Rice Bean: A Neglected and Underutilized Food Crop Emerges as a Repertory of Micronutrients Essential for Sustainable Food and Nutritional Security

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Contents

Abstract

Rice bean (*Vigna umbellata* syn. *Phaseolus calcarata* (Roxb.); *Azuki umbellata* (Thunb.) Owhi and Ohashi) is an obscure crop that is underexposed to the scientific investigation as yet. However, the crop has the essence of a potential crop, and it is considered a food and nutrition security grain for farmers of Southeast Asia, where rice bean is grown by small farm holders on marginal land with minimum agricultural inputs. Due to its potent nutrient profile, it is grown and diversified since its origin from Indo-China region; however, the crop till now has not received the requisite attention. The agronomic disadvantage like low palatability and indeterminate growth pattern with delayed flowering hampers the productivity and quality of the crop product and limits its spread, utilization, and commercialization. However, there has been a renewed interest in this underutilized crop, because it is a great genetic source of biotic and abiotic stress tolerance. Recent omics investigations and the literature available have highlighted the genes involved in the agronomically negative transactional traits.

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The identification of vital target genes is a prerequisite for trait improvement. Crop improvement and the identification of new target crops at the verge of population explosion, climatic, and environmental changes are crucial. The present endeavor has tried to highlight the importance of rice bean and recognize it as a crop for the future since staple crops are facing challenges for further improvement. We have discussed the work done in this direction along with the recent revelations and the need for genetic improvement for developing the rice bean as robust, high quality, and yielding crop.

Keywords

Rice bean · Underutilized crop · Nutrition · Genomic resource · Omics · Crop improvement

1 Introduction

A versatile, underutilized, less well-known legume known as the rice bean (*Vigna umbellata* syn. *Phaseolus calcarata* (Roxb.); *Azuki umbellata* (Thunb.) Owhi and Ohashi) has the potential to provide the rising human population with nutritious feed in the near future (Bhat and Karim 2009). It is a member of the Fabaceae (Leguminosae) family (Bhardwaj et al. 2021; Dahipahle et al. 2017) (Fig. 1). Therefore, it has the innate ability to assimilate biological nitrogen to restore soil fertility and serve as a substitute for intercropping. It is regarded as a resource for nutritious flour, dietary needs, and livestock feeding and fodder (Dahipahle et al. 2017; Khanal et al. 2009). (Tripathi et al. 2021). Although it holds such worthwhile agricultural capabilities and nutritional brilliancy, rice bean still has been abandoned by breeders. Attributions such as delay in flowering (Kaul et al. 2019a; Joshi et al. 2007; Takahashi et al. 2015) and unpalatableness (Basu and Scholten 2012) are two major constraints associated with cultivated varieties. More is concerned with the inadequate information on its nutritious advantage and the presence of anti-nutrients (Katoch 2020). Minimal advancement has been accomplished in achieving potentiality of rice bean due to the main matters associated to late induction of flowering (Joshi et al. 2007), unpalatableness (Kaul et al. 2019a), hard and coarse type of grain (Andersen 2012), shattering sensitivity (Parker et al. 2021), disease resilience (Pandiyan et al. 2008), and the presence of anti-nutrients (Bajaj 2014). Several kinds of literature evince rice beans' resiliency towards adverse environments consisting of some familiar biotic and abiotic stresses along with abilities to tolerate metal toxicity in the soil. *Vigna umbellata* has been identified by the Food Security, Rice Bean Research in India and Nepal (FOSRIN) network as one of the impending crops for the nutrified future (Andersen 2007; Basavaprabhu et al. 2013). Originated from Southern and Southwestern Asia (Bisht and Singh 2013), it had been adapted in Indo-China area (Doi et al. 2002) and became a conventional crop in East, Southeast, and South Asia (Tomooka et al. 2002; Seehalak et al. 2006). It is mostly cultivated in the belt of Indonesia, Vietnam, Myanmar, Bhutan, Southern China, Laos, Northern Thailand, East Timor, and India

Fig. 1 Life cycle of rice bean: (**a**) seedling stage; (**b**) reproductive stage: vine legume plants with yellow flowers and small edible beans; (**c**) inflorescence having flowers in different stages; and (**d**) variability of seed coat color and seed size (diameter of each unit is 4 cm) in rice bean. The vegetative parts can be fed to livestock as fresh or made into hay. Grain is generally used as dal/boiled soup for human consumption. Grain foliage is used as livestock fodder and manure

(Tian et al. 2013; Iangrai et al. 2017; Pattanayak et al. 2018). The wild type of rice bean, *V. umbellata* varieties *gracilis*, inhabiting the zone from Himalayan and Central Land of China to Malaysia (Seehalak et al. 2006; Rejaul et al. 2016), is presumed as the pioneer of today's cultivated crop. Although wild types exhibit intermediacy in qualities such as small seeds, free branching, and sensitivity towards photoperiod as compared to the cultivated varieties, till now, only the northern east area of India grow such wild-type intermediate varieties (Iangrai et al. 2017). Research on related members like *V. mungo* revealed the coevolution of this species during an individual domestication event in Thailand or Myanmar. Conspecific to the cultivated *V. umbellata* grown in South and Southeast Asia, this species is thought to have arisen from *V. umbellata* var. gracilis (Tomooka et al. 1991, 2002; Bisht et al. 2005; Seehalak et al. 2006). Rice bean has been embraced as a cover crop in places like Ghana, Sri Lanka, Indonesia, Jamaica, Haiti, Fiji, and Mexico, but it is only in limited cultivation in West Indies, Australia, Africa, Brazil, the United States, and Honduras (Wang et al. 2015; Khadka and Acharya 2009; Rajerison 2006; Burkill 1953) (Fig. 2). The location of the crop is mostly determined by the necessary growth factors; the rice bean thrives in regions with an annual rainfall of between 1000 and 1500 mm, although it also tolerates dry seasons to a reasonable extent. This crop can grow in the temperatures ranging between 18 °C and 30 °C, but it also can withstand cold temperatures as low as 10 °C with a vulnerability to more lower temperatures like frost, as well as temperatures as warmer as 40 °C. (Pattanayak et al. 2019). The screening of rice bean's germplasm for unexplored genomes may surface new approaches for unearthing neoteric traits and linked genes (Sarma et al. 1995). These agricultural endeavors favor generating robust and climate-resilient crops against the backdrop of adverse environments. The current circumstances of world hunger and the tendency of developing lifestyle-related severe disorders demand improvement and domestication of unexplored crops like rice bean to create unique sustainable landraces with increased productivity and lower levels of anti-nutrients. Rice bean may be enlisted as one of the crucial futuristic crops. In order to accelerate its domestication process, the crop necessitates more focused research. In comparison to other economically significant legumes including soybean, common bean, azuki bean, and mung bean, the absence of polymorphic molecular markers in rice bean has lagged in genomic investigations. So far, only a few papers have indicated intra- and inter-species molecular diversification of *V. umbellata* via application of simple sequence repeat (SSR), amplified fragment length polymorphism (AFLP), and random

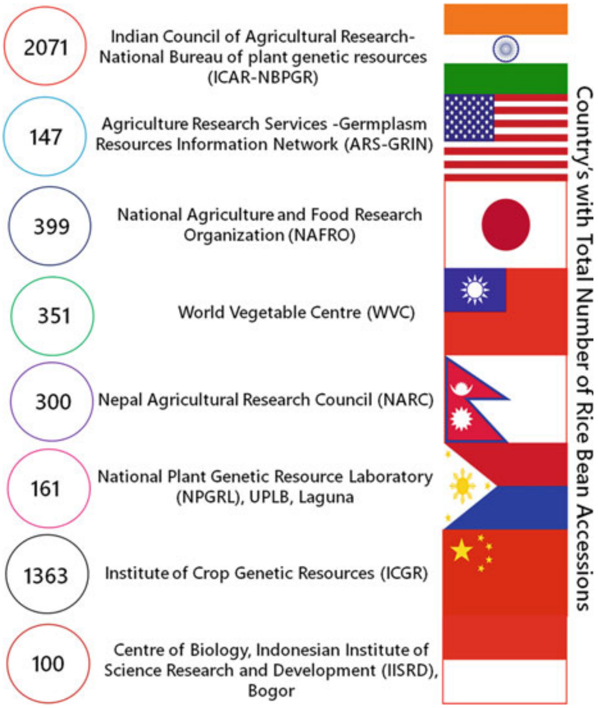

Fig. 2 Diagrammatic representation depicting the worldwide distribution of rice bean accessions in diverse agroecological microhabitats

amplified polymorphic DNA (RAPD) markers (Iangrai et al. 2017; Thakur et al. 2017; Tian et al. 2013; Bajracharya et al. 2008; Muthusamy et al. 2008). An in-depth draft genome assembly of rice bean will provide information on nucleotide polymorphism existing in the population, which will be turned into the resource of polymorphic SSRs applicable in determining how the marker linked to particular trait. The molecular breeding strategy for crop advancement can be efficiently regulated by the identification of genome-wide relevant trait-related markers, particularly markers linked to quantitative traits (Muthusamy et al. 2008). Landraces from various geographical areas must be included in order to fully represent the genetic variety. SSR markers addressed the greatest variation in an examination of 112 regionally collected different rice bean varieties from India and Nepal using 35 azuki bean's polymorphism markers (Bajracharya et al. 2008). To analyze the diversity indices for the target crop's genotype, polymorphic markers created for the orthologous crop can be used for the less-known sister crops. It is important to note that the first comprehensive SSR analysis, which included 84 wild and 388 cultivated accessions from 16 different geographic zones in Asia, revealed that the genetic diversity is highest in accessions from Nepal, Myanmar, Vietnam, and India (Tian et al. 2013). Among 65 accessions investigated using a cluster of 28 SSR markers, accessions were collected from Japan, Thailand, Korea, and China with significant diversified genetic characteristics. It is crucial to carefully examine the rice bean germplasm in order to benefit from the diversity that is intrinsically present there and to minimize the risks associated with farmers giving up the crop. Therefore, more emphasis on genetically governed key characteristics of rice beans is highly required for its adaptation, like taste, latency, and early floral induction to make this crop more feasible. This kind of approach permits the study of evolutionary components and the effects of domestication and breeding on rice bean molecular function (Fig. 1).

What necessitate the exploration of the underutilized crops? Will the endeavors be advantageous to resolve the problem of yield loss, biotic/abiotic stress vulnerability, and malnourishment? Invariably, these grave questions are relevant during a time when staple food crops are facing numerous challenges (Mayes et al. 2012; Andersen et al. 2009); moreover, the situation will escalate with the discrepancy in the current high population growth rate and low food productivity. Thus, with the upsurge to provide safe and healthy nutrition for underprivileged and deprived populations, food grain productivity must be increased urgently in order to feed the rapidly growing population. Considerably, the underutilized crops are more resilient to the changing environment or biotic/abiotic stress and well equipped to dwell on marginal lands with minimal investments of capital and agricultural products. Thus, the underutilized, neglected, or non-staple food crops are generally accepted alternatives to meet the Sustainable Development Goal (SDG).

2 Nutritional Composition of Rice Bean

Compared to other commercially grown crops, rice beans have a considerable amount of nutritional content and various health advantages. Furthermore, it holds tremendous potential to mitigate global micronutrient deficiency among the population. In South

Asian nations, rice bean is often eaten as a boiled soup or dal, as well as whole grain cooked by using dry heat and hot air, combined with wheat flour or chickpea. They provide a substantial quantity of nutritional fiber, tannin, slowly absorbed carbohydrates, significant minerals, and important amino acids. Rice bean has more iron (Fe), calcium (Ca), zinc (Zn), potassium (K), thiamine, riboflavin, and niacin compared to other leguminous crops. Moreover, it has a lower glycemic index (Katoch et al. 2014; Saharan et al. 2002). A large variety of bioactive compounds contain those that protect the liver, fight inflammation, lower blood pressure, improve immunity, fight cancer, fight infections and fungal growth, fight diabetes, inhibit HIV-1, and fight health hazards (Wei et al. 2015). In particular, ischemic heart disease, diabetes mellitus-type 2, colorectal cancer, and other metabolic ailments can be curbed and/or prevented by the bioactive phytochemical profile of rice beans (Tharanathan and Mahadevamma 2003). Rice bean is becoming an excellent choice for underdeveloped and developing countries because the nutritive profile holds huge health and nutritive benefits (Dhillon and Tanwar 2018; Katoch 2013; Parvathi and Kumar 2006). Digestible and non-digestible carbohydrates are the primary component of any legume (Priyadarshini et al. 2021). Rice bean contains more than 58% carbohydrate and up to 72% carbohydrate (Katoch 2013; Buergelt et al. 2009; Sadana et al. 2006), from 3.60% to ~5.56% of crude fiber (Bajaj 2014; Buergelt et al. 2009), while ~9 g per 100 g of acid detergent fiber (ADF) and ~13.0 g per 100 g of neutral detergent fiber (NDF) are present (Katoch 2013). Rice bean has 5–6 g/100 g of soluble sugars, 4.7–5.3 g/100 g of nonreducing sugars, and comparatively low starch (50–55 g/100 g) compared to other beans (Saharan et al. 2002). Rice bean has fewer oligosaccharides like raffinose, which ranges from 1.56% to 2.58%, while verbascose and stachyose are present in a percentage of 0.85–1.23 and 0.94–1.88, respectively. Food rich in raffinose and stachyose such as soybean, sword bean, and lima bean causes flatulence in the human body (Katoch 2013).

Rice bean has a total protein level ranging from 14% to 26% with better protein digestibility (86.1–89%) in vitro as compared to other legume crops (Bajaj 2014; Buergelt et al. 2009). Katoch (2013) reported rice beans have a greater amino acid profile, specifically tryptophan and methionine, whereas black and green gram have equivalent tyrosine, lysine, and valine levels. The reported fat content of 1.92–3.42% is also significantly lower than that of legumes (Bepary et al. 2017; Buergelt et al. 2009; Sadana et al. 2006). Rice bean can provide a resource for unsaturated fatty acids such as oleic acid and linoleic acid with a percentage of 15.6–17.91 and 17.24–18.98, respectively, while linolenic acid, stearic acid, and palmitic acid with a percentage of 39.89–44.36, 4.36–5.87, and 14.23–16.88, respectively (Katoch 2013; Pugalenthi et al. 2004). In rice bean, Katoch (2013) discovered 3.48–4.26 mg/100 g niacin and 15.33–29.00 mg/100 g ascorbic acid. Interestingly, phytic acid, a key anti-nutrient feature in legume grains, is present in trace amounts of 0.20–2.27% and is comparatively less than in other crops (Bepary et al. 2017; Bajaj et al. 2014). However, the anti-nutrient qualities, such as activities of phytic acid, polyphenols, trypsin inhibitors, and saponins, can be reduced by soaking and pressure cooking. As a result, its nutritional content may offer a hopeful addition of healthy and inexpensive value to impoverished and advanced nations in order to counter the food crisis (Dhillon and Tanwar 2018).

3 Problems with the Commercial Use of Rice Beans

Despite having health benefits, rice beans are considered an underdeveloped crop; however, it is difficult to pinpoint what characteristics make a crop underutilized: they are frequently linked to the cultural heritage of their region of origin; there is inadequate evidence of their farming and use; they are customized to specific marginal land and agroecological microhabitats; and there is no formal document for seed distribution mechanisms. Its anti-nutritional components, including phenolic compounds, alkaloids, phytate, enzyme inhibitors, late flowering, prolonged cooking time, inferior processing, and tough seed coatings, all contribute to its poorer usage. Additionally, its anti-nutritional contents, notably phenolic compounds, tannins, phytate, enzyme inhibitors, late flowering, extended cooking time, poor processing methods, and hard seed coats, contributes to its less utilization. Thereby, farmers are less eager to spend their time and resources on the expansion and production of underutilized crops (Nnamani et al. 2017; Popoola et al. 2020). In addition, rice bean is mostly grown by rural farmers who lack the resources, i.e., high-input farming practices required to raise essential crops (Conti et al. 2019). Additionally, their production has been limited by low market prices, low demand, a lack of purchasers, an inadequacy of improved varieties, and insufficient funding (Khan et al. 2021). In addition, light sensitivity and indeterminate vegetative developments due to delayed flowering have lost market attraction compared to crops like chickpeas, pigeon peas, lentils, peas, and black and green grams. Rice bean verities with prolonged vegetative development periods seem unpleasant, and the subsequent cropping is hampered by this prolonged period. Also, the tough and coarse grains limit daily consumption even after boiling (Andersen 2012). Early flowering may be accelerated by manipulating genes involved with the flowering pathway (González et al. 2016; Dhanasekar and Reddy 2014; Joshi et al. 2007). Furthermore, it is reported that rice beans may grow in a variety of climates. However, their cultivation is restricted by their need for moderate temperatures and rainfall and their sensitivity to prolonged exposure to harsh settings (Noda 1951). Rice bean cultivation is reduced in the cropping system due to the crop's rigid reaction to the mechanized cultivation system and lower harvest index, which contrast with other economically relevant pulses like lentils, peas, and soybean (Jayasundara 2015). Due to these serious issues, there are no legal channels for trade; still, it is locally marketed in Thailand, Nepal, India, and Myanmar through an unorganized trade.

4 Omics Approach: Identifying Novel Genes Associated with Stress Resistance and Nutritional Improvement

Due to the limited geographical distribution in congruence with restricted marketing channels and inadequate commercialization, rice bean has been unexplored for their underlying genetic richness. Thus, unraveling the rice bean' genome is critical, but it could provide ideal candidate genes for stress resilience and an extraordinary range of nutrients within the genus *Vigna* (*V. umbellata*) (Rana et al. 2014). Thereby, a major contribution has been made by Kaul et al. (2019a) with a 414 MBP genome draft assembly, i.e., NCBI.SRA.SRP132447 consisting of high confidence, identified 31,276 genes via analysis of 15,521 scaffolds. Primarily, it is critical to cover the whole genome. Functional coverage of almost 96.08% was attained via coverage of around 30X reads developed through Illumina along with the PacBio approach (Kaul et al. 2019a, 2022). The assembled genome indicated the closest relation of *Vigna umbellata* genome with *V. angularis*, followed by another closely related associate present in same genus, i.e., *Vigna radiata* and *Vigna unguiculata*. Collinearity block mapping, an alignment technique to compare crop genome assembly to other related plants' genomes, is employed and aligns the rice bean draft assembly with 13 complete genomes and 18 partial genomes available for legume crops. It revealed peculiar information about rice beans. The whole coding sequence (CDS) alignment also provided critically relevant findings. Moreover, with the application of LCB, i.e., locally collinear alignment block clusters, aligning with 17 medicinally relevant plant genomes incorporated in the National Institute of General Medical Sciences-NIH database, are able to decipher the 18,000 potential medicinally pertinent genes. In conclusion, the endeavors encompassing comparative genomics studies have highlighted the fundamental symplesiomorphic traits that have assisted in establishing the origin and relation of rice beans related to their genetic and functional lineage. Considerably, the major contribution of this study is the identification of neoteric palatability and late-flowering related genes and deciphering the position of a few of them in the mitochondria and chloroplast genomes. These genes are involved in functionally diverse metabolic pathways for the regulation of flavor, abiotic/biotic stress, disease resistance, photoperiod responsiveness, and more. The material and data have been made available at http://www.nicg.in to advance molecular breeding studies to produce rice beans as a potential resource. Kaul et al. (2022) reported the existence of genes that responded to stress from a variety of families, including stress-enhanced protein 1 (SEP-1), universal stress protein PHOS32 precursor (PHOS32), heat shock transcription factor HSF-02 (GMHSF-02), stress-responsive alpha-beta barrel domain-containing protein (GSU2970), and stress-enhanced protein 2 (SEP-2) in rice bean (Kaul et al. 2022). Targeting photoperiod-independent early flowering genes like the early flowering 3 (Elf3) gene, FLC-transcription factors, flowering locus T1 (Rft1), determinant stem 1 (DT1), ethylene-responsive transcription factor tiny (TINY), and Dead/dead box helicase domain-containing protein (PIE1) can increase yield by lowering vegetative and indeterminate growth. In India, the Nutritional Improvement of Crops (NIC) Group at ICGEB, New Delhi, has pioneered molecular studies in rice beans to add features including determinate habit, early flowering, and palatability using a clustered regularly interspaced short palindromic (CRIPSR)-based genome editing system (Fig. 3).

The advances in sequencing technology have made genomic exploration less challenging, which contributes primarily toward the visible paradigm shift in agriculture. Conventionally, till now, quantitative trait locus (QTL) mapping has harnessed the uncloaked capabilities of these underutilized crops and characters related to domestication via inter- and intraspecific mapping (Isemura et al. 2010). Rice bean projects resistance capability against mung bean yellow mosaic virus

Fig. 3 Schematic representation depicting the genome editing approach to target the palatability and late flowering genes to resolve the issues with the rice bean. Recent innovations like CRISPR/Cas9 could accelerate the breeding process

(Pandiyan et al. 2008, 2010; Sudha et al. 2013), pests actively affect storage conditions such as bruchid beetles (*Callosobruchus* spp.) (Tomooka et al. 2000; Kashiwaba et al. 2003; Somta et al. 2006) and bacterial disease like leaf spot (Arora et al. 1980). Generally, the underused crops are efficiently habituated to a variety of soil types. Specifically, the inherent capability of rice beans to secrete organic acids like citric acid and others curb the acidity of the soil and aluminum accumulation (Fan et al. 2014). MATE has identified resistance power to aluminum toxicity in rice beans, i.e., multidrug and toxic compound extrusion family organic acid efflux transporters such as VuMATE1 and VuMATE2 (Yang et al. 2006; Liu et al. 2018). Furthermore, the absorption of micronutrients like iron and zinc is reduced due to the prevalence of anti-nutrients such as polyphenols, saponins, tannin, phytic acid (PA), hemagglutination, and trypsin inhibitors. Thereby, the identified followed by functionally characterized micronutrient transporters can be targeted for the improvement of nutrition in rice beans such as iron-phytosiderophore transporter yellow stripe 1 (YS1), iron-regulated transporter-1(IRT1), constitutive photomorphogenic 1 (COP1), ferric reduction oxidase 2 (FRO2), nicotinamide synthase 1 (NAS1), and natural resistance-associated macrophage protein (NRAMP). In general, the PA residues form a complex with the micronutrient and thus make it inaccessible for absorption in the animal body too. Therefore, targeting genes such as phospholipase D (PLD) and inositol triphosphate kinase (ITPK6) can lead to a lower phytic acid concentration in rice bean grain. Likewise, the main reason for the low palatability index of rice beans is the presence of taste deterrents or pungent taste developers, for instance, polyphenols and tannins. Thereby, genes like N-(5-phosphoribosyl) anthranilate isomerase – a chloroplastic isoform, liquiritigenin 2-*O*-methyltransferase-like (ILMT), chalcone synthase 17-like (CHS-17), leucoanthocyanidin dioxygenase (LDOX), and spermidine hydroxycinnamoyl transferase-like (SHT) can be targeted due to their involvement in biosynthesis pathways of polyphenol and tannin. In accordance with this, the application of genome editing may lead the way to understanding the functional characterization of genes connected to critical agricultural factors determining crop habituation (Schenke and Cai 2020; Zafar et al. 2020).

5 Crop Improvement

If the underutilized crops are as superior as they are represented and promoted as having agro-economic, stress tolerance, and nutritious advantages, why then don't they reproduce on their own? Will they suffer if agriculture is increasingly commercialized and the food trade is more international? These barriers can be overcome using the traditional and molecular methods outlined below. These crops are frequently discussed in cross-disciplinary stakeholder/partnership efforts in agricultural progress (Padulosi and Hoeschle-Zeledon 2004, 2008), and as a result, they are covered under post-green revolution development policies. Both producers and consumers are unenlightened of rice beans' tremendous potential to enhance food and nutritional advantages, so, emphasizing its marketing and utility are highly significant. For novel varieties and flexibility in seed selection, old variety material should be exploited. For crop improvement and propagation, it demands a focus on breeding and on-farm trials. Seed providers should promote seed distribution and accessibility easily. By educating larger audiences about rice bean seed production in native places and handing out grains at trade fairs, access can be increased. In addition, quality assessment is vital (regarding germination and resilience to disease). Furthermore, timely circularization of information regarding the adaptability and technologies related to better production of rice beans is necessary. Alliance with the nongovernmental organization could be the marketing strategy to popularize the rice bean at chains of food hubs (Sthapit et al. 2010). Nutritional, chemical, and sensory analyses must be carried out at several intervals to gain data from various marketing surveys. These methods may create a unique hub for global consumption, achieving security in nutritious food and reducing malnutrition. Moreover, recent advances and implementation of high-throughput next-generation DNA sequencing approaches, like Illumina and Pac bio, have massively furnished the underlying potential of rice bean genomes with high confidence and accurately aligned data. Kang et al. (2014) released the draft genome of *V. radiata* (~genome size of almost 459 MB) with three genome assemblies and one sequencing read. They showed the draft genome of *V. angularis* with a genome size of ~455 MB with five assembled genomes and two sequencing reads by Kang et al. (2015). Similar findings involving *V. unguiculata* with an approximate genome size of 607 MB were reported by Muoz-Amatria et al. in 2017. The researchers developed the draft genome using two assembled genomes. Using next-generation sequencing (NGS) on the rice bean genome, Chen et al. (2016) were able to locate 3011 possible genetic/molecular SSR markers. But before drafting a genome to build confidence and partially annotate it, it is essential to perform an analysis of comparative genomes with the target genome. Kaul et al. (2019a, 2022) mapped the whole genome of rice beans using the anchoring elements of the functional and genetic orthologous sequences of *V. radiata*, *V. angularis*, and *V. unguiculata* as a basis for comparable functional properties. The blueprint of the draft genome, identification of genes, and translational annotation for the target *Vigna* *umbellata* can all be designed using the orthologous sequences as a reference. The probable protein-coding genes can also be found from the assembled sequence data utilizing the process, namely MAKER v2.31.9. (Campbell et al. 2014). It results in annotating genes via quality-dependent evidence. These eventually lead to the identification of the target gene or genes for trait modification and raise the market value of the neglected target crop (Kaul et al. 2019a). Genetic engineering techniques must be used to improve traits (Tabassum et al. 2021). Among the several genome editing techniques, CRISPR-dependent toolkits are the most effective, highly specific, and simple to generate editing techniques, which have recently gained attention in the researchers' community. The aforementioned method updates the targeted genome modification appropriately and suitably (Zhang et al. 2018; Ku and Ha 2020; Kaul et al. 2019b, 2020). These have been used extensively to discover traits and develop high-yield crops (Wang et al. 2018, 2019). Similar to this, rice bean characteristics such as less palatability, late regulation of flowering, and presence of anti-nutrients, alongside photoperiod sensitiveness, can be altered using CRISPR/Cas-dependent methods. As a result, it might be a ground plan to fix and eliminate the problems linked to the domestication of rice beans.

6 Conclusion

A long-term, affordable solution to the problem of malnutrition is to incorporate dietary heterogeneity into the food system in order to attain zero hunger. The rice bean is a rich source of high-quality protein, soluble fiber, minerals, and antioxidants, as well as a broad range of health supplements and pharmaceuticals that can cure or prevent diseases influenced by food. Due to its several uses as manure, fodder, and food for people, it is advantageous and economically viable for farms in underdeveloped areas. As a result, there are large gaps in current research on rice beans and marketing, necessitating increased effort. Farmers should be encouraged to participate in research projects on underutilized local plant varieties like rice beans, and policies should be developed to support this. Scientists should investigate the cultivars that both farmers and consumers favor and undertake awareness campaigns to emphasize the advantages of the crop for malnourished people in underdeveloped countries in order to encourage its planting. The aim is to increase crop yield, remove toxic anti-nutritional components, shorten the time needed to cook, gain consumer acceptance, acquire market approval, and address the protein- and food-insecurity problem. It requires a lot of effort to bring these nutrient-rich crops at the top of any country's food chain. However, recent innovations like CRISPR/Cas9, speed breeding, genomic selection, and other high-throughput approaches could expedite the breeding process (Fig. 3).

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