

# Potential Pulses

Genetic and Genomic Resources

Edited by  
**Rahul Chandra**  
**T. Basavaraja**  
**Aditya Pratap**



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## Potential Pulses: Genetic and Genomic Resources

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# Foreword

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The importance of grain legumes in global food and nutritional security, crop diversification, soil amelioration and environmental sustainability is well recognized. Their nutritional richness and adaptability to varied agro-ecosystems contribute significantly to the global agriculture, promoting especially the plant-based food systems. Owing to their properties, promoting widespread cultivation and consumption of food legumes can be one of the major drivers of the first three of the Sustainable Development Goals (SDGs), namely eliminating poverty, ending hunger and establishing good health and wellbeing. Among the grain legumes, the potential food legumes, also called underutilized or minor food legumes, hold a special significance as they are niche specific, can withstand harsher environments and provide an additional opportunity for the diversification of micro-climate cropping systems and diets.

A phenomenal economic growth has taken place in Asia and the Pacific in the past few decades, which has resulted in significant improvements in the socio-economic conditions in the region, positively impacting the lifestyle and living situations of the people. This has also resulted in expanding the food habits of the population and the evolution of a class of consumers preferring healthier and plant-based foods over animal products. In such a scenario, potential food legumes offer an obvious advantage due to their high and quality protein, low fat, low glycaemic index and plenty of antioxidants. Low input requirement during their cultivation, including an all-time scarce resource, water, also makes them a good choice for the smallholder and subsistence farmers. However, unfortunately, the focus has remained confined to a few major legumes until now channelling ample funding, research and policy support in the past three to four decades, marginalizing underutilized yet potential food legumes. Nevertheless, potential legumes present a substantial promise for improving food security, meeting dietary demands, and fostering agricultural growth. These offer a plethora of alternative protein crops, which are also resilient to changing climates and have an inherent fortified ability to withstand biotic and abiotic challenges. They also offer a viable avenue for crop diversification, contributing significantly to agricultural sustainability and a nation's overall economic prosperity. The nutritional analysis of minor pulses revealed their high nutrient density, sometimes even more than the major legumes for a few elements, encompassing crucial micronutrients, dietary fibre, resistant starch, proteins and bioactive compounds. It has been observed that the protein content of the minor pulses varies from 8.6% to 43%, surpassing even that of chickpea and soybean. While crops such as winged bean outdo all pulses with the highest protein content, its amino acid composition is comparable to soybean. Likewise, the African yam bean boasts of diverse proximate compositions, including carbohydrates, protein, ash, fat and fibre. Many of the minor pulses, such as winged bean, runner bean and cowpea, flaunt multiple edible parts within the same plant, making



available a range of nutrient sources. The potential pulses are not only inexpensive, but can also be grown in some of the areas where no other food legumes or even cereals can be grown. Therefore, there is a need to advocate strongly for the cause of potential pulses and promote them for healthier diets and the sustainability of the environment.

This book explores the potential and scope of underutilized pulses to greater depths and is very timely and well thought of in promoting this goldmine for global food and nutrition security. This volume, edited by three promising pulses researchers, offers a comprehensive and extensive treatise on the biology, ecology and breeding of the potential legumes besides providing an insight into the innovative developments that have changed our understanding of these neglected crops. Chapters on different minor pulses have been contributed by some of the best workers of these crops and have globally acknowledged research contributions. I am sure that the book will be widely read and the information contained in each individual chapter will be tremendously helpful to the researchers, students, teachers and extension workers.

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# Preface

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Welcome to *Potential Pulses: Genetic and Genomic Resources*, a comprehensive exploration of some of the world's most promising yet often overlooked crops. Pulses such as African yam bean, cowpea, adzuki bean, rice bean, runner bean, lima bean, faba bean, and grass pea have been dietary staples for centuries, valued for their nutritional richness and adaptability to various agroecological zones. However, despite their significant potential, these crops have not received the same level of research attention as other major pulses. Consequently, their cultivation and use have waned, leading to their classification as 'orphan', 'neglected', and 'underutilized' crops.

This book aims to change that narrative. By bringing together the knowledge and insights of leading experts from around the globe, *Potential Pulses: Genetic and Genomic Resources* seeks to unlock the potential of these vital crops. The 16 chapters within this volume delve into the genetic diversity, genomic tools, and biotechnological innovations essential for enhancing the productivity and resilience of these pulses. Each chapter provides a thorough examination of the nutritional values, usage patterns, origins, distribution, evolutionary relationships, roles in global food security, crop improvement strategies, cultivation practices, and future perspectives of these crops. Detailed tables and diagrams are included to facilitate a deeper understanding of the topics covered.

Our goal is to shine a spotlight on the untapped potential of these crops and inspire renewed interest and research within the scientific community and beyond. This book is designed to be an invaluable resource for researchers, agronomists, policymakers, and anyone dedicated to advancing sustainable agriculture and food security.

We extend our heartfelt gratitude to the contributors who have shared their expertise and passion, making this book a reality. Their collaborative efforts have resulted in a rich and diverse body of work that we believe will significantly advance our understanding of potential pulses and their role in sustainable agriculture and food security. We also express our sincere thanks to CAB International (UK) for their steadfast support and commitment to promoting scientific knowledge.

It is our hope that *Potential Pulses: Genetic and Genomic Resources* will serve as an essential reference and a source of inspiration for ongoing and future research in the realm of pulse crops.

**Rahul Chandora, T. Basavaraja and Aditya Pratap**

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# 1 Leveraging the Potential of Lesser-known Pulses for the Sustainability of Future Food Systems

T. Basavaraja<sup>1\*</sup>, Aditya Pratap<sup>1</sup> and Rahul Chandora<sup>2</sup>

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## Abstract

The rapid growth of the global population presents a daunting challenge to agriculture and natural resources, especially in the face of rising food demand. Hunger remains a crucial issue in various regions, particularly in South Asia and sub-Saharan Africa, where high rates of hunger and malnutrition persist. Despite improvements in agricultural practices, increasing hunger in 18 countries since 2015 highlights the need for innovative solutions. This book explores the potential of underutilized legume crops, often neglected in agriculture, to enhance food and nutritional security. With the world heavily reliant on a few staple crops, diversifying the food supply is crucial. These underutilized pulses, including adzuki bean, Bambara groundnut, African yam bean and winged bean, among others, offer rich nutritional profiles, high protein content and resilience to changing climates. Through genetic and genomic resources, including advanced sequencing technologies and marker-assisted selection, we can expedite the development of climate-resilient and nutritionally rich crop varieties. Harnessing the genetic diversity of these underutilized pulses is crucial in addressing food insecurity, improving agricultural sustainability and promoting diversified, nutrient-rich diets, offering a promising pathway to ensure global food security amidst the challenges posed by a growing population and changing climates.

**Keywords:** Potential legumes, orphan crops, genetic resources, underutilized, pulse genomics, sustainability

## 1.1 Introduction

Addressing the impact of the escalating global population on agriculture and natural resources in the 21st century requires a nuanced understanding of the challenges at hand. The 2023 Global Hunger Index (GHI) score of 18.3, though classified as moderate, highlights the persistent nature of hunger, particularly in 34 countries, with South Asia and sub-Saharan Africa facing the highest burden (Kousar *et al.*, 2021; von Grebmer

*et al.*, 2023). Despite incremental improvements, 18 countries have seen an increase in hunger since 2015, underscoring the urgency of addressing food and nutritional security, especially with the projected global population of 10 billion by 2050 (Singh *et al.*, 2022).

Compounding these challenges are limited agricultural land, which is further declining, changing climates, and the impact of abiotic and biotic factors on crop productivity (Mayes *et al.*, 2012; Devaux *et al.*, 2020). The scarcity of genetic

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diversity further complicates matters, hindering the development of enhanced varieties of orphan crops. Innovative solutions are imperative to tackle these multifaceted challenges.

### 1.1.1 Pulses for food and nutritional security

The threat posed by climate-change-induced erratic weather patterns to global food production necessitates a shift from the overreliance on a narrow range of crop genetic variability. With only 30 domesticated plant species dominating human diets, there is a pressing need to diversify beyond these key crops (Fghire *et al.*, 2022; Ali and Bhattacharjee, 2023). This diversification becomes critical to address food insecurity comprehensively.

The decline in crop diversity, unhealthy dietary habits and sedentary lifestyles have led to a dual nutritional crisis affecting around 2 billion individuals globally. This crisis causes malnutrition and obesity-related non-communicable diseases (Sreenivasulu and Fernie, 2022). The past decade has seen substantial research on alternative crops, particularly underutilized potential legumes. These crops, often overlooked in terms of research, investment and commercial output, hold significant promise in delivering valuable food, nutrition and economic benefits.

The importance of agrobiodiversity, which refers to the variety of crop species in a system, is gaining recognition for its role in sustainability, socio-economic resilience, and human health improvement (Dwivedi *et al.*, 2017; Tian *et al.*, 2021; Regmi *et al.*, 2023). Neglected and underutilized crop species are emerging as focal points owing to their potential to enhance nutritional value, promote agrobiodiversity, sustain hostile environs and withstand environmental stresses. Integrating these species into food production systems can enhance the resilience and diversity of food production with a reduced environmental footprint, and their integration into diets can mitigate non-communicable and diet-related diseases.

Despite the potential benefits, mainstreaming neglected crops faces obstacles such as insufficient research, low public awareness, inadequate government policies and limited public/private investments. Recent efforts have focused on

genetic conservation and enhancement of these crops to unlock their full potential.

### 1.1.2 Smart food crops: a path to sustainable agriculture

The focus on underutilized crops, aptly named 'smart food crops', aims to enhance food quality, reduce reliance on a limited set of staple crops, preserve cultural diet diversity, and explore climate-resilient alternatives (Ali and Bhattacharjee, 2023). The potential legume crops possess the capacity to thrive in diverse environmental challenges and changing climates due to their exceptional nitrogen-fixing capability. Beyond environmental adaptability, these crops boast higher nutritional content, making them instrumental in addressing nutrition deficiencies and ensuring food security in underserved regions (Joshi *et al.*, 2020; Ayilara *et al.*, 2022). As we navigate the complexities of global food security, investing in the potential of underutilized crops emerges as a critical avenue for sustainable and resilient agricultural practices.

## 1.2 Potential Pulse Crops: Nutrient Status, Consumption Pattern and Usage

The current global landscape is characterized by a grave situation marked by widespread hunger and significant loss of lives owing to malnutrition. The escalating shift towards vegetarian protein diets on a global scale has intensified the demand for alternative protein sources. In response, legumes have emerged as a viable and economically beneficial option to meet protein requirements (FAO, 2021; Singh *et al.*, 2022). These crops are highly esteemed globally for providing nutritional protein sustainably and cost-effectively, positioning them as the second most important dietary source after cereal grains (Nayak *et al.*, 2022). The pressing needs in the current context revolve around sustainable methods to enhance crop resilience to changing climates, fortify their ability to withstand biotic and abiotic challenges, and concurrently promote large-scale production and nutritional diversity. Underutilized pulses present substantial potential for improving food

security, meeting dietary demands and fostering agricultural growth. They offer a viable avenue for crop diversification, contributing significantly to agricultural sustainability and a nation's overall economic prosperity (Mayes *et al.*, 2012; Joshi *et al.*, 2020; Fghire *et al.*, 2022). A meticulous nutritional analysis of underutilized pulse crops unveils their high nutrient density, encompassing crucial micronutrients, dietary fibre, resistant starch, proteins and bioactive compounds (Table 1.1). The protein content of untapped pulses varies from 8.6% to 43%, surpassing that of soybeans (Ayilara *et al.*, 2022). Among these pulses, the winged bean seed stands out with the highest protein percentage (27–43%), and its amino acid composition is comparable to soybeans, with methionine and cysteine as the limiting amino acids. Horse gram seed boasts a protein level ranging from 18.5% to 22.5% (Savithramma and Shambulingappa, 1996). Crude protein in cowpea ranges from 25.38% to 27.56% (Gondwe *et al.*, 2019). Recent studies on African yam bean grains indicate diverse proximate compositions, including carbohydrates, protein, ash, fat and fibre (George *et al.*, 2020).

Underutilized pulses offer unique potential for addressing diverse nutritional needs, catering to various preferences. Many of these legumes feature multiple edible parts within the same plant, allowing for a range of nutrient sources. For example, winged bean provides edible components such as leaves, flowers, green pods, seeds and tuberous roots, all rich in protein and suitable for raw or cooked bean consumption (Ayilara *et al.*, 2022; Dwivedi *et al.*, 2023).

Cowpea, known for its versatility, includes young leaves, growing points, green pods and green seeds used as vegetables in South Africa. Its fresh leaves, ranked among the top four vegetables in various African and Asian countries, are well-suited for cultivation in high-rainfall agroecologies, aiding in reducing malnutrition (Mekonnen *et al.*, 2022). Hyacinth bean serves multiple purposes as a pulse, vegetable, livestock feed, green manure, and even a decorative or medicinal herb (Naeem *et al.*, 2020). Similarly, runner bean in South-east Europe is grown for dry seeds and consumed as immature green pods (Sinkovič *et al.*, 2019). Despite being underutilized, these legumes are recognized for producing delicious meals for domestic consumption, although consumption rates remain below their

nutritional potential. Common processing methods involve boiling after removing foreign ingredients and soaking in water, indicating opportunities for increased integration into everyday diets (Agyekum *et al.*, 2023). Potential pulses have high amounts of amino acids, minerals, proteins, vitamins, dietary fibres and some beneficial bioactive components, often on par with or even superior to those found in domesticated main pulses. These potential pulses are not only inexpensive, but they also provide an excellent source of protein, especially during times when the consumption of animal products has been minimized because of potential health risks. As a result, there has been a significant increase in the promotion of plant-based protein by researchers as an approach to fulfilling the population's nutritional needs.

### 1.3 Harnessing Genetic and Genomic Resources for Climate-resilient Agriculture

#### 1.3.1 Genetic resources

Germplasm collections serve as repositories of genetic diversity, encompassing phenotypic variations in agronomic features. Diverse genetic resources in crops play a crucial role in crop development and breeding efforts to improve resilience, yield potential, nutritional content and adaptability to changing environmental conditions (Silva *et al.*, 2019; Ulian *et al.*, 2020; Sserumaga *et al.*, 2021; Kanishka *et al.*, 2024).

Understanding phenotypic variations, assessing population structure and diversity, and characterizing genotype × environment interactions (GEI) in germplasm collections aid in identifying genetically varying, stable and agriculturally desirable germplasm. The International Institute of Tropical Agriculture (IITA) gene bank, for instance, houses a collection of 15,003 cultivated cowpea accessions from 89 countries, with a core collection of 2062 accessions developed based on geographical, agronomical and botanical descriptions (Boukar *et al.*, 2019). Sources of new traits continue to be discovered in cowpea germplasm, and the traits are being characterized at high genetic precision with the new genotyping methods available for detecting marker-trait



**Table 1.1.** An overview of potential pulse crops' nutritional profiles (per 100 g) (Dwivedi *et al.*, 2023) CC BY 4.0 DEED.

Potential pulses	Carbohydrate (%)	Crude protein (%)	Fat (%)	Energy (Kcal/100 g)	Crude fibre (%)	Ca (mg)	P (mg)	Fe (mg)
Adzuki bean	28.5–60.7	16.3–29.2	0.3–1.3	329	12.7	66	381	5
Bambara groundnut	53–69	17–25	6.5–8.5	1609	5–12	30–128	81–563	2–9
Grass pea	48–52	18–34	0.7–2.8	362	3.9–6.0	220–370	350–640	6.9–8.7
Horse gram	50–60	18.5–31.2	0.6–2.6	321	4.3–25.0	244–312	311–443	5.9–7.4
Faba bean	57.8–81.0	12.9–22.9	1.0–5.3	348	2.0–10.9	103–183	345–392	15
Hyacinth bean	29.6–66.3	20.5–35.5	0.3–9.7	344–383	3.7–14	94–132	317–428	1.7–9.4
Lima bean	49.4–77.34	8.6–30.3	0.5–5.9	338	2–16	68.7–81.0	4.3–11	91.6–128
Moth bean	61.5–66.0	22.0–26.0	1.6	343	–	1144–150	231–489	10.8–15.1
Rice bean	50–70	14–26	0.5–2.3	347	3.6–5.6	111–598	124–568	3.7–9.2
Tepary bean	65–69	21–25	0.9–1.2	360	2.1–3.1	28	450	7.1–8.3
Runner bean	62–83	27–32	1.0–1.8	372–458	1.2–1.8	72–138	59–559	10.3–12.0
Winged bean	12.7–42.2	27–43	13.9–26.7	409	3.4–27.0	102–850	310–637	4.9–6.0
Cowpea	50–60	23–32	5.4–11.2	336	3.9–10.6	85–93	438–498	10–11

associations, described in Akohoue *et al.* (2020). Tepary bean is a prominent legume crop with unique genes that can be introduced into common bean or *Phaseolus* species. The high levels of diversity reported in wild *Phaseolus acutifolius* and *Phaseolus parvifolius* suggest they contain beneficial genes for domesticated tepary bean genetic improvement (Mhlaba *et al.*, 2018). Lima bean (*Phaseolus lunatus* L.), one of the five domesticated *Phaseolus* bean crops, has extensive ecological adaptations from Mexico to Argentina. Garcia *et al.* (2021) successfully assembled a chromosome-level genome for the lima bean by combining long-read and short-read sequencing methods and using a dense genetic map derived from a biparental population. The high genetic variability of runner bean (*Phaseolus coccineus*) is valuable for breeding objectives, especially as a source of disease resistance and cold tolerance. Because *P. coccineus* germplasm has not been characterized, however, it cannot be used as a donor species for inter-specific hybridization (Guerra-García *et al.*, 2022). About 4685 runner bean accessions are documented worldwide, with the Austrian Agency for Health and Food Safety in Linz, Austria, maintaining 2674 accessions through the European Cooperative Programme for Plant Genetic Resources (Schwember *et al.*, 2017). Likewise, major moth bean *ex-situ* collections are maintained in the Indian National Gene Bank, ICAR–National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India, with a total of 3422 accessions, which have been utilized in extensive characterization and evaluation programmes to identify superior germplasm accessions such as IC36245, IC36555, IC36667, IC36577 and IC36604. The genetic stocks MH 65, MH 34/66, MH 45 and MH 66 exhibited the most promising traits, making them potentially beneficial candidates for integration into the moth bean varietal improvement programme (Chandora *et al.*, 2023).

Certain legumes, such as winged bean (*Psophocarpus tetragonolobus*), lima bean (*P. lunatus*), hyacinth bean (*Lablab purpureus*) and Bambara groundnut (*Vigna subterranea*), have received attention as potentially underutilized legumes within the diverse range of legume species cultivated in tropical countries. This recognition is due to their hardiness, immense nutritional qualities and notably high protein content, particularly in their seeds (Cheng *et al.*, 2019). Bambara

groundnut landraces exhibit highly significant variations in morpho-agronomic traits. Additionally, positive relationships are found between yield and traits associated with yield, indicating an opportunity for further enhancement of agronomic attributes in these landraces (Khan *et al.*, 2021; Uba *et al.*, 2021). Likewise, a total of 94 grass pea accessions were evaluated for three qualitative and 19 quantitative traits in lowland (Antalya, Turkey) and highland (Isparta, Turkey) environments. There were substantial variations between genotypes for all agronomic traits in lowland environments. The highest biological yields were found in GP104 and GP145, with 22.5 and 82.4 g values in the lowland and highland, respectively (Arslan *et al.*, 2022). The diversity found in the world's most extensive collection of grass pea and their relatives maintained at the ICARDA seed bank in Syria has been utilized by the ICARDA scientists. Extensive Lathyrus collections are conserved in France, and the NBPGR is in India, Bangladesh and Chile (Singh *et al.*, 2013).

### 1.3.2 Genomic resources

Molecular markers have become essential tools for evaluating germplasm, exploring genetic diversity, mapping genes and employing marker-assisted selection (MAS) to enhance crop quality. Although genomic research on underutilized pulses has lagged behind major pulse crops, recent breakthroughs in genome sequencing using next-generation sequencing (NGS) technology have accelerated progress (Varshney *et al.*, 2009).

The development of genomic resources for underutilized pulses has progressed more recently compared to major pulse crops such as chickpea, pigeon pea, lentil, mung bean and urd bean. Initial efforts focused on crop/germplasm domestication, collection and evaluation, utilizing various marker systems in genetic diversity investigations. This led to the rapid identification of molecular markers, including those linked to quantitative trait loci (QTL) associated with desirable characteristics in underutilized pulses (Table 1.2).

With the advancement of sequencing technology, single nucleotide polymorphisms (SNPs) have become the predominant molecular markers owing to their unbiased nature, especially when exploring closely related untapped pulse species (Feuillet *et al.*, 2011; Cheng *et al.*, 2019; Sahruzaini

**Table 1.2.** Details on germplasm, DNA markers, and primary output from molecular-based diversity studies of untapped pulses (modified from Dwivedi *et al.*, 2023) CC BY 4.0 DEED.

Germplasm no.	No. of markers	Output	Reference
<i>African yam bean (Sphenostylis stenocarpa)</i>			
169	1789 SNPs	Genetically differentiated sub-populations and a strong correlation between phenotype and genotype-based matrices are observed	Shitta <i>et al.</i> (2022)
93	3722 SNPs	Highly predictive genotypic–phenotypic diversity relationships	Aina <i>et al.</i> (2021)
77	AFLPs	Out of 227 AFLP bands, 59 were polymorphic, with genetic distances between 0.048 and 0.842. Four distinct clusters were identified, unrelated to geographical origin	Adewale <i>et al.</i> (2015)
<i>Adzuki bean (Vigna angularis)</i>			
261	110 SSR	North and South China accessions sufficiently differentiated	Chen <i>et al.</i> (2015)
96	26 SSR	The wild relatives of Chinese and Japanese origins possess enough similarity	Liu <i>et al.</i> (2014)
176	85 SSR	Higher allelic diversity in the wild than in cultivated germplasm	Wang <i>et al.</i> (2012)
<i>Bambara groundnut (Vigna subterranea)</i>			
100	5927 DArTseq SNPs	Two distinct clusters, with cluster I containing TVSu-1897, the remaining in cluster II based on DArTseq SNPs and stress tolerance index	Odesola <i>et al.</i> (2023)
100	5925 SNPs	Higher genetic diversity among Nigerian accessions	Osundare <i>et al.</i> (2023)
93	2286 SNPs + morpho-agronomic traits	Two heterotic groups and unique accessions with specific characteristics	Majola <i>et al.</i> (2022)
270	3343 DArT SNPs	Greater diversity among accessions from diverse regions	Uba <i>et al.</i> (2021)
78	19 SSR	Higher within landrace diversity than between landraces; significant gene flow among the landraces	Minnaar-Ontong <i>et al.</i> (2021)
96	32 ISSR	Moderate to high levels of genetic differentiation	Khan <i>et al.</i> (2021)
<i>Grass pea (Lathyrus sativus)</i>			
400	56 SSR	Highly polymorphic and diverse germplasm	Rahman <i>et al.</i> (2022)
22	31 SSR	A few genetically diverse germplasms with low $\beta$ -ODAP identified	Arslan <i>et al.</i> (2020)
118	18 EST-SSR	Sufficiently differentiated high- and low- $\beta$ -ODAP (neurotoxin) accessions	Gupta <i>et al.</i> (2018)
283	30 SSR	Wild relatives clustered separately from cultigens	Wang <i>et al.</i> (2015)
<i>Horse gram (Macrotyloma uniflorum)</i>			
58	150 SSR	Three to four distinct genetic stocks	Kumar <i>et al.</i> (2020a)
48	117 SSR	Within a population, genetic variance is greater than between populations	Kaldate <i>et al.</i> (2017)
360	33 SSR and 24 morphological descriptors	Two distinct gene pools with higher levels of accessions variability	Chahota <i>et al.</i> (2017)

Continued

**Table 1.2.** Continued.

Germplasm no.	No. of markers	Output	Reference
<i>Cow pea (Vigna unguiculata)</i>			
217	886 DArTseq	High level of differentiation among populations and morphotypes; eight distinct clusters	Kafoutchoni <i>et al.</i> (2021)
281	493 SNPs	Distinct subpopulation structures differentiated by seed coat colour and ecological regions	Akohoue <i>et al.</i> (2020)
<i>Hyacinth bean (Lablab purpureus)</i>			
166	2460 SNPs	Four distinct subpopulations differentiated by ecogeographic regions	Njaci <i>et al.</i> (2023)
142	1000 SNPs	Substantial among accessions diversity than within accession variance	Muktar <i>et al.</i> (2021)
65	9320 DArTseq-based SNPs and 15,719 SilicoDart markers	Lower discrimination; higher within-population variance than among the population	Sserumaga <i>et al.</i> (2021)
<i>Lima bean (Phaseolus lunatus)</i>			
183 landraces	12 SSR and 7 morphological descriptors	Sufficient discrimination and introgression between Andean and Mesoamerican gene pools	Silva <i>et al.</i> (2019)
46	73 ISSR	There is higher genetic diversity in Mayan lowlands than in Mayan highland landraces; Mayan culture shaped diversity	Camacho-Pérez <i>et al.</i> (2018)
<i>Rice bean (Vigna umbellata)</i>			
Sequence 440 landraces	1,400,862 SNPs	Identified loci harbouring orthologues of FUL (FRUITFULL), FT (FLOWERING LOCUS T), and PRR3 (PSEUDO-RESPONSE REGULATOR 3) contribute to the adaptation of rice bean from its low latitude centre of origin towards higher latitudes, and the landraces which pyramid early-flowering alleles for these loci display maximally short flowering times	Guan <i>et al.</i> (2022)
32 accessions	300 genic SSR markers	A total of 3011 genic SSRs were identified as potential molecular markers; of these loci, 23 primer pairs were polymorphic among 32 rice bean accessions	Chen <i>et al.</i> (2016)
353 accessions	2,145,937 SNPs	Constructed a rice bean pangenome size of 679.32 Mb by GWAS analysis	Francis <i>et al.</i> (2023)
<i>Tepary bean (Phaseolus acutifolius)</i>			
Wild <i>P. acutifolius</i> accession	2,247,877 SNPs	Reasonable heat stress tolerance and reduced disease resistance gene acquisition are signs of tepary bean adaptation to arid and hot environments	Moghaddam <i>et al.</i> (2021)
156 accessions	24 SNPs	High-throughput genotyping has facilitated large-scale SNP detection, resulting in the development of molecular markers with related sequence information	Gujaria-Verma <i>et al.</i> (2016)
87 genotypes	15,645 SNPs	A total of 90 flanking candidate genes were identified using 1-kb genomic windows centred in each associated SNP marker	López-Hernández <i>et al.</i> (2023)

Continued

**Table 1.2.** Continued.

Germplasm no.	No. of markers	Output	Reference
422 cultivated accessions	53,676 SNPs	Genome-wide association studies identified loci and candidate genes controlling biotic stress resistance, including quantitative trait loci for weevil resistance, common bacterial blight, Fusarium wilt, and bean common mosaic necrosis virus	Bornowski <i>et al.</i> (2023)
Runner bean ( <i>Phaseolus coccineus</i> )			
242 accessions	42,548 SNPs	Identified 24 SNPs associated with domestication, 13 with cultivar diversification, and eight with natural selection	Guerra-García <i>et al.</i> (2017)
113 genotypes	1190 SNPs	The genome-wide association analysis resulted in 18 high-quality SNPs that were subsequently used for the calculation of an estimated heat tolerance	Bomers <i>et al.</i> (2022)
237 accessions	79,286 SNPs	Introgression from wild to domesticated populations was detected, which might contribute to the recovery of the genetic variation	Guerra-García <i>et al.</i> (2022)
Moth bean ( <i>Vigna aconitifolia</i> )			
428 accessions	9078 SNPs	Analysed genetic relationships among the <i>Vigna</i> species using SNP markers	Yadav <i>et al.</i> (2023)
240 accessions	1287 SSRs and 5606 transcripts	Genes associated with moisture stress tolerance in moth bean have been discovered	Tiwari <i>et al.</i> (2018)
F2 population (188)	172 SSR markers	As a genetic linkage map was being developed, 50 QTLs and three genes linked to 20 traits related to domestication were identified	Yundaeng <i>et al.</i> (2019)
Winged bean ( <i>Psophocarpus tetragonolobus</i> )			
Two accessions (PI 491423 & PI 639033)	12,956 SSRs and 5190 SNPs	Gene discovery and marker development	Vatanparast <i>et al.</i> (2016)
F2 population (86)	1384 SNPs	The development of the first genetic linkage map for winged bean was accomplished	Chankaew <i>et al.</i> (2022)
Six accessions	9682 genic SSR	Developed assembly and validated genic SSR markers	Wong <i>et al.</i> (2017)

AFLP, amplified fragment length polymorphism; EST, expressed sequence tag; DArT, diversity array technology; ISSR, inter-simple sequence repeat; SNP, single nucleotide polymorphism; SSR, simple sequence repeat.

*et al.*, 2020). Notably, substantial levels of synteny (44 syntenic blocks) have been identified between *P. vulgaris* and *Glycine max*, providing valuable insights for comparative genomic and genome selection research in *Phaseolus* species. A comprehensive database, Phaseolus Genes (2016), has been established, encompassing legacy markers and genomics-based markers such as simple sequence repeats (SSRs), SNPs and indels, primarily focusing on the common bean. In the case of lima bean, the chloroplast genome was sequenced for the first-time using Illumina sequencing technology, revealing its structure

and organization (Tian *et al.*, 2021). Genomic studies by Garcia *et al.* (2021) and Wisser *et al.* (2021) resulted in a 623 Mb annotated assembly for lima bean, showcasing the combined efforts of sequencing, linkage and comparative analysis. The recent development of a tepary reference genome (Moghaddam *et al.*, 2021) provides valuable insights into linked loci conferring tolerance to biotic stresses (Bornowski *et al.*, 2023), given its unique breeding traits such as drought, heat, and salt stress tolerance (Gujaria-Verma *et al.*, 2016; Mhlaba *et al.*, 2018; Moghaddam *et al.*, 2021).

The genus *Vigna*, comprising five subgenera and over 100 wild species, has played a crucial role in domesticating seven distinct crops. Whole-genome sequences for these crops, including mung bean, black gram, rice bean, moth bean, cowpea, Bambara groundnut and adzuki bean, offer valuable genomic resources for achieving genetic progress in other *Vigna* species (Kang *et al.*, 2014; Yadav *et al.*, 2023). Comparative genomic studies have revealed substantial genome synteny among moth bean, mung bean, adzuki bean, rice bean and cowpea (Yundaeng *et al.*, 2019). Comprehensive sets of high-quality SNPs have been identified in rice bean and moth bean accessions through genotyping by sequencing (GBS) approaches (Suranjika *et al.*, 2023; Yadav *et al.*, 2023). Genome assemblies for moth bean have been generated, providing insights into stress-inducible genes associated with moisture stress tolerance (Tiwari *et al.*, 2018). Winged bean, despite its vast potential, has not received extensive research attention for molecular tool development supporting breeding programmes. However, recent efforts by Vatanparast *et al.* (2016) and Chankaew *et al.* (2022) have significantly expanded genetic resources for winged bean, including the identification of SSRs and

high-confidence SNPs. The development of the first genetic linkage map and the identification of QTLs further emphasizes the importance of genomic resources for elucidating complex trait architectures in underutilized pulse crops. The genomic resources established in major pulse crops offer an excellent platform for strengthening the genetic enhancement of potential pulse crops. Leveraging these resources enables researchers and breeders to expedite the enhancement of traits in underutilized pulse crops, thereby making substantial contributions to the overarching objectives of bolstering food security and promoting agricultural sustainability.

The integration of genetic and genomic resources has propelled our comprehension and refinement of underutilized pulse crops to unprecedented heights. These resources serve as the bedrock for expediting progress in breeding initiatives, thereby aligning with the enduring objectives of fortifying global food security and fostering sustainable agricultural practices. As we continue to delve into research and foster collaborative efforts, the potential of underutilized pulses becomes increasingly unlocked, solidifying their pivotal role in establishing resilient food systems amidst the challenges of a changing climate.

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