



Buckwheat: A critical approach towards assessment of its potential as a super crop

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Abstract

Buckwheat has attracted considerable interest amongst the global scientific community due to its nutritional and pharmaceutical properties. It is a low input crop whose cultivation has persisted through centuries of civilization in almost every country where cereals were cultivated. The crop is an important source of rutin, an important flavonoid which is known to have cardioprotective, vasoprotective, antihypertensive, anti-inflammation, cytoprotective and anti-diabetic properties. Grains of buckwheat are a rich source of protein with a balanced amino acid composition, gluten free flour, dietary fibre, vitamins, resistant starch, phytosterols, fagopyrins, fagopyritols and phenolic compounds. Buckwheat is a short season crop which completes its life cycle in 70-90 days and can grow in wide range of environmental conditions including marginal lands and rocky, poorly tilled soils. The protein content in buckwheat flour is higher than in commonly used cereals such as rice, wheat, millet, sorghum and maize. Buckwheat grain protein is rich in lysine and arginine, which are generally limiting in other cereals. Because of a low Lys/Arg and Met/Gly ratio, buckwheat protein has strong hypolipidemic activity. While Buckwheat is considered as a healthy food because of its nutraceutical properties, low yields due to seed shattering because of pedicel breaking and heterozygosity due to self-incompatibility as a consequence of dimorphic heterostylism have always remained major problems in achieving large scale incorporation of common buckwheat (*Fagopyrum esculentum*) in the agricultural portfolio. The present review highlights the multicore potential of buckwheat as a super crop to meet the challenges of food and nutritional security

Key words: Food security, Buckwheat, nutraceutical, rutin, functional food, domestication, genomics approach driven breeding

Introduction

Sustainable utilization of our limited natural resources

for maximizing food production is a serious challenge for attaining the sustainable development goal of “zero hunger”. An important approach towards addressing issues related to nutritional insecurity could be to mainstream the cultivation of crops that are currently grown in marginal areas. These crops are nutritionally dense and have the capacity to grow in soils with poor fertility. FAO has identified 39 nutrition-sensitive and climate resilient crops as “Future Smart Foods”. These include buckwheat, millets, sorghum, grain amaranth, quinoa, taro, swamp taro, yam, sweet potato, grasspea, fababean, cowpea, mungbean, blackbean, ricebean, lentil, horsebean, soybean, drumstick, chayote, fenugreek, snake gourd, pumpkin, roselle, Indian gooseberry, jackfruit, wood apple, linseed, walnut, Nepali butter tree, and Perilla. Buckwheat has attracted considerable interest amongst the global scientific community due to its nutritional and pharmaceutical properties. It is a low input crop whose cultivation has persisted through centuries of civilization in almost every country where cereals were cultivated. Seeds of buckwheat are a rich source of high biological value protein with a balanced amino acid composition. Buckwheat seeds are also rich in dietary fiber, minerals and flavonoids and phenolic compounds. Seeds of buckwheat are a good source of gluten free flour and hence important for patients with celiac disease. Buckwheat seeds have high anti-oxidative properties because of the presence of α -, β - and γ -tocopherols, rutin and quercetin. Rutin has cardioprotective, vasoprotective, anti-hypertensive, anti-inflammation, cytoprotective and anti-diabetic properties. Buckwheat is a short season crop which completes its life cycle in 70-90 days and can grow in a wide range of environmental conditions including

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marginal lands and rocky, poorly tilled soils. The protein content in buckwheat flour is higher than in commonly used cereals such as rice, wheat, millet, sorghum and maize. Buckwheat grain protein is rich in lysine and arginine, which are generally limiting in other cereals. Because of a low Lys/Arg and Met/Gly ratio, buckwheat protein has strong hypolipidemic activity.

While Buckwheat is considered as a healthy food because of its nutraceutical properties, low yield due to seed shattering because of pedicel breaking and heterozygosity due to self-incompatibility as a consequence of dimorphic heterostylism have always remained as major problems in achieving large scale incorporation of this crop in the agricultural portfolio. Even though buckwheat breeding has a difficult history, modern tools of genomics-driven breeding has lead to the identification of QTLs for many quality traits and also the development of several high yielding varieties. The emergence of whole genome sequences of buckwheat, has paved the way for the development of breeding pipelines that integrate phenomics and genomics tools for quality trait improvement in buckwheat. Unlocking the real potential of buckwheat as a super crop by an integrated approach involving cultivation practices, genomics driven breeding and appropriate policy framework of marketing and crop popularization would unleash tremendous gains in achieving the millennium goal of food and nutritional security.

Food security: A complex issue

Food security is a complex issue with many facets. By definition, "Food security" is the measure of availability of food and an individual's abilities to access it. During the early part of the 20th century the "food" debate centred on food security, drawing on the widely accepted concept from the 1996 World Food Summit, which defined food security as a situation "when all people, at all times, have physical, economic and social access to sufficient, safe and nutritious food to meet their dietary needs and food preferences for an active and healthy life". While the original concept of food security focussed on averting hunger, inclusion of the adjective "nutritious" signalled the emphasis of the "quality of food" as an important contributor to food security. More recently, as the nature and severity of malnutrition, especially stunting and wasting in children, become more apparent, the concept of food security has undergone a change to include other factors such as "adequate sanitation and health services", as important contributors towards nutritional security

(FAO 2012). FAO (2018) has noted that despite significant advances made over the years towards achieving the millennium goal of "Zero hunger", globally over 820 million people are still facing food insecurity and at least 2 billion are facing nutritional insecurity. FAO has identified "population gap" and "nutrition gap" as the two major gaps in the current agriculture sector which would constrain the achievement of "Zero hunger" status by 2050. FAO in its report published in the year 2018 has estimated that a 30 per cent increase in global population by 2050 would require a nearly 60 percent increase in food production. Since wheat, rice and maize, grown under current day agriculture, seem to be near to near 80 per cent of their yield potential, it is highly unlikely that increase production of staple crops alone would meet the increased demand for food. Hence reliance on these crops alone would not be sufficient to close the gap between demand and supply. The narrow agricultural portfolio also raises serious questions on how effectively major crops alone can contribute towards achieving the millennium goal of zero hunger.

An important approach towards addressing issues related to nutritional insecurity could be to mainstream the cultivation of crops that are currently grown in marginal areas. Also known as "underutilized/neglected" crops, these crops are grown in areas with poor soil fertility, limited rainfall and limited agricultural inputs. Although the reasons for marginalization or neglect of these crops may vary (Padulosi et al. 2002; Padulosi and Hoeschle-Zeledon 2004), the fundamental role played by these species in income generation (Chadha and Oluoch 2007; Hughes 2009; Mahyao et al. 2009), adaptation to climate change (Padulosi et al. 2011) and food and nutrition security (Frison et al. 2006; Hawtin 2007; Smith and Longvah 2009) is broadly acknowledged. Pulse crops constitute a significant source of protein for the resource-poor population of Asia, Africa and Mediterranean regions of the world. In particular, the underutilized pulses which are also rich in protein, can play a significant role in alleviating the hunger and malnutrition among the poor of the region. Cowpea [*Vigna unguiculata* (L.) Walp.], a short duration crop, can very well fit in the wheat-rice system in the north India and the rice fallows in the central and southern India (Singh 2016). Similarly, grasspea (*Lathyrus sativus* L.) a multi-purpose, climate smart legume crop which can sustain drought, waterlogging and salinity has been supplementing the diet of the resource poor farmers and consumers of South-Asian countries (Rizvi et al. 2016). The minor

pulses, namely, mothbean [*Vigna acountifolia* L. (Jacq.) Marechal], horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] and ricebean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi], which are grown in limited area in dry and hot conditions of semi-arid regions of tropics in South Asia, Africa and Mediterranean regions also

action plan for Plant Genetic Resources for Food and Agriculture” (FAO 2012) and the “Cordoba Declaration” (2013) envisaged a set of timelines for developing policy framework for conservation and sustainable utilization of underutilized/neglected crops (Fig. 1).

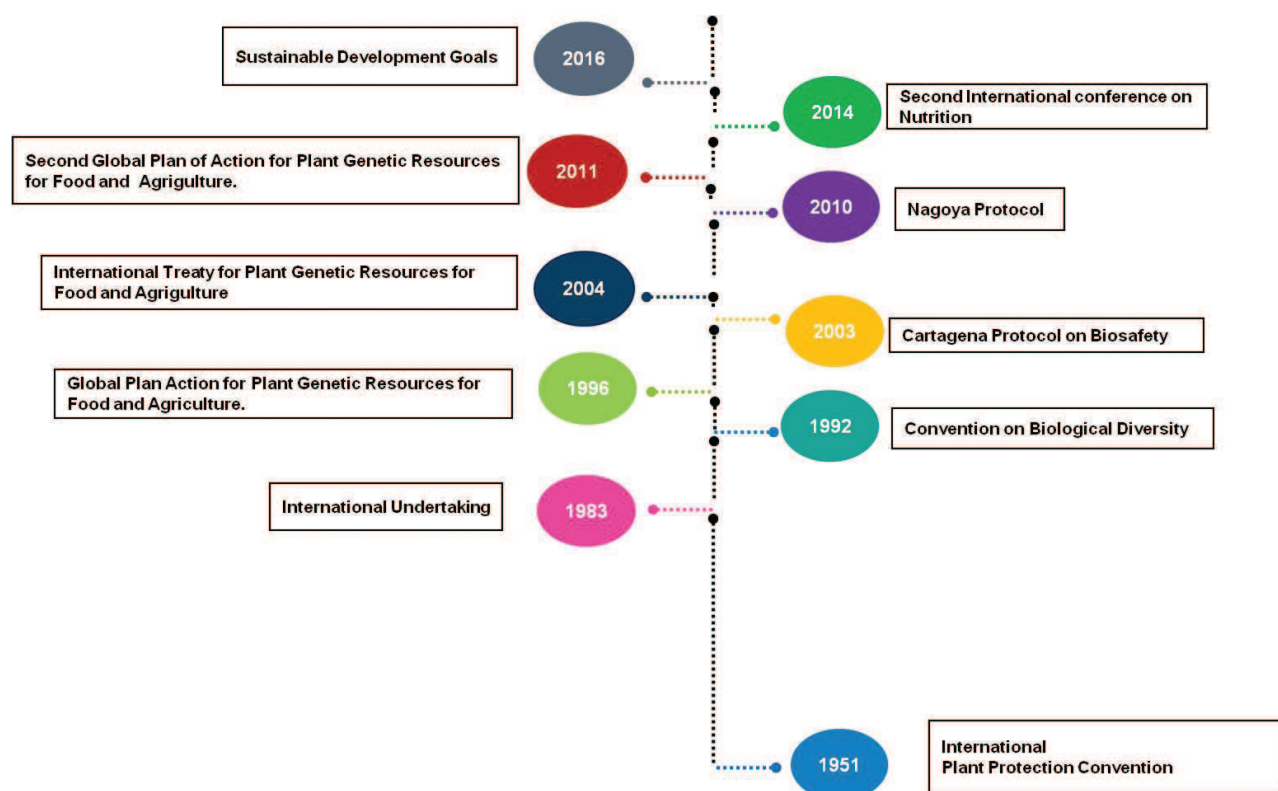


Fig. 1. FAO identified timelines for developing a policy framework for conservation and sustainable utilization of underutilized/neglected crops

plays a great role in supplementing the diet of the resource poor farmers and consumers (Viswanatha et al. 2016).

Many of these crops are nutritionally dense and represent an important source of germplasm for genomics approach driven breeding to design “smart crops” for the future (Padulosi 1999; Boukid et al. 2017). While the importance of underutilized crops in meeting the nutritional requirements of mankind has been recognized by the global scientific community for long (Stamp et al. 2012; Kahane et al. 2013; Khoury et al. 2014; Nyadanu et al. 2016; Rutto et al. 2016), development of a policy framework and its implementation has often been noted as the missing key in promoting their utilization (Noorani et al. 2015). The first “Global action plan for conservation and sustainable utilization of Plant Genetic Resources for Food and Agriculture” (FAO 1996), the second “Global

Role of underutilized crops in nutritional security

In spite of the benefits reaped by mankind because of green, white and blue revolutions, many regions of the world still face the twin challenge of hunger and malnutrition. Currently, over 60 % of the global calorie requirements are met by just three crops - rice, wheat and maize. This is a paradox, considering the fact that more than 4,00,000 vascular plant species are available globally (Royal Botanic Gardens, Kew, UK. State of the Worlds Plants 2016) and about 6000 species have been actively cultivated for human consumption (<http://mansfeld.ipk-gatersleben.de/apex/f?p=185:3>). Significantly, rice, maize and wheat are the staple diet of more than 4000 million people (<http://www.fao.org/3/u8480e/u8480e07.htm>). While these crops are an essential part of various diets, they are devoid of many essential micronutrients, thereby raising health concerns over high dependence on such

crops (FAO 2013). Therefore, achieving the SDG of “Zero hunger” necessitates a substantial increase in the diversity of agricultural portfolios in the coming decades. This would also require incorporation of socially inclusive, economically productive and environmentally sustainable food systems into the agricultural portfolio. While the global averages of crops under agriculture mask the diversity that exists at local or regional levels, it also underlines the need for bringing into agricultural portfolio other climate change-resilient and nutritionally dense crops to meet the demands of the growing population. Although such crops constitute a large component of agrobiodiversity, they are often ignored due to the importance given to maize, wheat, rice and potato. However, policy makers are now increasingly recognizing the fact that securing future food and nutrition security requires mainstreaming the cultivation of the large diversity of crops which have till date remained confined to marginal farming only. The International Network of Food Data Systems (INFOODS) of the Food and Agriculture Organization (FAO) has drawn a list of such crop species available in different parts of the globe (<http://www.fao.org/infoods/infoods/food-biodiversity/en/>). Since many of these species are well adapted to extreme environments their role in the current scenario of climate change becomes extremely important. While these crops continue to be maintained by socio-cultural preferences and user practices, they remain inadequately characterized for their traits. Underutilized crops have the potential to play several roles in achieving the millennium goal of “zero hunger”. These include reducing the risk of over-reliance on very limited numbers of major crops, enhanced nutritional quality of food, preservation of cultural and dietary diversity at local level and increased sustainability of agriculture through a reduction in inputs. Many crops, however, face bottlenecks such as unstable yields, presence of anti-nutritional factors, poor taste or unpleasant texture, low post-harvest shelf life, poorly developed markets and a lack of value-added products which may limit their value. Given the vast repository of underutilized/neglected crops, how can those with enough potential to justify investing the very limited resources available for their improvement best be identified? One possible strategy is to identify crops with trait values that exceed the equivalent trait in fully domesticated crops and have the potential to achieve high value markets due to their quality characteristics. Crops for the Future, a global organization formed following the merger between

International Centre for Underutilized Crops and Global Facilitation Unit for Underutilized Species has identified *Chenopods*, *Fagopyrum*, millettes, *Perilla* and grain amaranth, as some of the potential crops for mitigating food and nutritional insecurity of the growing population. *Chenopodium quinoa*, *Fagopyrum esculentum*, *Fagopyrum tataricum*, pearl millet (*Pennisetum glaucum*), Finger millet (*Eleusine coracana*), proso millet (*Panicum miliaceum*) and foxtail millet (*Setaria italica*) are currently a part of the agricultural portfolio under subsistence farming in many regions of the globe. These crops do not require high agricultural inputs, can be grown on marginal lands and easily intercropped or rotated with other staple crops. Since these crops are adapted to marginal conditions, they can make production systems more sustainable and climate resilient. *Chenopodium quinoa*, *Panicum miliaceum*, *Setaria italica* have already gained large scale acceptance in the agricultural portfolio. While high nutritional value, palatability and cooking qualities were important factors in greater acceptability of quinoa as a food crop, extensive research efforts aimed at (i) development of core collections, (ii) quality trait assessment and improvement (iii) development of seed production systems, (iv) development of processes for post harvest processing including value addition and creation of supportive policy framework accelerated the evolution of *Chenopodium quinoa* as a commercially important food crop. FAO (2018) has highlighted the fact that while potential future super crops such as quinoa, buckwheat and millets contribute only a small portion to the food basket at the National level, their contribution towards nutritional security at household levels in small and marginal farming communities is quite high. Buckwheat and quinoa are also used extensively as functional foods by elite communities. While the consumption of buckwheat has shown a slow but consistent increase over the years, limitations of investment in research and development of processes for post harvest processing, including value addition, have hampered any large scale incorporation of buckwheat into the agricultural portfolio as a super crop. Domestication of most of the current day staple crops started 8,000-10,000 years ago and was followed by a process of adaptation and optimization (Harlan 1992). Subsequently selection, breeding, and application of agronomic practices have allowed these species to produce more stable or greater yields than when they were grown near its centre of domestication. It is noteworthy that no such processes of adaptation, improvement, and optimization of agronomic management practices have

been applied to many of the underutilized crops which, to a large extent, have remain confined to their centres of origin. It would therefore be logical to assume that, based on a strategic mix of improved management/agronomy and selective breeding; it is possible to improve upon the existing traits of at least a few of the underutilized crops which have the potential to transform into super crops.

Buckwheat (*Fagopyrum* spp.), is an important non-poaceous pseudocereal belonging to the family Polygonaceae. Out of the nearly 30 species belonging to the genus *Fagopyrum*, only two species viz., *Fagopyrum esculentum* (common buckwheat) and *Fagopyrum tataricum* (tartary buckwheat) are cultivated. While *F. esculentum* is cultivated primarily

in the temperate regions of the northern hemisphere, *F. tataricum* is principally a crop of high altitudes (Rana 2004). Buckwheat is cultivated mainly in the northern hemisphere from Eastern Europe to Japan. Buckwheat is also cultivated as a subsistence crop under low agricultural inputs in North America and Brazil (Fig. 2a). In India, buckwheat is cultivated along the Himalayan foot hills from Ladakh in the North to Arunachal Pradesh in East (Fig. 2b). The importance of buckwheat as a nutraceutical can be ascertained from the fact that it possesses high value biological proteins, antioxidants, essential vitamins and minerals. Buckwheat is also rich in dietary fiber and flavonoids such as rutin, which is known for its antioxidant, vasoprotective, antihypertensive, and cardioprotective properties (Krkoskova and Mrazova 2005; Alamprese

Table 1. List of known wild and cultivated species of the genus *Fagopyrum*

S.No.	Latin name	Group	Ploidy	Mating system*	Reference
1	<i>F. esculentum</i>	Cymosum	2n = 2x = 16	SI	Moench (1794)
2	<i>F. esculentum</i> ssp. <i>Ancestralis</i>	Cymosum	2n = 2x = 16	SI	Ohnishi (1991)
3	<i>F. tataricum</i>	Cymosum	2n = 2x = 16	SC	Gaertner (1791)
4	<i>F. cymosum</i>	Cymosum	2n = 2x = 16	SI	Meisner (1857)
5	<i>F. homotropicum</i>	Cymosum	2n = 2x = 16	SC	Ohnishi (1998a)
6	<i>F. pilus</i>	Cymosum	2n=4x=32	SI	Chen (1999)
7	<i>F. megaspartanum</i>	Cymosum	2n = 4x = 32	SI	Chen (1999)
8	<i>F. zuogongense</i>	Cymosum	2n = 2x = 16	SC	Chen (1999)
9	<i>F. hailuogouense</i>	Cymosum	2n = 4x = 32	SC	Zhou et al. (2015)
10	<i>F. wenchuanense</i>	Cymosum	2n = 2x = 16	SC	Shao et al. (2011)
11	<i>F. longzhoushanense</i>	Cymosum	2n = 2x = 16	SC	Wang et al. (2017)
12	<i>F. urophyllum</i>	Urophyllum	2n = 2x = 16	SI	Gross (1913)
13	<i>F. stative</i>	Urophyllum	2n = 2x = 16	SI	Gross (1913)
14	<i>F. gilesii</i>	Urophyllum	2n = 2x = 16	SI	Hedberg (1946)
15	<i>F. lineare</i>	Urophyllum	2n = 2x = 16	SI	Haraldson (1978)
16	<i>F. gracilipes</i>	Urophyllum	2n = 4x = 32	SC	Diels (1901)
17	<i>F. leptopodum</i>	Urophyllum	2n = 2x = 16	SI	Hedberg (1946)
18	<i>F. densovillosum</i>	Urophyllum	2n = 2x = 16	SC	Liu et al. (2008a)
19	<i>F. tibeticum</i>	Urophyllum	2n = 6x = 48	INA	Tian et al., (2011)
20	<i>F. pleioramosum</i>	Urophyllum	2n = 2x = 16	SC	Ohnishi (1998a)
21	<i>F. callianthum</i>	Urophyllum	2n = 2x = 16	SC	Ohnishi (1998a)
22	<i>F. capillatum</i>	Urophyllum	2n = 2x = 16	SI	Ohnishi (1998a)
23	<i>F. jinshaense</i>	Urophyllum	2n = 2x = 16	SI	Ohsako et al. (2002)
24	<i>F. gracilipedoides</i>	Urophyllum	2n = 2x = 16	SI	Ohsako et al. (2002)
25	<i>F. rubifolium</i>	Urophyllum	2n = 2x = 16; 2n=4x=32	SC	Ohsako and Ohnishi (1998)
26	<i>F. macrocarpum</i>	urophyllum	2n = 2x = 16	SC	Ohsako and Ohnishi (1998)
27	<i>F. crispatifolium</i>	urophyllum	2n = 4x = 32	SC	Liu et al. (2008)
28	<i>F. pugense</i>	urophyllum	2n = 2x = 16	SC	Tang et al. (2010)
29	<i>F. qiangcai</i>	urophyllum	2n = 2x = 16	SC	Shao et al. (2011)
30	<i>F. luojishanense</i>	urophyllum	2n = 2x = 16	SC	Hou et al. (2015)



Fig. 2. (a) World map showing areas (filled with dots) where buckwheat is cultivated. (b) Areas under buckwheat cultivation in India

et al. 2007; Gimenz-Bastida and Zielinski 2015; Ganeshpurkar and Saluja 2017). Buckwheat extracts especially those from leaves have high anti-oxidative properties because of the presence of α -, β - and γ -tocopherols, rutin and quercetin. However, low yields due to seed shattering and heterozygosity due to self-incompatibility as a consequence of dimorphic heterostylism have always remained a major problem in common buckwheat. On the other hand, tartary buckwheat is an annual self-pollinated species. Seeds of tartary buckwheat have strongly adhering hull. The dough prepared from flour of tartary buckwheat is bitter in taste because of presence of quercetin, which is one of the hydrolysis products of rutin as a consequence of activation of rutinoidase upon addition of water (Suzuki et al. 2014; Suzuki and Morishita 2016). In spite of the self-compatible nature and high rutin

Table 2. Comparison of nutritional composition of buckwheat with rice, wheat and maize*

Nutrients	Crop			
	Buckwheat	Rice	Wheat	Maize
Proximate composition (100 gm grain⁻¹)				
Energy (Kcal)	355.0	345.0	346.0	365.0
Crude protein (%)	13.3	6.8	11.8	9.4
Total carbohydrates (g)	72.9	78.2	71.2	74.3
Total fibre (%)	17.8	4.5	12.5	7.5
Fat (g)	7.4	1.5	2.5	4.7
Moisture (%)	11.0	13.7	12.8	10.4
Minerals and trace elements (mg per 100gm grain⁻¹)				
Calcium	110.0	10.0	38.0	7.0
Iron	4.0	0.7	3.9	2.7
Magnesium	390.0	65.0	120.0	127.0
Phosphorus	330.0	160.0	298.0	210.0
Manganese	3.4	0.5	2.3	1.9
Zinc	0.8	1.3	2.9	2.3
Potassium	450.0	268.0	340.0	287.0
Essential amino acids (mg 100mg protein⁻¹)				
Lysine	5.7	3.9	2.3	2.7
Methionine	2.3	1.7	1.2	1.9
Tryptophan	2.0	1.3	2.4	0.5
Leucine	5.9	8.1	6.3	12.4
Vitamins (mg 100gm grain⁻¹)				
Thiamine	3.3	0.41	0.47	0.4
Ribofavin	10.6	0.02	0.09	0.2
Niacin	18.0	5.80	8.20	3.6
Vitamin E (Alpha Tocopherols)	40.0	0.10	1.40	—

* Source: Campbell (1997); Tomotake et al. (2006); McKevith (2004)

content, tartary buckwheat has not received much favor for cultivation because of the tightly adhering hull and bitter taste. Some of the other limitations in buckwheat such as unstable yields, indeterminate growth habit, lodging, presence of allergenic compounds restrict its popularity amongst the farmers.

Buckwheat as a potential super crop

Fagopyrum is a small genus comprised of about 30 species. While traditionally, *Fagopyrum* has been known to comprise about 19 species (Ohsako et al. 2002), during the last 10 years, a number of species have been added to this genus, thereby taking the total number of species to 30 (Table 1). The genus is comprised of both perennial as well as annual species with diploid ($2n = 2x = 16$) as well as tetraploid ($2n = 4x = 32$) cytotypes. Whereas most of the wild species of the genus *Fagopyrum* have shown narrow distribution along the south-eastern edge of Qinghai-Tibetan Plateau (Ohnishi 1998a), common buckwheat is cultivated extensively in the mountainous regions of India (Fig. 3), China, Russia, Ukraine, Kazakhstan, parts of Eastern Europe, Canada, Japan, Korea and Nepal. Cultivation of tartary buckwheat is, however, mainly confined to the hilly and mountainous regions of China and the Himalayas (Zhou et al. 2018). Buckwheat is a gluten-free grain crop and hence forms an important component of diet for patients with celiac

disease (Mazza and Oomah 2005; Sytar et al. 2016). From a nutritional perspective, buckwheat is an excellent source of high-quality protein, dietary fiber, essential amino acids, vitamins and flavonoids (Table 2). Compared to cereals, seeds of buckwheat are a rich source of magnesium, calcium, zinc, iron, copper, phosphorus, vitamin A, B2, B6, E, C, niacin, folic acid and flavonoids such as kaempferol, rutin and quercetin (Pomeranz 1983; Steadman et al. 2001). Buckwheat seeds have been reported to accumulate up to 3.30 mg 100 gm⁻¹ of catechin, 20.5 mg 100 gm⁻¹ of epicatechin and 1.27 mg 100 gm⁻¹ of epicatechin gallate (Danila et al. 2007). Many of the therapeutic properties of buckwheat have been attributed to the high flavonoid, more specifically rutin, content of its seeds (Table 3). Rutin (3,3',4',5,7-pentahydroxy-flavone-3-rhamnoglucoside) has several health benefits, which include modulation of hypercholesterolemia, prevention of oxidative damage in aortic endothelial cells by lowering nitrotyrosine immune-reactivity, anti-platelet aggregation prevention of cognitive impairments like Alzheimer's disease by ameliorating oxidative stress and prevention of splenocyte apoptosis (Kreft et al. 2002; Javed et al. 2012). Rutin is also known to have cardioprotective, anti-inflammation, cytoprotective and antidiabetic properties (Ganeshpurkar and Saluja 2017; Calderon-Montano et al. 2013). It has been reported to inhibit

Table 3. Nutraceutical properties of buckwheat

Phytochemical compound	Nutraceutical properties	Reference
Protein (13S Globulin, 8S vicilin, 2S albumins)	Nutritionally balanced amino acid composition. High proportion of essential amino acids, especially lysine, lowers hepatic and plasma cholesterol levels	Metzger et al. (2007) Milisavljević et al. (2004), Radović et al. (1999).
Carotenoids (β -carotene, lutein)	Strong antioxidant potential, Amelioration of oxidative stress	Tuan et al. (2013)
Flavonoids (Rutin, quercetin, vitexin, isovitexin, kaempferol)	Ameliorating oxidative stress, modulation of hypercholesterolemia, prevention of oxidative damage in aortic endothelial cells by lowering nitrotyrosine immune-reactivity, antiplatelet aggregation, prevention of cognitive impairments like Alzheimer's disease, prevention of splenocyte apoptosis. Anti-inflammatory, cytoprotective and antidiabetic. Inhibition of transcription of more than 20 genes coding for critical pro-inflammatory factors such as TNF- α , IL-1 and IL-8.	Kreft et al. (2002), Jiang et al. (2007). Javed et al. (2012)
Dietary fibre	Reduction in serum cholesterol and glucose levels	Slavin (2013)
Micronutrients and trace elements, vitamin A, B2, B6, E, C, niacin, folic acid	Cofactors of various enzymes	Zheng et al. (2011)
Tocopherols	Antioxidants	Przybylski et al. (1998)
Fagopyritols	Fagopyritol A1 is an active constituent in insulin signaling is therefore helpful in treatment of type II diabetes and polycystic ovarian syndrome	Janet et al. (2005)

the transcription of genes coding for critical pro-inflammatory factors such as TNF- α , IL-1 and IL-8 (Choi et al. 2013). Due to its ability to inhibit COX-2 inhibition, rutin could possibly serve as an alternative to aspirin. The flavone C-glycosides, anthocyanins, proanthocyanins and tocopherols make buckwheat seeds a good source of antioxidants for human consumption. Rutin has been reported to represent 54, 29, and 82% of the total flavonoid content in *F. esculentum*, *F. homotropicum*, and *F. tataricum*, respectively (Li and Zhang 2001; Jiang et al. 2007). Amongst the two cultivated species of buckwheat, tartary buckwheat (IC-421601) accumulates upto 1.133% rutin in its seeds, which is five-fold higher than that of common buckwheat. Tartary buckwheat also contains higher levels of quercetin and rutinase activity in its seeds than that in common buckwheat (Suzuki and Morishita 2016). However, quercetin, which is a hydrolysis product of rutin as a consequence of rutinase activity, gives a strong bitter taste to dough prepared from buckwheat flour. Bai et al. (2015) have demonstrated the role of lectins present in seeds of tartary buckwheat in the induction of apoptosis in human leukaemia cells (U937) in a dose dependent manner, thereby indicating its role in reducing the proliferation of spontaneous and induced tumors. Likewise, seven phenylpropanoid glycosides isolated from the extracts of *F. tataricum* roots have been demonstrated to have potential cytotoxic effects on several cancer cell lines including A-549, HCT116, ZR-75-30 and HL-60, thereby indicating potential anti-cancer properties of these glycosides (Zheng et al. 2012).

Buckwheat seeds contain 12-15 per cent protein, which is comparable with major cereals (Eggum et al. 1980; Bonafaccia et al. 2003; Suzuki et al. 2020). The major seed storage protein in buckwheat is a 13S globulin which contains 5.9% lysine and 2.3% methionine (Rout and Chrungoo 1996; Bharali and Chrungoo 2003; Bonafaccia et al. 2003). The protein also has significantly lower ratios of lysine to arginine and methionine to glycine than that of other plant proteins (Krkošková and Mrázová 2005). Such rare plant proteins are widely recognized for their cholesterol-lowering effects in blood and serve as a healthy food for patients suffering from hypercholesterolemia (Metzger et al. 2007). Carroll and Hamilton (1975) have ascribed the cholesterol lowering properties of buckwheat proteins to the ratios of lysine to arginine and methionine to glycine as these amino acids are involved in the regulation of the formation of

hepatic low density lipoproteins (LDL). In addition to 13S (280kD) globulin, buckwheat seeds have also been reported to contain 8S (57-58kD) vicilin (Milisavljević et al. 2004) and 2S (8-16kD) albumins (Radovic et al. 1999). Whereas globulins comprise 70% of the total seed protein fraction, albumins, glutelin and prolamins respectively constitute 12.5%, 8.0% and 2.9% of the total protein content in the seeds (Radovic et al. 1999; Ikeda 2002). With 92.3% of the value of non-fat milk solids and 81.4% of the whole egg solids, buckwheat seed proteins are amongst the best known sources of high biological value proteins in the plant kingdom (Pomeranz and Robbins 1972). Even though buckwheat seeds are a good source of high value protein, they also contain certain anti-nutritional factors such as protease inhibitors, which lower the digestibility of buckwheat proteins (Farrell 1978; Eggum et al. 1980; Ikeda et al. 1986; Kreft et al. 2020). Germination of buckwheat seeds has been shown to result in a significant reduction in the activity of protease inhibitors (Kreft 1983). This makes buckwheat sprouts a good source of nutrition and antioxidants for healthy growth.

Buckwheat flour and groat are used for preparation of a wide variety of dishes. While in Asia, buckwheat flour is used for the preparation of noodles, dumplings and pancakes, in Europe, particularly Eastern Europe, roasted dehulled buckwheat seeds are cracked into coarse granules, known as 'kasha' which is used in the preparation of porridge and soups. Buckwheat flour has been blended with other flours to produce multigrain pasta, energy bars, waffles, cereal flakes, bagels, and bread. The crop stands apart from other cereals or plant sources as it contains immensely more nutraceuticals that can ameliorate many chronic and life style based health problems. Rutin-rich herb tea is an extensively consumed buckwheat herbal product in Japan (Fabjan et al. 2003). Buckwheat honey is highly nutritious honey made by bees who collect nectar from buckwheat flowers. The honey contains high amounts of flavonoids and other phenolic components and is known to protect human blood lipoproteins against oxidation more effectively than sucrose analogs (Gheldof et al. 2003).

Growth, Development and agronomic attributes of buckwheat

Buckwheat is a short season crop which completes its life cycle in 70-90 days (Campbell 1997). Although buckwheat can grow in wide range of environmental conditions including marginal lands and rocky, poorly

tilled soils, it thrives well on sandy soils having acidic pH (Jung et al. 2015). The crop is sensitive to high temperatures and dry winds especially during flowering. Temperature $>30^{\circ}\text{C}$ during flowering has been reported to cause abortion of ovule, embryo sac malformation, fruit desiccation and poor yield (Gang and Yu 1998; Drazic et al. 2016). Sowing of buckwheat requires advance preparation of the land by removal of weeds to increase soil porosity and allow for proper drainage. In India, the sowing of buckwheat generally begins with the onset of monsoon and continues up to August (Hore and Rath 2002). The optimum sowing time of buckwheat in different buckwheat growing regions of India is given in Table 4. Buckwheat sowing

Table 4. Sowing time of buckwheat in different parts of India*

Region	Sowing time
North-Western hills	June-July (Rainy season); March-April (spring season)
North-Eastern hills	August-September including Assam
Sikkim	October-November
Nilgiri hills(TamilNadu)	April-May
Plani hills (Tamil Nadu) and Kerala	January
Chhattisgarh	September-November

Source: Joshi (1999); Babu et al. (2016)

is carried out in line as well as in broadcast mode (Björkman 2008). A seed rate of 20kg ha^{-1} has been found to be the best for optimum growth and yield. Campbell and Gubbels (1978) have recommended a seed sowing rate of $35\text{-}40\text{kg ha}^{-1}$ for optimum yield. Under optimum climatic conditions (soil temperature of $18\text{-}22^{\circ}\text{C}$), seedlings emerge in 4-5 days and plants show profuse vegetative growth from 3rd to 6th week. Flowering starts between the 6th-7th week after sowing and the seeds start to mature in the 10th-12th week after sowing. While common buckwheat has been reported to give maximum yield under rain fed conditions and planting geometry of $30\text{ cm} \times 10\text{ cm}$ at a depth of 4-6 cm (Babu et al. 2016b; Hulihalli and Shantveerayya 2018), tartary buckwheat has been reported to give maximum yield under planting geometry of $40\text{ cm} \times 10\text{ cm}$ at a depth of 4-6 cm (Rana et al. 2005). Buckwheat has a very low nutrient requirement. Campbell and Gubbels (1978) have recommended 47kg N , 22kg P and 40kg K ha^{-1} for

obtaining optimum yields. However, Phogat and Sharma (2000) have a recommended 50kg N , 20kg P and 40kg K or $1500\text{-}2000\text{kg FYM ha}^{-1}$ for obtaining optimum yields in Indian Himalayan foothills. Plants grown under high dose of soil N have been reported to exhibit lodging which results in low yield. Higher dose of P has, however, been shown to alleviate this effect (Inamullah et al. 2012). Buckwheat is a crop of indeterminate growth habits. Hence choosing the right time for harvesting has always remained a question mark. Farooq et al. (2016) have suggested harvesting of the crop when 70-75% of the seeds have reached physiological maturity. This stage corresponds with the start of seed shattering in this crop.

Although buckwheat finds an important place in the basket of functional foods, one of the major problems associated with its cultivation is yield instability due to flower abortion and seed shattering. Seed shattering in buckwheat has been ascribed to presence of brittle and weak pedicles, a trait controlled by two complementary dominant genes, *Sht1* and *Sht2* (Matsui et al. 2004) and the formation of an abscission layer across the brittle pedicle (Wang et al. 2005). Tetraploid buckwheat has been reported to show less shattering than the diploid forms (Hayashi 1992; Fujimura et al. 2001). However, the reasons for differences in extent of seed shattering between diploid and tetraploid forms are not clear. Moreover, seed shattering has been shown to exhibit a linked inheritance with the number of vegetative nodes on the main stem. Using a wide crossing program between *Fagopyrum homotropicum* and *F. esculentum*, Wang et al. (2005) have demonstrated that *F. esculentum* possesses recessive alleles at two or three loci that affected the development of the abscission layer. The F_1 interspecific hybrids expressed seed shattering, indicating the dominance of shattering trait over non-shattering trait. The F_2 populations from individual F_1 plants segregated in the ratios of 3:1, 9:7, and 27:37, supporting the control of shattering by three complementary dominant genes. These results established the multiple gene control system in defining shattering in common buckwheat. However, non-shattering populations of common buckwheat carried only a single recessive gene, thereby conferring resistance to shattering. In the case of *F. tataricum* at least two such genes have been reported to control shattering. Mutation of either of these genes led to a non-shattering phenotype. Currently, several varieties of shattering resistant buckwheat are reported. Suzuki et al. (2012) have reported a non-shattering

green flower mutant (W/SK86GF) from Russian populations of buckwheat. This mutant is considered a useful genetic resource of seed-shattering resistance because of strong pedicles. Genetic analysis of morphological characters has revealed that homostyly, shattering, and acute achenes are controlled by different dominant single genes and that the shattering gene has a 7.81% linkage to the homostyly locus (Li and Chen 2014).

In addition to seed shattering, one of the major causes of low yields in common buckwheat is flower abortion. Woo et al. (2004) have identified (i) abnormal flower morphogenesis resulting in undersized and sterile gynoecia, (ii) early failure of seed set in pollinated flowers with normal gynoecia due to incompatibility reactions, and (iii) indeterminate growth habit caused by the morphogenetic processes that are involved in the establishment of reproductive structures as some of the probable factors responsible for flower abortion in *F. esculentum*. Taylor and Obendorf (2001) have reported the absence of seed set in 35-97% flowers of common buckwheat even in the absence of any limitation due to pollination. They ascribed the failure to form seeds to either male/female sterility or embryo abortion. In view of high (>90%) viability of pollen, Cawoy et al. (2006) and Chen et al. (2007) concluded that male sterility could only be considered a marginal factor in low seed set in common buckwheat. Their arguments pointed towards deficiency of female reproductive structures as a factor influencing seed set in common buckwheat. According to Cawoy et al. (2007), the occurrence of undersized and sterile gynoecia is dependent on the position of the flower in a raceme, the phenomenon being more frequent in distal than in proximal cymes. In their endeavor to differentiate between early abortion of embryo and sterility of female organs, Taylor and Obendorf (2001) observed that early (24 h post pollination) abortion of embryo occurred only in 10% of the pollinated flowers. They concluded that early abortion could not be considered as the important limiting factor which affected seed set in common buckwheat. While 20% of flowers showed a non-viable mega-gametophyte at anthesis, 30% of flowers at the beginning and 60% at the end of flowering showed a normal embryo sac without fertilization after 24 hours of pollination. According to Taylor and Obendorf (2001), this could be explained by a wrong alignment of the canal of the style and the micropyle. Cawoy et al. (2007) ascribed this aberration, which is dependent on the position of flower in the raceme as well as the

occurrence of undersized gynoecia, to altered floral morphogenesis in response to a limitation of resource availability in a developing cyme. They suggested that the distal flowers faced higher resource limitation than the proximal ones because of a decrease in the diameter of sieve-tube cells. While excision of selected inflorescences, leading to alteration of source/sink ratio, enhanced the number of flowers in an inflorescence, the increased number of flowers could not fully compensate the loss of racemes. Despite the increase of resource availability, the excision did not change the final distribution between wilted pollinated flowers with a normal sized gynoecium, flowers with an undersized gynoecium, aborted seeds and ripe seeds. These observations led Cawoy et al. (2007) to hypothesize the occurrence of other internal mechanisms, besides assimilate distribution, in determining the fate of a flower in an inflorescence.

Genetic resources of buckwheat in India

Buckwheat harbors a wide range of diversity. More than 10,000 diverse accessions of buckwheat are being maintained in different repositories across the globe and nearly half of them are maintained in gene banks located in East and South Asian countries (Zhou et al. 2018). In the Indian subcontinent, buckwheat is cultivated in Himalayan foothills from Ladakh in north to Arunachal Pradesh in the east. Most of the cultivation of buckwheat in India has been reported from Ladakh, Gurez valley (J&K), Pangi, Lahul and Pin valleys (Himachal Pradesh), Pindari and Darma valleys (Uttarakhand), Cooch Behar, Darjeeling (West Bengal), Lachen, Lachung (Sikkim), Tawang, Bomdila and Dirang (Arunachal Pradesh). The crop is also cultivated to a small extent in Nilgiris and Palani hills in the South (Rana et al. 2012). Depending on the region, the crop is known as kutu (Hindi), Phaphar (Garwhali) and Oggal (Kumaoni). Out of all the species of buckwheat reported in literature, 7 species viz. *F. esculentum*, *F. emarginatum*, *F. tataricum*, *F. tataricum* var. *himalianum*, *F. kashmirianum*, *F. giganteum* and *F. cymosum* have been reported from Indian Himalayas. While the Western Himalayan species, *F. kashmirianum* (Munshi 1982) has been shown to be morphologically akin to *F. tataricum* var. *himalianum* (Gohil et al. 1983; Farooq and Tahir 1987), *F. emarginatum* has been treated as conspecific with *F. esculentum* (Arora and Engels 1992). *F. tataricum* ssp. *annum* is more common in the Eastern Himalayas and *F. tataricum* ssp. *potanini* in Tibet, Kashmir Himalayas and northern Pakistan (Ohnishi 1989, 1991, 1992). The geographical heterogeneity of Indian

Himalayas offers a great variability in various traits of economic importance in the genus *Fagopyrum*. Misra et al. (2019) have recorded significant variations in agronomically important traits including days to 50% flowering, days to 80% maturity, primary branches plant⁻¹, plant height and 100-seed weight. While 1055 accessions of the crop are being maintained *ex situ* in various gene banks of National Bureau of Plant Genetic Resources (NBPGR), 837 accessions are maintained for long term storage at the National Gene Bank of NBPGR. Apart from this, more than 300 working collections are maintained as field collections by other organizations such as the G. B. Pant Agricultural University, Hill Campus, Ranichauri, Vivekananda Parvatiya Krishi Anusandhan Shala, Almora, Regional Stations of Agricultural University, Palampur at Sangla and Kukumseri, North Eastern regional station of NBPGR at Umiam (Meghalaya), North Eastern Hill University, Shillong and University of Kashmir, Srinagar. The entire collection has been evaluated for various agronomic traits such as cyme length, days to maturity, yield, seed size, seed weight,

tolerance to lodging, resistance to powdery mildew and leaf spot and promising accessions have been identified (Table 5). Multi-location testing of 13 elite varieties, carried out by Indian Council of Agricultural Research (ICAR) under an All India Coordinated Research programme on underutilized crops, has led to release of 5 high yielding varieties of buckwheat (Table 6). Assessment of genetic variations amongst different accessions of buckwheat across the Himalayas have revealed a higher level of inter-population variability with a higher heterozygosity in *F. esculentum* landraces from central Himalayas than that in the Western and Eastern Himalayas. Characterization of the germplasm has led to identification of variability in various agronomic traits such as plant type, leaf architecture, flower colour, days to maturity, grain morphology, resistance to diseases (leaf spot caused by *Cercospora fagopyri* and powdery mildew caused by *Erysiphe polygoni*) and tolerance to lodging (Joshi and Paroda 1991; Rana 2004).

Table 5. Agronomic traits of some promising accessions of buckwheat germplasm*

Accession(s)	Agronomic trait	value
<i>Fagopyrum esculentum</i>		
IC265491, IC27260, IC42401, IC341631, IC318859, EC125357, EC58322	No. of primary branches	>8.0
IC265491, IC27260, IC42401, IC341631, IC318859, EC125357, EC58322	Cyme length (cm)	>6.5
EC323731, EC323729, VL7, IC329568, IC381130, IC13412, IC16558, IC42411, IC24301, EC323731, EC323729	Days of maturity (no.)	<80
IC188701, IC16550, IC204085, IC329404 IC467923, IC447689, IC540858, EC218740	Seed yield plant ⁻¹ (gm)	>22.0
EC58322, EC18864, EC125397, EC125940, IC360829, IC360846, IC361359, EC216685, EC213682	Seed Weight (gm 100 seeds ⁻¹)	>2.4
EC323724, EC323729, VL7, PRB1, EC125938, IC261963, IC341674, IC109729	Seed Protein content (mg 100gm ⁻¹)	>12.2
<i>Fagopyrum tataricum</i>		
IC107964, IC107961, IC107627, IC360826, IC547549, IC547346, IC547396, IC361635	No. of primary branches	>8.0
IC107964, IC107961, IC107627, IC360826, IC547549, IC547346,	Cyme length (cm)	>7.5
IC24299, IC24301, IC28756, IC26755, IC329568 IC381130, IC13412, IC16558, IC42411	Days of maturity (no.)	<75
IC18869, IC18889, IC107964, IC107965, IC18869, IC18889, IC318859, IC329401	Seed yield plant ⁻¹ (gm)	>15.5
IC201481, IC243184, IC318859, IC381077, IC381098, IC381049, IC58322, EC323724	Seed Weight (gm 100 seeds ⁻¹)	>2.4
IC108499, IC108500, IC128519, IC107989, IC382287, IC310104, IC341671	Seed Protein content (mg 100gm ⁻¹)	>14.0
IC42421, IC14889, IC14253, IC107962, IC310045	Rutin content (µg gm ⁻¹ seed)	>17.0

Table 6. Agronomic traits of varieties of buckwheat developed and released by different research Institutes in India[‡]

Variety	Species	Plant height (cm)*	Dry matter (gm plant ⁻¹)*	Days taken to 50 % flowering	Yield (qt ha ⁻¹)	No. of primary branches plant ⁻¹	No. of secondary branches plant ⁻¹
Himpriya	<i>Fagopyrum tataricum</i>	99.9	21.4	55.0	18.80	2.63	5.25
Himgiri	<i>Fagopyrum tataricum</i>	92.9	18.2	55.0	17.80	2.63	5.58
Sangla B1	<i>Fagopyrum tataricum</i>	89.9	19.0	57.5	15.60	2.13	4.71
PRB 1	<i>Fagopyrum esculentum</i>	93.1	23.1	56.0	20.00	2.75	5.75
VL7	<i>Fagopyrum esculentum</i>	101.8	20.1	53.5	18.40	2.88	5.62
SE±		1.11	0.34	0.20	0.38	0.12	0.20
CD (P _{0.05})		3.23	0.98	0.58	1.12	0.35	0.59

[‡]Source: Paul and Nandi (2020); *60 days after sowing

In spite of a large number of accessions of buckwheat available globally and the development of a key for species identification in buckwheat (Ohnishi 1995), there appears to be little agreement on important traits to be documented for characterization of different accessions of the crop. Preparation of a list of Buckwheat Descriptors (Engels and Arora 1994) has been the only major step forward in the development of passport data on this crop. Since most of the traits used as descriptors can be influenced by the environment, the data has not led to the development of reliable morphological markers for determination of diversity in buckwheat. Analysis of morphological variations among 32 accessions/ cultivars of different species of *Fagopyrum* from Indian Himalayas using 10 diagnostic morphological traits has established the accession IC13145, which was identified as "*F. himalayanum*", as conspecific to *F. esculentum* (Rout and Chrungoo 2007). Similarly IC13141, which was identified as *F. tataricum* (Joshi and Paroda 1991), appears to be an accession of *F. esculentum* (Rout and Chrungoo 2007). The similarity matrix based on ten morphological traits among the 32 accessions of *Fagopyrum* revealed a range of coefficient of similarity from 0.10 to 1.0, thereby indicating the diverse nature of collected germplasm. Based on cluster analysis using Ward's minimum variance, Senthilkumaran et al. (2008) have classified populations of buckwheat from North-Western Himalayas into four major groups which showed a fair degree of association with geographical location. Their results have shown a higher level of inter-population variations in accessions from Uttaranchal than that from Himachal Pradesh. On the basis of their observations on variations in SDSPAGE profiles of endosperm proteins, Rout and Chrungoo (2007) have argued for a closer relationship between that *F. esculentum* and *F. tataricum*. Yang et

al. (2008) have supported this contention. Rout and Chrungoo (2007) have emphasized that the current practice of accessioning based on IPGRI defined descriptors could lead to erroneous cataloguing. Rout and Chrungoo (2007) could not detect any variations in the SDS PAGE profiles of endosperm proteins in the "Sangla" group of cultivars, which belong to tartary buckwheat and are cultivated exclusively in Western Himalayas, and IC412663, which is a tartary buckwheat from Eastern Himalayas. Principal component analysis carried out on a combination of variations in qualitative morphological traits, SDSPAGE profiles of endosperm proteins and RAPD analysis supports the taxonomic treatment of the three species and the relationship within accessions within the genus *Fagopyrum* (Rout and Chrungoo 2007). One of the significant features revealed by PCA was the emergence of VL7 and EC323729 as accessions distinct from other accessions of the same species. While VL7 is a high yielding and early maturing cultivar released by VPKAS, Almora, EC323729 is an East European accession. Rout (2007) has reported the exclusive presence of a 41/39 kDa duplex of proteins in SDS-PAGE profile of endosperm proteins of the cultivar VL7, which is a high yielding and early maturing variety, suitable for cultivation in the middle hills. Joshi and Rana (1995a) have identified IC13141, IC13374, IC42430, IC18869, IC136804, IC36914, IC42403 and NC64039 as the most diverse and promising lines of buckwheat in India. They have also identified IC13374, IC13411, Kulu Gangri, and VL7 as high yielding and most stable lines (Joshi and Rana 1995b). Whereas IC341671, EC323729 and EC323731 mature in 60-65 days, seeds of IC329457 and IC341679 have a loose hull that can be removed just by rubbing with hands (Rana et al. 2012).

Genomics driven breeding of buckwheat

Even though the cultivation of buckwheat has been going on for long time, its breeding has a difficult history. While a major focus of buckwheat research has been the identification and characterization of its bioactive molecules, not much work has been carried out on development of molecular markers and genome resources for QTLs in this crop. Further, most of the research on molecular genetics and breeding in this crop has focused on common buckwheat. Emergence of whole genome sequences of buckwheat, has paved the way for development of breeding pipelines that can integrate the phenomics and genomics tools for quality trait improvement in buckwheat. Programs aimed at genetic improvement of buckwheat through conventional breeding have achieved limited success because of heteromorphic self incompatibility associated with common buckwheat. To overcome this problem, remote hybridization has been attempted by crossing with a monomorphic self-compatible wild species, *F. homotropicum* (Campbell 1995; Woo and Adachi 1997). The hybrids were successfully produced through embryo rescue and forwarded to successive generations by selfing as well as back crossing, i.e. introgressive hybridization. Common buckwheat is a distylous, self incompatible species. It has long-styled flowers with short stamens (Pin type) and short-styled flowers with long stamens (Thrum type). Therefore, understanding the molecular mechanism of floral heteromorphism is essential to control the mating behaviour in breeding and development of self-compatible (SC) lines. Heterostylism in buckwheat is controlled by a single locus *S* with three alleles, *S*, *S^h* and *s*, which respectively control the *F. homotropicum* homotype *S^hS^h*, *F. esculentum* (thrum) *Ss* and pin *ss*. Adachi et al. (2000) identified three RAPD markers which showed tight linkage with the *Sh* gene and converted them into SCARs. Out of these two markers were found to be present only in *F. homotropicum*, thereby indicating their applicability in differentiating heterozygosity from both types of homozygote. While Nagano et al. (2000) used the *F₂* progeny of *F. esculentum* and *F. homotropicum* for fine mapping of the *S^h* allele (homostylar locus) with the help of AFLP markers, Yasui et al. (2016) have identified novel candidate genes controlling heteromorphic self-incompatibility of buckwheat using the buckwheat genome sequence as the reference database.

Although buckwheat finds an important place in the functional food sector it suffers from unstable yields due to seed shattering which has been ascribed to the

presence of brittle or weak pedicels. Matsui et al. (2003) investigated the inheritance of brittle pedicels using 2 self-compatible lines (01AMU2 with brittle pedicels and KSC2 with non-brittle pedicels), produced by an interspecific cross between *Fagopyrum esculentum* cv botansoba (non-brittle) and *F. homotropicum* (brittle). While the *F₁* plants derived from crosses between Botansoba × 01AMU2 and Botansoba × KSC2 had brittle pedicels, the *F₂* population derived from the cross between Botansoba × 01AMU2 showed segregation of brittle and non brittle pedicels in the ratio of 3:1. On the basis of this ratio, Matsui et al. (2003) suggested that non-brittle pedicel trait in Botansoba was controlled by a single recessive gene (*sht1*). On the other hand, the *F₂* population derived from cross between Botansoba × KSC2, showed segregation of brittle and non-brittle pedicels in the ratio of 9:7, thereby indicating that the non-brittle pedicel trait in KSC2 was controlled by a different single recessive gene (*sht2*). Matsui et al. (2004) developed 5 AFLP markers which were linked to the *sht1* locus and converted two of them into STS markers for MAS of non-brittle pedicel plants.

Self-incompatibility is an obstacle in the generation of pure lines and the fixation of agronomically useful traits. The *S^h* allele, conferring the self-compatibility trait, is dominant over the *s* allele but recessive to the *S* allele. Thus, to obtain *F₁* plants with the self-compatibility trait, plants with pin type flowers and self compatible lines need to be crossed. However, efforts made in this direction have achieved limited success till date (Table 7). The first interspecific hybrid in the genus *Fagopyrum* was an artificial allopolyploid *Fagopyrum giganteum* which was obtained as a result of conventional crossing between *F. tataricum* and *F. cymosum* (Krotov and Golubeva 1973). However, in almost all the cases of interspecific hybridizations, the hybrids were unable to form mature seeds and produce progenies without recycling of ovule rescue. The only successes recorded in the direction of overcoming breeding barriers in buckwheat has been achieved by successful interspecific hybridization between *F. esculentum* and *F. homotropicum* wherein the self-compatibility trait was transferred from *F. homotropicum* to *F. esculentum* (Campbell 1995; Woo et al. 1999; Matsui et al. 2003). Successful interspecific cross between *F. esculentum* and *F. homotropicum* at diploid level has opened new possibilities for improvement of common buckwheat.

While the major focus of breeding efforts in common as well as tartary buckwheat has been on

Table 7. Progress in interspecific hybridizations in buckwheat

Species crossed	Method of hybridization	Outcome	Reference
<i>F. tataricum</i> × <i>F. cymosum</i>	Conventional cross	Fertile hybrids which was subsequently designated as <i>F. giganteum</i>	Krotov and Golubeva (1973)
<i>F. esculentum</i> × <i>F. cymosum</i>	Ovule culture	Hybrids showing perennial growth habit and heterostyly Sterile hybrids. Flowers produced by the hybrid plants were homomorphic as in tartary buckwheat, but with white sepals like common buckwheat	Hirose et al. (1995) Samimy et al. (1996)
<i>F. tataricum</i> (female parent) × <i>F. esculentum</i> (male parent)	Ovule culture		
<i>F. esculentum</i> × <i>F. cymosum</i>	Embryo rescue	Hybrids reached flowering stage. All the hybrids were vigorous in their growth and produced flowers which were self-sterile	Woo et al. (1999)
<i>F. esculentum</i> × <i>F. Homotopicum</i> (C2026)	Conventional cross	The phenotype of interspecific hybrids and backcrosses <i>F. esculentum</i> × F ₁ , being heterozygous at DET/det, SHT/sht loci and a homostyly gene of <i>F. homotopicum</i> , was like a recessive homozygote for at least one of these genes, thereby indicating silencing of the dominant alleles. Pollen tube growth was normal. However, the fertilized embryo could grow to the rod or early globular stage (2-3 days after pollination). The hybrid embryos showed various post fertilization ultra-structural abnormalities such as failure of endosperm development, vacuolated embryo cells with degenerated endosperm	Fesenko and Fesenko (2001), Shaikh et al. (2002)
<i>F. esculentum</i> × <i>F. cymosum</i>	Conventional cross		
<i>F. tataricum</i> × <i>F. esculentum</i>	Ovule rescue	Sterile hybrids	Samimy et al. (1996) Hirose et al. (1995), Wang et al. (2002), Azaduzzaman et al. (2009), Campbell (1995); Wang et al. (2005c)
<i>F. tataricum</i> × <i>F. esculentum</i>	Ovule rescue	The fertile hybrids produced F ₁ and F ₂ generations	
<i>F. tataricum</i> × <i>F. esculentum</i> × <i>F. homotopicum</i>	Embryo rescue	The F ₁ hybrids generally resembled the male parent (<i>F. homotopicum</i>), in morphology, The hybrids showed homostylous flowers. Male sterile flowers	
<i>F. tataricum</i> × <i>F. giganteum</i>	Conventional cross	Early maturing, self-fertilizing which was subsequently designated as <i>F. hybridum</i>	Fesenko and Fesenko (2010)
[(<i>F. esculentum</i> × <i>F. cymosum</i>) × <i>F. homotopicum</i>] × <i>F. Homotopicum</i>	Ovule culture	Mostly sterile hybrids	Suvorova (2016)

yield stability and development of self-compatible lines, optimization of their nutritional quality, and development of loose hulled cultivars of tartary buckwheat has received greater attention in the recent past (Kreft et al. 2020). Tartary buckwheat has received more attention because it has higher and more stable yield attributes due to low-seed abortion, homomorphic self-compatibility and frost tolerance (Wang and

Campbell 2007). Compared to common buckwheat, seeds of tartary buckwheat also have higher flavonoid content especially rutin (Bonafaccia et al. 2003). However, seeds of tartary buckwheat have a tightly adhering hull which is hard to remove (Wang and Campbell 2007). Tartary buckwheat has a bitter taste because of hydrolysis of rutin to quercetin by the activity of rutinase present in the hull. Major

breeding objectives for tartary buckwheat improvement include development of high yielding varieties which have low rutosidase activity and large seeds with a non-adhering hull for efficient processing. Improvement of tartary buckwheat has been previously achieved through the introduction of landraces and selection of natural or artificial mutants in the past. There have been only a few successful cases of hybridization breeding, which has been severely limited by the small size of its flowers. Wang et al. (1996) have reported a particular type of tartary buckwheat, called rice-tartary buckwheat, which has seeds with three length-wise splits in its hull compared to tartary buckwheat, which has three grooves in the hull of its grains. The presence of the three splits makes dehulling easier. It would be possible to develop tartary buckwheat with loose hulled seeds by introgression of genetic component of non-adhering hull of rice-tartary into tartary buckwheat genome. Wang and Campbell (2007) have attempted transfer of the non-adhering hull trait of rice-tartary buckwheat to tartary buckwheat through breeding by hybridization between tartary buckwheat and rice-tartary buckwheat. Based on progeny analysis of the F₁, F₂, and F₃ generations, they reported that the presence of splits on the sides of the seeds in rice-tartary buckwheat was controlled by a single homozygous recessive gene. Wang and Campbell (2007) have reported the development of advanced lines of tartary buckwheat having seeds with non-adhering hulls. On the other hand, based on the Bulk Segregant Analysis (BSA) of whole genome sequence data of two parents (tartary buckwheat and rice-tartary buckwheat) and samples from the F₂ population derived from the parents, Zhang et al. (2020) have identified a candidate genetic region, containing 45 impact SNPs/indels and 36 genes, that might control the non-adhering hull trait of rice-tartary buckwheat. Zhang et al (2020) suggested that this region could be the target for breeding easy dehulling Tartary buckwheat.

Improvement of yields, palatability, development of self compatible lines, removal of allergins in grain flour have been important objectives in buckwheat. AFLP, SSR, EST and array based markers have provided important leads in regard to mapping of loci involved in various agronomic traits (Yasui et al. 2004; Konishi and Ohnishi 2006; Hara et al. 2011; Yabe et al. 2018). While AFLP markers have not yet been converted to single locus markers in the buckwheat genome, amplification of specific gene loci based on SSR markers has proved to be difficult in *Fagopyrum*

esculentum because of the high level of genetic diversity between the cultivars. Yasui et al. (2016) have generated a draft assembly of common buckwheat (*Fagopyrum esculentum*) genome using short reads obtained by next-generation sequencing. They have annotated the functions of 35,816 CDSs, excluding those for transposable elements. However, the major drawback of the draft genome is its truncated nature and the large number of scaffolds. Variability in buckwheat germplasm can be seen as a source of novel genes for the improvement of other crops. Rout et al. (1996) have isolated a 26kDa basic subunit of the 13S globulin which has more 5.9% lysine and about 2.3% methionine. The gene coding for this protein could be a valuable source for improving the nutritional imbalances in cereals which are generally deficient in lysine.

With the emerging insights in molecular genetics of buckwheat, it is high time to target efforts for identifying genes or alleles governing proven traits of importance in wild species for use in improvement of cultivated species of buckwheat. Precise editing of genes through the CRISPR/Cas9 approach would facilitate development of varieties with improved agronomic traits. This approach, even though not tried in buckwheat till this day, would minimize breeding timelines and facilitate the early release of varieties. Even though biparental QTL mapping has been undertaken in common buckwheat, for some growth and morphological traits, the allogamous reproductive system in this species acts as a barrier due to difficulties in the generation of suitable mapping populations. In order to perform QTL analysis to investigate photoperiodic sensitivity, Hara et al. (2011) constructed a linkage map using 63 expressed sequence tag (EST) markers and three candidate genes. They identified a single candidate gene and two ESTs that were associated with the target trait. In a similar approach, Yabe et al. (2014a) used pseudo-test cross mapping strategy, in which a map is constructed for each parent and then two maps are bridged, and high-density markers, to construct a high-density linkage map for a population of common buckwheat. The map was used for QTL analysis for main stem length. While these studies highlight the usefulness of linkage maps, even for populations of an allogamous species, genomic selection could become the most promising tool in breeding programmes involving common buckwheat. It would be worthwhile to mention that, even though common buckwheat possesses high genetic diversity, which

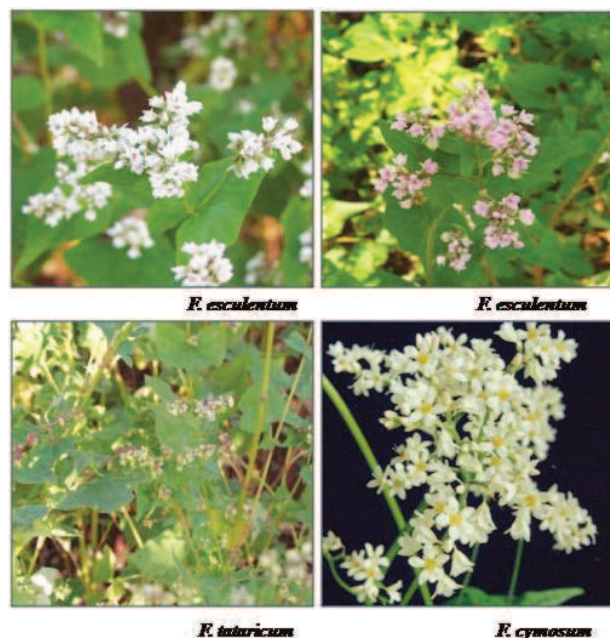


Fig. 3. Variations in flower colour in buckwheat

is beneficial for GS, the low LD of allogamous species could actually hinder GS. Combination of simulations and empirical GS breeding can be a better tool to achieve rapid genetic improvement in common buckwheat.

However, it is important to identify an optimal breeding program in advance because of paucity of information on genomics-assisted breeding in buckwheat. In brief, enhanced research on efforts for breeding better varieties with determinate growth habit, self compatibility, reduced seed shattering, low rutinoidase activity, low allergenicity, improved technologies for value addition for along with public awareness on nutritive value and government support for marketing could certainly make buckwheat as a golden crop of the future. A schematic representation of an integrative genomics and breeding approaches for accelerated genetic improvement of buckwheat is proposed in Fig. 4.

Future perspectives

The potential challenge of trying to provide food security in the future can in no way be underestimated. In the absence of well developed models to predict the exact effects of population growth and climate change on agricultural output, it seems highly likely that agriculture in large regions of the world may need to undergo significant adjustment over the coming decades in order to keep pace with food and nutritional

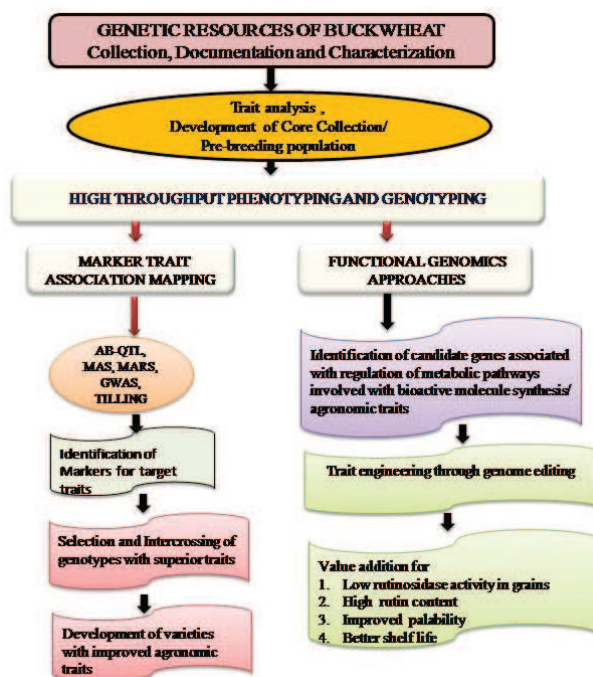


Fig. 4. Schematic representation of an integrative genomics driven approach for buckwheat improvement

requirements of the growing population. While this would include the diversification of the food basket, it would be also important to visualize the nutritionally dense underutilized crops as part of a food mix for a particular region, rather than as 'stand-alone' crops. Using combinations of underutilized crops as additions to the existing staples could help make nutritional and food security an achievable goal. However, since such crops have remained neglected in research and breeding programmes, they would need investments in research efforts to achieve the expected output.

Although quinoa overweighs buckwheat in several agronomic traits such as growth habit, yield, palatability and areas under cultivation, the nutraceutical qualities of buckwheat are superior to that of quinoa or grain amaranth. Because of the high level of several bioactive molecules, buckwheat also has a strong pharmaceutical potential. Because of its immense nutraceutical properties, buckwheat is also projected as the "Golden crop" of future. Yet, the years of neglect and grading as a marginal crop, has led to a consistent decrease in the area under its cultivation. One of the major reasons for the declining cultivation of buckwheat is the poorly characterized analysis of its agronomic traits which limits the capability to measure its true potential *vis-a-vis* the major staple

crops. Absence of high quality QTL maps has also hindered GS based screening of the existing diversity for identification cultivars with better agronomic traits. Our current knowledge of its physiology, genetics and cultivation practices can provide the necessary framework for harnessing its potential as a super food. Although buckwheat is regarded as a subsistence crop in major parts of the globe, expanding its cultivation and use will create nutritional synergy with the major staples. A better understanding of the genetic makeup responsible for various agronomic traits such as determinate growth habit, flower abortion, seed shattering, palatability as well as optimizing post-harvesting technologies for value addition to create functional foods from buckwheat seeds will create the avenues for developing a super crop out of buckwheat. Amongst the two cultivated species, tartary buckwheat, by virtue of its better agronomic traits such as self-compatibility and higher rutin content, offers greater potential for development into a super crop. Tartary buckwheat has received relatively less favor amongst the farmers and consumers because of the bitter taste of its flour due to the presence of quercetin, which is a hydrolysis products of rutin as a consequence of activation of rutosidase upon addition of water. Seeds of tartary buckwheat have tightly adhering hull which makes dehulling difficult. Thus, breeding for *F. tataricum* having non-adhering hulls and low rutosidase activity would be crucial for enhancing the utilization of tartary buckwheat.

Buckwheat has been used as an important raw material for the development of functional foods such as buckwheat enhanced breads, biscuits, snacks, noodles, pasta, tea, tarhana, sprouts, buckwheat honey. The emerging consumer demands for food products with improved nutritional values/health benefits are expected to stimulate progress in agriculture through the selection of raw materials and optimization of production process. Advancing the utilization of buckwheat would require an integrated approach involving marker assisted selection of genotypes showing quality traits, mutagenic approach aimed at elimination of immune-dominant allergenic proteins from its grains and screening of the entire gene pool of buckwheat, including its wild species, for genes which could be used for improvement of the cultivated species through biotechnological approaches. With the emerging insights in molecular genetics of buckwheat and modest progress in interspecific hybridization between genetically distant species of buckwheat species one would expect

significant developments in genomics assisted breeding in buckwheat in near future. Precise editing of genes through the CRISPR/Cas9 approach can facilitate generation of varieties with improved agronomic traits. This approach, even though not tried in buckwheat till this day, would minimize breeding timelines and facilitate the early release of varieties.

Authors' contribution

Both the authors have contributed equally in collecting the information and preparation of the manuscript.

Declaration

The authors declare no conflict of interest.

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