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REVIEW PAPER

Buckwheat (*Fagopyrum* sp.) genetic resources: What can they contribute towards nutritional security of changing world?

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Abstract The global population depends on fairly a small number of crops including wheat, rice and maize for food and nutrition, leaving a wealth of genetic resources neglected. Owing to ever increasing demands of the growing world, food production must be increased but research evidences suggests that climate change has adversely affected crop yields, thereby impacting whole agriculture. Exploring the potential reservoir of underutilized crops would provide a highly diversified agricultural production system in sustaining food and nutritional security under climate change. Buckwheat (*Fagopyrum* sp.) is one such crop representing a broad gene pool harboring diverse genetic resources for future agriculture due to their suitability to marginalized environments. Research advancements suggest that buckwheat has immense potential of commercialization due to presence of essential nutrients and therapeutics. With a balance of bioactive components and nutraceuticals, it has the ability to withstand various environmental stresses to make it a suitable candidate crop for future nutritional security initiatives. Despite such potential, efforts pertaining to genetic improvement, including breeding and molecular techniques are not exemplary. In this review, we present a comprehensive coverage of buckwheat germplasm research done till date along with a tangible perspective of integrating breeding and omics-driven approaches to accelerate higher genetic gains. The implementation of this strategy could enhance the nutritional benefits and adaptation to changing climates for future needs.

Keywords Buckwheat · Genetic resources · Conservation · Climate change · Nutritional security

Introduction

Globalization of agriculture and consequent industrialization along with changing climate scenario has diminished the genetic diversity in general and, food and agriculture in particular. Adoption of monoculturing practices and technological advancements have ousted the traditional cropping practices, thereby, making the global food security and economic growth dependent on limited number of crop species. With an ever increasing human population ($\sim$ 9 billion by the year 2050) and its nutritional requirements, there is an urgent need to combat food and feed deficiencies which are developing in the form of hidden hunger as per estimates of Sustainable Development Goals (Barrett 2010; FAO 2017; Allen and de Brauw 2018). According to the EASAC Policy Report

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(2011), the underutilized crops can be strategically exploited to ensure the effective management of eco-efficient production of nutritious and functional food along with minimal land usage and inputs. Being resilient to a large number of biotic and abiotic stresses, these can mitigate the effect of climate change (Massawe et al. 2015; Mabhaudhi et al. 2019). Among various underutilized crops occurring worldwide, buckwheat (*Fagopyrum* sp.) offers unique combination of biologically valuable compounds to ensure its usefulness as an extraordinary super food having nutraceutical and pharmaceutical potential.

Buckwheat is a dicotyledonous crop belonging to the Polygonaceae family and *Fagopyrum* genus which is comprised of both perennial and annual species having diploid (2n = 2x = 16) and tetraploid (2n = 4x = 32) chromosome numbers with a haploid genome size of ~ 1.2 Gb (Yasui et al. 2016). Out of the 34 reported species till date, it is recognized primarily by two cultivated species, common buckwheat (*F. esculentum* Moench) and tartary buckwheat (*F. tataricum* Gaertn) along with a wild species *F. cymosum* (Trev.) Meisn (Fig. 1) occurring in highlands of Euro-Asian regions (Farooq and Tahir 1987; Ohnishi 1995; Chen 1999; Tsuji et al. 1999; Chen et al. 2001; Rana 2004; Lui et al. 2001; Shao et al. 2011; Kalinova and Dadakova 2013; Tang et al. 2014; Zhou et al. 2015; Hou et al. 2015; Chen et al. 2018). Buckwheat is said to have been originated in temperate Central Asia (Morris 1947; Tsvetoukhine 1952) and China is considered as center of its origin (Farooq et al. 2016; Zhou et al. 2018a, b). Globally, the countries responsible for buckwheat production are Brazil, Canada, France, Poland, Russia, Ukraine and USA, including China and India (Campbell 1997; Di Fabio and Parraga 2016). It is cultivated in 2.4 Mha area worldwide with average production and productivity of 2.4 million tonnes and 1000 kg/ha, respectively. France has the distinction of having highest buckwheat productivity (3735 kg/ha) in the world (FAOSTAT 2018a, b). In India, the estimates for buckwheat production are not available separately, although it is distributed in Jammu & Kashmir in the North to Arunachal Pradesh in the East and Tamil Nadu in the South.

Since buckwheat has the wide adaptability to grow in any kind of environment, it has gained considerable interest among socio-scientific communities worldwide to improve food and nutritional security by increasing agricultural diversification and minimizing environmental degradation. Owing to presence of various bioactive constituents, crop-specific traits and physiological responses, buckwheat research has seen significant advances in context of crop cultivation and food applications (Ahmed et al. 2013; Alencar and Oliveria 2019; Pirzadah et al. 2019). In this article, we review the nutraceutical potential, origin and species distribution, genetic resources management, breeding and genomic advancements along with future prospects of buckwheat research. Our initiative will help in promotion and conservation of underutilized crops including buckwheat which will play an important role in providing food and nutritional security to the developing world under changing climate scenario.

Multifarious uses and health benefits

Buckwheat has been widely recognized as a future crop having multifarious uses ranging from restoring

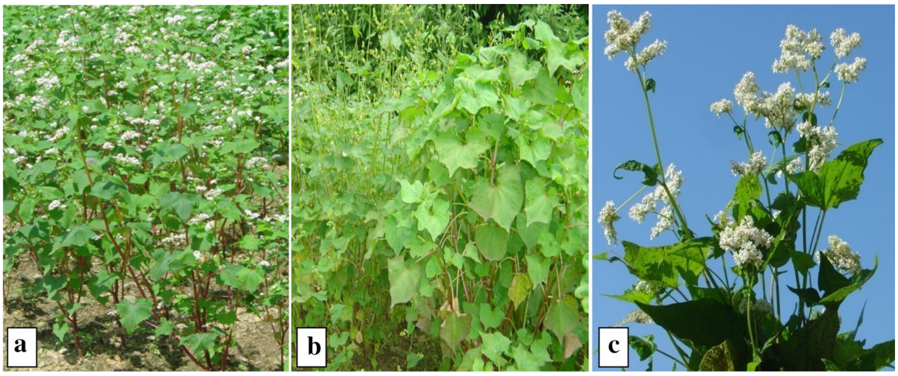

Fig. 1 View of cultivated **a** *F. esculentum* **b** *F. tataricum* and wild **c** *F. cymosum* species of buckwheat

soil productivity to nutraceutical properties and sustaining livelihood security of world population (Babu et al. 2018). It is an ephemeral green manure crop which tightens up the on-farm nutrient cycle by soaking up the leachable nutrients, thereby enhancing soil aggregate stability and nutrient scavenging mechanism (Clark 2007; Bjorkman and Shail 2010). The crop also has the potential to suppress root pathogens and insect-pests cycle (Magdoff and van Es 2009). Being an excellent phosphorus scavenger, buckwheat is often regarded as natural phosphorus pump having 10 times higher uptake capacity than wheat (Zhu et al. 2002). The roots exudates of buckwheat contain several mild acids which mineralize the slow release of organic fertilizers to subsequent crops (Bjorkman and Shail 2010; Tolaini et al. 2016).

The economic importance of buckwheat is due to presence of bioactive compounds such as flavonoids including rutin- the major marker compound along with nutritional characteristics. The flavonoids such as rutin, orientin, homoorientin, quercetin, vitexin and isovitexin present in flowers, leaves and seeds impart nutraceutical value to this crop (Zielinska et al. 2012; Raina and Gupta 2015). Rutin has been widely used in treatment of edema, haemorrhagic diseases, hypertension and inflammation (Omidbaigi and Mastro 2004; Nile and Park 2014). It is also known to avert Alzheimer's disease by ameliorating oxidative stress (Javed et al. 2012). On the other hand, quercetin possesses health effects like rutin and reduces inflammation (Sikder et al. 2014). Buckwheat also contains fagopyrin which is used in photodynamic therapy for the treatment of cancer, diabetic and microbial cells (Dai et al. 2009; Amezqueta et al. 2012; Tavčar et al. 2014). Also, the occurrence of polyphenolic antioxidants like caffeic acid, gallic acid and salicylic acid in this crop is helpful in curing various metabolic diseases (Oniszczuk 2016). The distinct aroma of its grains is due to the presence of salicylaldehyde (Janes and Kreft 2008). In addition, the gluten-free buckwheat flour is used in preventing celiac disease in human population (Wronkowska et al. 2013; Costantini et al. 2014; Giménez-Bastida et al. 2015; Kaur et al. 2015; Tummaramatti et al. 2016). Buckwheat contains a variety of nutrients viz. carbohydrates, proteins, lipids, minerals and vitamins whose concentrations are higher than most of the major cereal crops (Table 1). The total content of components depends on the variety vis-à-vis environmental factors (Bárta et al. 2004). Buckwheat proteins are known to reduce cholesterol concentration in the serum by increasing the fecal excretion of the steroids (Takahama and Hirota 2011) and they also suppress colon carcinogenesis by reducing cell proliferation (Liu et al. 2001). Buckwheat can also be harnessed for production of functional foods with high starch and flavonoid contents having low glycemic and insulin indexes (Stokić et al. 2015; Gao et al. 2016). The presence of higher levels of amino acids especially arginine, aspartate and lysine than cereals which are generally considered deficient in essential amino acids makes buckwheat a promising alternative for super food applications (Wijngaard and Arendt 2006; Janssen et al. 2016; Sytar et al. 2018). Additionally, it is also considered as a mineral source having high concentrations of copper, magnesium, phosphorus, potassium and zinc compared to major cereals (Campbell 1997; Wijngaard and Arendt 2006) along with the presence of well documented useful vitamins (Alvarez-Jubete et al. 2010). Moreover, it also possess high antioxidant activity, including DPPH radical scavenging activity which may help in optimization of processing conditions in health promoting products (Şensoy et al. 2006; Tang et al. 2009). Thus, it can also be blended with other cereal grains to produce multigrain bread, pasta and waffles (Lin et al. 2009). The investigations of Prestamo et al. (2003) showed the effect of buckwheat ingestion in rat increasing aerobic and lactic acid bacteria in its intestine with simultaneous decrease in pathogenic bacteria, thus justifying the role of buckwheat products as potential prebiotics for human consumption. Lately, buckwheat flowers have been used in preparation of organic tea (Qin et al. 2011; Thwe et al. 2013). Overall, buckwheat provides high commercial value and unique functional and nutritional benefits to the civil society. Therefore, the evaluation of genetic resources is prerequisite to identify promising genotypes/cultivars and their exploitations for developing elite varieties using appropriate breeding strategies. These resources could also be taken well as super food having pharmacological usage to resolve the problem of malnutrition.

Gene pool, origin and distribution

The taxonomic studies of buckwheat were first reported by Gross (1913) on the basis of distinct

Table 1 Comparison of nutritional and nutraceutical status of buckwheat with some major cereal crops (Partially adapted from Bonafaccia and Fabjan 2003; Przybylski and Gruczyńska 2009; Kumar et al. 2016; Joshi et al. 2019)

Nutrients	Buckwheat	Barley	Maize	Rye	Wheat
Amino acids (g/100 g)					
Cysteine	2.2	2.3	2.2	–	1.8
Histidine	2.5	2.2	2.4	–	2.3
Lysine	5.7	3.7	2.8	–	2.5
Methionine	2.3	1.8	2.4	–	1.8
Phenylalanine	4.3	4.9	4.5	–	4.4
Minerals (mg/100 g)					
Calcium	18	33	7	33	25
Copper	1.1	0.5	0.3	0.5	0.4
Iron	2.2	3.6	2.7	2.7	3.6
Magnesium	231	133	127	121	124
Phosphorus	347	264	210	374	332
Zinc	2.4	2.8	2.2	3.7	2.8
Proximate (%)					
Carbohydrates	72.9	73.5	74.3	69.8	71.1
Fibers	8.5	17.3	7.3	14.6	11.2
Lipids	7.4	2.3	4.7	2.5	2.5
Moisture	10.0	9.4	10.4	10.9	10.9
Proteins	12.0	12.5	9.4	14.8	13.7
Nutraceuticals					
Flavonoids (µg/g)					
Catechin	31.3	–	–	–	–
Epicatechin	203.5	–	–	–	–
Orientin	8.6	–	–	–	–
Quercetin	4.5	–	–	–	–
Rutin	176.5	–	–	–	–
Vitexin	17.8	–	–	–	–
Vitamins (mg/100 g)					
Niacin	6.15	4.61	3.63	4.27	5.71
Pyridoxine	0.58	0.32	0.62	0.29	0.34
Riboflavin	0.19	0.29	0.21	0.25	0.11
Thiamin	0.42	0.65	0.39	0.32	0.51

morphological identification which forms the basis of gene pool classification (Fig. 2). The genus *Fagopyrum* consists of about 34 species of which only two species viz. *F. esculentum* and *F. tataricum* are cultivated and classified under *cymosum* group while *F. acutatum, F. callianthum, F. capillatum, F. caudatum, F. crispatifolium, F. cymosum, F. densovillosum, F. dibotrys, F. emarginatum, F. giganteum, F. gilesii, F. gracilipedoides, F. gracillipes, F. hailuogouense, F. hybridum, F. homotropicum, F. jinshaense, F. leptopodium, F. lineare, F. luojishanense, F. macrocarpum, F. megaspartanium, F. pilus, F. pleioremosum, F. pugense, F. qiangcai, F. rubifolium, F. static, F. sagittatum, F. urophyllum, F. wenchuanense, F. zuogongense* are wild types occurring under *urophyllum* group (Farooq and Tahir 1987; Ohnishi 1995; Chen 1999; Tsuji et al. 1999; Chen et al. 2001; Rana 2004; Lui et al. 2001; Shao et al. 2011; Kalinova and Dadakova 2013; Tang et al. 2014; Zhou et al. 2015; Hou et al. 2015; Chen et al. 2018). The genus *Fagopyrum* is comprised of both self and cross-pollinated species and the rate of dimorphic heterostyly results in self incompatibility among species (Chrungoo et al. 2012; Farooq et al. 2016).

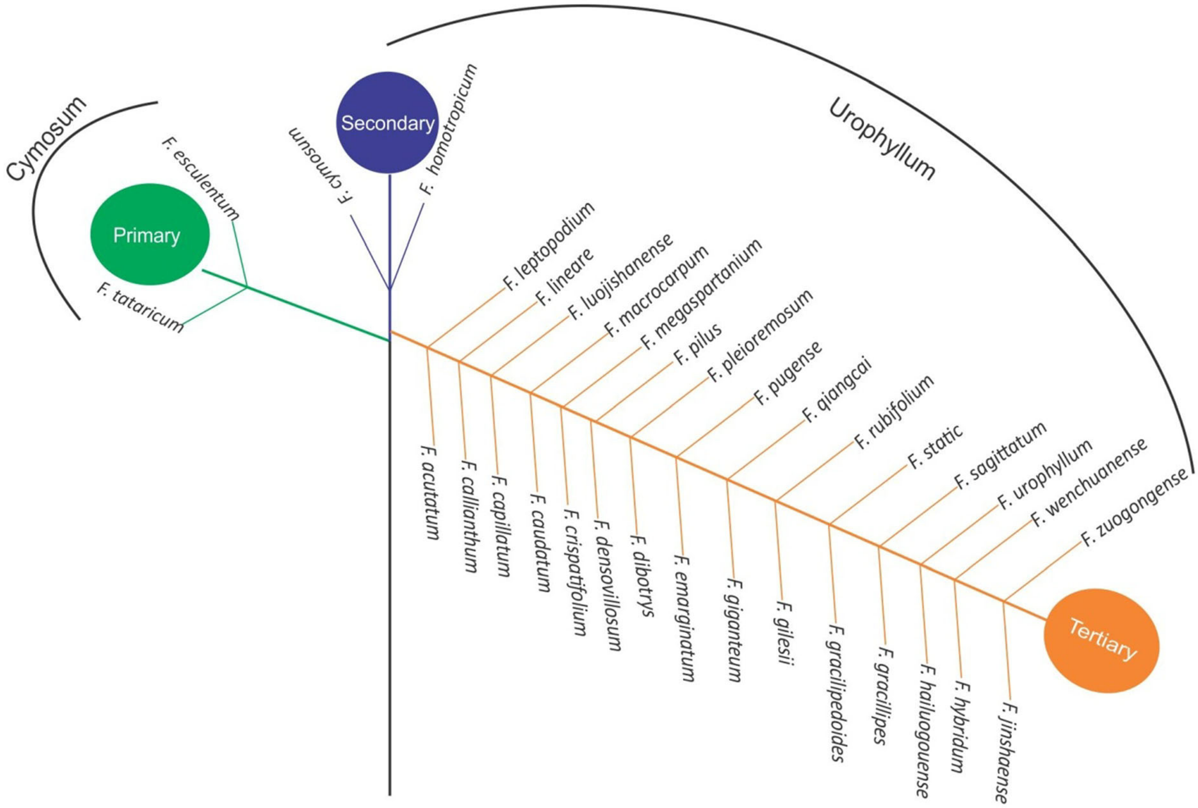

Fig. 2 Buckwheat gene pool

Buckwheat is said to have been originated in temperate Central Asia (Morris 1947 and Tsvetoukhine 1952). The oldest remains of buckwheat were found in China (Yururi and Zhongging 1984; Ahmad et al. 2018) and are known to have been cultivated in 1st and 2nd centuries BC (Li and Yang 1992) on the contrary to Hunt (1910) who believed them to be not so ancient. In (1957), Nakao ascertained De Candolle's (1883) hypothesis on origin of buckwheat in Northern China or Siberia which was contradictory to Steward's (1930) distribution of wild *Fagopyrum* species as reported by Ohnishi (1995). In (1992), Li and Yang suggested Yunnan region as the origin of common buckwheat and Jiang and Jia (1992) reported Daliangshan region as the origin of tartary buckwheat. Ohnishi (1995) ascertained two hot spots for differentiation of *Fagopyrum* species; the Yunnan province and the upper Min river basin. As stated by Campbell (1976), *F. cymosum* is not the ancestor of cultivated buckwheat but is distantly related, stating *F. esculentum* ssp. *ancestralis* Ohnishi as the wild ancestor of common buckwheat and *F. tataricum* ssp. *potanini* Batalin as the wild ancestor of tartary buckwheat (Ohnishi 1998). The studies related to allozyme analysis and DNA polymorphism revealed possibility of *F. megaspartanium* and *F. pilus* as the progenitors of common buckwheat and tartary buckwheat, respectively (Chen et al. 2004; Li et al. 2013). Domestication of common and tartary buckwheat took place in the western Yunnan and Sichuan region of China (Ahmad et al. 2018). With the availability of draft genome, the evaluation of genome-wide diversity using genotyping-by-sequencing has resulted in elucidating the evolutionary history of buckwheat suggesting multiple origins pertaining to Asian and European continents (Yasui et al. 2016; Mizuno and Yasui 2019).

Buckwheat is widely distributed in the intricated geographical environment of South-West China. Common buckwheat was first cultivated in inland South-East Asia from where it was expanded to Central Asia, Europe, Middle East and Tibet via

Russia (Kreft 2001; Woo et al. 2010; Ahmad et al. 2018). From South-West China it was distributed to Bhutan, Nepal, India and Pakistan (Kreft 2001). From Northern China via Korean peninsula, buckwheat was introduced in Japan (Nagatomo 1984 and Ohnishi 1995). Later, from Asia and Europe, buckwheat cultivation was started in Argentina, Brazil, Canada, South Africa and USA (Kreft 2001). Dispersal around the globe was completed by 2006 (Ahmad et al. 2018). With passage of time, it became an important crop in mountainous regions of China, India, Kazakhstan, Russia, Ukraine and parts of Canada, Japan, Korea and Nepal (Wei et al. 2003; Stibilj et al. 2004; Sangma and Chrungoo 2010). In India, the important segments of buckwheat cultivation are Jammu & Kashmir, Himachal Pradesh and Uttarakhand in the North; Arunachal Pradesh, Manipur, Meghalaya and West Bengal in the East; and parts of Nilgiri and Palani hills in the south (Rana et al. 2012).

Genetic resources and ex situ conservation

Buckwheat genetic resources are comprised of released cultivars, advanced breeding lines, landraces and wild species which are distributed globally. With the dawn of modern agriculture, replacement of local landraces by other high yielding crop varieties and adverse effects of changing climate, these have become prone to genetic erosion. Food and Agriculture Organization (FAO) in 1945 was the first body to perceive the danger of genetic erosion of valued resources and consequently started conservation activities to prevent it. In 1974, FAO established International Board for Plant Genetic Resources (IBPGR) with the mandate for conservation and sustainable use of genetic diversity. Subsequently, germplasm conservation activities have been undertaken at Regional, National and International levels.

Many global gene banks are actively involved in the conservation of buckwheat resources like Crops Genetic Resources Institute of Chinese Academy of Agricultural Sciences (CAAS), China (largest repository with > 2800 accessions); Genebank of the Crop Research Institute (CRI), Czech Republic; National Bureau of Plant Genetic Resources (NBPGR), India; National Agriculture Genetic Resource Centre (NAGRC), Nepal; and N.I. Vavilov Research Institute of Plant Industry (VIR) in Russia (Suvorova and Zhou 2018). These genetic resources are conserved in long-term storage (LTS) (−20 °C and 5% RH) or mid-term storage (MTS) (5 °C and 35% RH) depending on their usability. In 1980s, CAAS began to collect buckwheat germplasm with other institutes in 24 provinces and stored them in its gene bank with current holding of > 2800 accessions (Tang et al. 2016). Simultaneously, NBPGR in India also started buckwheat introduction, collection and conservation activities resulting in 1050 germplasm collections stored in the LTS at New Delhi as base collection and the same set of germplasm storage at its regional station in Shimla as working collection. The list of global gene bank holding the buckwheat germplasm has been presented in Table 2.

Although on-farm conservation of buckwheat germplasm has been initiated globally, detailed reports regarding the same are still limited except studies in Indian Himalayan region (Rana et al. 2016), Nepal (Luitel et al. 2017) and South-West China (Huang et al. 2017b; Song et al. 2019, 2020). These studies have revealed that traditional farming systems are of utmost importance for maintenance of local genetic diversity along with sustainable livelihood and food security. Nevertheless, general awareness camps and brainstorming sessions at grass root level can aid in successful conservation of buckwheat genetic resources along with initiation of new breeding initiatives.

Germplasm characterization and evaluation

The characterization and evaluation of genetic resources is a pre-requisite for conducting a successful crop improvement programme with a view to introgress desired traits for developing potential cultivars. Buckwheat germplasm has been characterized globally for various qualitative and quantitative traits using the plant descriptors jointly developed by International Plant Genetic Resources Institute (IPGRI), now Bioversity International, NBPGR and others. A wide range of variability has been observed in germplasm for different yield contributing characters worldwide (Ujihara 1983; Choi et al. 1992; Baniya et al. 1995; Rana and Sharma 2000; Rana 2004). Countries like China, India, Japan, Nepal and North Korea have evaluated agronomic traits of buckwheat such as plant height, number of branches, number of flowers,

Table 2 Buckwheat genetic resources conserved in the major global gene banks

Organization	Country	Germplasm collection	References
Crop Genetic Resources Institute of Chinese Academy of Agricultural Science (CAAS)	China	2804	Zhou et al. (2018a, b)
Genebank of the Crop Research Institute (CRI)	Czech Republic	170	Cepková et al. (2009)
National Bureau of Plant Genetic Resources (NBPGR)	India	1050	Rana et al. (2016)
National Institute of Agro-biological Sciences (NIAS)	Japan	226	Katsube-Tanaka (2016)
Central Plant Breeding and Biotechnology Division	Nepal	172	Arora et al. (1995)
National Agricultural Research Council (NARC)	Nepal	488	Arora et al. (1995)
National Hill Crops Research Program	Nepal	411	Arora et al. (1995)
N.I. Vavilov Research Institute of Plant Industry (VIR)	Russia	2230	Romanova et al. (2018)
Podillya State Agricultural University	Ukraine	900	Zhou et al. (2018a, b)
V.Y Yuryev Institute of Plant Production	Ukraine	1600	Zhou et al. (2018a, b)

1000-seed weight, plant type, stem color, flower color, seed color and seed shape along with important quality characters (Chauhan et al. 2010).

Buckwheat varieties usually differ from each other in plant type, stem color, leaf color, flower color, grain color, grain shape etc., thus, abundant diversity has been reported in various accessions pertaining to *F. esculentum* and *F. tataricum* (Yang 1992; Baniya et al. 1995). The CAAS has identified important agronomic characters in 964 *F. esculentum* accessions (Yang and Lu 1992) and Baniya et al. (1995) evaluated them in 309 accessions. Similarly, Yang (1995) reported variability in 550 *F. tataricum* accessions while Joshi et al. (2011) also reported the same in 192 accessions for different agro-morphological characters. Recently, a study by Rauf et al. (2020) led to characterization of 251 *F. esculentum* accessions demonstrating high diversity pertaining to seed color, 80% maturity, and 1000-seed weight under the spring cultivation. Likewise, the wild species of buckwheat harbors rich genetic diversity in terms of nutritional and medicinal composition viz. amino acids, carbohydrates, flavonoids, minerals and proteins. Reports have suggested that wild *F. cymosum* contains highest amount of amino acids, minerals, proteins and vitamins among buckwheat species (Lu et al. 1996; Zhang et al. 1999; Zhao et al. 2002; Tang et al. 2011). Common buckwheat contains 18 kinds of amino acids which differ significantly in terms of content as reported by Yang (1992) who also observed variation in minerals (0.054–3682 ppm) and vitamins (0.09–9.84 mg/100 g) among 906 accessions of *F. esculentum*. Furthermore, tartary buckwheat is a rich source of various nutrients including amino acids, lipids, minerals, proteins, vitamins and bioactive substances. Chinese researchers in early 1990s have measured the contents of amino acids and trace elements like Ca, Mn, P, Se, Zn etc. in $>$ 500 *F. tataricum* accessions which ranged from 7040 to 15,830 mg/100 g for amino acids and 0.05–3762 ppm for minerals. Zheng et al. (2011) reported the presence of Se in buckwheat (0.0406 mg/g) which imparts resistance to various cancers and cardiovascular diseases among humans, thereby making buckwheat an ideal candidate for exploiting Se to make biofortified products to promote nutritional security. Further, rutin being the major marker compound in buckwheat known for various pharmacological properties has been measured in *F. esculentum* and *F. tataricum*. Park et al. (2004) reported that highest rutin content was observed in flowers and lowest in roots among both *Fagopyrum* sp. Similarly, Jiang et al. (2006) demonstrated the variation in rutin content along with antioxidant activity decreasing from *F. tataricum* to *F. esculentum*. Results have also shown that the rutin content of *F. tartaricum* is more than that of *F. esculentum* ranging from 6–30 μg/mg and 0.145–0.189 μg/mg in *F. tataricum* and *F. esculentum*, respectively (Kitabayashi et al. 1995; Campbell 1997; Yan et al. 2004; Gupta et al. 2012). Gupta et al. (2011) found that the germplasm with high rutin content is stable, thus implying the importance of genetic differences in *F. tartaricum* accessions which can be used for developing elite buckwheat chemotypes. Reports have revealed that metabolite contents of buckwheat germplasm vary due to environmental factors (Nam et al. 2018), sowing time (Hyun et al. 2018), varietal changes (Kiprovski et al. 2015) and so on. A study by Yu et al. (2019) showed significant variation in rutin and quercetin contents in *F. tataricum* accessions, suggesting effect of geographical location on the same. Further, among *F. esculentum* germplasm, 10 accessions with high rutin content (~ 0.35 µg/mg) and 3 accessions with high quercetin content (~ 0.01 µg/mg) have also been reported in recent times (Rauf et al. 2020). Overall, trait-specific accessions of buckwheat germplasm for different agro-morphological and biochemical characteristics have been identified over the years (Table 3). In general, characterization and evaluation of buckwheat germplasm has led to screening and identification of novel buckwheat genetic resources which have immense potential for their utilization in buckwheat breeding.

Development of cultivars and germplasm registration

The need for recognition of improved crop genotypes is widely considered as an important aspect for sustainable utilization of genetic resources in crop improvement. This becomes critically imperative during changing global scenario in view of Intellectual Property Rights' (IPRs) regimes. Recent years have seen rapid advances in development and registration of buckwheat genotypes worldwide. Globally, Belarus had registered 12 buckwheat varieties while Russia had registered 48 (Suvorova and Zhou 2018). China registered high yielding perennial tartary buckwheat varieties 'Gui Duoku 003', 'Gui Duoku 60' and 'Gui Duoku 74' developed by wide hybridization between tartary buckwheat variety 'Daku No. 1' and perennial buckwheat variety 'Hongxin Jinqiaomai' having low shattering, high seed number and better genetic stability (Chen et al. 2018). Japan had registered 32 varieties of common buckwheat between the years 1919–2010 (Hayashi 2011). Ukraine had registered 20 varieties based on genetic recombination and phenotypic selection criteria (Taranenko et al. 2004). Two accessions, IC3789 and IC3823 from Eastern Ukraine are considered as the most resistant accessions for shedding (Joshi and Paroda 1991).

In India, buckwheat varieties 'Himpriya' and 'Himgiri' were developed by NBPGR Regional Station, Shimla as a pure line selection from IC13374 and EC321978 in 1991. Further, 'VL UGAL 7' variety was developed in 1991 by Vivekanand Parvatiya Krishi Anusandhan Sansthan (VPKAS), Almora, India through mass selection (Joshi and Rana 1995). In 1997, 'PRB 1' developed for high seed yield was registered by GB Pant University of Agriculture and Technology, Pantnagar, India. Then, an easy dehulling accession IC258233 was registered by NBPGR Regional Station, Shimla in 2004. Later in 2005, Himachal Pradesh Agriculture University (CSKHPKV), Palampur, India developed variety 'Sangla B1' through pure line selection for high seed yield (Rana et al. 2016). Earlier, Joshi and Paroda (1991) evaluated 108 accessions of buckwheat from Himalayan region and considered accession IC13145

Table 3 Sources of useful traits identified in buckwheat germplasm

Trait of interest	Value	Species	References
Days to flowering	< 40 days	*F. tataricum*	Chauhan et al. (2010)
Days to maturity	< 80 days	*F. esculentum, F. tataricum*	Rana et al. (2016), Rauf et al. (2020)
Seed yield per plant	> 100 g	*F. tataricum*	Rana et al. (2016)
1000-seed weight	> 25 g	*F. esculentum, F. tataricum*	Chauhan et al. (2010), Rauf et al. (2020)
Lysine content	> 4.50%	*F. tataricum*	Zheng et al. (2011), Rana et al. (2016)
Total phenols	> 1.60%	*F. cymosum, F. tataricum*	Rana and Sharma (2000), Zhao et al. (2002)
Total proteins	> 14%	*F. cymosum, F. esculentum*	Przybylski and Gruczynska (2009), Tang et al. (2011)
Quercetin content	> 0.2 µg/mg	*F. esculentum, F. tataricum*	Yu et al. (2019), Rauf et al. (2020)
Rutin content	> 17 µg/mg	*F. tataricum*	Gupta et al. (2012), Yu et al. (2019)

as *F. himalianum* which was later listed by IPGRI as *F. tataricum* var. *himalianum*.

NBPGR initiatives—mainstreaming buckwheat landraces into production system

The study was focused on on-farm conservation and mainstreaming of important crop landraces which are becoming extinct due to climate change and onslaught of cash crops. In this direction, efforts were made to promote buckwheat landraces belonging to cold desert regions of India.

The study was focused on systems-level analysis of substantial intensification of agriculture with participatory farm household resources and economic environments for conservation and management of traditional buckwheat landraces. Biochemical profiling for the identification of bioactive substances responsible for nutritional and health benefits was also done for identification of elite plant material, thereby generating knowledge paradigm among farming communities. It was shown that protein content in *F. esculentum* and *F. tataricum* seeds was 115 mg/g and 105 mg/g, respectively while starch activity was 4.8 U/µM/30 min. and 6 U/µM/30 min., respectively. Similarly, high performance liquid chromatography (HPLC) analysis showed presence of 3 mg/g flavonoid in *F. esculentum* seeds as compared to 20.5 mg/g in *F. tataricum* seeds. The cultivated buckwheat varieties, *F. esculentum* and *F. tataricum* were also documented for registration with the Protection of Plant Varieties and Farmers' Rights Authority (PPVFRA), New Delhi to record the unique landrace diversity carrying important trait of interest. The results demonstrated integration of on-farm conservation for traditional landraces along with biochemical analysis, registration of farmers' varieties and establishment of Community Seed Banks (CSBs) which will aid in systems level analysis for long term sustainability of plant genetic resources from cold-arid agro-ecosystem for achieving nutritional security under changing climate scenario. Hence, creating seed chain system through on-farm conservation and CSBs vis-à-vis characterization and evaluation of elite farmers' varieties for novel traits will bring the potential crops in general and buckwheat in particular under mainstream agriculture, thus strengthening their sustainable conservation and utilization (Fig. 3; unpublished data).

Progress in breeding strategies

Buckwheat breeding program has always been associated with numerous problems pertaining to apomixis, low seed availability, self/cross-incompatibility, shattering, sterility etc. Despite such breeding barriers, different plans aimed at buckwheat genetic improvement were initiated by various international organizations. The major breeding advancements in buckwheat have been summarized in Table 4. In 1938, the first buckwheat variety 'Bogatyr' was released and developed through mass selection from Russian landrace populations (Suvorova and Zhou 2018). Studies aimed at broadening the genetic base of buckwheat along with improvement of existing varieties and introgression of new characters were started when interspecific crosses were attempted. Morris (1951) reported a cross between *F. esculentum* and *F. tataricum* which resulted in immature embryos if *F. tataricum* was used as the female parent. The first interspecific hybrid, *F. giganteum* Krotov was obtained by crossing *F. cymosum* and *F. tataricum* (Krotov and Golubeva 1973). Because of the self-incompatibility of *F. esculentum*, several attempts were made to obtain its hybrids through ovule culture (Ujihara et al. 1990). Later in 1995, with the identification of wild progenitor *F. homotropicum*, self fertile species extended the possibilities of interspecific crossing of common buckwheat. This led to a successful interspecific cross between *F. esculentum*

Fig. 3 Buckwheat on-farm conservation site in Sangla valley of Himachal Pradesh, India

Table 4 Progress of breeding in buckwheat

Study/Problem	Organ used	Result	References
Anther culture	Anther	Induction of haploid or diploid plants	Bohanec et al. (1993)
Interspecific hybridization using embryo rescue	Embryo	Successful production of interspecific hybrids from crosses between *F. cymosum* × *F. esculentum* and *F. esculentum* × *F. tataricum*	Woo et al. (1995), Woo et al. (2002), Niroula et al. (2006)
Gametophyte selection	Pollen	Pollen competition influenced genetic structure and vigor of buckwheat mapping population	Bjorkman (1995)
Self-incompatibility in interspecific crosses	Pollen	Occurrence of unilateral incompatibility and dimorphic self-incompatibility	Hirose et al. (1995)
In vitro germination and viability	Pollen	Temperature and flower age influenced pollen longevity	Adhikari and Campbell (1998)
Inflorescence	Pollen	Light affected photosynthetic rate and flowering time	Quinet et al. (2004)
Cytogenetics	Pollen	Crossing autotetraploid plants with diploid parent produced autotriploid and trisomic progenies	Chen et al. (2007)
Embryo development in interspecific crosses	Pollen	Highly compatible pollination occurred between *F. esculentum* × *F. cymosum* and *F. esculentum* × *F. homotropicum*	Woo et al. (2008)
Enhanced seed development by backcross	Pollen	Desirable agronomic traits from wild *F. homotropicum* transferred to cultivated *F. esculentum*	Shin et al. (2009)

and *F. homotropicum* (Campbell 1995). After several breeding efforts, a common buckwheat breeding line 'Norin-PL1' was developed by crossing *F. esculentum* cv. Botansoba and *F. homotropicum* accession from Yunnan followed by recurrent backcrossing of F_1 hybrid with *F. esculentum* (Matsui et al. 2008).

Subsequently, various crosses of *F. cymosum* x *F. esculentum* and *F. esculentum* x *F. tataricum* were developed using embryo rescue technique (Hirose et al. 1995; Woo et al. 1999, 2008), although certain reports on unsuccessful interspecific crosses are available in literature (Wagatsuma and Un-no 1995; Wang and Campbell 1998). Despite the difficulty of embryo abortion in *F. esculentum* and *F. tataricum* crosses, researchers continued the search to overcome the incompatibility barriers. To improve the success of interspecific hybridization between the two cultivated species, Samimy et al. (1996), Wang et al. (2002), Niroula et al. (2006), and Azaduzzaman et al. (2009) carried out various hybridization experiments independently. A hybrid was produced using polyethylene glycol-mediated fusion of mesophyll protoplasts of *F. esculentum* and hypocotyl protoplast of *F. tataricum* (Samimy et al. 1996). Then, more than 30 embryos were produced by crossing *F. esculentum* and *F. tataricum* (Suvorova 2001). To improve the seed setting and shattering, 'Hongxin Jinqiao', a tetraploid variety was developed in 2007 using *F. cymosum* accessions with less shattering (Chen et al. 2018). A tri-species hybrid of *F. cymosum*, *F. esculentum* and *F. homotropicum* was obtained as a result of multiple crossing and ovule rescue technique (Suvorova 2001, 2010). The plants obtained were vigorous in growth but were not able to produce mature seeds without ovule culture. Lastly, a new species *F. tartricymosum* was obtained by interspecific cross between *F. cymosum* and *F. tataricum* (Ren and Chen 2016). Earlier, Mukasa (2011) standardized hot water emasculation in common buckwheat (42 °C for 5 min) and tartary buckwheat (44 °C for 3 min) for artificial hybridization and large scale production of hybrids.

In India, buckwheat breeding programs is being carried out under AICRP on potential crops to obtain improved breeding materials (Hore and Rathi 2002). Several attempts were made to hybridize buckwheat using different protocols but limited success has been achieved till now. NBPGR Regional Station, Shimla has attempted to hybridize two registered buckwheat varieties, 'Himpriya' and 'Shimla B1' using two emasculation techniques viz. hot water treatment and hand emasculation. Result showed development of viable hybrid seeds using hand emasculation which is under further analysis (unpublished data). Nevertheless, more efficient and reliable breeding methods are required for genetic improvement of buckwheat to cope with changing world.

Progress in biotechnological interventions

During the last 20 years, the application of modern biotechnology in buckwheat research has attracted the concern of scientists globally. The development and use of molecular markers has significantly addressed various aspects of molecular genetics which forms the basis for utilization of DNA polymorphism (Cullis 2002). Different genome-wide markers have been employed to study the diversity and evolutionary history of buckwheat gene pool. The origin of common buckwheat has been studied by using random amplified polymorphic DNA (RAPD) markers (Murai and Ohnishi 1996) and amplified fragment length polymorphism (AFLP) markers (Konishi et al. 2005). Lately, the development of simple sequence repeat (SSR) markers led to significant genetic differentiation among common buckwheat cultivars (Iwata et al. 2005), although only few SSR markers are reported in buckwheat (Konishi et al. 2006; Joshi et al. 2006; Ma et al. 2009). Thereafter, Yasui et al. (2008) constructed a bacterial artificial chromosome (BAC) library for rapid enrichment of buckwheat genetic resources. Further, reports by Chauhan et al. (2010) and Rana et al. (2016) suggested the use of expressed sequenced tags (ESTs) for rapid development of molecular markers in buckwheat. They also reported identification of rutin biosynthetic pathway genes in *F. esculentum* and *F. tataricum* by utilizing comparative genomics approach. Lately, the substantial advances in genomics applications led to development of high quality reference genomes of *F. esculentum* (Yasui et al. 2016) and *F. tataricum* (Zhang et al. 2017) with genome sizes of 1.2 Gb and 0.48 Gb, respectively followed by two chloroplast genome sequences (Liu et al. 2016; Wang et al. 2017). The studies related to marker-assisted selection in buckwheat have been summarized in Table 5.

The comprehensive analysis of the association between agronomic traits for marker-assisted selection and quantitative trait loci (QTLs) is primarily associated with genetic maps (Chauhan et al. 2010). The availability of genetic maps for common buckwheat (Yasui et al. 2004; Pan and Chen 2010) and tartary buckwheat (Xiaolei et al. 2013) led to identification of QTLs governing photoperiod sensitivity (Hara et al. 2011) and stem length (Yabe et al. 2014), but limited efforts have been made till date to generate genetic mapping populations of buckwheat in terms of rapid advancements made in other crops associated with production of Multiple Advanced Generation Intercross (MAGIC), Nested Associated Mapping (NAM) and Recombinant Inbred Lines (RILs) population. Of late, speed breeding has also been deployed for rapid cultivar development in major crop species to manage six crop cycles per year than one or two cycles under normal conditions (Watson et al. 2018). Since growing season of buckwheat lasts 3–4 months (Joshi et al. 2019), this technique could be helpful in achieving six crop cycles annually. Besides, an immediate thrust is required for enhancing buckwheat production by integrating genomics-assisted breeding approaches. Although the potential of genomic selection to complement mass selection in buckwheat has been demonstrated recently (Yabe et al. 2018), utilization of CRISPR/Cas9-mediated genome editing will aid in improving nutraceutical value and yield in buckwheat.

The last decade has also witnessed the use of transcriptome-based gene expression profiling for characterization of the candidate genes regulating various biological processes (Kumar et al. 2016). In buckwheat, comprehensive transcriptome analysis for floral structure, aluminum toxicity and salt tolerance have been reported by Logacheva et al. (2011), Xu et al. (2017) and Wu et al. (2017), respectively. Huang et al. (2017a) identified 11,676 differentially expressed genes by transcriptome analysis of seed development stages in tartary buckwheat. Moreover, proteomics-based analysis of buckwheat has also helped in better understanding of developmental processes to facilitate deeper analysis by functional genomics (Lee et al. 2016). Likewise, hairy root culture-induced metabolic profiling of tartary buckwheat led to increase production of flavonoids along with the identification of 47 secondary metabolites by gas chromatography-mass spectrometry (GC–MS) analysis (Thwe et al. 2013, 2016).

Table 5 Progress of marker-assisted selection in buckwheat

Study	Marker used	Result	References
Population genetics of *F. esculentum*	RAPD	Construction of phylogenetic trees for landraces from all over the world	Murai and Ohnishi (1996)
Identification of molecular markers linked to the homostylar (Ho) gene	RAPD	Generation of F_2 population from an interspecific cross between *F. esculentum* and *F. homotropicum*	Ali et al. (1998)
Origin of *F. tataricum*	RAPD	Construction of phylogenetic tree based on RAPD markers	Tsuji and Ohnishi (2000)
PCR-based DNA fingerprinting	RAPD	Uncovering of species relationship between 28 different accessions belonging to 14 different species	Sharma and Jana (2002)
Characterization of interspecific hybrids between *F. esculentum* and *F. tataricum*	RAPD	Production of hybrids from interspecific crosses using ovule rescue method	Asaduzzaman et al. (2009)
Genetic mapping of *F. esculentum*	RAPD	Construction of linkage map involving RAPD markers	Pan and Chen (2010)
Conversion of AFLP marker to a simple PCR-based marker	AFLP	Identification of tightly linked markers associated with cell compatibility	Nagano et al. (2001)
Identification of AFLP markers linked to non-seed shattering (Sht 1) locus	AFLP	Identification of 5 AFLP markers linked to Sht 1 locus	Matsui et al. (2004)
AFLP linkage analysis of cultivated *F. esculentum* and wild *F. homotropicum*	SSR	Development of interspecific linkage map and SSR markers	Yasui et al. (2004)
Development of SSR markers	SSR	Development of 136 SSR markers in *F. esculentum*	Ma et al. (2009)
Assessment of genetic diversity and population structure	SSR	Low genetic differentiation due to out-crossing and self-incompatibility	Song et al. (2011)

Further, due to its immense nutraceutical importance, there is a greater significance for in vitro production of plant metabolites in buckwheat. Vegetative propagation of many economic plants has so far been achieved through tissue culture methods (Murashige and Skoog 1977). Previous results showed that isolated hypocotyls and cotyledons of buckwheat could be induced to develop calluses, with the capacity for organogenesis and restoration of plantlets (Yamane 1974). Moreover, research was conducted on common buckwheat to develop a plant regeneration system for future application of genetic transformation (Woo et al. 2000a, b). Somatic embryogenesis has also been reported by culturing of immature embryos of common buckwheat (Neskovic et al. 1987; Rumyantseva et al. 1989) and tartary buckwheat (Lachmann and Adachi 1990; Rumyantseva et al. 1989). Research on somatic embryogenesis and plant regeneration has been carried out using hypocotyl segments as explant of the cultivated buckwheat species *F. esculentum* to develop an efficient protocol for plant regeneration for common buckwheat (Kwon et al. 2013). Several studies have also been conducted to develop a potential technique for the isolation of viable protoplasts from egg cells (Woo et al. 1999) so that egg cells of buckwheat can be fused with somatic protoplasts and other gametoplasts because of their biological function; a technique has also been developed for the isolation of viable protoplasts from sperm cells (Woo et al. 2000a, b). Additionally, genetic engineering through *A. tumefaciens* and *A. rhizogenes*-mediated transformation is well established in both common and tartary buckwheat as suggested by findings of Kojima et al. (2000), Kim et al. (2001, 2010) and Gabr et al. (2012). These studies have paved the way for development of transgenics in buckwheat vis-à-vis production of higher amount of flavonoids which can have a perpetual impact on global food and nutritional security.

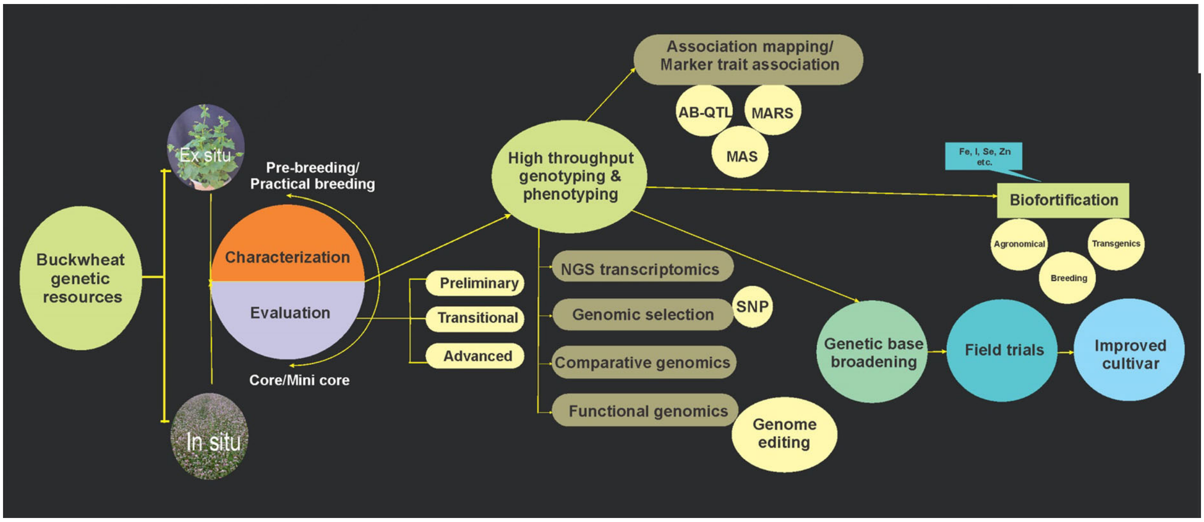

Fig. 4 Integrated approach for achieving higher genetic gains using buckwheat genetic resources

Conclusions and future perspectives

Buckwheat is a nutritionally rich and well suited pseudocereal crop to diversify our cropping systems and adapt to changing environments. The increasing awareness about the nutritional properties, health benefits and other important uses of buckwheat has resulted in the renaissance of the crop. The genetic variability available in the buckwheat gene pool including traditional crop landraces permits the development and improvement of nutritionally rich varieties. The phenotypic diversity for economic traits of interest are also needed to be assessed using multilocational testing for identifying stability within promising germplasm resources. Despite the detailed coverage of almost all aspects of buckwheat resources, there seems to be a huge gap for mainstreaming and popularizing this potential crop. With the availability of crop wild relatives within the *Fagopyrum* genus, extensive efforts are required to obtain desirable agronomical traits and breeding interventions among buckwheat populations. Similarly, several reports on biotechnological advancements reviewed recently by Joshi et al. (2020) have shown significant developments in buckwheat genomics, but these efforts seem to be underachieved in comparison to other food crops. Therefore, multivisionary research is needed for promoting this potential crop via amalgamation of high throughput genomics approaches. Further, being the store house of diverse functional properties in the form of nutritional profile and bioactive compounds, buckwheat provides high commercial value and wide applicability among human population. The comprehensive research on biofortification and value addition along with molecular farming is the need of the hour for accelerating buckwheat research. The development of biofortified buckwheat cultivars and commercial products could result in wide implications to counteract nutritional deficiencies in the form of hidden hunger, although some groups have recently demonstrated effects of biofortification on biochemical and physiological characteristics of buckwheat (Jiang et al. 2018; Germ et al. 2019). A schema of integrating multidisciplinary approaches for enhancing higher genetic gains has been represented in Fig. 4. Lastly, specific and targeted interventions at scientific and societal levels are required to make buckwheat a crop for the future to cope with nutritional security and climate change. Overall, diversifying the prosperous legacy of genetic materials nurtured by buckwheat resources can play a vital role in edifying an economically feasible and resilient production system to protract food and nutritional security of changing world.

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Authors' contribution MS, NM conceived the idea, coordinated the manuscript layout and wrote the article; KS assisted in data collection and literature survey. All the authors have read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest Authors declare that they have no conflict of interest.

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