excellent nutritional values and be a significant source of vitamins, fiber, minerals, and unsaturated fats; they could also have essential therapeutic potential (Cavender 2006). For food-insecure impoverished people in underdeveloped countries, wild edible plants always were an important and widely available food source (Pieroni et al. 2007; Dansi et al. 2008). They are essential for family ensuring food security in some remote regions, where they are used to complement basic

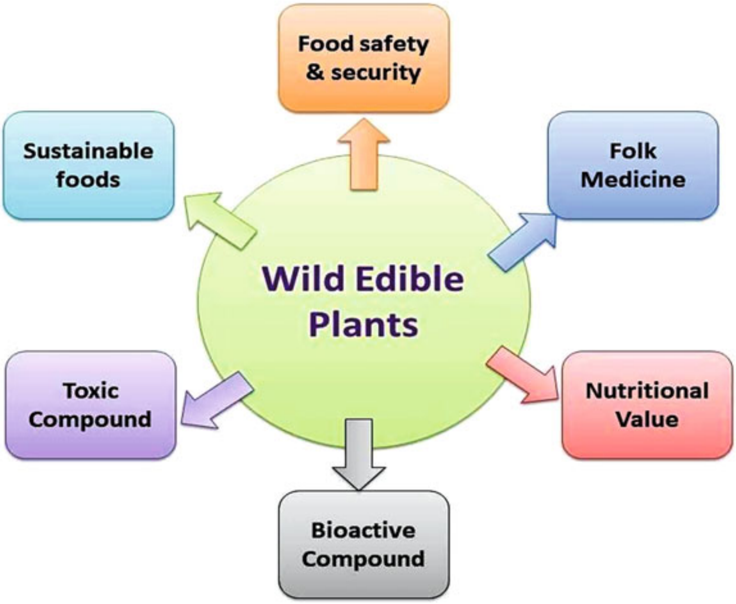

Fig. 18.1 Importance of wild edible plants

foods, overcome chronic food insecurity, and act as emergency supplies in times of starvation (Mavengahama et al. 2013). They are also essential for several remote villages and even metropolitan communities, particularly among the impoverished and underprivileged (Yumkham et al. 2017). Wild edible plants play a significant role in providing a massive food supply in all regions of the world region (Chakravarty et al. 2016). Daily, over one billion individuals throughout the world consume wild plants food (Lulekal et al. 2011). Wild edible plants are nutritious and can be used to complement vitamins and micronutrients in particular (Sunderland 2011; Fraval et al. 2018). Because of their higher nutrient content, they can help complement nutritional needs (Berihun and Molla 2017; Feyssa et al. 2011). Some of the importance of wild edible plants are shown (Fig. 18.1). Furthermore, certain fruits include the so-called “anti-nutritional” components (e.g., phytic acid and tannins) that might reduce nutrient absorption, especially if they are present in high concentrations (Spiller 2001). Plants that grow in WEPs contain a wide diversity of life forms and botanical features such as annual or perennial herbaceous plants, vines with needlelike leaves, sedges and rushes, and broadleaved shrubs with needlelike or scalelike leaves (Carvalho and Barata 2017).

Apart from nutritional benefits, the retail or trade of their fruits, leaf, pulp, and native beverages can provide money and employment (Grivetti and Ogle 2000). Wild plants are used as cheap and abundant remedies to the significant number of the world’s rural population. According to research, many wild edible plants have now been discovered to be high in one or so more medically essential components, such as proteins, carbohydrates, vitamins, and minerals. Along with the nutritional components, some of them include significant quantities of a range of health-promoting substances, such as phenolics (Guinand and Lemessa 2001; Pardo-de-Santayana et al. 2007; Fentahun and Hager 2009).

The dietary, nutritional, and therapeutic contributions of wild edible plants have not been investigated comprehensively worldwide. As a result, the objectives of this chapter are to explore the existing knowledge on the nutritional contributions, supplemental role, and therapeutic value of wild edible plants.

18.2 Diversity and Conservation

National contributions to the Food and Agriculture Organization of the United Nations' recent "State of the World's Biodiversity for Food and Agriculture" confirm the usage of wild edible plants in several nations in their diet (Belanger and Pilling 2019). With wild edible plants gradually disappearing from nature and diets, the challenge is how to significantly boost their long-term usage, while also conserving them for food and nutrition security. WEPs have high amount of nutritional values, and because of these nutritious contents, WEP helps in eradication of poverty, increases resources for income, guarantees the security for availability of food, alleviates malnutrition, and diversifies the agriculture practices (Urso et al. 2016; Kaoma and Shackleton 2015; Rathore 2009). As the WEP safeguards scarcity of food, famine, or conflict, they reduce the food insecurities in local markets (Termote et al. 2010; van Andel 2006; Seifu et al. 2017).

In India various climatic zones and diversified ecology are present, and this helps in creating rich phytodiversity of WEPs occupying important position in the cultural, religious, and health sector and ethnic and rural lives of Indians. These facts were studied and confirmed by many researchers of India (Cruz-Garcia 2017). Historically, humans may have exploited more than 7000 WEPs (Barbier 2010), but many such food resources and valuable plants are still to be explored (Uprety et al. 2012).

Furthermore, because certain species' germplasm and other plant material (e.g., tissues, embryo, etc.) may not be appropriate for ex situ conservation, both in situ and ex situ conservation should be combined for best outcomes (Hawkes et al. 2012; Borelli et al. 2020). In situ conservation strategies can complement ex situ conservation and allow WFPs to continue to evolve obtained results in their natural environments, while benefiting those who need them most, particularly in areas where high diversity, rural poverty, and malnutrition coexist. The main reasons for threats to wild edible plants include land-use changes, forest destruction and dilapidation, agronomic change, use of chemicals, overexploitation, or untenable processing. The loss of cultural management practices was used by societies to increase the number of wild edible plants. Other challenges to WFP usage and value have included insufficient knowledge (diet, health, hygiene, economic, and environmental); a deficiency of harvests, preservation, and value-adding research and technology; and an unawareness, training, and involvement in programs and policies (Zhang et al. 2018; Borelli et al. 2020).

By decreasing the risk of overdependence on a small number of crops, edible wild plants can help to enhance sustainability. Some of the world's poorest rural communities have relied heavily on these wild edible plants to meet their food and nutritional needs and improve their health (Joshi et al. 2018). Because they appear to need fewer expenditures than other commercially produced plants, a path has been created for their prospective cultivation. Furthermore, customer demand for new natural-source goods that are both sustainable and ecologically branded has aided WEP recovery and market acceptance (Pereira et al. 2020).

In the poor countries, protein deficiency is a serious public health issue. Because the main food crops are roots and tubers, the diets in these areas are mostly starchy. The trace elements, along with other important nutrients, are required for development, normal physiological function, and the maintenance of life; they cannot be synthesized by the body and must be obtained from diet (Ali and Deokule 2009). Although the distinction between trace and macrominerals isn't always obvious, traces are frequently thought of as minerals that the body requires in levels less than 100 mg/day to boost the immune system; otherwise maybe different types of microorganism will cause diseases like coronavirus (Rocha et al. 2021). Minerals are essential in the diet for optimal growth and well-being. Calcium, phosphorus, magnesium, potassium, sulfur, sodium, and chlorine are required in macro proportions, whereas iron, iodine, copper, cobalt, chromium, manganese, selenium, zinc, fluorine, and molybdenum are required in micro amounts. The minerals calcium, phosphorus, magnesium, potassium, iron, and sodium are abundant in cruciferous and other vegetables, and the majority of these minerals are present in their most bioavailable form. Fruit and vegetable trace mineral content is determined by the quantity of trace minerals present in the soil where the plant was grown. Vitamins and minerals in the diet are essential for appropriate development and metabolism, as well as influencing the absorption of other nutrients like protein. A shortage of vital vitamins or minerals causes a variety of physiological problems and diseases, as well as delayed development and protein deposition in tissues. For proper protein usage, a sufficient amount of B-complex vitamins is required. We may employ edible proteins from plants such as vegetables and fruits in the food industry and as nourishment. In addition to total proteins and nitrogen, there are also albumins, globulins, and free amino acids. Omics technologies must be used for all the plants to know the better understanding about the plant nutrition and edibility (Singh et al. 2021a, b, c; Kumar et al. 2020). Essential amino acid proteins have a high nutritional value and are thus acceptable for intake since the body cells require them.

Many plants that are used and cultivated by civilized societies nowadays were originally identified and developed through indigenous knowledge. WEPs are freely available, they are preferred culturally and religiously, so they are being used by rural populace since antiquity. So it is prime need of our generation to collect the information and document the traditional knowledge of WEPs with their ethnomedicinal uses (Battiste and Youngblood 2000; Singh et al. 2019).

Plants, which contain phytochemicals with potent antioxidant properties, have gotten a lot of attention in recent years. Antioxidants, which prevent organic molecules from oxidizing, are essential not just for food preservation but also for the protection of biological systems against oxidative stress (Masuda et al. 2003). By donating a hydrogen atom from a phenolic hydroxyl group, phenolic antioxidants stop the propagation of the free radical autoxidation chain, resulting in the creation of a relatively stable free radical that does not begin or propagate additional oxidation processes (Kaur and Kapoor 2001). Dietary fiber (DF) helps to reduce the risk of constipation, diabetes, cardiovascular disease (CVD), diverticulosis, and obesity, among other conditions (Tamang et al. 2019). Dietary fiber is found in plant grains. Dietary fiber contains all of the main components of plant cell walls (cellulose, lignin, hemicellulose, pectin, gums, and mucilage). Cereals, pulses, green leafy vegetables (GLV), roots, tubers, other vegetables, fruits, oil seeds, spices, and sauces are all common ingredients in local food. Fruits come in a variety of forms, including fresh, dried, frozen, and tinned. Dietary polysaccharides make up a significant portion of the diet. In healthy human volunteers, fiber in fruits and vegetables is helpful because it reduces plasma cholesterol levels (Table 18.1) (Gillman et al. 1995).

18.3 Edible Plants from Wetlands in North East India

Among the world's biodiversity hotspots are the wetlands of the Northeast Indian subcontinent. As a result of the fact that their fundamental worth to humanity has been undervalued, insufficient attention has been paid to preserving them. Wetlands play a vital role in indigenous cultures' survival. Wetlands encompass about 6% of the earth's surface, or 8.6 million km^2 (Maltby and Turner 1983). As the ecotone between terrestrial and aquatic ecosystems, they perform unique hydrologic activities and are heavily relied upon to provide food, medicine, and shelter to all living species. There are several types of wetland regions that may be wet all year round or only during specific times of the year. Globally, wetlands are expected to provide products and services worth US$70 billion annually (Vijayan 2004). A considerable number of wetlands are found in Northeast India, which is part of the Indo-Burma hotspot. There is extensive tribal knowledge of wetland species in the region, but there is a scarcity of information on such knowledge, which could otherwise serve as a basis for their conservation and sustainable management. Wetland regions provide a diverse range of edible plants to locals for both food and medicine. They also provide additional services like aesthetics, revenue, food for animals, and crafts (Jain et al. 2004, 2005). For individuals in isolated rural communities where vegetable production was not common, wild food items were a key source of vitamins and minerals (Misra et al. 2008). A significant protein content was observed in the early shoots and leaves. *Lemanea australis* had a high amount of important nutrients (fat, carbohydrate, protein, and nitrogen) as well as a high amount of micronutrients (Zn and Cu), and the carbohydrate content of the roots of *Nelumbo nucifera* and *Colocasia esculenta* was found to be high (Jain et al. 2011). These species were also found to have a high nutritional value. Wild edible plant resources were an essential element of native diets in mountain locations, and they

Table 18.1 List of economically and medicinally important wild edible plants (WEPs) is listed with their botanical name, family name, and their uses

S. No.	Botanical name	Family	Uses	References
1.	*Acacia catechu* Willd	Leguminosae	Tea; medicinal	Ray et al. (2006)
2.	*Aegle marmelos*	Rutaceae	Sharbat and jam	Ruhil et al. (2011)
3.	*Aerva lanata*	Amaranthaceae	Leaves are eaten during famine, used during cough and diabetes	Goyal et al. (2011)
4.	*Alternanthera sessilis*	Amaranthaceae	Tribal use as vegetable, used to treat eye diseases	Walter et al. (2014)
5.	*Amaranthus viridis*	Amaranthaceae	Edible, antidiabetic, antihyperlipidemic	Kumar et al. (2012a)
6.	*Artemisia scoparia*	Compositae	Leaves eaten during jaundice, fever, inflammation	Safaei-Ghomi et al. (2005)
7.	*Artocarpus lacucha*	Moraceae	Fruits as pickled, antiviral, for stomachache, anti-tyrosinase	Islam et al. (2019)
8.	*Asparagus adscendens* Roxb.	Asparagaceae	Pickled, used as salad, for abdominal troubles, antifilarial	Mehta and Subramanian (2005)
9.	*Bauhinia vahlii*	Leguminosae	Seeds are fried with rectified butter and eaten, antidiabetic, anti-inflammatory	Bhandari et al. (2020)
10.	*Bombax ceiba*	Malvaceae	Flower receptacle as vegetable, antimicrobial activity	Chaudhary and Khadabadi (2012)
11.	*Borassus flabellifer*	Arecaceae	Endosperm is eaten. Young seedling (param) is edible	Davis and Johnson (1987)
12.	*Buchanania cochinchinensis*	Anacardiaceae	Seeds are edible	Dixit et al. (2019)
13.	*Buglossoides arvensis*	Boraginaceae	Fruits are eaten raw	Zahariev et al. (2016)
14.	*Butea monosperma*	Leguminosae	Flower decoction is taken as sharbat for cooling purpose	Sindhia and Bairwa (2010)
15.	*Capsella bursa-pastoris*	Brassicaceae	Eaten as cooked or raw vegetable	Al-Snafi (2015)
16.	*Capparis zeylanica*	Capparaceae	Fruits are made into vegetable and eaten	Ghule et al. (2007)
17.	*Cardamine impatiens*	Brassicaceae	Seed as vegetable	Glenn and Barringer (2004)

(continued)

Table 18.1 (continued)

S. No.	Botanical name	Family	Uses	References
18.	*Carissa spinarum*	Apocynaceae	Seeds as spice condiment	Sanwal and Chaudhary (2011)
19.	*Carum carvi* L.	Apiaceae	Herbs to control aflatoxins	Iacobellis et al. (2005)
20.	*Celastrus paniculatus* Willd	Celastraceae	Fruits are eaten as raw	Shashank et al. (2017)
21.	*Chenopodium album* L.	Amaranthaceae	Tribal people use it as vegetable	Poonia and Upadhayay (2015)
22.	*Cissampelos glaberrima*	Menispermaceae	Leaves as Pakora, chutney	da Silva Mendes et al. (2020)
23.	*Citrus aurantiifolia*	Rutaceae	Jambiri tree fruit juice is added to chutneys, eaten raw	Fagodia et al. (2017)
24.	*Citrus medica*	Rutaceae	Fruits pickled, juice is added to chutneys	Panara et al. (2012)
25.	*Carissa spinarum*	Apocynaceae	Pickle is prepared from fruits	Laddimath (2021)
26.	*Celosia argentea*	Amaranthaceae	Leaves are edible	
27.	*Chenopodium album*	Cucurbitaceae	Leaves are edible	
28.	*Cocculus hirsutus*	Menispermaceae	Leaves are edible	
29.	*Cryptolepis dubia*	Apocynaceae	Used for preparation of pickle, paratha, curry, etc.	
30.	*Dioscorea belophylla*	Dioscoreaceae	Tubers as vegetable, pickle	Dobriyal and Dobriyal (2014)
31.	*Diplazium esculentum*	Athyriaceae	Fronds as vegetable, pickled	
32.	*Duchesnea indica*	Rosaceae	Fruits are eaten as raw	
33.	*Dendrocalamus strictus*	Poaceae	Bamboo shoots (Karel) are edible	
34.	*Diospyros melanoxylon*	Ebenaceae	Fruits are edible	
35.	*Euphorbia royleana* Boiss	Euphorbiaceae	Young shoots are boiled, cut into small pieces, and added to yogurt to make raita	Kumari et al. (2018)
36.	*Fagopyrum acutatum*	Polygonaceae	Seeds as vegetable; chapatti of flour is eaten during severe cold	
37.	*Ficus auriculata*	Moraceae	Fruits are eaten raw	Ambreen et al. (2019)
38.	*Ficus palmata*	Moraceae	Leaves are cooked with diluted yogurt to make curry, leaves are also cooked with	

(continued)

Table 18.1 (continued)

S. No.	Botanical name	Family	Uses	References
			meat; fruits are eaten as raw	
39.	*Ficus racemosa* L.	Moraceae	Fruits are eaten as raw	
40.	*Flacourtia indica*	Salicaceae	Fruits are eaten raw; tea	Bharadwaj and Seth (2017)
41.	*Flemingia prostrate*	Leguminosae	Fruits, seeds chutney (prepared by grinding fruits and seeds)	
42.	*Fumaria indica*	Papaveraceae	Herb leaves as vegetable; medicinal	
43.	*Ficus religiosa*	Moraceae	Fruits are edible	
44.	*Grewia asiatica*	Malvaceae	Fruits are edible	Zia-Ul-Haq et al. (2013)
45.	*Gymnosporia emarginata*	Celastraceae	Leaves are edible	Khichar et al. (2019)
46.	*Holoptelea integrifolia*	Ulmaceae	Seed are edible	Kumar et al. (2012b)
47.	*Hygrophila auriculata*	Acanthaceae	Leaves are edible	Sethiya et al. (2018)
48.	*Lathyrus aphaca*	Leguminosae	Seeds and fruits are eaten as raw	Dahiya et al. (2019)
49.	*Lannea coromandelica*	Anacardiaceae	Gum is edible	Yun et al. (2014)
50.	*Lantana camara*	Verbenaceae	Flower nectar is edible; antimicrobial	Mansoori et al. (2020)
51.	*Medicago polymorpha*	Leguminosae	Vegetable and as biofertilizer	Algandaby and Salama (2018)
52.	*Mentha longifolia*	Lamiaceae	Chutney; tea; medicinal	Hussain et al. (2021)
53.	*Moringa oleifera*	Moringaceae	Vegetable, pickle; medicinal	
54.	*Morus alba*	Moraceae	Fruits are eaten raw; medicinal	
55.	*Morus nigra*	Moraceae	Fruits are eaten raw; medicinal	
56.	*Murraya koenigii*	Rutaceae	Leaves as spice; medicinal	Handral et al. (2012)
57.	*Madhuca longifolia*	Sapotaceae	Flowers and fruits are edible. Fruit oil is used for cooking purpose. Flowers are used for making country liquor	Akshatha et al. (2013)

(continued)

Table 18.1 (continued)

S. No.	Botanical name	Family	Uses	References
58.	*Marsilea aegyptiaca* Willd	Marsileaceae	Leaves are edible	Schaefer et al. (2011), Sathiyanarayanan and Arulmozhi (2007)
59.	*Marsilea minuta*	Marsileaceae	Leaves are edible	
60.	*Mucuna pruriens*	Leguminosae	Seed are edible	
61.	*Opuntia elatior*	Cactaceae	Fruits are eaten	Juyal and Ghildiyal (2013)
62.	*Oxalis corniculata*	Oxalidaceae	Leaves are edible	
63.	*Plantago lanceolata*	Polygonaceae	Used as tea and syrup	
64.	*Prunus armeniaca*	Rosaceae	Fruits are eaten raw	Takeoka et al. (1990), Pande et al. (2007)
65.	*Prunus persica*	Rosaceae	Fruits are eaten raw	
66.	*Pueraria tuberosa*	Leguminosae	Fruits are eaten raw and cooked as vegetable	
67.	*Punica granatum*	Lythraceae	Seed fruits are eaten as raw, anaardana (dried seeds) are grinded to make chutney	
68.	*Pergularia daemia*	Apocynaceae	Flowers are edible	Reddy et al. (2019)
69.	*Phoenix sylvestris*	Arecaceae	Fruits are edible	
70.	*Physalis angulata*	Solanaceae	Fruits are edible	
71.	*Rumex dentatus*	Polygonaceae	Used as vegetable rich of vitamins	Nisa et al. (2013)
72.	*Scandix pectin-veneris*	Apiaceae	Vegetable of young shoots	Soheili et al. (2013)
73.	*Silene conoidea*	Caryophyllaceae	Fruits are eaten raw	
74.	*Syzygium cumini*	Myrtaceae	Fruits are eaten as raw	Thapa et al. (2014)
75.	*Semecarpus anacardium*	Anacardiaceae	Fruits are edible	
76.	*Sonchus oleraceus*	Compositae	Leaves are eaten during famine	
77.	*Terminalia bellirica*	Combretaceae	Fruits are eaten raw after removing outer covering	Pande et al. (2007)
78.	*Terminalia chebula*	Combretaceae	Vegetable, curry	
79.	*Trifolium pratense*	Leguminosae	Used as vegetable	
80.	*Trifolium repens*	Leguminosae	Tubers are eaten raw	
81.	*Tamarindus indica*	Leguminosae	Leaves made in to chutney and eaten	
82.	*Urtica dioica*	Urticaceae	Used as beverage	Joshi et al. (2014)

(continued)

Table 18.1 (continued)

S. No.	Botanical name	Family	Uses	References
83.	*Veronica persica*	Plantaginaceae	Young leaves and shoots as vegetable are prepared in yogurt	Heidarian et al. (2019)
84.	*Vicia hirsuta*	Leguminosae	Pods are eaten as raw	
85.	*Viola odorata*	Violaceae	Flowers as tea	
86.	*Woodfordia fruticosa*	Lythraceae	Flowers and nectaries are edible	Ahmed (2019), Amjad et al. (2016)
87.	*Acacia catechu* Willd	Leguminosae	Tea; medicinal	Ray et al. (2006)
88.	*Aegle marmelos*	Rutaceae	sharbat and jam	Ruhil et al. (2011)
89.	*Aerva lanata*	Amaranthaceae	Leaves are eaten during famine, used during cough and diabetes	Goyal et al. (2011)
90.	*Zanthoxylum armatum*	Rutaceae	Chutney is prepared from seeds; fruits are sun dried, fried in oil, and used as pickle	
91.	*Ziziphus jujuba*	Rhamnaceae	Fruits are eaten as raw	
92.	*Ziziphus oenoplia*	Rhamnaceae	Fruits are edible	
93.	*Schefflera vinosa*	Araliaceae	Used as fertilizer, as antimicrobial	Singh et al. (2021a)
94.	*Thespesia lampas*	Malvaceae	Used as vegetables	Singh et al. (2021b)

also helped to maintain nutritional balance among tribal populations (Sundriyal and Sundriyal 2001; Sundriyal and Sundriyal 2004). *Euryale ferox*, *Colocasia esculenta*, *Nelumbo nucifera*, *Oenanthe javanica*, etc. were the most often traded marsh plants.

Due to its unique topography and ecological marginal circumstances, the northern portion of India has a large variety of medicinal plants. Northern India's ancient medical systems are part of a long-standing culture that is still respected today. For more than 3000 years, these traditional techniques have been used to treat complicated diseases (Ulett et al. 1998). Most of the plant populations have been reduced due to the fast increase in demand for these therapeutic herbs, showing a lack of ecological understanding among communities who use the plants (Yu et al. 2006). Differences in geographical location, kinds of wild edible plants, and societal culture may all have a role in the marketability of wild food plants (Tables 18.2 and 18.3).

18.4 Wild Green Vegetables

In poor nations, the shortage, high cost, and unpredictable supply of healthy food have resulted in a search for low-cost and alternative sources of good and nutritious food. For many regions of the globe, wild edible plants (WEPs) constitute an

Table 18.2 Edible plants prevalent in wetlands

S. No	Name of the plant	Dietary consumption and preparation	Reference
1.	*Alocasia cucullata*	Traditional salad known as singju (a combination of fermented fish, chili, and other plants)	Jain et al. (2011)
2.	*Alpinia galanga*	For lunch and supper, the decoction of the rhizomes is mashed with fermented fish and chili.	Joshi et al. (2018)
3.	*Centella asiatica*	Whole plant is cooked, then mashed with potato and fermented fish, and then consumed as a whole	Aryal et al. (2018)
4.	*Commelina benghalensis*	Shoot cooked-eaten once in a while (also used as fodder)	Ray et al. (2020)
5.	*Eleocharis dulcis*	Root is used to cook with molasses and consumed as a snack	
6.	*Fagopyrum esculentum*	Cooked leaves and shoots are consumed as vegetables (and goat fodder)	
7.	*Ipomoea aquatica*	Shoots cooked and eaten	
	Polygonum barbatum		
	Spilanthes acmella		
	Stellaria media		
	Viola pilosa Blume		
8.	*Lemanea australis*	Chutney made from dried and roasted filaments (the plant gives off a fishy odor when roasted in the fire, thus it may be used as a fish replacement)	
9.	*Nelumbo nucifera*	A raw salad is made from the flowers, delicate shoots, leaves, and roots, while the roots are boiled with molasses and served as snacks	
10.	*Nymphaea alba*	Eaten as a salad, the flower and petiole	
	N. nouchali		
	Nymphaea pubescens		
	Nymphaea stellate		
	Nymphoides indicum		
11.	*Oenanthe javanica*	Shoot and leaf are one of the most important and widely used species in the production of fish fermentation	
12.	*Oxalis corniculata*	For both lunch and dinner, plant is cooked with pea seeds (*Pisum sativum*)	

(continued)

Table 18.2 (continued)

S. No	Name of the plant	Dietary consumption and preparation	Reference
13.	*Polygonum molle*	Cooked and consumed leaf and shoot	
	Polygonum plebeium		
	Rumex nepalensis		

essential alternative source of healthful and nutritious food. NE India is a biodiversity hotspot in the world. Among the locals, wild edible plants (WEPs) are commonly consumed in their everyday diet. WEPs are essential for the survival of ethnic communities, as well as a source of revenue for the communities themselves, In contrast, WEPs have received less attention in research, economic growth, and biodiversity protection. Many of them are largely overlooked and undiscovered. WEPs must be properly utilized, exploited, and managed in order to reduce the gap in traditional knowledge and access the hidden potential resources for sustainable development. As a result of the existence of biologically active chemicals, some studies have shown that many WEPs have nutritional or therapeutic value and hence may be classified as food medicine and quality food (Pereira et al. 2011). As a result, several traditional leafy vegetables have better nutritional contents than some well-known cultivated plants (Sundriyal and Sundriyal 2001). *Leguminosae*, *Compositae*, *Poaceae*, *Malvaceae*, and *Rosaceae* were the families with the most species, while others were prized for their many edible plant components (Ray et al. 2020). Over 53 million tribes from 550 distinct groups utilize 9500 wild plants in the Indian subcontinent for food, medicine, fodder, fiber, fuel, essential, cultural, and other uses (Jain et al. 2012). In comparison to conventionally cultivated veggies, wild plants contain a wider range of nutrients. *Taraxacum campylodes* is a high-protein, calcium-, phosphorus-, and fiber-rich vegetable (Escudero et al. 2003). In India and other areas of the world, *Urtica dioica* has a high local value as a vegetable (Lopatkin et al. 2005; Rutto et al. 2013). It is high in vitamin A, calcium, iron, crude proteins, fiber, fat, and carbohydrates (Table 18.4).

18.5 Wild Fruits

WEPs have a significant role in eradicating poverty, ensuring food security, diversifying agriculture, generating economic resources, and reducing hunger (Bhatia et al. 2018). Incorporating WEPs into the diet can significantly reduce hunger, one of the most pressing issues of current generation. Plant species that are neither grown or domesticated but are available from diverse natural habitations and consumed as food are referred to as wild edible plant fruit (Beluhan and Ranogajec 2011). Fruits are mostly eaten uncooked. *Phyllanthus emblica*, *Punica*

Table 18.3 Wetland flora that have medicinal properties

S. No	Name of a scientific entity	Conventional applications	Reference
1.	*Alpinia galanga*	The paste is used to cure intestinal worms, as an abortifacient, and as a topical treatment for leukoderma, among other things	Jain et al. (2011)
2.	*Alternanthera philoxeroides*	Cuts and wounds are treated using paste	Joshi et al. (2018)
3.	*Amomum aromaticum*	High blood pressure is treated using a powder	Aryal et al. (2018)
4.	*Cardamine hirsuta*	Cuts and injuries are treated using paste	Ray et al. (2020)
5.	*Centella asiatica*	Extract is used as a tonic in the treatment of coughs and diabetes	
6.	*Colocasia esculenta*	Cuts and injuries are treated with juice	
7.	*Commelina bengalensis*	Boils and burns are treated using a decoction paste. Muscle sprains are treated using hot fermented plants	
8.	*Dryopteris marginata*	To treat wounds, burns, and other ailments with a paste	
9.	*Eclipta alba*	It is an expectorant and an antispasmodic that is astringent	
10.	*Enhydra fluctuans*	In diabetes, it is used as a treatment	
11.	*Euryale ferox*	Raw fruit is used to treat diabetes; leaf petiole paste is used to treat burns and boils	
12.	*Gynura cusimbua*	A paste is applied to wounds, and a cooked leaf is consumed to treat diabetes and high blood pressure	
13.	*Hedychium coronarium*	Cough and fever are treated with rhizome paste, while throat complaints are treated with leaf extract	
14.	*Hedyotis auricularia*	Dysentery and cough are treated with extract.	
15.	*Ipomoea aquatica*	Ear drops made from boiled leaves are used to cure earaches, while leaf paste is applied to bug bites	
16.	*Jussiaea repens*	Cuts and injuries, as well as sore gums, are treated with paste	
17.	*Jussiaea suffruticosa*	Paste is applied to new cuts and wounds to prevent infection and speed recovery	
18.	*Lemanea australis*	When a plant is cooked and the soup is consumed, diabetes can be cured	
19.	*Marsilea minuta*	A plant paste is applied to boils and burns as a topical treatment	
20.	*Nasturtium indicum*	Paste is used to treat wounds and skin disorders such as eczema	
21.	*Nelumbo nucifera*	On blisters and burns, petiole paste is administered	

(continued)

Table 18.3 (continued)

S. No	Name of a scientific entity	Conventional applications	Reference
22.	*Neptunia oleracea*	When you have dysentery or intestinal illnesses, you can eat it uncooked	
23.	*Nymphoides indica*	Boils and burns are treated with the extract	
24.	*Oenanthe javanica*	The filtrate is boiled in a little amount of water and used as an ear drop to treat earache	
25.	*Oxalis corniculata*	In dyspepsia, it is used as a paste to treat boil and burn wounds, and it is fried and consumed	
26.	*Persicaria posumbu*	Consumed for the treatment of diabetes and intestinal disorders	
27.	*Pistia stratiotes*	Boils and blisters are treated with paste	
28.	*Plantago erosa*	Fever is treated with a powder containing a little amount of honey, while a boiled plant is used to treat muscle sprain	
29.	*Polygonum barbatum*	For the treatment of gastrointestinal disorders and dysentery, paste is used	
30.	*Polygonum chinense*	Gastrointestinal problems and dysentery are treated with paste	
31.	*Polygonum molle*	Shoots are crushed and used to wounds as a dressing	
32.	*Polygonum plebeium*	On wounds, a paste is administered	
33.	*Sagittaria sagittifolia*	If you have a cough, you'll be offered honey paste and paste	
34.	*Spilanthes acmella*	To cure jaundice and sore throat, paste is used	
35.	*Stellaria media*	Decoction of the plant is used to treat new wounds, itchy skin, and nosebleeds	
36.	*Trapa natans*	Consumed to improve blood circulation	
37.	*Viola pilosa*	For the treatment of cough, runny nose, and stomach ulcer	
38.	*Zizania latifolia*	Fire-roasted, infected inflorescences are consumed for dyspepsia	
39.	*Acacia catechu*	Gastrointestinal issues, respiratory illnesses, diarrhea, dysentery, bronchitis, and menstrual irregularities	
40.	*Cassia fistula*	Antiseptic, asthma, bronchitis, bronchitis, bronchitis	
41.	*Rhododendron arboreum*	Diseases of the digestive and respiratory tract	
42.	*Quercus leucotrichophora*	Gonorrheal and gastrointestinal conditions	
43.	*Terminalia bellirica*	Triphala has fruit as a key component	
44.	*Adhatoda vasica*	The symptoms of a cold, bronchitis, pulmonary diseases, and a cough	

(continued)

Table 18.3 (continued)

S. No	Name of a scientific entity	Conventional applications	Reference
45.	*Calotropis procera*	Asthma, expectorant, cough, cold	
46.	*Indigofera gerardiana*	Cough, diarrhea, and dysentery	
47.	*Achyranthes aspera*	Malaria, delivery, dropsy, and bronchitis are all symptoms of malarial fever	
48.	*Anagallis arvensis*	Leprosy, dropsy, and cerebral diseases are all examples of eprosy	
49.	*Euphorbia hirta*	Asthma, bronchitis, and warts are all symptoms of a bronchial infection	
50.	*Mentha arvensis*	Indigestion and vomiting	
51.	*Mentha suaveolens*	Digestion problems, headaches, low blood pressure, acne, and nasal congestion can all be treated (2020)	
52.	*Phyllanthus amarus*	Febrifuge, astringent, stomachic, diuretic	
53.	*Vernonia anthelmintica*	Irritable bowel syndrome, fever, and skin problems are all symptoms of digestive problems	
54.	*Acorus calamus*	Rhizome that has been dried and used to cure sore throats, coughs, and colds	
55.	*Glechoma hederacea*	Treat respiratory problems including asthma, bronchitis, colds, coughs, and throat irritation, as well as gastrointestinal problems like indigestion, stomachaches, and diabetes	

granatum, *Cordia dichotoma*, *Syzygium cumini*, *Ficus palmata*, *Berberis lycium*, *Prunus armeniaca*, *Prunus persica*, *Pyrus pashia*, *Rubus ellipticus*, and other fruits were popular among the inhabitants. In comparison to cultivated species, wild fruits have more fiber, higher vitamin concentrations, and a wider diversity of secondary metabolites (Table 18.5).

18.6 WEPs as a Medicine

Many of the wild foods have been described as dietary medicine. Wild edibles are widely utilized as medicines across the world (Menendez et al. 2015), and these plants are generally referred to as nutraceuticals (Hook 1993). These species, which can be a wild vegetable or fruit, are consumed as needed or on special occasions. For example, locals prepare *Taraxacum campylodes* leaves as a vegetable, particularly as a pre- and post-pregnancy meal to help women overcome frailty. It's high in protein, boron, calcium, choline, copper, iron, manganese, magnesium, potassium, silicon, and zinc (Vallverdu et al. 2015), as well as vitamins A, B complex, C, and D (Balaswamy et al. 2004). *Mentha* spp. are a vast genus containing species that can be confusing; nevertheless, they can be distinguished because each variation

Table 18.4 Edible wild plant vegetable

S. No.	Name of a scientific entity	Method of use or preparation	Reference
1.	*Ipomoea aquatica*	Cooked and consumed as a vegetable	Jain et al. (2011)
2.	*Oenanthe javanica*	Prepared as a mixed vegetable	Joshi et al. (2018)
3.	*Alocasia cucullata*	Cooked with dried fish and potatoes	Aryal et al. (2018)
4.	*Polygonum barbatum*	Cooked and consumed as a vegetable	Ray et al. (2020)
5.	*Nelumbo nucifera*	Raw snack consumed	
6.	*Neptunia oleracea*	Cooked in the presence of additional ingredients	
7.	*Chenopodium album*	When cooked, it is consumed with other vegetables	
8.	*Stellaria media*	Served as a vegetable	
9.	*Zizania latifolia*	Snack on it raw, roast it, prepare it as a vegetable, and cook it with milk, honey, and black rice	
10.	*Gnaphalium indicum*	Raw as a condiment, cooked as a vegetable	
11.	*Solanum torvum*	Cooked and consumed as a vegetable	
12.	*Passiflora edulis*	Cooked and eaten as a vegetable; also used in meat curry	
13.	*Clerodendrum indicum*	Boiling with salt or cooking with other veggies	
14.	*Polygonum molle*	Cooked and consumed as a vegetable	
15.	*Agaricus campestris*	To produce vegetables, fresh fruiting bodies are cooked in water, decanted in hot water, and then fried in edible oil	
16.	*Agave americana*	Used to make vegetables	
17.	*Allium atropurpureum*	Used to make vegetables	
18.	*Allium jacquemontii*	Used to make vegetables	
19.	*Allium roylei*	As a vegetable or spice, bulbs and leaves are utilized	
20.	*Bauhinia variegata*	Flower buds are eaten as a vegetable, while the petals are used to make curd	
21.	*Benincasa hispida*	Used to make vegetables	
22.	*Chaerophyllum villosum*	Edible as vegetable	

(continued)

Table 18.4 (continued)

S. No.	Name of a scientific entity	Method of use or preparation	Reference
23.	*Dioscorea deltoidea*	Vegetable-friendly	
24.	*Fagopyrum cymosum*	Edible as vegetable	
25.	*Indigofera pulchella*	Edible as vegetable	
26.	*Polystichum aculeatum*	Used to make vegetables	
27.	*Rheum australe*	Vegetables made from leaves	
28.	*Sechium edule*	Used to make vegetables	
29.	*Silene conoidea*	Shoots and leaves are used as a vegetable in cooking	
30.	*Typhonium diversifolium*	Used to make vegetables	
31.	*Urtica dioica*	Used to make vegetables	
32.	*Fagopyrum esculentum*	Used to make vegetables	
33.	*Taraxacum campylodes*	Used to make vegetables	

has its own essential oil, the composition of which is modified by growth and environmental conditions. *Mentha suaveolens* is a species of significant interest since it has traditionally been used as a culinary component and has medical uses, including the treatment of digestive problems, migraines, reduced blood pressure, acne, and nasal congestion. All of these characteristics are attributable to the existence of bioactive chemicals, which may be extracted using various methods. As a result, obtaining and purifying them is an important and practical step, not only because of their health benefits but also because they may be used as more natural and nutritious food preservatives. These chemicals exhibit cytotoxicity, antimicrobial, antioxidative, anti-inflammatory, hypotensive, antifungal, hepatoprotective, and insecticidal properties, among other bioactivities (Bichra and Benkhalti 2012). The reported species are important for giving family income, glorifying local festivals, and providing construction material, in addition to supplying food and medicinal applications and producing fermented starter beverages and sweets in accordance to different seasons. Wild edible plants are found in the forest. So, management of forest biodiversity is also very important.

18.7 Forest Ecosystem Management

Forests provide critical ecosystem services for global agriculture's long-term viability; their importance is frequently recognized but hardly included into agricultural and food security strategy. Greater scientific studies need to be conducted to

Table 18.5 Edible wild plant fruits

S. No.	Botanical name	Method of use or preparation	Reference
1.	*Sesbania sesban*	Fruit that has been cooked	Jain et al. (2011)
2.	*Phyllanthus emblica*	Fruits that are edible	Joshi et al. (2018)
3.	*Punica granatum*	Fruits that are edible	Aryal et al. (2018)
4.	*Syzygium cumini*	Fruits that are edible	Ray et al. (2020)
5.	*Ficus palmata*	Fruits that are edible	
6.	*Berberis lycium*	Fruits that are edible	
7.	*Prunus armeniaca*	Fruits that are edible	
8.	*Pyrus pashia*	Fruits that are edible	
9.	*Rubus ellipticus*	Fruits that are edible	
10.	*Prunus persica*	Fruits that are edible	
11.	*Cordia dichotoma*	Fruits that are edible	
12.	*Zehneria scabra*	Cooked with a pinch of salt in boiling water	
13.	*Cyclanthera pedata*	Raw as a snack or cooked as a vegetable	
14.	*Solanum betaceum*	As a vegetable or in a chutney	
15.	*Aegle marmelos*	Eating ripe fruits and using them in the preparation of sweet drink	
16.	*Benthamidia capitata*	Fruits that are edible	
17.	*Castanea sativa*	Fruits that are edible	
18.	*Celtis australis*	Ripe fruits are consumed	
19.	*Corylus jacquemontii*	Fruits that are edible	
20.	*Dendrophthoe falcata*	Ripe fruits are consumed	
21.	*Ficus palmata*	Ripe fruits are consumed	
22.	*Ficus auriculata*	Ripe fruits are consumed	
23.	*Fragaria indica*	Ripe fruits are consumed	
24.	*Garuga pinnata*	Fruits that are edible	
25.	*Grewia optiva*	Ripe fruits are consumed	
26.	*Hippophae tibetana*	Fruits that are edible	
27.	*Madhuca indica*	Fruits that are edible	
28.	*Morus serrata*	Ripe fruits are consumed	
29.	*Prunus cerasoides*	Ripe fruits are consumed	
30.	*Pyracantha crenulata*	Ripe fruits are consumed	

(continued)

Table 18.5 (continued)

S. No.	Botanical name	Method of use or preparation	Reference
31.	*Rhamnus triquetra*	Ripe fruits are consumed	
32.	*Rosa macrophylla*	Ripe fruits are consumed	
33.	*Solanum nigrum*	Ripe fruits are consumed	
34.	*Sorbus cuspidata*	Ripe fruits are consumed	
35.	*Viburnum cotinifolium*	Ripe fruits are consumed	
36.	*Ziziphus jujube*	Ripe fruits are consumed	
37.	*Portulaca oleracea*	Fruits that are edible	

investigate sustainable forest management strategies which might contribute to the preservation of threatened species. Forest ecosystems maintain a large percentage of species that are threatened with extinction. The decline of natural ecosystems can affect nutrition in both the long and short term. Because forest and agroforests are critical for the reproduction of under-consumed as well as nutritionally essential food groups like plant-based foods, maintaining these agricultural forms well within landscapes will be critical for ensuring a sustainable, highly nutritious global food system. Food systems that are nutrition-sensitive must assure the availability, accessibility, and consumption of nutrient-dense items as well as dietary diversity (Palkovacs et al. 2018). This will be critical to build market linkages for nutritional and functional tree and forest foods so that they might reach far-flung customers, while being affordable to all. Forests, agroforests, biodiversity, tree cover, and forest patches within agroecosystems are all important but often overlooked features of food and agriculture system sustainability. In nutrition-sensitive agroecosystems, the relevance of wild species diversity as well as forests in ensuring sustainability, dietary diversity, and resilience must not be neglected.

18.8 Genetic Tools for Trait Development

The advances in genetic techniques for managing wild plant communities has received rare attention in the case of wild plants, till date. However, there are many wild species from diverse families that offer beneficial features but have not yet been domesticated. We can use more efficient selection to conserve more wild plant species as we learn more about the genetic and biological basis of domestication processes. Because many wild groups are regionally suited to specific ecosystems and contain high genetic variety, this could lead to the development of novel plants and aid in the development of more ecologically sustainable agriculture in the face of climate change.

Gene editing technologies are the most visible of the rapidly emerging tools. Other current multiomics technologies, on the other hand, may be valuable to those attempting to neo-domesticate a plant species. Genome sequencing and resequencing that help to characterize molecular diversity, genome-wide association studies (GWAS) to uncover connections between traits of interest and genes, and genomic selection to promote multigenic traits are just a few examples (Sood et al. 2021). These measures will aid in the fight against poverty and malnutrition, while also benefiting farmers and others involved in wild species cultivation.

18.9 Conclusion

Due to the increasing demand of food security for the future generation, studies of wild species plants are very important. There is need for highlighting the roadmap to strengthen wild species cultivation such as finding varieties suitable for specific habitats and then using multiomics techniques to focus trait improvement.

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