

Chapter 12

Tackling Climate Change: A Breeder's Perspective



P. K. Singh and R. S. Singh

Abstract The threat of climate change is well evident by the fact of increasing temperature and more frequent severe drought and floods in recent times, and higher incidence of insects-pest and diseases impacting agriculture and food production. This situation has aggravated the scarcity of food and hunger around the world. To mitigate the ill effects of climate change, developing climate resilient varieties for heat, cold, drought and flood stresses is one of the options, where breeders can play major role. Several Institutions in the world are engaged in developing viable strategies. This will require a much better understanding of our genetic resources, the underlying mechanism of gene interactions and pyramiding multi-stress related genes for developing new variety or improving the already cultivated variety. The most suited approaches should involve conventional breeding as well as new emerging technologies like doubled haploidy, marker-assisted selection, high throughput phenotyping and bioinformatics to hasten the crop improvement. For breeders, ample opportunity lies in developing climate resilient high-yielding varieties, resistant/tolerant to biotic and abiotic stresses that help increasing food production and productivity, thus ease the cultivation under climate change regime. In this direction, several international institutes have initiated work on developing climate resilient crops, for example, the International Rice Research Institute (IRRI) has released 44 varieties of rice that are resilient to the effects of climate change and work is underway on a tripartite rice variation to cope with stresses like droughts, floods and saltiness. Even, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) identified 40 germplasm lines of chickpea with resistance to extreme weather conditions such as drought, high temperature and salinity. In India, various ICAR institutes and state agricultural universities, under National Innovations on Climate Resilient Agriculture (NICRA) programme, made the concerted efforts to develop different high yielding cultivars with enhanced tolerance to heat, drought, flooding, chilling and salinity stresses for different agro-climatic zones. Thus, effect of climate change can be withstand to a greater extent with a

P. K. Singh (✉) · R. S. Singh

Department of Plant Breeding and Genetics, Bihar Agricultural University,
Bhagalpur, Bihar, India

suitable genetic blue print in our cultivars and that need more focussed research and development from breeder's side.

Keywords Climate change · Plant breeding · Genetic resources · Climate resilient varieties

12.1 Introduction

Climate change is very obvious now, we see increasing temperature, increasing CO₂ concentration, melting of glacier and rising global average sea level. The threat of climate change is well evident also by the fact of more frequent and severe drought and floods in recent times, and higher incidence of insects-pest and diseases impacting agriculture and food production. For breeders, ample opportunity lies in developing eco-friendly and high-yielding varieties, resistant to pests and diseases that could increase food productivity and production, thus ease the cultivation under climate change regime. Modern breeding methods enable faster and more efficient breeding of crops adapted to specific regions. Breeding a particular variety for a specific situation gets further boost with the help of genomics-based approaches.

The International Rice Research Institute (IRRI) has released 44 varieties of rice that are resilient to the effects of climate change and work is underway on a tripartite rice variation to cope with stresses like droughts, floods and saltiness. Even, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) identified 40 germplasm lines of chickpea with resistance to extreme weather conditions such as drought, high temperature and salinity. Similarly, International Centre for Agricultural Research in the Dry Areas (ICARDA) has started evolutionary participatory programmes for barley and durum wheat. In our country, various ICAR institutes and state agricultural universities, under National Innovations on Climate Resilient Agriculture (NICRA) programme, made the concerted efforts to develop different high yielding cultivars with enhanced tolerance to heat, drought, flooding, chilling and salinity stresses for different agro-climatic zones. Thus, effect of climate change can be withstand to greater extent with a suitable genetic blue print in our cultivars and that need more focussed research and development from breeder's side.

12.2 Climate Change Impact on Agriculture

Increased intensity and frequency of storms, drought and flooding, altered hydrological cycles and precipitation variance have implications for future food availability. The potential impacts on rainfed agriculture *vis-à-vis* irrigated systems are still not well understood. The developing world already contends with chronic food problems. Climate change presents yet another significant challenge to be met.

While overall food production may not be threatened, those least able to cope will likely bear additional adverse impacts (WRI 2005). In developing countries, 11 percent of arable land could be affected by climate change, including a reduction of cereal production in up to 65 countries and about 16 per cent of agricultural GDP (FAO, Committee on Food Security Report 2005).

Enhanced frequency and duration of extreme weather events such as flood, drought, cyclone, cold and heat wave as a result of climate change may adversely affect agricultural productivity. This is projected to reduce the crop yield in India, like in irrigated rice by ~4% in 2025 and rainfed rice yield by 6%; wheat by 6 to 23%; mustard by 2%; potato by ~2.5%, rainfed sorghum by 2.5%; maize yield in Kharif season by 18% (www.nicra.iari.res.in).

The growing concentration of CO₂ in the atmosphere, global warming and a higher frequency of extreme weather events mean increasing fluctuations in yields from agricultural crops and growing yield losses. The initial effects of the shift in climatic zones, vegetation zones and habitats are already visible: Pest and disease pressure on crops is growing. Global population is increasing while arable land area reducing day-by-day due to industrialization and human encroachment, and at the same time water shortages like situation, decreases the efficiency of agricultural production. In the short to medium term, agriculture can adapt by means of agronomical measures, such as tilling, crop rotation and optimized fertilization methods, and plant protection measures to safeguard the plants.

Each and every sphere of agriculture get affected by climate change be it crops, pasture, forests and livestock, land, soil and water resources, weed and pest, besides socio-economic impacts. The increased temperature (2–4 °C) by 2100, rise in CO₂ concentration, droughts and floods might be frequent events of future therefore, emphasis needs to be on climate smart agriculture with the aim of reduction of greenhouse gas emissions enhanced resilience and reduced wastes with the increase in the productivity of small and large scale farmers (Ahmed et al. 2013).

12.3 How Can Plant Breeding Help?

Increasing frequency of biotic stress is also highly probable. Plant breeding has addressed both abiotic and biotic stresses for a long time. Strategies in the face of climate changes may be based more on plant architectural changes to plant nutrient use efficiency, photoperiod and temperature responsiveness, with different maturity period to escape or avoid the unfavourable situation crop life cycles. Development of new more climate-resilient crop varieties will always be critical. All the cereals, oilseed, pulses, vegetables, flowers and fruits that is part of our day today life come from varieties developed by plant breeders and grown by farmers across the world. Now, with the intervention of modern genomics and biotechnology tool, the development of new adapted varieties has become a more precise and rapid process that contributes in feeding the world and tackling Climate Change at the same time. In the present scenario, the most suited approaches should involve conventional

breeding as well as new emerging technologies like doubled haploidy, marker-assisted selection, high throughput phenotyping and bioinformatics to hasten the crop improvement.

For long time, plant breeders have been applying mutagenesis to induce genetic variation for increasing crop yield and improving the adaptability of crop plants. In the beginning, the X-ray radiation and gamma-ray radiation were used to induce point mutations and chromosomal mutations (Muller 1927, Devreux and Scarascia Mugnozza 1964. Designing crop breeding system suited for climate change with the help of superior combinations of genes into new varieties for new cropping systems and new environments. Environmentally friendly varieties such as improved varieties resistant to pests require fewer pesticides. Increase food production per unit area and alleviate pressure to add more arable land to production systems. The new improved varieties should be environmentally friendly, ensuring food security, while conserving the environment. Designing the crop breeding systems (1) to study the useful traits in response to various climatic factors such high CO₂ and high temperature, (2) a non-invasive phenotyping methods for specific traits, and (3) simulation of phenotypes will be helpful in plant breeding programs.

12.4 Exploring Plant Genetic Resources

Utilizing our plant genetic resources as source of traits/genes for resilience to changing environmental conditions and stresses could be a good option. Biodiversity itself is capable of providing genetic resources resilience to changing environmental conditions and stresses. The concerted effort on their bio-prospection is needed. The variability is the essence of plant breeding and the exploitation of plant ecosystems has resulted in loss of many valuable genetic resources. Plant breeders in recent time can take the advantage of genetics and genomics in characterizing the genetic resources so that enhanced breeding materials could be developed. The institution like National Bureau of Plant Genetic Resources (ICAR-NBPGR) does the task of several jobs related to plant genetic resources from introduction, exploration and collection, documentation, quarantine, maintenance and sharing. The gene bank maintained at NBPGR is good resource for exploring the genetic resources for traits suitable for high temperature, drought, and flooding, high salt content in soil, pest and disease resistance have been harnessed for new crop varieties by national and International programmes.

Developing genetic responses to climate change is incumbent on effective evaluation and exploitation of the existing genetic variability. Use of molecular markers to predict adaptive variability is rather ineffective because little correlation exists between molecular genetic diversity and quantitative genetic variation (Gilligan et al. 2005). Genomics possesses the potential to increase the diversity of alleles available to breeders through mining the gene pools of crop wild relatives. Genomics tools also enable rapid identification and selection of novel beneficial genes and their controlled incorporation into novel germplasm. In the genomics era, this technology

will be used to safeguard the future through improved food security. Taken together, the application of genomics for crop germplasm enhancement offers the greatest potential to increase food production in the coming decades. With continued rapid advances in genome technologies, the application of genomics to identify and transfer valuable agronomic genes from allied gene pools and crop relatives to elite crops will increase in pace and assist in meeting the challenge of global food security.

12.5 Conventional Breeding Approaches

One of the strategies for introgressing traits to mitigate the effect of climate change on plants performance for sustainable food production is identifying and incorporating suitable alleles by means of conventional breeding approaches. For this purpose, crop relatives have been used for decades for breeding, in particular to transfer genes of resistance or tolerance to pests, diseases or abiotic stress to the cultivated species (Hajjar and Hodgkin 2007; Honnay et al. 2012). In case of non-availability or no known source of suitable alleles, mutation breeding is one of the choice upon which breeder's can rely. By exposing seeds to mutagenic chemicals or radiation the mutants are generated with desirable traits to be bred with other cultivars. In radiation-based approaches, FAO/IAEA reported in 2014 that over 1000 mutant varieties of major staple crops were being grown worldwide.

In India, Bhabha Atomic Research Centre (BARC) has contributed a lot by induced mutation (mostly using gamma rays)-based varietal development programme in different crops for example, groundnut, mungbean, blackgram, soybean, redgram, cowpea, mustard, rice and jute. Mutation breeding using radiation technology for crop improvement is an active area of research at the Bhabha Atomic Research Centre (BARC), Trombay, Mumbai. (<http://dae.nic.in>). Using radiation induced mutation and cross-breeding, 39 new crop varieties (Trombay varieties) developed at BARC have been released. These include 20 in oil seeds (14-groundnut, 3-mustard, 2 soybean, 1 sunflower), 17 in pulses (8-greengram, 4-blackgram, 4-pigeonpea, 1-cowpea) and one each in rice and jute for high yield, some with additional desirable characters like disease resistance, early maturity, suitability to rice fallows, improved quality parameters etc. (Table 12.1).

ICAR-National Rice Research Institute, Cuttack, has development blast tolerant mutants of rice (CRM 49, CRM 51 and CRM 53) from IR 50 (a blast susceptible variety) through mutation breeding (chemical-based mutagenesis). CRM 49 and CRM 51 were isolated from sodium azide-treated populations, while CRM 53 from ethyl methane sulfonate (EMS)-treated populations. These mutants possessed semi-dwarf stature, long slender grains and with a yield potential of 5 t/ha.

In mutational programme, the work on calmodulin-binding protein gene family involved in abiotic stress responses in rice is going on at BAU, Sabour. More than 1, 50, 000 M₃ mutant rice (Gamma irradiated) plants of Rajendra Mahsuri-1 and Rajendra Kasturi were grown and screened for drought stress in field condition.

Table 12.1 Varieties developed by mutation breeding for various stresses

Crop	Recommended for states	Features (including stress tolerance)
Groundnut		
TG 26	Gujarat North Maharashtra Madhya Pradesh	Earliness, high harvest index, 20 days seed dormancy, smooth pods, salinity tolerance, high harvest index
TG 37A	Haryana, Rajasthan, Punjab, Uttar Pradesh, Gujarat, Orissa, West Bengal, Assam, North Eastern states	High yield, smooth pods, wider adaptability, collar rot and drought tolerance
Sunflower		
TAS-82	Maharashtra	Black seed coat, tolerant to drought
Pigeonpea		
TJT- 501	Madhya Pradesh, Gujarat, Maharashtra, Chhattisgarh	High yielding, early maturing, tolerant to Phytophthora blight
Mungbean (Green gram)		
TJM-3	Madhya Pradesh	Resistant to powdery mildew, yellow mosaic virus and Rhizoctonia root –rot diseases.
TM 2000–2	Chhattisgarh	Suitable for rice fallows and resistant to powdery mildew
TMB-37	Eastern Uttar Pradesh, Bihar, Jharkhand, West Bengal, Assam	Tolerant to yellow mosaic virus
Urdbean (Black gram)		
TU 94–2	Andhra Pradesh, Karnataka, Kerala, Tamil Nadu	Resistant to yellow mosaic virus

Source: <http://dae.nic.in>

Rice mutants (R. Mahsuri-1) were showing different phenotypes like early flowering, increased L/B ration and any marked visual changes were selected.

12.6 Breeding Strategies for Major Climate Change Effect

The breeding strategies to tackle the adverse climate change effect on crops should encompass the development of stress tolerant genotypes together with sustainable crop and natural resources management along with sound implementation of policies. Meanwhile, development of resistance genotypes to biotic/abiotic stresses, choice of crops, change in the cropping patterns, rotation, time of planting and avoidance, nutrient use efficiency and the approaches like wide hybridization, mutagenesis, genomics-assisted breeding and transgenic will be very helpful to achieve the goal of yield sustainability.

Under “National Innovation in Climate Resilient Agriculture” (NICRA), IARI has developed new crop varieties with higher yield potential and resistant to multiple

stresses (heat, drought, flood, salinity) that will be the key to maintain yield stability. Two germplasm, Nerica L44 and N22 were identified as novel sources of heat tolerance in rice by the Institute. Further, in an effort to map the QTLs governing heat tolerance recombinant inbred line mapping populations are being generated involving heat tolerant genotypes namely L44 and N22, which are in F4 generation. Marker assisted backcross breeding was carried out using molecular marker linked to the QTL governing drought tolerance, qDTY1.1 into Pusa Basmati 1 and qDTY3.1 into Pusa 44 and 41 (in Pusa Basmati 1 background), 36 (in Pusa 44 background). Similarly, in wheat the standardized physiological trait-based phenotyping protocol for screening for heat and drought tolerance in wheat and also, maize genotypes tolerant to low and high temperature tolerance were identified.

Maize inbred lines were also screened for multiple disease resistance. In tomato, two wild species i.e., *L. peruvianum* and *L. pimpinellifolium* crossable to cultivated tomato have been identified for temperature stress tolerance. Among cultivated genotypes (Pusa Sadabahar and TH-348) and hybrids (DTH-9 and DTH-10) were identified for heat stress tolerance.

Under Cereal Systems Initiative for South Asia (CSISA) programme, at BAU Sabour, with rigorous effort of scientists, Rajendra Mansuri has been identified as suitable for direct seeded rice (DSR) cultivar that would save labour and water. This variety can be recommended for water deficit region and would help in climate change regime.

Plant breeding programmes at ICAR-IARI has led to release of several varieties in different crops for stress tolerance (Table 12.2).

12.6.1 Flood and Salinity Tolerant

Climate induced weather extremes, such as flooding, submergence and salinity impacts crops adversely. About 20 million hectares of rice land is prone to flooding in Asia, which is major rice growing continent. Of this, India and Bangladesh share more than 5 million hectares of rice field, flooded during most of the planting seasons (<http://irri.org>). Progressive salt accumulation due to excessive irrigation with poor water quality coupled with poor or improper drainage results in high salt levels (Ismail et al. 2007). Excess water in the soil reduces oxygen availability to the plant (Kozłowski 1984). The extended deep submersion can cause plant death because of a lack of oxygen required to sustain plant growth and an accumulation of toxic substances, such as organic acids, NO_2^- , Mn^{2+} , Fe^{2+} , and H_2S (Kozłowski 1984; Janiesch 1991).

Generally, the traits like the vigorous roots and less evapo-transpiration could be developed in plants that can help maintaining water balance up to some extent. The past decade has witnessed an increase in studies related to detection of quantitative trait loci (QTL) for drought-related traits, and the first encouraging results in QTL cloning have been reported (Salvi and Tuberosa 2005). Thus, development of more flood-tolerant cultivars is critical for enhancing sustainable production of crops. For

Table 12.2 List of varieties released by ICAR-IARI for various stresses

Crops	Variety	Stress
Maize	Pusa Composite3, Pusa Composite4	Moisture stress
Karan rai	Pusa Swarnim (IGC01), Pusa Aditya (NPC9)	
Pearl millet	Pusa Composite 383, Pusa Composite 443,	
	Pusa Composite 612	
Pigeonpea	Pusa 991	Salinity
Indian mustard	Pusa Vijay (NPJ93)	High temperature tolerance
Wheat	Kaushambi (HW 2045), Pusa Gold (WR544),	
	Pusa Basant (HD2985), Pusa Wheat111, (HD2932), Harshita (HI1531)	
Chickpea	Pusa 547	
Mungbean	Pusa 9531	
Indian mustard	Pusa Agrani (SEJ2), Pusa Mahak (JD6), Pusa Vijay (NPJ93), Pusa Tarak (EJ13), Pusa Mustard25, (NPJ112), Pusa Mustard26, (NPJ113), Pusa Mustard27 (EJ17)	
Mungbean	Pusa 0672	
Maize	AH421 (PEHM5)	Water logging
Cotton	PSS2 (Arvinda)	Hot and humid conditions
Wheat	VSM (HD 2733), Kaushambi (HW 2045)	Diseases-pest
Chickpea	Pusa 1088 (Kabuli)	

Source: <http://www.iari.res.in>

example, rice dies within 5–6 days of complete submergence, resulting in total crop loss. These losses affect rice farmers in rainfed and flood-affected areas where alternative livelihoods are limited. After the gene called Sub1 gene was found, it was infused into popularly grown rice varieties in rice-growing countries in Asia (<http://irri.org/>). IRRI has developed a rice variety using Sub1 gene through marker-assisted backcrossing, Swarna-sub1 in 2005 that can withstand being submerged under water for two weeks.

Soil salinity is a major cause of concerns in rice growing areas. In India nearly 6.72 million ha of total land are salt affected out of which 2.95 million ha are saline (including coastal) and 3.77 million ha are alkaline (IAB 2000). In Bangladesh's coastal areas, salinity affects about one million hectares of land that can otherwise be used for rice farming. Rice productivity in salt-affected areas is very low less than 1.5 tons per hectare. But this can potentially increase by at least two tons per hectare with improved varieties that can withstand soil salinity.

IRRI scientists have identified a major region of the rice genome called Saltol that gives the rice plant tolerance to salinity. Saltol is being used to develop varieties that can cope with exposure to salt during the seedling and reproductive stages of the plant. Recent work at IRRI has shown that the SUB1 gene and Saltol can be combined in the same variety of rice, increasing the rice plant's tolerance to salinity

and submergence. Plant breeders have incorporated Saltol in popular rice varieties such as the BRRI Dhan 11, 28, 29 varieties released in Bangladesh. To date, IRRI, with the help of its national partners, has developed more than 100 salinity-tolerant elite lines. These elite lines possess superior traits such as high yield, good eating quality, resistance to pests and diseases, and tolerance of stresses, and are ready for testing in farmer's fields.

Central Soil Salinity Research Institute, Karnal, India (CSSRI) has identified several promising salt-tolerant crops such as salt-tolerant varieties of rice, for example, CSR 10, CSR 11, CSR 13, CSR 27 for inland situations and CST 7-1, CSR 4 and CSR 6 for coastal areas. Likewise, salt-tolerant varieties for wheat, KRL 1-4 and mustard, CS-52, CS-330 have been developed and released (Dagar 2005).

12.6.2 Cold, Heat and Drought tolerance

Tolerance to freezing temperatures is the most important component for winter survival, but also of considerable importance is the capability to withstand combinations of stresses due to desiccation, wind, ice-encasement, low light, snow cover, winter pathogens, and fluctuating temperatures. Resistance to desiccation through the maintenance of cell membrane integrity and retention of cellular water is essential, and it is unsurprising that the same genetic response to the onset of freezing temperatures is often observed with drought or salinity stress (Yue et al. 2006). Indeed, cold acclimation can frequently improve adaptation to a mild drought stress and vice versa (Seki et al. 2002). Higher temperatures are speculated to reduce rice grain yields through two main pathways: (i) high maximum temperatures that in combination with high humidity cause spikelet sterility, and (ii) increased night time temperatures, which may reduce assimilate accumulation (Wassmann and Jagadish 2009).

Cold tolerance is a complex trait controlled by many genes. IRRI scientists have identified three regions of the rice genome that have a direct link to cold tolerance at the plant's reproductive stage. Cold stress at critical times of reproduction hinders the formation of fertile pollen that is crucial for fertilization and consequently the rice plant may fail to produce grains. In pigeonpea at BAU, Sabour, it was found that the pigeonpea lines starts dropping flowers and newly developed pod when temperature goes below 10 °C. In this context, 120 pigeonpea genotypes planted in augmented design with four checks. Genotypes categorized into cold escape, cold tolerant and susceptible. It has been found that the early group of pigeonpea genotypes which completed their reproductive cycle before temperature down below 10 °C was not affected by temperature considered cold escape such as, ICP-13359, ICP-11627, ICP-11059, ICP-11477. Other long to medium duration genotypes ICP-15382, ICP-7076, ICP-7076 and ICP-14229, i.e., also developed pods normally since temperatures were not critically low during winter season. Hence conclusion cannot be made this year due to normal winter season.

IRRI scientists are looking for rice that can tolerate high temperatures by screening improved and traditional rice varieties. These donors are used in a crossing program to incorporate tolerance of high temperature into elite rice lines that are then tested for heat tolerance in 'hot and dry' and 'hot and humid' countries. Some of the development that can help fight against climate change, for example, discovery of a cold-tolerant breeding line called IR66160-121-4-4-2 that inherited cold tolerance genes from Indonesia's tropical japonica variety Jimbrug and northern China's temperate japonica variety, Shen-Nung89-366 by IRRI's and South Korea's Rural Development Administration.

Drought is the most widespread and damaging of all environmental stresses, affecting 23 million hectares of rainfed rice in South and Southeast Asia. In some states in India, severe drought can cause as much as 40% yield loss, amounting to \$800 million. In all cases, the emphasis will be on identifying and using sources of genetic variation for tolerance/ resistance to a higher level of abiotic stresses. The two most obvious sources of novel genetic variation are the gene banks (ICARDA has one of the largest gene banks with more than 120,000 accessions of several species including important food and feed crops such as barley, wheat, lentil, chickpea, vetch, etc.) and/or the farmers' fields. Currently, there are several international projects aiming at the identification of genes associated with superior adaptation to higher temperatures and drought. At ICARDA, as elsewhere, it has been found that landraces and, when available, wild relatives harbour a large amount of genetic variation some of which is of immediate use in breeding for drought and high temperature resistance (Ceccarelli et al. 1991; Grando et al. 2001).

Sabour Ardhajal, a drought tolerant variety of rice developed at BAU, Sabour under Stress-Tolerant Rice for Africa and South Asia (STRASA) programme, which contains QTL for reproductive stage drought tolerance would be important climate change scenario. Further, under the same project at BAU Sabour, several multi-environmental trials (MET) underway on aspect of breeding for drought, heat and cold tolerance, in H-MET total 14 entries were evaluated including local check R. Mahsuri-1. Yield differences were found to be significant and varied from 2827 kg/ha (CGZR-1) to 4971 kg/ha (IR 91953-141-2-1-2(R-119)). Two entries IR 91953-141-2-1-2(R-119) and IR 92937-178-2-2(R-155) recorded yield significantly superior to R. Mahsuri-1 (3752 kg/ha). While in MET-2 (Loc-1), total seven entries were evaluated including local check Prabhat. Yield differences were found to be significant and varied from 2183 kg/ha (Prabhat) to 3638 kg/ha (MTU1010). Entry R-RHZ-7 recorded yield significantly superior to Prabhat (2183 kg/ha). In MET-2 (Loc-3), total seven entries were evaluated including local check Prabhat. Yield differences were found to be significant and varied from 2123 kg/ha (Prabhat) to 3437 kg/ha (MTU1010). Entry R-RHZ-7 recorded yield significantly superior to Prabhat (2123 kg/ha). In Swarna Sub-1+ drought (control), total 16 entries were evaluated including two checks namely S. Sub-1 and Swarna. Yield differences were found to be varied from 6696 kg/ha (IR 96321-315-294-B-1-1-1) to 9494 kg/ha (IR 96321-558-563-B-2-1-3). However, none of the entry could statistically surpass the best check Swarna (9063 kg/ha). In Swarna Sub-1+ drought (Drought), total 16 entries were evaluated including two checks namely

S. Sub-1 and Swarna. To identify suitable drought donors, a total 24 entries were evaluated including checks. Yield differences were found to be varied from 949 kg/ha (Koi Murali) to 4348 kg/ha (Binuhangin). Top three yielder donors were Binuhangin, Dular and Uri. Donors were crossed with the locally adapted varieties.

Under Heat stress Tolerant Maize (HTMA) for Asia project at BAU, Sabour, 20 entries (in AMDWTC-17" trial) were tested and significant differences were observed among the entries for grain yield. Grain yield ranged from 2400–6930 kg/ha but none of the entry showed significantly higher yield than the best check "PIO3396" (6930 kg/ha).

In another programme on improvement of pigeonpea for plant type, early maturity, pod borer resistance and moisture stress tolerance at BAU, Sabour, 250 pigeonpea germplasm received from NBPGR were planted with four checks (Asha, Patam, Pusa 9 and Bahar) to screen genotype against pod borer at flowering and podding. For this experiment was left without chemical treatment (insecticide/ pesticide). Plants (5/row) were tagged to monitor damage by pod borer. Before harvest pods were plucked from individual plant and counted. The damage pods were counted separately and percent infestation were recorded on plant basis. It has been found that out of 250 entries 23 genotypes showed less infestation (< 30%) with minimum 7%. However, maximum infestation went up to 90%.

In chickpea programme at BAU, Sabour, the evaluation of advanced generation chickpea genotypes for yield and abiotic / biotic stress tolerance (Desi) were done involving nine chickpea advanced breeding lines including PG 186 as check were evaluated in RCBD (Timely sown condition). Varietal difference with respect to grain yield was found significantly superior which ranged from 1555 kg/h to 2043.2 kg/ha. Highest grain yield (2043.2 kg/ha) was recorded by cross no 14 (ICCV 10 x ICCV 97105) which was 15% superior to check PG 186, while two entries were at par with check. The trials were planted under normal moisture condition; however disease and insects infestation was less than 10%. Also characterization and evaluation of eighty chickpea genotypes (Desi) including four checks for heat tolerance (late sown and normal sown condition) is underway. The varietal difference with respect to grain yield was found significantly superior which ranged from 300 kg/h to 1905.2 kg/ha. Highest grain yield was recorded by ICCV 4958 followed by IPC 10–59, JG 14, PG 186, JG 18 under late sown condition.

The work on understanding heat and drought tolerance mechanism in lentil and its improvement by over-expression of antioxidant genes is also being carried out keeping in view climate change at BAU, Sabour. Under *in vitro* condition shoot cultures of four genotypes viz. Noori, HUL 57, Arun and SBO Local were established. Shoot regeneration for Noori and HUL 57 have been standardized from embryonal axis. Pot experiments were conducted using 14 contrast genotypes under heat and drought stress condition.

The evaluation of linseed germplasm under utera (sowing in standing paddy crop) condition is being carried out that may help climate resilience by early harvest of linseed. One hundred eight entries were evaluated along with two checks (T-397 & R-552), twenty five entries were found promising as they recorded more yield than the best check, T-397 (825 kg/ha). The top ranker five entries were BRLS-112-2

(1497 kg/ha), BRLS-113 (1454 kg/ha), BRLS-110-2 (1453 kg/ha), BRLS-109-2 (1428 kg/ha), BRLS-111-2 (1312 kg/ha). One of the variety released recently Linseed variety “Sabour Tisi-1” has been released for utera condition.

In rapeseed-mustard breeding programme, to combine traits of interest viz. early and late sowing, bold seed, semi compact canopy, lodging and shattering resistant, TW high, MR to AB & aphid, high yield, profuse branch, semi-appressed, non-glossy stem and upright branches in popular varieties is being carried out. Also, inter-specific crosses (*Brassica juncea* X *Brassica carinata*) for drought tolerance and better growth under late sown condition were done.

In safflower, Brassinosteroid-mediated increase in seed yield and enhanced abiotic stress tolerance Safflower (A1 variety) were transformed with CaMV:DWF4:NOS gene construct by *Agrobacterium* transformation. The presence of transgene in transgenic safflower lines (T1 and T2) were confirmed using PCR analysis. RT-PCR was carried out to confirm the expression of transgene. Sub-cellular localization experiment showed that the expression of DWF4 in cytoplasm.

12.6.3 Diseases and Pest

To date, research on the impact of climate change on plant diseases has been limited, with many studies focusing on the effects of a single atmospheric constituent or meteorological variable on the host, pathogen, or the interaction of the two, under controlled conditions. Rising temperature and atmospheric CO₂ are also indirectly affecting crops through their effects on pests and diseases. These interactions are complex, and their full impact on crop yield is yet to be fully appreciated. Impacts of warming or drought on resistance of crops to specific diseases may be through the increased pathogenicity of organisms or by mutations induced by environmental stresses (Gregory et al. 2009). The influence of climate change on plant pathogens and their consequent diseases has been reviewed extensively (Coakley et al. 1999; Chakraborty 2005). Different individual parameters associated with climate change, such as warming, increased levels of CO₂, decreased rainfall, and erratic pattern of rainfall, have been studied for their influence on different aspects of pathogens and diseases across various crops (Chakraborty 2005).

At BAU, Sabour, the engineered resistance in rice against fungal pathogens is underway. Rice calli of Rajendra Kasturi were transformed using *Dwfl* gene construct using *Agrobacterium* mediated transformation. The presence of transgene in transgenic rice lines (T₁ and T₂) were confirmed using PCR analysis. RT-PCR was carried out to confirm the expression of transgene. While in lentil, for biotic stress the work on identification of donor parents resistant to *Fusarium* wilt is going on. In this, a trial consisting 16 released varieties including check from different states were tested for the performance for its adaptability in different ecological regions of Bihar. HUL 57 (1250 Kg/ha) was the best check, three entries were found significantly superior than the check. Out of 16 entries BRL-3 has yielded out

highest (1860 Kg/ha) followed by BRL-1 (1629 Kg/ha) and BRL-2 (1539 Kg/ha), other varieties were at par with the best check HUL 57 (1250 Kg/ha).

In wheat, for biotic tolerance the work on development of spot blotch resistant genotypes of spring wheat for eastern Gangetic plain of India using double haploid (DH) technology was undertaken keeping in view climate change. For this purpose, spot blotch resistant genotypes viz. Chirya 3, Chirya 7, MACS 2496, GW373, HD 3118, RAJ 3765, WH730, BH1146 were procured. Crosses were made involving Spot blotch resistance genotypes and high yielding locally adapted genotypes. Procedures and physical conditions were optimized for pseudo seeds production. Nutrient media and physical conditions were standardized for haploid production.

12.7 Genomics Assisted-breeding and Biotechnological Intervention for Climate Change

Potential of Genomics-assisted Breeding in Producing Climate Resilient Crops
Genomics offers tools to address the challenge of increasing food yield, quality and stability of production through advanced breeding techniques. Advances in plant genomics provide further means to improve the understandings of crop diversity at species and gene levels, and offer DNA markers to accelerate the pace of genetic improvement (Muthamilarasan et al. 2014). A genomics-led breeding strategy for the development of new cultivars that are “climate change ready” (Varshney et al. 2005) commences by defining the stress that will likely affect crop production and productivity under certain climate change scenarios.

The ideotype breeding coupled with DNA fingerprinting, and gene/ quantitative trait loci (QTL) will assist in selecting screening promising accessions against specific stress. Similarly, precise phenotypic assessments and appropriate biometric analysis will assist in identifying unique responses of a set of genotypes in a given physiological stage influenced by variation of weather patterns. This information will be further used in genomics aided breeding approaches such as genome-wide selection of promising germplasm for further use in crop breeding aiming at both population improvement and cultivar release. Genetic mapping and QTL analysis, via bi-parental or association mapping (AM) populations, have accelerated the dissection of genetic control of agricultural traits, potentially allowing MAS, QTL, and AM studies or direct calculation and genomic selection (GS) of high value genotypes to be made in the context of breeding programs (Kulwal et al. 2011).

With the advent of next-generation sequencing (NGS) methods has facilitated the development of large numbers of genetic markers, such as single nucleotide polymorphisms (SNP), insertion-deletions (InDels), etc. even in relatively research-neglected crop species. Discovery of novel genes/alleles for any given trait could be then performed through genotyping-by-sequencing (GBS) approaches. Similarly, genome-wide association studies (GWAS) could be used to identify the genomic regions governing traits of interest by performing statistical associations between

DNA polymorphisms and trait variations in diverse collection of germplasm that are genotyped and phenotyped for traits of interest.

Compared to radiation methods, chemical mutagens tend to induce SNPs rather than chromosomal mutations. Currently, chemical mutagens, such as Ethyl methanesulfonate (EMS) are being used to induce random mutations into the genome and have become a useful complement to the isolation of nuclear DNA from mutated lines by TILLING (Targeting Induced Local Lesions in Genomes) technology and screening of the M_2 population at the DNA level using advanced molecular techniques.

At BAU, Sabour, the work on architectural modification of Katarni rice through marker assisted selection is underway. The work will bring down the height of Katarni rice resulting in lodging resistance and help the crop stand against storm or high wind and rain. Survey of parental polymorphism between Katarni, IR-64, Rajendra Sweta and BPT 5204 was undertaken through the set of 25 additional SSR markers in rice were conducted. Validation of F_1 plants of Katarni/BPT5204 through parental polymorphic SSR was done in PCR. Backcrossing of 8 validated Katarni/BPT5204 F_1 s with recurrent parent Katarni was done to obtain the BC_1F_1 seeds. 388 BC_1F_1 plants of Katarni/R.Sweta//Katarni were raised out of which 107 plants were selected based on the foreground selection using *badh2* gene specific primer (Bradbury 2005). Out of 107 fragrant allele positive plants, 87 were found to be positive for *sd1* gene through PCR using *sd1* gene specific primer as suggested by Spielmeier et al. (2002). On the basis of grain and leaf aroma KOH sensory test, 15 plants were selected out of the 87 positive plants for *sd1* gene. These 15 plants will be evaluated for the presence of aroma, *sd1* gene with early flowering trait in next segregating generation. Out of about 10,000 F_2 plants of Katarni/R.Sweta, 410 plants were selected based on KOH sensory test, plant height and early date of flowering. Out of about 6000 F_2 plants of Katarni/IR64, 350 plants were selected on the basis of plant height and date of flowering.

For the first time, the germin-like protein multi-gene family in tomato has been identified in our lab at Plant Breeding and Genetics lab, BAU Sabour. Through detailed bioinformatics analysis, a potent candidate gene (annotated in this study as *SIGLPH*) has been identified. The *SIGLPH* transcript has been detected in leaf, stem, flower and fruit tissues of tomato. Relative abundance of the *SIGLPH* transcript has been found to be significantly increased under abiotic stress conditions. The coding DNA sequence of the *SIGLPH* gene has been amplified from tomato (cultivar: Pusa Ruby) genomic DNA and verified through custom sequencing. A genetic construct for over-expression of the *SIGLPH* gene has been prepared, mobilized to *Agrobacterium* and plant transformation (tomato and brinjal) has been initiated.

12.8 Conclusion

Plant breeders need to focus on traits with the greatest potential to increase yield. Hence, new technologies must be developed to accelerate breeding through improving genotyping and phenotyping methods and by increasing the available genetic diversity in breeding germplasm. Crop improvement through breeding brings immense value relative to investment and offers an effective approach to improving food security. Many new improved varieties are environmentally friendly, ensuring food security, while conserving the environment. The holistic approach in tackling climate change should encompass the climate resilient genotypes coupled with a suitable crop and natural resources management and sound implementation policies that could lead to climate-smart agriculture.

References

- Ahmed, M., Asif, M., Sajad, M., Khattak, J. Z. K., Ijaz, W., Fayyaz-ul-Hassan, W., A., & Chun, J. A. (2013). Could agricultural system be adapted to climate change? Review. *Australian Journal of Crop Sciences*, 7(11), 1642–1653.
- Bradbury, L. M. T., Fitzgerald, T. L., Henry, R. J., Jin, Q. S., & Waters, D. L. E. (2005). The gene for fragrance in rice. *Plant Biotechnology*, 3(3), 363–370.
- Ceccarelli, S., Valkoun, J., Erskine, W., Weigand, S., Miller, R., & Van Leur, J. A. G. (1991). Plant genetic resources and plant improvement as tools to develop sustainable agriculture. *Experimental Agriculture*, 28, 89–98.
- Chakraborty, S. (2005). Potential impact of climate change on plant-pathogen interactions. *Australasian Plant Pathology*, 34, 443–448.
- Coakley, S. M., Scherm, H., & Chakraborty, S. (1999). Climate change and plant disease management. *Annual Review of Phytopathology*, 37, 399–426.
- Dagar, J. C. (2005). Salinity Research in India: An Overview [In: Gupta et al. (Editors), Ecology and Environmental Management: Issues and Research Needs] Bulletin of the National Institute of Ecology 15: 69–80.
- Devreux, M., & Scarascia Mugnozza, G. T. (1964). Effects of gamma radiation of the gametes, zygote and proembryo in *Nicotiana tabacum* L. *Radiation Botany*, 4, 373–386.
- FAO. (2005). Impact of climate change, pests and diseases on food security and poverty reduction. Special event background document for the 31st Session of the Committee on World Food Security. Rome. May 2005 p. 23–26
- Gilligan, D. M., Briscoe, D. A., & Frankham, R. (2005). Comparative losses of quantitative and molecular genetic variation in finite populations of *Drosophila*. *Genetical Research*, 85, 47–55.
- Grando, S., Von Bothmer, R., & Ceccarelli, S. (2001). Genetic diversity of barley: use of locally adapted germplasm to enhance yield and yield stability of barley in dry areas. In H. D. Cooper, C. Spillane, & T. Hodgink (Eds.), *Broadening the Genetic Base of Crop Production* (pp. 351–372).
- Gregory, P. J., Johnson, S. N., Newton, A. C., & Ingram, J. S. I. (2009). Integrating pests and pathogens into the climate change/food security debate. *Journal of Experimental Botany*, 60, 2827–2838.
- Hajjar, R., & Hodgkin, T. (2007). The use of wild relatives in crop improvement: a survey of developments over the last 20 years. *Euphytica*, 156, 1–13.
- Honnay, O., Jacquemyn, H., & Aerts, R. (2012). Crop wild relatives: more common ground for breeders and ecologists. *Frontiers in Ecology and the Environment*, 10, 121–121.

- IAB. (2000). *Indian Agriculture in Brief* (27th ed.). New Delhi: Agriculture Statistics Division, Ministry of Agriculture, Govt. of India.
- Ismail, A. M., Heuer, S., Thomson, M. J., & Wissuwa, M. (2007). Genetic and genomic approaches to develop rice germplasm for problem soils. *Plant Molecular Biology*, *65*, 547–570.
- Janiesch, P. (1991). Eco-physiological adaptation of higher plants in natural communities to water logging. In J. Rozema & J. A. C. Verkleij (Eds.), *Ecological Responses to Environmental Stresses* (pp. 50–60). The Netherlands: Kluwer Academic Publishers.
- Kozłowski, T. T. (1984). Plant responses to flooding of soil. *Bioscience*, *34*, 162–167.
- Kulwal, P. L., Thudi, M., & Varshney, R. K. (2011). Genomics interventions in crop breeding for sustainable agriculture. In R. A. Meyers (Ed.), *Encyclopedia of Sustainability Science and Technology* (pp. 2527–2540). New York: Springer.
- Muller, H. J. (1927). Artificial transmutation of the gene. *Science*, *66*, 84–87. <https://doi.org/10.1126/science.66.1699.84>. New York/Rome: CABI/FAO/IPRI.
- Muthamilarasan, M., Venkata Suresh, B., Pandey, G., Kumari, K., Parida, S. K., & Prasad, M. (2014). Development of 5123 intron-length polymorphic markers for large-scale genotyping applications in foxtail millet. *DNA Research*, *21*, 41–52.
- Salvi, S., & Tuberosa, R. (2005). To clone or not to clone plant QTLs: present and future challenges. *TRENDS in Plant Science*, *10*(6), 297–304.
- Seki, M., Narusaka, M., Ishida, J., Nanjo, T., Fujita, M., Oono, Y., et al. (2002). Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. *The Plant Journal*, *31*, 279–292.
- Spielmeier, W., Ellis, M. H., & Chandler, P. M. (2002). Semidwarf (sd-1), “green revolution” rice, contains a defective gibberellin 20-oxidase gene. *Proceedings of National Academy of Sciences USA*, *99*, 9043–9048.
- Varshney, R. K., Graner, A., & Sorrells, M. E. (2005). Genomics-assisted breeding for crop improvement. *Trends in Plant Science*, *10*, 621–630.
- Wassmann, R., & Jagadish, S. (2009). Regional vulnerability of climate change impacts on Asian rice production and scope for adaptation. *Advances in Agronomy*, *102*, 91–133.
- World Resources Institute (WRI) in collaboration with United Nations Development Programme, United Nations Environment Programme, and World Bank, (2005): World Resources 2005: The Wealth of the Poor—Managing Ecosystems to Fight Poverty. Washington, DC
- Yue, B., Xue, W., Xiong, L., Yu, X., Luo, L., Cui, K., et al. (2006). Genetic basis of drought resistance at reproductive stage in rice: separation of drought tolerance from drought avoidance. *Genetics*, *172*, 1213–1228.