Mungbean and Urdbean Breeding

Parul Sharma, Shreya Vashisht, Bhawandeep Kaur, Dikshita Saikia, Asmita Sirari, Ashok Kumar, R K Gill, B.S. Gill, Inderjit Singh and Sarvjeet Singh

Mungbean (*Vigna radiata*) and urdbean (*Vigna mungo*) are important pulse crops widely cultivated in India and other Asian countries due to their high protein content, short growth duration, adaptability, and suitability for diverse cropping systems. Besides contributing to food and nutritional security, they improve soil fertility through biological nitrogen fixation and are extensively used in intercropping and rice-fallow systems. Both crops originated in the Indian subcontinent and belong to the family Fabaceae. They are self-pollinated diploid species (2n = 22) with seeds containing 22–28% protein along with essential carbohydrates, minerals, vitamins, and bioactive compounds. Conserved germplasm and wild relatives provide valuable genetic resources for improving resistance to diseases, insect pests, and abiotic stresses. Breeding efforts focus on developing high-yielding, early-maturing, climate-resilient cultivars with improved nutritional quality, desirable plant architecture, lodging and pod shattering resistance, and suitability for mechanized harvesting. Major breeding targets include resistance to yellow mosaic disease, powdery mildew, Cercospora leaf spot, anthracnose, bruchids, stem fly, and tolerance to drought, heat, salinity, cold, and waterlogging. Recent advances in genomics, molecular breeding, marker-assisted selection, genome-wide association studies, genomic selection, CRISPR/Cas genome editing, and high-throughput phenotyping have accelerated crop improvement. Integrating these approaches with conventional breeding will facilitate the development of high-yielding, nutritionally superior, and climate-smart cultivars to ensure sustainable pulse production and food security.

Keywords: *DNA markers, MAS, Plant Breeding, Crop Improvement, Underutilized crop*

Parul Sharma[1], Shreya Vashisht[1], Bhawandeep Kaur[1], Dikshita Saikia[1], Asmita Sirari[1], Ashok Kumar[2], R K Gill[1], B.S. Gill[1], Inderjit Singh[1], Sarvjeet Singh[1*]
[1]Punjab Agricultural University, Ludhiana, India.
[2]RRS Gurdaspur, Punjab Agricultural University, Ludhiana, India.

[*]Email: sarvjeet62@pau.edu

Publisher: Cornous Publications LLP., Puducherry, India.
Handbook of Plant Breeding
Editor: Dr. Selvakumar Gurunathan
ISBN: 978-81-993853-0-6
DOI: https://doi.org/10.37446/edibook152024/91-137

Introduction

Economic importance of mungbean and urdbean

Mungbean (*Vigna radiata* (L.) Wilczek) and urdbean (*Vigna mungo* (L.) Hepper), commonly known as green gram and black gram, respectively are among the most significant pulse crops cultivated in India and several Asian countries. Both crops play an important role in ensuring food and nutritional security, supporting rural livelihoods, and promoting sustainable agriculture due to their rich nutritional composition, short crop duration, adaptability, and suitability for diverse cropping systems (Nair et al., 2019). Mungbean has considerable commercial importance owing to its utilization as dry grains, sprouts, noodles, and processed food products; while urdbean is highly valued in traditional fermented foods and for its superior protein quality and lysine-rich amino acid composition, which effectively supplements cereal-based diets. Both crops are also agronomically important due to their ability to fix atmospheric nitrogen through symbiotic relationship with *Rhizobium*, which enhances soil fertility and reduces the need for chemical fertilizers. Additionally, their short duration and drought tolerance make them suitable for intercropping, rice-fallow cultivation, and multiple cropping systems. Mungbean and urdbean are used as green manure, fodder, and catch crops, contributing to enhanced soil health, cropping intensity, and farm profitability (ICAR-IIPR, 2023).

Origin and domestication

Mungbean and urdbean are closely related pulse crops that are considered to have originated from the Indian subcontinent. Archaeobotanical evidence supports their indigenous origin, as charred grains of both crops have been recovered from the Chalcolithic site of Navdatoli (1500–1000 BC), while carbonized remains of their wild forms were reported from Daimabad, Maharashtra (2200–1000 BC) (Kajale, 1974). The India-Myanmar region is recognized as a major centre of diversity for the genus *Vigna*, and classical studies by de Candolle (1884) and Vavilov (1926) identified India as the primary centre of origin. India continues to harbour an extensive diversity of both cultivated and wild forms of genus *Vigna* (Chandel et al., 1984; Singh et al., 1974).

Evidence suggests that both crops were domesticated from their corresponding wild forms, *V. radiata* var. *sublobata* Verdc. and *V. mungo* var. *silvestris* (Lukoki et al., 1980). Although earlier considered variants of a single species, they were later recognized as distinct species based on morphological and biochemical differences (Singh, 1982). Domestication involved selection for desirable traits such as erect growth habit, photoperiod insensitivity, increased pod number, and higher seed yield, while undesirable wild traits, including pod shattering, hard seed coat, and asynchronous maturity, were progressively eliminated. Urdbean is estimated to have been domesticated about 4,500 years ago in India, particularly in Gujarat and the northern peninsular region, followed by its spread to Myanmar and Thailand (Chandel et al., 1984; Verma et al., 2022). Mungbean domestication is associated with the India–Myanmar region, where extensive polymorphism in wild forms facilitated diversification and evolution of cultivated types (Singh, 2014).

Taxonomy and Classification

Mungbean and urdbean are important grain legumes belonging to the family Fabaceae (Leguminosae), subfamily Faboideae and tribe Phaseoleae. Both are self-pollinated diploid species with a chromosome number 2n = 22 (Jansen, 2006; Heuzé et al., 2015; Heuzé et al., 2016). Taxonomically, both crops belong to

the subgenus *Ceratotropis*, which also includes moth bean (*Vigna aconitifolia*), adzuki bean (*Vigna angularis*), and rice bean (*Vigna umbellata*) (Kaewwongwal et al., 2015). Earlier, these pulse crops were classified under the genus *Phaseolus* because of their close morphological resemblance. However, morphological, cytogenetic, and chemotaxonomic studies confirmed them as distinct species with separate evolutionary lineages (Chandel et al., 1984). Consequently, several Asiatic pulse crops were transferred from *Phaseolus* to *Vigna* following the classification reported by Maréchal et al. (1978). The phylogenetic relationships among important species of the genus *Vigna* are presented in Figure 1. The accepted botanical names are therefore *Vigna radiata* (L.) Wilczek for mungbean and *Vigna mungo* (L.) Hepper for urdbean. The taxonomic classification hierarchy of mungbean and urdbean from kingdom to intraspecific varieties is presented in Figure 2.

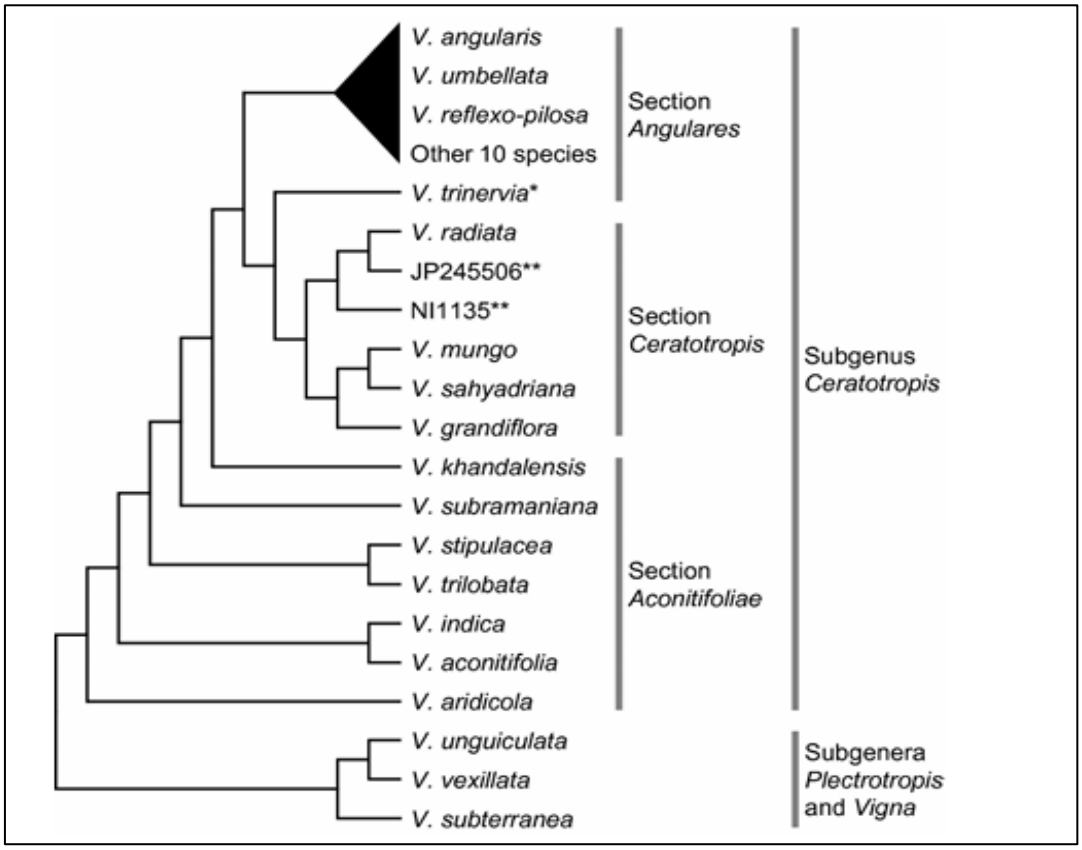

Figure1. Phylogenetic classification of species belonging to the genus *Vigna* (adapted from Takahashi & Tomooka, 2020)

Vigna radiata

Several intraspecific forms and botanical varieties of *Vigna radiata* have been described in the literature, including var. *radiata*, var. *aurea*, var. *grandis*, var. *brunnea*, and var. *glabra* (Heuzé et al., 2015; Swamy, 2023). The wild progenitor of cultivated mungbean is recognized to be *Vigna radiata* var. *sublobata* (Roxb.) Verdc., which occurs naturally in India, Southeast Asia, East Africa, Madagascar, and northern Australia (Siemonsma & Lampang, 2016). Historically, mungbean was referred to as *Phaseolus aureus* Roxb. and *Phaseolus radiatus* L. (Heuzé et al., 2015).

Vigna mungo

Urdbean is taxonomically recognized as *Vigna mungo* (L.) Hepper. The cultivated form is classified as *Vigna mungo* var. *mungo*, whereas the wild ancestral form is *Vigna mungo* var. *silvestris* Lukoki, Maréchal and Otoul (Lukoki et al., 1980). Some researchers have also recognized var. *viridis*, which includes green-seeded forms (Kanade, 2006). Urdbean differs from mungbean in possessing bright yellow flowers, shorter erect pods, and black seeds (Jansen, 2006). Important synonyms associated with urdbean include *Phaseolus mungo* L. and *Azukia mungo* (L.) Masam. (Heuzé et al., 2016).

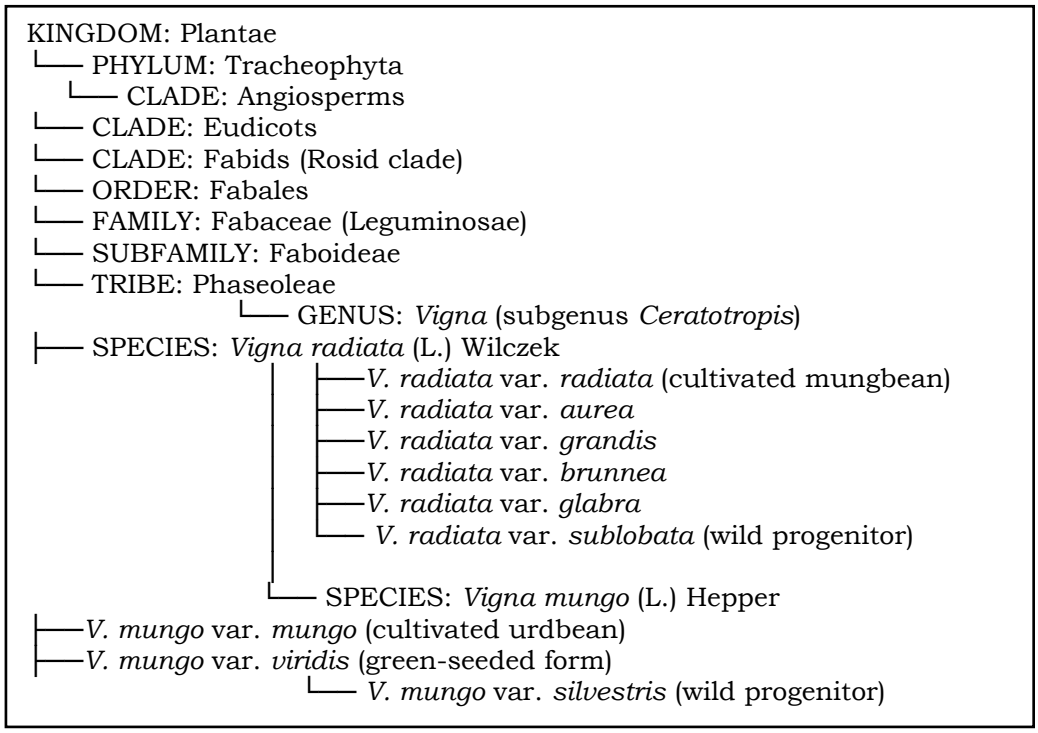

Figure 2. Taxonomic classification hierarchy of mungbean and urdbean from kingdom to intraspecific varieties

Distribution and production

Owing to their adaptability and nutritional significance, both crops are widely grown across diverse agroecological regions. Mungbean and urdbean are extensively cultivated in India, Pakistan, Thailand, Bangladesh, Myanmar, Sri Lanka and other Asian countries (Vavilov, 1926; Smartt, 1990; Jansen, 2006). Their cultivation has also expanded to Africa, Australia, and the United States because of their short duration, adaptability, and tolerance to drought stress (Nair et al., 2019; Tomooka et al., 1991). Recent estimates suggest that mungbean is grown worldwide on approximately 7.3 million hectares, producing about 5.3 million tonnes with an average yield of 721 kg ha^{-1}. In comparison, urdbean is cultivated on approximately 4.0–4.5 million hectares, with a production of 2.5–2.8 million tonnes and an average productivity of around 600 kg ha^{-1} (Nair et al., 2019; Directorate of Economics and Statistics, 2021). Among all countries, India holds the leading position in both the production and consumption of these crops (Keatinge et al., 2011). In India, mungbean is cultivated over an area of about 3.19 million hectares, yielding nearly 1.51 million tonnes and contributing around 10% of the country's total pulse acreage. Urdbean, on the other hand, covers

approximately 4.63 million hectares with a production of 2.78 million tonnes and an average yield of 600 kg ha^{-1} (ICAR-IIPR, 2024; Agricultural Statistics Division, DES, MoAF&W, 2022). Rajasthan is the leading mungbean-producing state, whereas Madhya Pradesh and Uttar Pradesh are major urdbean-growing states. Besides India, Myanmar is an important producer and exporter of both crops, while Australia, Tanzania, and Mozambique also contribute to international trade (Fujita & Okamoto, 2006). Both crops are mainly cultivated in rice- and cereal-based cropping systems and contribute significantly to sustainable agriculture through biological nitrogen fixation and soil fertility improvement.

Nutritional significance

The grains of green gram and black gram are traditionally consumed in South and Southeast Asia as whole seeds, split dhal, sprouts, soups, curries, fermented foods, snacks and flour-based products because of their high nutritional value, taste and health-promoting properties. Urdbean is extensively used in traditional fermented foods such as idli, dosa, vada, and papad, whereas mungbean sprouts are valued for their digestibility and nutritional richness. Both crops are excellent sources of vitamins, dietary fibre, proteins, carbohydrates, and minerals. Mungbean seeds contain about 22-28% protein and 55-65% carbohydrates, while urdbean contains approximately 23-26% protein and 58–61% carbohydrates on a dry matter basis (Heuzé et al., 2015; Heuzé et al., 2016; Mehandi et al., 2019). Their proteins possess considerable essential amino acids such as isoleucine, lysine, valine, and leucine, making them major supplements to cereal-based diets. Both pulses are also important sources of calcium, iron, magnesium, phosphorus, potassium, folate, and B-complex vitamins. These crops also contain bioactive compounds, including antioxidants, flavonoids, and phenolic acids, which exhibit anti-inflammatory, antidiabetic, and cardioprotective attributes (Cao et al., 2011). Traditional processing methods improve nutrient availability and digestibility (Hou et al., 2019).

Floral Biology

Mungbean and urdbean, two important grain legumes of the family Fabaceae, possess typical papilionaceous flowers and largely follow a self-pollinated mode of reproduction. The unique floral structure, consisting of specialized petals such as the standard, wings and keel, encloses the reproductive organs and promotes self-pollination (Figure 3). In many cases, pollination occurs even before the flower fully opens (a condition known as cleistogamy), which helps in retaining a high level of genetic purity (Chen et al., 2016).

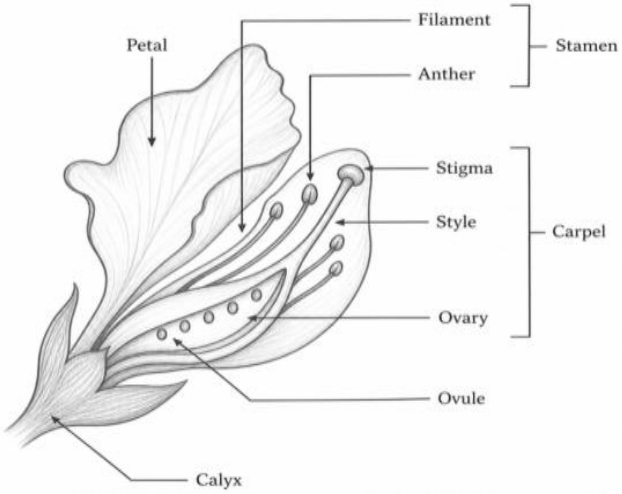

Figure 3. Structure of Legume flower

Floral biology of mungbean and urdbean

Mungbean and urdbean are closely related pulse crops belonging to the family Fabaceae and share many common floral characteristics. In both species, flowers are borne on axillary inflorescences and are bisexual, zygomorphic and hypogynous in nature. The flowers possess a typical papilionaceous arrangement consisting of two wing petals, one standard petal, and two fused keel petals that enclose the reproductive parts. The androecium contains ten stamens arranged in a diadelphous manner (9+1) while the gynoecium is monocarpellary with a superior ovary and hairy stigma, which assists in pollen reception (Chhabra, 2006; Fakir et al., 2011; Gupta et al., 2022).

Although both crops exhibit similar floral organization, certain features clearly differentiate them. In mungbean, flowers are produced in elongated axillary racemes containing around 10–30 flowers; urdbean bears flowers in compact clustered inflorescences on short peduncles. Mungbean flowers are generally smaller with a comparatively simple keel structure, while urdbean flowers are more prominently yellow and possess spirally twisted keel petals with a horn-like tip. The style and ovary in urdbean are comparatively more hairy and twisted than those of mungbean. Differences are also observed in pod and seed characteristics after fertilization. Urdbean produces shorter, thicker and densely hairy pods with relatively larger seeds; mungbean pods are comparatively slender and less hairy (Bhattacharjee et al., 2024).

Both crops are predominantly self-pollinated; however, their flowering behaviour differs slightly. In mungbean, pollination usually takes place before flower opening due to cleistogamy, with anther dehiscence occurring during late night or early morning hours. As a result, fertilization is generally completed before the flowers open, ensuring high self-fertility and genetic purity. In urdbean, flowers open shortly after sunrise and remain receptive for a brief period during the morning hours (Gupta & Das, 2021). These floral and reproductive traits serve as important distinguishing features between the two closely related *Vigna* species.

Plant Genetic Resources

Plant genetic resources comprise the genetic material of plants that possess actual or potential value for food production, agriculture and crop improvement. In mungbean and urdbean, these resources include a diverse array of genetic materials, such as landraces, traditional and obsolete cultivars, advanced breeding lines, wild relatives and related species within the genus *Vigna*. The collection, conservation and effective utilization of these genetic resources are essential for crop improvement.

In mungbean and urdbean, genetic diversity has evolved through adaptation to diverse agro-climatic conditions and continuous selection by farmers and breeders for desirable traits such as nutritional quality, yield, and stress tolerance. India is considered an important center of diversity for various legumes, which include mungbean and urdbean (Zeven & Zhukovsky, 1975; Hawkes, 1983). Systematic efforts for germplasm conservation and collection began with the foundation of the ICAR-National Bureau of Plant Genetic Resources in 1976, which has since played a crucial role in conserving huge collections of pulse germplasm under *ex situ* conditions and facilitating their utilization in breeding programmes (Rana et al., 2016).

Germplasm collection and conservation
Mungbean

Mungbean genetic resources are extensively conserved across national and international gene banks, reflecting the broad spectrum of germplasm. One of the oldest and most significant collections is sustained at the N. I. Vavilov Research Institute of Plant Industry, Russia, which houses several early-collected mungbean accessions (Gayacharan et al., 2019). Worldwide, more than 43,000 greengram germplasm accessions are conserved under *ex situ* conditions, indicating the broad genetic base and importance of this crop in diverse agro-ecological regions (Gayacharan et al., 2019; Irfan et al., 2025).

Within India, the greengram germplasm collection began as early as 1925; however, systematic and organized efforts were initiated after the setup of the ICAR-National Bureau of Plant Genetic Resources (NBPGR) in 1976. The National Gene Bank at NBPGR, New Delhi, serves as the central repository for germplasm collection, introduction and conservation. It currently conserves more than 11,000 mungbean accessions, which include both exotic and indigenous collections, which are sustained under prolonged storage conditions at –20°C (Bisht et al., 2004; Gayacharan et al., 2019). Besides these large collections, the ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, keeps an active working collection of 1,060 mungbean accessions, which are primarily utilized in breeding and crop improvement programmes.

At the international level, the World Vegetable Center conserve one of the wide-ranging collections of green gram genetic resources, with approximately 6,700 accessions (Schafleitner et al., 2015). Other important repositories include the USDA National Plant Germplasm System as well as national gene banks in countries such as Thailand, Japan, Austria, Australia and China, all of which contribute significantly to global conservation efforts. Furthermore, a substantial number of mungbean accessions are preserved as safety duplicates in the Svalbard Global Seed Vault, ensuring long-term security against genetic erosion (Bisht et al., 2004; Gayacharan et al., 2019). Collectively, these national and international efforts play an important role in safeguarding mungbean genetic diversity and provide a significant resource base for crop improvement programmes intended to develop nutritionally improved, stress-resilient and high-yielding cultivars.

Urdbean

Urdbean germplasm is preserved and maintained in several national and international gene banks, with India recognized as the primary center of diversity for this crop (Verma et al., 2022). The ICAR-NBPGR, New Delhi, serves as the principal repository for urdbean germplasm in India. Earlier reports indicated the conservation of approximately 3,153 urdbean accessions (Kaewwongwal et al., 2015; Verma et al., 2022). However, recent estimates suggest that the collection has increased to around 3,200–3,300 accessions by 2025–2026 due to continuous exploration, collection and conservation efforts (Verma et al., 2022; Swamy, 2023). Complementing this, the ICAR-IIPR, Kanpur, maintains an active working collection of about 310 urdbean accessions, which are extensively used in breeding programmes and varietal development.

At the global level, urdbean germplasm is relatively limited compared to mungbean, comprising approximately 6,500–7,000 accessions (Schafleitner et al., 2015). These are distributed across major repositories in countries such as Thailand (1,200 accessions), Pakistan (950 accessions), Taiwan (900 accessions), the World Vegetable Center, Japan (450 accessions) and the United States (300 accessions)

(Verma et al., 2022; Swamy, 2023). These collections represent a valuable pool of genetic diversity that is important for breeding programmes aimed at developing improved cultivars with valuable traits, which includes disease resistance, determinate growth habit, early maturity, and adaptability to diverse agro-climatic conditions (Verma et al., 2022). The availability and effective utilization of this germplasm collection have significantly contributed to varietal improvement and continue to support ongoing genetic enhancement efforts in urdbean.

Wild relatives

Crop wild relatives are a rich source of genetic variations and provide valuable traits that can be exploited in breeding programmes. In mungbean and urdbean, a number of wild *Vigna* species have been identified as important genetic resources for the development of improved cultivars with enhanced productivity and adaptability.

Wild relatives of mungbean & urdbean

Two important legumes of the subgenus *Ceratotropis* of the genus *Vigna*, mungbean and urdbean, possess several wild relatives that serve as rich sources of genetic diversity for breeding programmes. The cultivated mungbean is believed to have originated from *Vigna radiata* var. *sublobata*, while *Vigna mungo* var. *silvestris* is considered the immediate wild progenitor of black gram (Lukoki et al., 1980). These wild forms generally exhibit primitive characteristics such as seed shattering, indeterminate growth habit and small seeds, but they are highly important because they possess valuable genes for disease resistance, tolerance to abiotic stresses and insect pest resistance (Tomooka et al., 1992; Nair et al., 2024; Chandel et al., 1984).

In addition to their direct progenitors, some *Vigna* species, such as *Vigna trilobata*, *Vigna vexillata* and the cultivated species *Vigna umbellata* (rice bean), have been identified as important genetic resources for both mungbean and urdbean improvement programmes. These species contribute desirable traits including resistance to mungbean yellow mosaic disease (MYMD), bruchid resistance, drought and salinity tolerance and wider adaptability to diverse agro-climatic conditions (Kaewwongwal et al., 2015; Bisht et al., 2004). Among these, *Vigna umbellata* has been particularly useful in urdbean improvement through interspecific hybridization for transferring disease resistance and yield-related traits (Dana, 1998; Singh & Bains, 2006; Singh et al., 2013).

Although mungbean and urdbean share several common wild relatives, some differences exist in their utilization. In mungbean, wild species are mainly exploited for improving the capacity to endure biotic and abiotic stresses and broadening the genetic base, whereas in urdbean, emphasis has also been placed on improving seed traits and yield components. However, the use of wild forms in both crops is often constrained by cross-compatibility barriers and reduced hybrid fertility. Despite these limitations, wild *Vigna* species continue to play a major role in enhancing genetic variation and developing improved cultivars with better stress tolerance and adaptability (Gupta & Kumar, 2006).

Gene Pool

The gene pools of mungbean and urdbean are classified into primary, secondary and tertiary groups according to the concept of genetic relationships and cross ability suggested by Harlan and de Wet (1971). In both

crops, the primary gene pool (GP1) comprises the cultivated species along with their immediate wild progenitors. In mungbean, GP1 includes cultivated *Vigna radiata* and *Vigna radiata* var. *sublobata* (Singh et al., 2022), in urdbean, it comprises *Vigna mungo* var. *mungo* and its wild form *Vigna mungo* var. *silvestris*. These species are easily crossable and generally produce fertile progenies, making them highly useful in breeding programmes (Singh & Bains, 2006; Kaewwongwal et al., 2015).

The secondary gene pool (GP2) includes closely related *Vigna* species such as *Vigna mungo, Vigna radiata*, *Vigna trilobata* and *Vigna umbellata* (rice bean). Hybridization among these species is possible; however, it is often associated with partial sterility, reduced fertility and other crossability barriers due to genetic or cyto-genetic incompatibility (Dana & Karmarkar, 1990; Sharma et al., 2022).

The tertiary gene pool (GP3) of both crops includes distantly related species such as *Vigna vexillata*, where gene transfer becomes difficult because of strong reproductive barriers (Evans et al., 1976; Smart, 1981; Chandel & Laster, 1991). Introgression of useful genes from these species generally requires advanced breeding programmes such as embryo rescue and other biotechnological techniques (Singh & Bains, 2006). Overall, the gene pool classification of mungbean and urdbean provides an important framework for identifying suitable genetic resources and broadening the genetic base for crop improvement programmes.

Breeding Objectives

Yield improvement

The major aim of breeding programmes for mungbean and urdbean is to develop climate-smart, high-yielding cultivars, as these crops are typically grown in low-input, stress-prone environments. Yield is a complex quantitative trait governed by numerous genes and strongly influenced by environmental conditions. Consequently, selection in mungbean breeding is often based on traits that contribute directly to yield improvement (Du et al., 2025). Key traits under selection include seed weight, the number of pods / plants, and the number of seeds/pod, in addition to improved branching, higher flowering nodes, better pod setting, and reduced flower drop. In both crops, the main obstacles to higher yields are the limited genetic variability, the lack of favourable crop ideotypes for diverse cropping patterns, low harvest index, and vulnerability to different stresses. Additionally, the accessibility of quality seeds of better-quality varieties remains a challenge. Notwithstanding persistent challenges, the last decade has witnessed substantial advancements, with breeding efforts increasingly targeted toward enhancing biotic stress resistance and maximizing yield potential (Nair et al., 2020). Modern approaches, including interspecific hybridization assisted with MAS, are being deployed to overcome traditional bottlenecks and accelerate genetic gains.

Early maturity

Early maturity in pulse crops is an important breeding and agronomic trait that allows crops to complete their life cycle within the available growing window. Early-maturing mungbean varieties are highly suitable for intensive cropping systems like rice–wheat and rice–rice rotations, where only a short window is available between major crops. Early types in urdbean are particularly important in rainfed and rice-fallow ecosystems where soil moisture becomes limited after the monsoon. Their short duration allows farmers to fit an additional crop into the cycle without delaying the main seasonal crops. It helps the crop in evading terminal drought, high temperature stress and late-season pest & disease attacks. It also enables timely sowing of the next crop, improving cropping intensity and resource use efficiency. Moreover, fitting of a short-duration

legume crop like mungbean or urdbean also adds nitrogen through the symbiotic inherent ability of the soil for the next cereal crop.

Early-maturing mungbean varieties generally take about 55–65 days to mature. Several widely adopted early-maturing varieties have been developed by leading research institutions. These include SML 668 from Punjab Agricultural University (Ludhiana), IPM 02-3, Virat and Samrat from the ICAR- IIPR (Kanpur), Pant Mung 5 from GB Pant University (Pantnagar), HUM 12 from Banaras Hindu University (Varanasi) and TMB 37 from BARC (Mumbai). These varieties are popular because of their adaptability, consistent performance and suitability across diverse agro-climatic zones. Over time, many such short-duration varieties have been released for different regions, giving farmers flexibility to choose cultivars that match their local climate, soil type, and cropping system (Mishra et al., 2025).

Early-maturing urdbean varieties mature in about 60–70 days compared to 80–90 days in medium and late types. Popular early maturing varieties include Mash 1137, Mash 1008, T-9, PU-31, Pant U-19, PU-35, LBG 752, PDU-1 and UG 218. Many potential donors like STY 2848, PLU 710, IPU 31-5, L 25-7 and IPU 96-3, have also been identified for early maturity for use in breeding programmes of urdbean (Gupta et al., 2001). In urdbean, early maturing types are generally dwarf with short internodes, often maturing after the first flush of flowers, and require good early vigour for better performance. Based on several agro-morphological attributes, 46 urdbean cultivars were grouped (Katiyar et al., 2010). Among these, T-9 was found to be particularly appropriate for spring. Moreover, lower plant height is also a crucial trait for early maturing varieties and about 20 varieties, in addition to T-9, were placed in this category (Katiyar et al., 2010). However, newer genotypes like IPU 19-27 show even earlier maturity (60–65 days) and improved performance in certain regions (Gupta et al., 2020).

In addition to early maturity, mungbean breeding programmes focus on incorporating resistance to lodging and pod shattering, together with an erect and uniform plant architecture, to enhance suitability for mechanical harvesting. These traits contribute to improved harvest efficiency by reducing pre- and post-harvest seed losses, ensuring greater harvestability, and facilitating a once-over harvest. The development of such ideotypes helps reduce labour requirements and production costs while improving harvest index, operational efficiency, and overall economic returns.

Resistance breeding

Biotic stresses

At present, the productivity of both legume crops is significantly impacted by several biotic stresses that include viral, fungal, and bacterial diseases, as well as insect pests. Major constraints include YMD, powdery mildew, anthracnose, cercospora leaf spot, dry root rot, bacterial leaf spot and bruchid infestation. Although chemical control measures are available, they are often costly and environmentally hazardous. Therefore, HPR (host plant resistance) remains the most cost-effective, eco-friendly and sustainable strategy against these stresses.

Yellow Mosaic Disease

Yellow Mosaic Disease (YMD), caused by Mungbean Yellow Mosaic Virus (MYMV) and Mungbean Yellow Mosaic India Virus (MYMIV), is the most devastating viral disease of both crops, causing severe

yield losses. Since chemical control of the whitefly vector is often ineffective and environmentally undesirable, host plant resistance remains the most sustainable management strategy. Extensive screening has identified several resistant sources in mungbean, *viz.*, Pusa 0672, HUM16, IPM-02-03, IPM-02-14, ML-5, PM-2, PDM 139 (Subedi et al., 2016; Paul et al., 2013; Bhanu et al., 2017; Datta et al., 2012; Nair et al., 2020; Asthana,1998; Mohan et al., 2014). The mungbean donors registered with NBPGR for YMD resistance are IPM526-11 (IC641993) and LGG 607 (IC639816). For urdbean, the most consistently reported and repeatedly validated donors for resistance to YMD are PU 31, PU 35, LBG 20, Uttara, NDU12-1, NIRB002, NIRB003, NIRB004, IPU96-6, IPU99-220, IPU13-7, NP21, IPU13-3 and PLU99-10. The urdbean donors registered with NBPGR for YMD resistance are PU06-14 (IC570262), PU06-23 (IC570264), PU6-24 (IC570265), PU06-19 (IC570267), PU06-20 (IC570268), IC572, IC11613, IC485638, IPU19-27 (IC636672), LBG 884 (IC639815). Wild species such as *Vigna radiata* var. *sublobata*, *V. trilobata*, and *V. mungo* var. *silvestris* have also been recognized as rich sources of resistance genes (Pandiyan et al., 2017). The inheritance of YMD resistance is highly variable, with reports of monogenic dominant, monogenic recessive, digenic dominant, digenic recessive, complementary recessive, and polygenic inheritance, depending on the genotype and virus strain (Dhole & Reddy, 2012; Nair et al., 2020). The use of interspecific hybridization for integrating novel resistance genes from wild *Vigna* species remains a key strategy for developing durable YMD-resistant mungbean and urdbean varieties.

Powdery mildew

Powdery mildew, caused primarily by *Erysiphe polygoni* DC. and occasionally by *Oidium* spp., is a significant fungal disease of mungbean and urdbean that can cause substantial economic losses under favourable environmental conditions. Among the various management practices, the production and cultivation of improved elite varieties remain the most effective and environmentally sustainable management strategy. In mungbean, several resistant sources have been identified, including PMR-1, VC1560D, VC6144A, ML 1720, ML 818, and IPM series genotypes, while the wild relative *V. radiata* var. *sublobata* has provided valuable novel resistance genes for breeding programmes (Reddy et al., 1994; Chankaew et al., 2013). Similarly, in urdbean, genotypes such as LBG-20, PU-31, LBG-17, Pant U-30, IPU 02-43, Pant U-19 and VBN (Bg) 4 have demonstrated stable resistance across environments (Basandrai et al., 2011; Singh et al., 2015; Gupta et al., 2020). Genetic studies have shown that powdery mildew resistance is predominantly governed by a single dominant gene in many resistant sources, although oligogenic or polygenic inheritance with the influence of minor modifier genes depending on the genetic background and pathogen variability has also been reported (Reddy et al., 1994; Basandrai et al., 2011). The availability of diverse resistant donors, coupled with a deeper understanding of the inheritance of powdery mildew resistance, has greatly facilitated the transfer of resistance into elite genetic backgrounds. Through the application of conventional breeding, marker-assisted selection, and gene pyramiding approaches, substantial progress has been made in developing durable powdery mildew-resistant cultivars of both legumes.

Cercospora leaf spot (CLS)

Cercospora leaf spot (CLS), caused mainly by *Cercospora canescens* and *C. cruenta*/*Pseudocercospora cruenta*, is a major foliar disease of both legumes, causing significant yield losses through reduced photosynthetic area, premature defoliation, and poor pod filling. HPR is the most economical and sustainable management approach. In mungbean, resistance is predominantly quantitative in nature, involving polygenic or oligogenic inheritance with additive and epistatic gene effects. Resistant sources such as VC3960A,

ML1037, HUM12, and several recently identified germplasm accessions have been utilized in breeding programmes (Asadullah et al., 2024). In urdbean, resistant and moderately resistant genotypes including HPBU 51, P 38, TEU 95-1, BLG 0069-1, BLG 0068-2, and other advanced breeding lines have been identified as suitable donors for resistance breeding (Saha et al., 2017; Shrestha et al., 2024). Recent progress in black gram genomics, including genome sequencing, SNP discovery, and molecular marker development, is expected to accelerate the identification of resistance loci and the development of durable CLS-resistant cultivars through MAS (Nair et al., 2024).

Anthracnose

Anthracnose, caused primarily by *Colletotrichum truncatum*, is an important fungal disease of mungbean and urdbean that affects leaves, stems, petioles, and pods, which leads to economic and quality losses under congenial conditions. In mungbean, resistance is generally quantitative in nature, involving multiple genes, although monogenic resistance has been reported in some sources. Resistant genotypes such as VC1973A, VC2750A, and other AVRDC-derived lines have been recognized and utilized in crop improvement programmes. Wild relatives, particularly *Vigna radiata* var. *sublobata*, also serve as valuable sources of novel resistance genes. In urdbean, anthracnose resistance has been suggested to be governed predominantly by major dominant genes. Studies involving resistant donors KUG-216 and IPU-05-13 demonstrated dominant inheritance of resistance based on segregation patterns observed in F_1, F_2, and backcross generations (Bindra, 2016). Several resistant genotypes, including HPBU 71, HPBU 125, KUG-216, and IPU-05-13, have been identified as useful donors in breeding programmes. However, the existence of pathogenic variability and multiple races of *C. truncatum* necessitates the deployment of broad-spectrum resistance sources (Katoch et al., 2016). Recent advances in molecular breeding, including the use of SSR and SNP markers, QTL mapping, and MAS, are facilitating the rapid development of durable anthracnose-resistant cultivars in both mungbean and urdbean.

Insect resistance

The key insect-pests affecting mungbean can broadly be categorized into field pests and storage pests. Field pests include whitefly, aphids, stem fly, thrips, jassids, and pod borers. Whitefly is particularly important because it acts as the vector of MYMV. Stem fly infestation causes tunnelling within stems, resulting in poor plant vigour and reduced yield. Thrips and aphids damage flowers and foliage by sap sucking, thereby reducing pod formation. Bruchids are the most destructive storage pests of mungbean. Infestation may begin *in-vivo* and continue during storage, where larvae feed internally on seeds, causing substantial deterioration in seed quality, weight, germination, and market value. Because chemical control during storage raises concerns related to residues, resistance breeding has received significant attention. Extensive germplasm screening programmes conducted at the World Vegetable Center and other research institutions identified several resistant sources against major insect pests. The wild accession TC1966 (*Vigna radiata* var. *sublobata*) from Madagascar was the first highly resistant donor reported against *Callosobruchus* spp. showing complete resistance to both *C. chinensis* and *C. maculatus*. Subsequently, resistant cultivated lines such as V2802, V2817, V1128 and V2709 were identified and utilized in breeding programmes. Talekar and Lin (1992) extensively screened mungbean germplasm and reported that resistant genotypes significantly reduced oviposition, larval development, and adult emergence of bruchids. However, incorporation of resistance from wild species often resulted in linkage drag, particularly pod shattering and poor agronomic

traits. Resistance sources against the stem fly were identified by AVRDC and CIAT. Genotypes such as V2396, V3495, V4281, G05253, G05776, and Co 3 showed resistant reactions under field conditions.

Early genetic studies demonstrated that resistance derived from TC1966 was governed by a single dominant gene designated as Br. Fujii and Miyazaki (1987), Kitamura et al. (1988), and Fujii et al. (1989) independently confirmed monogenic dominant inheritance for resistance to *Callosobruchus* spp. Further investigations revealed that resistance may involve different genes depending on the donor source. Somta et al. (2007, 2008) reported multiple quantitative trait loci (QTLs) associated with bruchid resistance in cultivated and wild mungbean accessions. Some resistant lines exhibited complementary gene interactions, while others showed polygenic inheritance. Young et al. (1992) conducted one of the earliest molecular mapping studies in mungbean and mapped the major bruchid resistance gene using RFLP markers on linkage group VIII. The resistance locus was located about 3.6 cM from the closest marker, facilitating marker-assisted breeding. Subsequent studies identified tightly linked SSR and SNP markers associated with resistance loci, significantly improving selection efficiency in breeding programmes. Marker-assisted introgression has enabled the transfer of resistance genes into elite backgrounds while minimizing linkage drag.

Compared with bruchid resistance, relatively limited information is available regarding the inheritance of stem fly resistance. Most studies indicate quantitative inheritance involving additive gene effects. Resistance is generally associated with stem toughness, trichome density, and biochemical constituents that reduce larval penetration and development. Some reports suggested that additive gene action predominates, thereby making recurrent selection and pedigree breeding effective for improving resistance. Environmental influence on stem fly incidence often complicates inheritance studies.

Whitefly resistance is generally considered quantitatively inherited and influenced by multiple genes. Morphological characters such as leaf pubescence, leaf thickness, and biochemical compounds contribute to antixenosis and antibiosis mechanisms. Studies involving segregating populations demonstrated partial dominance and additive gene effects for whitefly resistance. Because whitefly also transmits MYMV, breeding programmes often target combined resistance to both vector and virus.

Abiotic Stresses

Abiotic stresses are among the major factors limiting crop productivity across the world. In pulses like mungbean and urdbean, their impact is even more pronounced because these crops are often cultivated under rainfed on marginal lands. Key stresses such as drought, high temperature, salinity and waterlogging collectively cause substantial yield losses well below their potential (Chauhan & Williams, 2018). In recent years, due to changes in climatic conditions and increasing environmental fluctuations, these stresses have further intensified by making growing conditions more uncertain and challenging. These stresses interfere with the plant's ability to efficiently use essential resources like water, nutrients and light, thereby affecting growth and development at various levels (Haeften et al., 2023). Plants respond to such stresses through a range of molecular, biochemical, physiological and morphological adjustments which ultimately determine their productivity. Therefore, a clear understanding of these responses is crucial for developing effective breeding strategies focused on enlightening abiotic stress tolerance in both legumes (Chauhan & Williams, 2018; Nair et al., 2019). In this context, the foremost abiotic stresses distressing mungbean and urdbean, namely heat, water scarcity, cold, waterlogging and salinity, are discussed in the following sections.

Heat Stress

Mungbean and urdbean are adapted to warm climates, but exposure to high temperatures above 35–40°C, especially during flowering and pod formation, can sharply reduce yield. Heat stress mainly affects the reproductive stage by lowering pollen viability, disturbing fertilization and increasing flower and pod drop, which together lead to major yield losses (Chauhan et al., 2010; Hanif & Wahid, 2018; Chaudhary et al., 2022). High temperature also disrupts the key functional processes, namely photosynthesis, chlorophyll content and stomatal function, resulting in reduced biomass and early leaf senescence (Sharma et al., 2016; Priya et al., 2019; Chaudhary et al., 2022). In addition, high temperatures accelerate crop development, shortening the flowering and grain filling period and limiting assimilate supply for seed formation (Basu et al., 2019). To improve heat tolerance, breeding efforts focus on traits like early maturity, stable seed set and efficient root systems, while management practices such as adjusting sowing time can help crops escape terminal heat stress (Iqbal et al., 2021; Yadav et al., 2022). Overall, heat stress remains a major constraint in both crops, particularly during reproductive growth stages (Haeften et al., 2023).

Drought Stress

Drought is another critical abiotic stress affecting mungbean and urdbean as these legume crops are primarily cultivated under rainfed conditions. Water deficit, particularly during flowering and pod development, can cause severe yield losses often greater than those observed at the vegetative stage (Uprety & Bhatia, 1989; Sadeghipour, 2009). Drought stress reduces leaf water status, leading to stomatal closure, decreased photosynthesis and chlorophyll degradation, ultimately limiting plant growth and productivity (Baroowa et al., 2016). It also restricts canopy development by reducing leaf area and plant height, which lowers radiation interception and biomass accumulation. However, maintaining leaf area and efficient water use are important adaptive traits under stress conditions. Plants cope with drought through mechanisms such as better stomatal regulation, higher leaf water potential and improved root systems that enhance water uptake from deeper soil layers (Aski et al., 2021; Singh & Bell, 2021). Early maturing genotypes with rapid root and shoot growth may perform better by escaping terminal drought. Despite these insights, research in mungbean and urdbean is still limited, particularly in integrating above and below-ground traits and further evaluation of diverse germplasm using advanced phenotyping tools is needed to support effective breeding for drought tolerance (Haeften et al., 2023; Tardieu et al., 2018).

Cold Stress

Mungbean and urdbean are also sensitive to low temperatures, especially when grown outside their optimal season or region. Exposure to cold conditions (around 15°C) during flowering can reduce growth and yield by affecting chlorophyll content, photosynthesis and key yield components (Hu et al., 2022). Prolonged cold stress can further disrupt physiological processes, including gene expression related to chlorophyll synthesis, leading to poor plant performance. In some regions, late sowing may expose crops to frost during reproductive stages, which can damage flowers and immature pods, reducing grain quality and yield (Gentry, 2010). Since these crops are usually grown in warm seasons, early flowering genotypes can help escape cold or frost stress. In many parts of India, these crops are grown as a spring crop where sowing coincides with low temperatures that reduce or delay germination and plant growth is stunted after germination. However, research progress on cold stress tolerance in mungbean and urdbean is still limited, particularly under field

conditions. Hence, this is the need of the hour to characterize varied germplasm to identify useful traits and donors for cold-tolerant varieties (Hu et al., 2022; Christy et al., 2022; Haeften et al., 2023).

Waterlogging Stress

Waterlogging is caused by excess rainfall or poor drainage, which results in a scarcity of oxygen in the root zone and poses a serious constraint to mungbean and urdbean cultivation, particularly during the reproductive stage. Excess soil moisture generates hypoxic or anoxic circumstances in the root zone, which severely restrict root respiration and metabolic activity. This lack of oxygen adversely affects root growth and nodulation, thereby impairing biological nitrogen fixation, which is a critical process for these legumes. As a result, plants exhibit poor germination and establishment, reduced vigour, and diminished growth (Pratap et al., 2013).

However, these crops can tolerate short-term flooding, but prolonged waterlogging significantly reduces yield by affecting root growth, nutrient uptake and overall plant vigour (Islam et al., 2008; Pan et al., 2021). Waterlogging stress during the flowering stage and pod filling often results in pod abortion, poor seed set and reduced grain size and quality. This also decreases root length and biomass due to root damage, which limits the supply of nutrients and assimilates required for pod development (Garrity & Pernito, 1996). Some tolerant genotypes exhibit adaptive attributes like the adventitious roots formation and the ability to recover photosynthetic activity after stress, which helps in maintaining biomass under flooded conditions (Ahmed et al., 2002). For climate change and events like increasing occurrence of drastic rainfall, improving screening methods and developing waterlogging-tolerant varieties will be crucial for sustaining mungbean and urdbean production and productivity (Setter et al., 2009; Haeften et al., 2023).

Salinity Stress

Salinity is an increasing constraint in mungbean and urdbean production, particularly in arid and semi-arid areas where soil degradation is a common problem. High salt levels reduce plant growth by limiting water intake due to osmotic stress and causing ion toxicity from excessive salt accumulation in plant tissues (Munns & Tester, 2008; HanumanthaRao et al., 2016). In legumes, salinity also interferes with biological nitrogen fixation, which affects productivity. Most studies have focused on early growth stages, where salinity delays germination and reduces root and shoot development (Misra et al., 1996; Saha et al., 2010).

However, salt tolerance at early stages does not necessarily ensure tolerance during reproductive development. Limited research indicates that salinity at later stages can lead to leaf chlorosis, reduced chlorophyll content and decreased biomass, ultimately lowering the yield (Wahid et al., 2004; Haeften et al., 2023). Hence, more research on diverse genotypes and across growth stages is needed to better understand and improve tolerance to salinity in mungbean and urdbean (Ahmed et al., 2009).

Breeding Strategies and Molecular Approaches for Abiotic Stress Tolerance

Breeding for abiotic stress tolerance in mungbean and urdbean is complex due to the quantitative nature of stress-responsive attributes and their interaction with the environment. Conventional approaches have focused on selecting tolerant germplasm and developing early maturing varieties to escape terminal stresses such as drought and heat.

In addition, key physiological traits like efficient water use, membrane stability and strong root systems are increasingly targeted to enhance resilience. The incorporation of molecular tools, including MAS, has further enhanced the effectiveness and precision of breeding programmes. The stress-tolerant genotypes identified through these approaches serve as valuable donor parents for future crop improvement programmes (Sehgal et al., 2018). The major sources of abiotic stress tolerance in mungbean and urdbean are summarized in Table 1.

Table 1. Major sources of abiotic stress tolerance in mungbean and urdbean

Abiotic stress	Source of Tolerance in Mungbean	Source of Tolerance in Urdbean	References
Drought	ML 2082, K-851, IC-325770 and VC-6173-C	PU 19, PU 31, LBG 623, VBN(Bg)4, CBG-09-13, Vamban 2 and VBN(Bg)6	Solanki et al. (2011), Dutta et al. (2016), Prakash et al. (2017), Pandiyan et al. (2017), Dutta & Bera (2008)
High temperature stress	Harsha, ML1299, EC693369, EC693358 and EC693357	IPU 94-2, Pant Urd 31, BGP 247, NO-5731, IPU 98/36, UPU 85-86 and PGRU 95016	Sharma et al. (2016), Bindumadhava et al. (2018), Gupta et al. (2021), Nair et al. (2024)
Low temperature stress	Perennial accessions of *V. radiata* var. *sublobata* and PAU911	IPU 94-1, BGP 247, VBG-06-010, UPU 85-86 and PGRU 95016	Gupta et al. (2021), Manasa et al. (2023)
Waterlogging	V 3372, V 3092, V 2984, and V 1968	Mash 114, Uttara, EC319031–33, TC-100190, TC-100193 and TC-100353	AVRDC (1979), Negi & Muneem (1998), Rana et al. (2016)
Salinity	BB92R, TCR86, PLM380, WGG37, K-851 , IC615, IC2056, IC10492, PLM32, PLM891 and PLM562	VBN (Bg) 4, CO 5 and ADT 3	Sehrawat et al. (2014), Gayacharan et al. (2023)

With the advancement of modern approaches, breeding strategies are increasingly integrating molecular and genomic methods to accelerate the development of stress-resilient cultivars. MAS, along with genomics, proteomics and metabolomics strategies, has facilitated the recognition of stress-responsive genes and QTLs associated with tolerance mechanisms.

Furthermore, the adoption of high-throughput phenotyping platforms, including imaging and automation-based systems, has improved the precision and efficiency of trait evaluation under stress conditions. Despite these advancements, breeding success remains constrained by factors such as the interaction of multiple stresses, difficulty in accurate phenotyping of complex attributes and the relatively narrow genetic base of cultivated germplasm (Nair et al., 2019).

Quality Improvement

Both mungbean and urdbean are major parts of the daily diets of vegetarians in several countries, including India. Based on their uses for various culinary purposes, different quality parameters are important for nutritional security. For quality improvement, the major aims focus on enhancing nutritional value while lowering anti-nutritional compounds through breeding and genetic techniques. Besides protein, a major quality trait, the other important traits include increasing grain iron (Fe) and zinc (Zn) levels to help reduce micronutrient deficiencies, and decreasing phytic acid and tannin content, which interfere with nutrient absorption. In urdbean, other compounds such as trypsin inhibitors reduce protein digestibility by inhibiting digestive enzymes, while oligosaccharides like raffinose and stachyose can cause flatulence. Recent advances in molecular technologies such as GBS, SNP identification, and association mapping have made it easier to locate particular genomic regions and genes responsible for these traits, supporting the development of elite varieties of both legume crops with better nutritional benefits.

The study analyzed genetic diversity for iron, zinc, phytic acid, and tannin components in mungbean using 127 genotypes and identified 14,447 SNPs through GBS. Two genotypes, IPM 02-19 and PUSA 1333, showed high nutrients and low anti-nutrients. Association mapping revealed significant SNPs and 185 candidate genes linked to these traits, providing useful markers for improving nutritional quality in mungbean breeding (Sinha et al., 2023). The germplasm useful for enhancing nutritional quality in urdbean has been identified by many workers (Nair et al., 2024). Many genotypes like LBG17, K1, Malabiri local, Boudha local, G. Udayagiri local, IPU 11-02, HIM Mash, UG-218 and UG-218 with high protein content have been reported in different studies (Kole et al., 2002; Rana et al., 2016). There is a wide scope for biofortification in urdbean, and a large number of accessions have been reported, out of which, iron- and zinc-rich accessions have been identified that can be utilized to develop biofortified cultivars aimed at improving nutritional quality and reducing mineral deficiencies (Singh et al., 2017).

Genetics of Important Traits

Precise knowledge of genetics, along with the availability of sufficient variability, is fundamental to directed crop improvement programmes. Understanding the inheritance of economically important traits is essential because information on the same assists breeders in formulating efficient breeding and selection strategies for the development of elite cultivars. Knowledge of the mode of inheritance also helps in determining whether a trait is governed by simple or complex genetic mechanisms, thereby facilitating the choice of appropriate breeding approaches for trait improvement. Overall, numerous investigations on the genetic analysis of both oligogenic and polygenic traits in mungbean have provided valuable insights into their inheritance patterns and gene actions, thereby contributing significantly to the formulation of effective crop improvement strategies (Tables 2a, b).

Table 2a. Genetic control of economically important quantitative and qualitative traits in mungbean

Trait	Donor	Genetic Control	References
Growth habit and Plant type	T44 × NP36; spreading × erect derivatives	Twining growth habit - Single dominant/ recessive gene; semi-spreading is dominant over erect habit	Pathak & Singh (1963); Sen & Ghosh (1959)

Lobbed Leaf	Lobed leaf mutant selection from indigenous mungbean germplasm	Single dominant gene; Dominant: Large leaflet, lobbed Recessive: Small leaflet, entire type	Singh (1980), Talukdar & Talukdar (2003)
Incised leaflet and Ovate leaflet	Incised leaflet mutant lines	Dominant gene and its alleles	Pokle (1972)
Unifoliate and multifoliate Leaflets	Multifoliate mutant derivatives	Recessive genes	Santos (1969)
Trilobite leaf	Trilobite mutant accession	Dominant gene over normal monolobate	Sareen (1985)
Pubescence	NP36 × T44	Single dominant gene	Sen & Ghosh (1959), Murty & Patel (1973),
Seed Coat	NP36 × Type 1; green × black seeded lines	Two complementary genes	Murty & Patel (1973), Sen & Ghosh (1959), Bose (1939)
Blue sap colour	Blue sap pigmented mutant	Single dominant gene	Sen & Ghosh (1959)
Buff sap colour	Buff sap mutant line	Single recessive gene	
Green and spotted seed colour	Spotted seeded accessions from African germplasm	Dominant genes	van Rheenen (1965)
Black spot	Black spotted mutant line	Single dominant gene	Singh & Singh (1970)
Seed coat colour	VC1973A and related AVRDC lines	Oligogenic; Mottling: single gene	Lambrides et al. (2004), Chen & Liu (2001), Khattak et al. (1999)
Flower colour	Bryta yellow and naphthalene yellow mutants	Allelic series of three genes	Murty & Patel (1973)
Pod colour	Green pod × pigmented pod crosses	Single dominant gene	Murty & Patel (1973), Sen & Ghosh (1959), Bose (1939)
Purple pigmentation in the vertical suture of unripe pods	Purple sutured pod mutant	Single dominant gene	
Light popcorn and almond biscuit color	Seed colour mutants from AVRDC germplasm	Two independent recessive genes	
Black pod Color	Black pod mutant line	Two dominant alleles	

Brown pubescence	Brown pubescent accession	Recessive gene	Sen & Ghosh (1959)
Colour less pubescence	Colour less pubescent mutant	Two dominant alleles	
Anthocyanin in hypocotyl	T1 × NP36	Single dominant/recessive gene, Two supplementary genes	Mukherjee & Pradhan (2002), Mishra et al. (1970), Pathak & Singh (1963)
Red color of cotyledon, hypocotyl and top of the leaf stalk	Red pigmented mutant lines	Single dominant gene Multiple allelic series	van Rheenen (1965), Sen & Ghosh (1959)
Purple hypocotyl	Purple hypocotyl mutant	Single dominant gene	Swindell & Poehlman (1978)
Anthocyanin pigmentation in the hypocotyl, stem, petiole and Peduncle	Pigmented local accession	Single recessive gene	AppaRao & Jana (1973)
Cotyledon Colour	Green cotyledon mutant	Single recessive: green colour	Thakare et al. (1988)
Inflorescence Type	Compound × simple inflorescence types	Simple types: two dominant genes Compound types: double recessive homozygous; number of clusters: single gene	Singh & Singh (1970), Sen & Ghosh (1959)
Stem fasciation	Fasciated mutant from Pusa lines	Single recessive gene	Dwiwedi & Singh (1990)
Hard-seededness	TC1966; wild *Vigna radiata* var. *sublobata* accessions	Oligogenic	Humphry et al. (2005), Singh (1983), Lambrides (1996)
Pod shattering	Wild × cultivated derivatives	Single dominant gene	Verma & Krishi (1969)
Seed weight	Small seeded × bold seeded crosses	Dominant: Small	Humphry et al. (2005), Fatokun et al. (1992), Sen and Murty (1960)

Pre-harvest sprouting	Contrasting germplasm lines	Gene action: Additive and non-additive; High G x E interaction	Durga & Kumar (1997)
Nodulation	High nodulating × low nodulating lines	Gene action: Additive and non-additive	Singh et al. (1985)
Crop duration	Early maturing × late maturing lines	Gene action: Additive, non-additive, epistatic	Khattak et al. (2001)
Protein content	High protein × low protein lines	Gene action: Additive and non-additive	Chandra & Tickoo (1998)
Yield components	Pusa Baisakhi × ML 5 and related crosses	Gene action: Additive and non-additive	Khattak et al. (2002), Dasgupta et al. (1998), Yohe & Poehlman (1975), Singh & Singh (1972)
YMD resistance	ML 818 × susceptible lines; NM 92; HUM 8	Monogenic dominant	Sandhu et al. (1985); Gupta et al. (2005)
	VRM (Gg) 1 × CO 5	Digenic dominant	Mahalingam et al. (2018)
	Kopergaon × susceptible cultivars	Digenic recessive	Bhanu et al. (2018), Singh et al. (2013) ole & Reddy (2012)
	PIMS 1 × susceptible parent	Complementary recessive genes	Shukla & Pandya (1985), Thamodhran et al. (1988),
	Resistant local donor derivatives	Three recessive genes	Mishra & Asthana (1996)
Cercospora leaf spot (CLS) resistance	ML 172; V4718; AVRDC resistant lines	Single dominant gene	AVRDC (1981a, b), Thakur et al. (1977a, b, c), Singh & Patel (1977), Lee (1980),
	Resistant indigenous accessions	Single recessive gene	Singh et al. (2008), Mishra et al. (1988), Thakur et al. (1980)
	AVRDC breeding populations	Polygenic genes	Chankaew et al. (2011)

Bacterial leaf spot (BLS) resistance	Local resistant germplasm selections	Single recessive gene	Yadav et al. (1981)
Powdery mildew resistance	VC2750A; AVRDC resistant lines	Single dominant gene	AVRDC (1979)
	Resistant × susceptible crosses	Genes with additive effects	Young et al. (1993), Yohe & Poehlman, (1975), Sorajjapinun et al. (2005)
	AVRDC resistant derivatives	Recessive polygenes	AVRDC (1981a, b)
	CN72 and related Thai accessions	Non-allelic dominant gene	Khajudparn et al. (2007)
Bruchids (*Callosobruchus* spp.) resistance	TC1966	Monogenic dominant	Fujii & Miyazaki (1987), Kitamura et al. (1988)
		Single dominant gene	Kitamura et al. (1988), Ishimoto & Kitamura (1993), Lei et al. (2008), Sarkar & Bhattacharya (2014)
	V2709, V2802	Quantitative/major gene	Somta et al. (2008)

Table 2b. Genetic control of economically important quantitative and qualitative traits in urdbean

Trait	Donor/Source	Genetic Control	Reference
Growth habit (twining)	T9, local landraces	Single dominant gene for twining growth	Pathak & Singh (1963), Sen & Ghosh (1959),
Plant height	Various germplasm lines	Quantitative; predominantly additive gene action	Singh & Singh (1979), Panigrahi et al. (2014)
Days to flowering	PU-19, T9, Pant U-30	Polygenic inheritance with additive and dominance effects	Ghafoor et al. (2000)
Days to maturity	Pant U-19, TU 94-2	Quantitative inheritance; additive gene action important	Khajudparn et al. (2012)
Pod length	VMU-4, PU-31	Polygenic inheritance with additive effects	Ghafoor et al. (2000)
Pods per plant	T9, Pant U-35	Quantitative trait Gene action: additive and non-additive gene effects	Panigrahi et al. (2014), Makeen et al. (2007)

Seeds per pod	PU-31, LBG-623	Polygenic inheritance; additive effects predominant	Singh & Singh (1979)
100-seed weight	Mash-114, PU-31	Mainly additive gene action; moderate heritability	Ghafoor et al. (2000), Panigrahi et al. (2014)
Seed yield per plant	Various elite cultivars	A complex quantitative trait controlled by multiple genes with additive and dominance effects	Singh & Singh (1979), Makeen et al. (2007)
Protein content	IC-145202, IC-436519	Polygenic inheritance with additive gene effects	Gupta et al. (2008)
Seed coat colour (black)	T9, Mash cultivars	Single dominant gene for black seed coat	Pathak & Singh (1963), Khattak et al. (1999)
Seed coat colour (green)	Green-seeded mutants	Recessive inheritance	Khattak et al. (1999)
Leaf shape (lobed leaf)	Lobed leaf mutants	Single dominant gene	Gupta & Singh (1984)
Leaf size	Large-leaf genotypes	Large leaflet is dominant over small leaflet	Gupta & Singh (1984)
Yellow Mosaic Disease (YMD) resistance	PU-31, VMU-4, Mash-114	Single recessive gene, duplicate recessive genes, and oligogenic inheritance reported depending on source	Singh (1980), Basak et al. (2004)
Powdery mildew resistance	IC-76381, IC-39822, PU-31	Single dominant gene in several resistant sources	Singh & Singh (1988), Souframanien & Gopalakrishna (2006)
Cercospora leaf spot resistance	IC-145202, PU-31	Quantitative inheritance with additive effects	Singh et al. (2015)
Anthracnose resistance	KUG-216, IPU-05-13	Single dominant gene	Bindra (2016)
Urdbean Leaf Crinkle Disease (ULCD) resistance	TU-94-2, Pant U-31	Monogenic recessive and oligogenic inheritance reported	Bashir et al. (2005)
Bruchid resistance	Wild *Vigna mungo* accessions	Quantitative inheritance; resistance associated with seed biochemical factors	Somta et al. (2007), Talekar & Lin (1992)
Drought tolerance	Wild relatives and landraces	Polygenic inheritance with additive effects	Singh et al. (2011)

Breeding Methods

Conventional Method

The structured varietal improvement programmes were initiated following the setup of the All India Coordinated Pulses Improvement Project (AICPIP) in 1967. In the early phase, the main focus was on the genetic improvement of locally adapted yet heterogeneous populations through pure line and mass selection, primarily targeting adaptive and agronomic traits rather than yield attributing traits. This approach led to the development and release of numerous pure line cultivars, and a few of them remain in cultivation in specific

agro-ecological zones. Subsequently, breeding strategies shifted towards hybridization followed by selection, and in recent decades, these efforts have expanded to include distant hybridization aimed at broadening the genetic base and facilitating the introgression of beneficial traits.

Intensive breeding efforts in mungbean in India initially relied on direct selection from indigenous landraces and introduced germplasm, beginning with the release of 'Mung Type 1' in 1936 from Muzaffarpur, Bihar, which later served as a key parent in developing many other varieties. Hybridization efforts also led to varieties like Mohini (S 8) and KM-1, the latter derived using Iranian germplasm and becoming widely popular in southern India. The AVRDC has played a key role globally by providing diverse germplasm (plant genetic resources), especially for mungbean, which is instrumental for the development of high-yielding short-duration cultivars such as SML 668, Pusa Vishal and Pant Moong 5.

Indigenous landraces played a pivotal role in early urdbean breeding in India, with half of all varieties released between 1949 and 2000 originating from local genetic selections. The heavy reliance on these adapted local resources highlights their foundational importance in breeding efforts during this period. A prime example is the T9 variety, developed from a landrace in Bareilly (Uttar Pradesh), which became a widely used parent in numerous breeding programmes, notes a 2010 report (Goyal and Khan, 2010; Katiyar et al., 2017). Then by using pure line selection from local germplasm, varieties such as ADT 3, ADT 1, CO 5, CO 2, CO1, CO 3 were developed (Gupta and Kumar, 2006; Tickoo et al., 2006), and these varieties were widely cultivated and extensively used in hybridization to develop second-generation improved lines (Gupta et al., 2001). For instance, derivatives of T9 like UPU 1 and UPU 2 contributed to the development of short-duration and MYMV-resistant varieties, Pant Urd 30 and Pant Urd 19. Subsequently, breeding strategies shifted toward hybridization-based approaches to generate genetic variability and facilitate the pyramiding of desirable traits within single genotypes, thereby enhancing adaptability across diverse agro-ecological conditions (Gupta et al., 2020). In this context, KM 1 represents the first black gram cultivar in India developed through hybridization in 1977.

Regardless of persistent efforts in conventional breeding, genetic advancement in both pulses has remained constrained. This limitation is primarily attributed to the complex, polygenic architecture of important agronomic traits and the substantial influence of genotype × environment (G×E) interactions, which collectively hinder selection efficiency and predictability. These challenges necessitate a strategic transition toward integrative breeding frameworks that integrate traditional methodologies with advanced genomic technologies to improve selection precision and expedite crop improvement.

Molecular Breeding Approaches

Initial studies by Young et al. (1992), Menancio-Hautea et al. (1993) and Fatokun et al. (1992) established the foundation for genetic mapping in mungbean. These early linkage maps facilitated the identification of new genomic regions linked with seed size, insect resistance, and disease resistance. Comparative mapping studies further revealed extensive synteny between mungbean and other crops like soybean, cowpea and common bean. During the period from 1993 to 2010, only a limited number of linkage maps were developed because of the scarcity of polymorphic molecular markers. Most maps were based on RFLP and SSR markers derived from related legume species and were primarily used for mapping resistance to bruchids, bean bug, powdery mildew, seed dormancy, and seed size traits.

The development of SSR markers and next-generation sequencing technologies after 2010 significantly accelerated mungbean genomics research. Several SSR-based linkage maps with improved genome coverage were developed and utilized for QTL mapping of agronomic attributes, domestication-related characteristics, seed quality parameters, and resistance to different stresses. A major milestone was achieved when linkage maps developed by Kajonphol et al. (2012) and Isemura et al. (2012) successfully resolved all eleven mungbean chromosomes. Subsequently, the release of the first draft reference genome of variety VC1973A by Kang et al. (2014) provided a comprehensive genomic framework for gene discovery, comparative genomics, and marker-assisted breeding. The assembled genome comprised approximately 431 Mb, organized into eleven pseudochromosomes and contained more than 22,000 predicted protein-coding genes. WGS of wild and cultivated accessions further facilitated large-scale SNP discovery and accelerated molecular breeding efforts.

Recent developments have transformed mungbean genomics from linkage mapping to genome-enabled breeding. High-quality chromosome-scale genome assemblies generated using PacBio SMRT and Oxford Nanopore sequencing technologies have substantially improved genome completeness and assembly accuracy. Improved genome assemblies of VC1973A and other cultivated accessions have revealed extensive structural variation, gene copy number variation, and domestication-related genomic regions (Ha et al., 2025). The development of mungbean pan-genomes has provided insights into core and dispensable genes controlling adaptation, stress tolerance, and yield-related traits. Pan-genomic analyses have identified numerous presence–absence variations and structural variants that are not represented in a single reference genome, thereby expanding the available genetic diversity for crop improvement (Nair et al., 2020).

GWAS using diverse germplasm panels and high-density SNP markers have increasingly complemented traditional bi-parental QTL mapping. GWAS has facilitated the identification of loci associated with flowering time, seed size, yield components, drought tolerance, heat tolerance, mineral nutrition, and disease resistance. High-throughput genotyping platforms, including GBS and whole-genome resequencing, have enabled the development of dense SNP-based linkage maps and genomic prediction models.

More recently, genomic selection, haplotype-based breeding, and machine-learning-assisted genomic prediction have emerged as promising approaches for accelerating genetic gain in mungbean. Incorporation of genomics with metabolomics, transcriptomics and high-throughput phenotyping is increasingly being used to identify candidate genes and regulatory networks governing complex traits. In addition, CRISPR/Cas genome-editing technologies are being explored for targeted improvement of disease resistance, stress tolerance, flowering behaviour, and nutritional quality traits, although practical deployment in mungbean breeding remains at an early stage.

Molecular breeding in urdbean has evolved considerably over the last three decades and has become a crucial aspect of plant breeding aimed at enhancing disease resistance, yield, seed quality traits and stress tolerance. Early breeding efforts relied largely on conventional selection methods, but progress was often constrained by narrow genetic diversity, low levels of polymorphism within cultivated germplasm, complex inheritance of quantitative traits, and strong genotype × environment interactions.

The introduction of molecular markers during the 1990s and early 2000s provided new opportunities for genetic analysis and marker-assisted breeding. Initially, marker systems such as RAPD, AFLP, RFLP, and ISSR were employed to assess genetic diversity, characterize germplasm collections, and identify resistant

genotypes. Subsequently, SSR markers became the preferred marker system because of their high reproducibility, co-dominant inheritance, and genome-wide distribution. Since genomic resources in urdbean were limited, many SSR markers developed from related *Vigna* species, particularly mungbean and adzuki bean, were successfully used for diversity analysis, linkage mapping, and MAS.

Primary targets of molecular breeding in urdbean have been resistance to MYMD, caused by begomoviruses such as MYMIV and MYMV. Numerous studies identified RAPD-, ISSR-, SCAR-, and SSR-based markers linked to resistance loci, facilitating the screening of resistant germplasm and the development of segregating populations for resistance breeding. Marker-assisted selection became increasingly important for the rapid introgression of resistance genes into elite cultivars. Similar efforts were undertaken for resistance to powdery mildew, Cercospora leaf spot, leaf crinkle disease, and other economically important diseases.

During the same period, linkage mapping studies began to identify QTLs linked with yield traits, flowering time, maturity duration, plant architecture, and stress tolerance. The availability of transcriptome sequencing further accelerated marker development through the discovery of large numbers of SSRs and SNPs, while comparative genomics with mungbean revealed extensive synteny and enabled the transfer of genomic information across species. These developments laid the foundation for genomics-assisted breeding in urdbean (Gupta et al., 2008; Gupta et al., 2013; Souframanien & Gopalakrishna, 2004).

During the past few years, urdbean genomics has entered a new phase with the development of genome-scale resources and high-throughput sequencing technologies. Draft genome assemblies and large-scale transcriptome datasets have substantially expanded the available genomic information, enabling genome-wide discovery of SNPs, insertion–deletion polymorphisms, repetitive elements, and candidate genes associated with agronomically important traits. Advances in NGS, GBS, and whole-genome resequencing have facilitated the construction of high-density linkage maps and improved the resolution of QTL mapping studies.

These resources have enabled the identification of genomic regions controlling resistance to MYMD, powdery mildew, drought stress, and yield-related traits with greater precision than was previously possible. GWAS are increasingly being employed in diverse urdbean germplasm collections to identify marker–trait associations for complex quantitative traits. Compared with traditional bi-parental mapping, GWAS provides higher mapping resolution and facilitates the identification of candidate genes underlying economically important characteristics. Concurrently, transcriptomic analyses under different stress conditions have identified numerous differentially expressed genes involved in pathogen defence, hormone signalling, oxidative stress regulation, and stress adaptation.

Numerous transcription factor families, including AP2/ERF, MYB, NAC, bZIP, and WRKY, have been implicated in regulating defence responses and environmental stress tolerance. Recent research has also focused on integrating genomics with transcriptomics, proteomics, metabolomics, and high-throughput phenotyping to better understand the molecular mechanisms underlying complex traits. Comparative genomics and pan-genomic studies across *Vigna* species have revealed extensive structural variation and gene-content diversity that can be exploited for crop improvement. Furthermore, genomic selection and haplotype-based breeding approaches are beginning to emerge as promising strategies for accelerating genetic gain in urdbean breeding programmes (Singh et al., 2013). The utilization of genome editing approaches like CRISPR/Cas, although still in its infancy in urdbean, offers significant potential for targeted

modification of genes controlling disease resistance, flowering time, stress tolerance, and seed nutritional quality. Collectively, these advances are transforming urdbean improvement from marker-assisted breeding towards precision breeding based on genome-wide information, thereby enhancing the prospects for developing high-yielding, climate-resilient, and nutritionally superior cultivars. The timeline for mapping genes or QTLs for important traits of mungbean and urdbean is given in Figure 4.

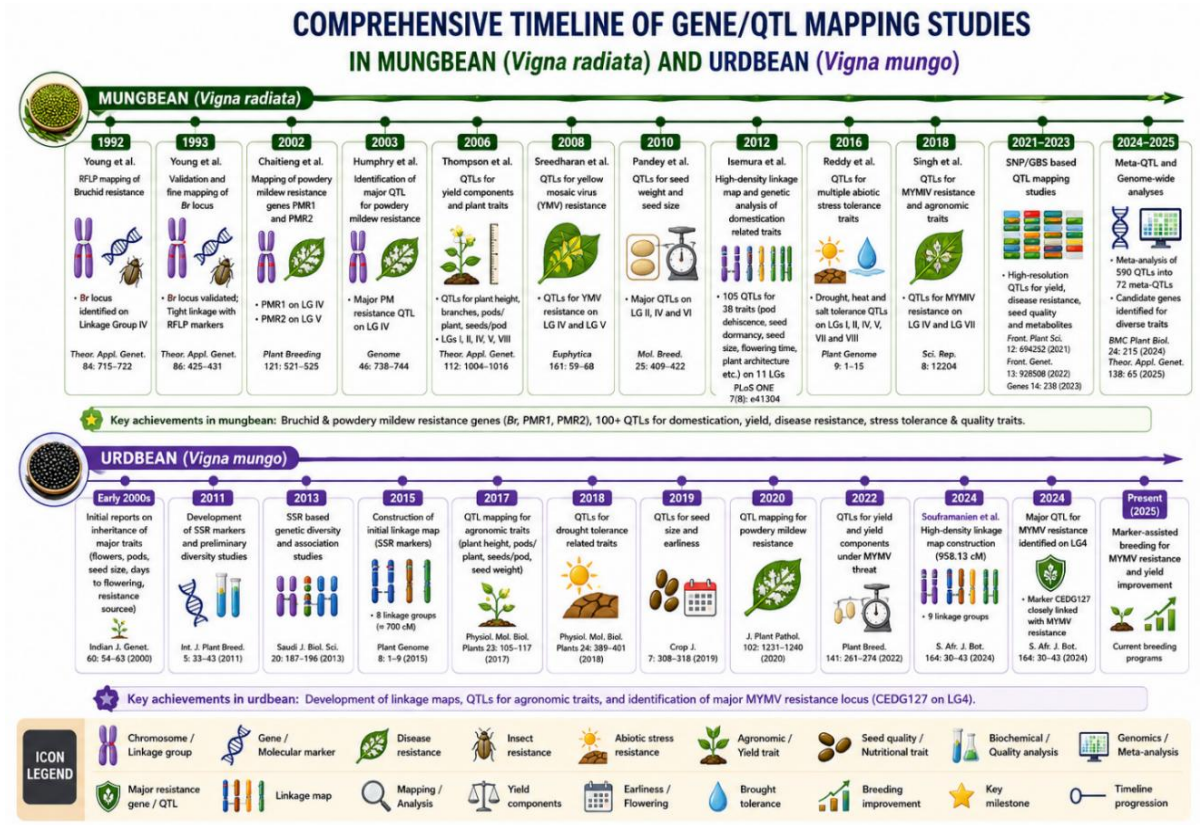

Figure 4. Timeline for mapping genes/QTLs for crucial traits in mungbean and urdbean

Biotechnological Approaches

Biotechnological approaches in mungbean and urdbean breeding have become increasingly important to complement conventional breeding methods and to overcome limitations such as narrow genetic variability, poor crossability with wild relatives, long breeding cycles, and vulnerability to different major stresses. These crops are particularly affected by diseases such as YMD, powdery mildew, and various insect pests, along with stresses such as drought and heat, which significantly reduce productivity. Biotechnology provides advanced tools to accelerate genetic improvement, enhance precision in selection, and introduce novel attributes that are problematic to achieve through traditional breeding alone. The major biotechnological interventions in these crops include plant tissue culture, somatic hybridization, molecular MAS, genetic transformation, and modern genome editing techniques. Together, these tools are helping to reshape mungbean and urdbean improvement programmes by increasing efficiency and expanding the genetic base.

Mungbean and urdbean were earlier considered as orphan crops because very limited genomic information was available compared to other important legume crops. Due to this, the use of modern breeding techniques remained restricted, and the progress in their genetic improvement was relatively slow. A major advancement

occurred when the first draft genome sequences of mungbean and urdbean were published, respectively in 2014 and 2021 (Kang et al., 2014; Souframanien et al., 2021). This achievement provided detailed insight into the genetic structure of the crops and opened up new opportunities for scientific research and crop improvement. Recent advancements in mungbean genetics have focused on crucial traits, including drought resistance, yield, pod shattering, domestication, and nutritional composition. The GWAS have proven effective for trait mapping, even in the absence of complete genome data. Moreover, various linkage maps have been established using molecular markers like RAPD, RFLP, SSR (Fatokun et al., 1993; Shanmugasundaram et al., 2010; Chen et al., 2015). The recent availability of WGS has further accelerated the identification and mapping of key agronomic traits (Pratap et al., 2016; Pratap et al., 2017).

The application of MAS to introgress YMV resistance into elite mungbean varieties marks a significant milestone in Indian agricultural research, facilitating the development of resistant, high-yielding lines. By utilizing specific molecular markers such as Resistance Gene Analogues (RGAs) like CYR-1 and VMR-1 or SSR markers- breeders can efficiently identify resistant genotypes, accelerating the breeding process and overcoming the limitations of conventional screening, particularly in key production areas where YMV causes substantial yield losses (Maiti et al., 2011; Nandini et al., 2025). MAS has played a key role in transferring resistant genes from *Vigna radiata* var. *sublobata* into cultivated mungbean, resulting in cultivars such as VBN 4 with stable performance (Tamilzharasi et al., 2019). Moreover, molecular studies have identified QTLs and molecular markers associated with key traits like bruchid resistance, seed size and drought tolerance. CRISPR/Cas9 technology has emerged as a transformative tool for the genetic improvement of mungbean, primarily focusing on introducing resistance to devastating viral diseases such as MYMV (Talakayala et al., 2022). Recent developments in CRISPR/Cas9 technology have demonstrated significant potential in improving agricultural productivity, with trials targeting specific pod number genes resulting in yield increases of 10-15% (Kumar et al., 2023). Molecular markers, such as the SSR marker CEDG180, are powerful tools in modern plant breeding, providing a precise, DNA-based method to identify and select desirable traits without waiting for phenotypic expression. However, their widespread adoption is hindered by significant financial and infrastructure bottlenecks (Nair et al., 2024). The sequencing of the mungbean genome has provided valuable genomic resources, significantly advancing gene identification and comparative genomic research. While molecular breeding in mungbean remains at a relatively early stage compared with cereal crops, its incorporation into conventional and mutation breeding programmes is contributing to more precise and efficient genetic improvement. Consequently, substantial progress is being made towards the development of high-yielding, climate-resilient and nutritionally enriched cultivars.

Legume breeding has been revolutionized by high-quality genome assemblies and germplasm variation studies, enabling novel tools like MAS, MABC, and GS. While urdbean formerly lacked the dense molecular markers needed for comprehensive gene and QTL mapping, the creation of genetic linkage maps now acts as a foundation for identifying key traits. In the case of urdbean, the initial genetic map, spanning 783 cM and organizing 148 markers into 11 linkage groups, was developed by Chaitieng et al. (2006) using a BC_1F_1 population of 180 individuals derived from a cross between a large-seeded accession (JP219132) and *V. mungo* var. *silvestris* (JP107873). Subsequently, Gupta et al. (2008) constructed a map from 104 RILs derived from an inter-subspecific cross between a susceptible cultivar, TU94-2, and a resistant wild genotype, *V. mungo* var. *silvestris.* Somta et al. (2019) reported a high-density linkage map comprising 3,675 SNP markers, generated via specific-locus amplified fragment sequencing. These maps used a population derived from a cultivated and wild urdbean cross, with most gene and QTL mapping studies focusing on resistance

to bruchid (*C. maculatus*) and MYMD. Transgenic urdbean was produced using a protocol involving *Agrobacterium tumefaciens* (strain EHA105) and the pKSB binary vector to transform shoot apices, building on the earlier *in vitro* regeneration methods established by Saini et al. (2003) and Saini & Jaiwal (2005). The rapid development of CRISPR/Cas9 has provided a powerful toolkit for functional genomics, enabling everything from simple knockouts to complex multiplexing (Arora & Narula, 2017). Despite rising adoption in global agriculture (Chen & Gao, 2014), applying this to legumes presents unique, though increasingly overcome challenges. Key successes have already been achieved in crops like soybean, chickpea, cowpea, and *Medicago truncatula*. Looking forward, these genome-editing tools offer vital pathways to enhance legume productivity and stress resilience, particularly for crops like urdbean (Mahto et al., 2022; Singh et al., 2023). Recently, genomic selection (GS) and genome editing technologies have emerged as promising tools for urdbean improvement. Genomic selection utilizes genome-wide marker information to predict breeding values for complex traits controlled by multiple minor-effect loci. This approach has the potential to accelerate breeding cycles and improve selection accuracy. Similarly, CRISPR/Cas-mediated genome editing offers opportunities for precise modification of genes associated with disease susceptibility, stress tolerance, and yield traits. Although genome editing in urdbean is still in its early stages due to limitations in transformation efficiency and regeneration protocols, ongoing research is expected to enhance its applicability in future breeding programmes. Despite substantial progress, several challenges continue to limit molecular breeding in urdbean. The narrow genetic base of cultivated germplasm, limited availability of high-quality reference genomes, insufficient high-throughput phenotyping infrastructure, and low transformation efficiency remain major bottlenecks. In addition, many identified QTLs and candidate genes require functional validation before large-scale deployment in breeding programmes. Future research will likely focus on pan-genomics, multi-omics integration, genomic prediction models, speed breeding, and AI-assisted breeding approaches to accelerate genetic gain in urdbean. The timeline of major genomics and biotechnology milestones in mungbean and urdbean is given in Figure 5.

Varietal development in Mungbean and Urdbean

In India, the crop improvement work initiated on mungbean through selection as early as first quarter of 20th century at Pusa Bihar and more systematic efforts for varietal improvement were started under the Pulse Scheme: in Uttar Pradesh in 1943. Mung type 1, a selection from Muzaffarpur (Bihar) was released in 1936 in UP, but multiplied on large scale only after 1948 (Mehta & Sahai, 1955), However, later it served as a key parent in developing varieties like T 2, K 851, T 44, and Sunaina. In the initial stage, more emphasis was on improving genetically diverse locally adapted populations through mass and pure line selection leading in release of several improved cultivars and a few of them are still being grown such as T9 of urdbean. Moong 54 and Moong 305 were selected from locally adapted population mixtures in Punjab and released in 1947 while Co 1, a selection from local available germplasm was released in Tamil Nadu in 1952. In Maharashtra, Kopergaon was released in 1956 through selection from local germplasm and Jalgaon 781 was selected from China Mung and was released in 1957. Many other varieties like Pusa 105, Pusa 9531, G 65, Krishna II were released through selections and were very popular. Gradually the efforts had been shifted towards hybridization which led to the development of ML 1 and ML 5 at PAU, Ludhiana in the 1970s, and further contributed to the development of improved varieties such as ML 267, ML 131 and ML 337. All these varieties were early maturing and had genes for wider adaptation and suitable seed traits. Later in the beginning of 21st century, many germplasm lines were introduced through NBPGR from AVRDC, Taiwan, and after selections, some were released as varieties like SML 668, Pusa Vishal and Pant Moong 5. All of these varieties are large-seeded.

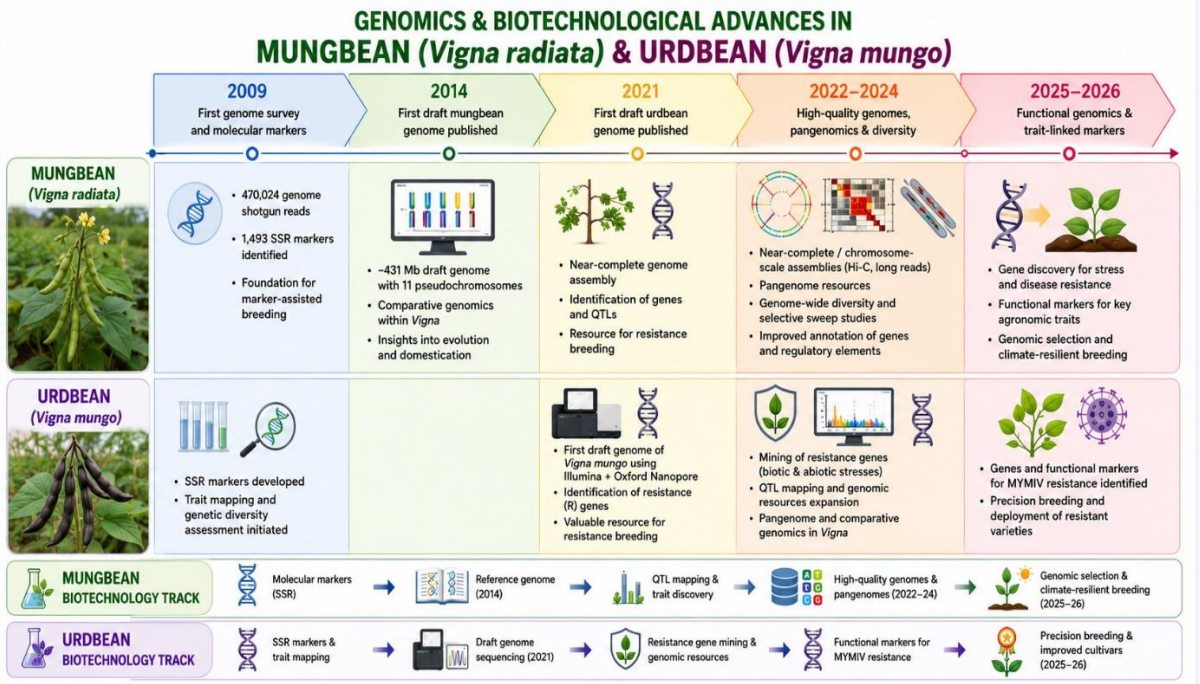

Figure 5. Timeline depicting major genomics and biotechnology milestones in mungbean and Urdbean

In case of inter-varietal hybridization in mungbean, the first and foremost varieties were Type 44 in UP, Kanke in Bihar and Kharif Sona in West Bengal developed from Type 1 × China Mung 781-7, Type 1 × Sona Mung crosses, and Type 2 × Type 49, respectively. At IIPR Kanpur, using IPM99-125 as one of the parents, genotypes IPM02-1, and IPM03-1 were developed in mungbean, which were further used for the development of two extra early mungbean genotypes, IPM205-7 and IPM 409-4, which matures in about 52-55 days (Pratap et al., 2013). At, PAU the kharif varieties ML 267 and ML 613 release in 1986 and 1995, respectively were very popular. In recent decades, breeding has focused on developing short-duration, photo- and thermo-insensitive varieties with resistance to major diseases significantly boosting production. Notably improved varieties include KM 2241, HUM 16, MH 2-15, TMB 37, IPM 02-3 (suited for both spring and kharif), IPM 410-3 (Shikha), and IPM 2-14. The large-seeded short-duration variety SML 668 released in 2004 and dominated breeder seed demand until 2014–15. It was surpassed by IPM 02-3 in 2015–16, reflecting a shift toward newer, more adaptable and disease-resistant varieties (Singh et al., 2016).

In urdbean, Type 9, selected from Bareilly Local and released in 1948, was one of the earliest improved varieties. Several other varieties, including Gwalior 2, Type 65, Type 27, Type 77, BR 68, and BR 76, were also developed through selection from local germplasm and were well suited for intercropping due to their indeterminate and spreading growth habit. Hybridization breeding began with the release of KM 1 (1977) and ADT 2 (1979), followed by varieties like TMB 1 and KM 2. Type 9 and its derivatives were widely used as parents in breeding programmes, contributing to the development of elite cultivars such as Pant U 30 and Pant U 19. Both of these were developed from cross UPU1 x UPU2 which are selections of T9. More recently, varieties such as Mash 114, Mash 1137, Mash 1008, TU 40, VBN 6, 7, 8, 9, 10, and 11 have been developed either through intra-specific or inter-specific hybridization followed by rigorous selection (Geetha et al., 2020; Gupta et al., 2022). Further Pant U 19 used as one of the parents to develop Mash 479 and Mash 878 released for NWPZ. Thereafter, many improved cultivars possessing a high level of resistance to MYMV,

were developed and released for kharif season. For instance, Shekhar 1 (KU 301) developed from cross G 31 × Type 9 at CSAUAT, Kanpur and TU 94-2 developed from cross TPU 3 × TAU 3 at BARC Trombay were released in 1998 for cultivation during rabi season in SZ of India.

Interspecific hybridization has played significant role in varietal development programme. As a result of interspecific hybridization among *Vigna* species at GB Pant University, Pantnagar, Pant Moong 4 was released in 1997, the first variety developed from interspecific hybridization between *V. radiata* x *Vigna mungo.* PAU, Ludhiana, developed a kharif urdbean variety Mash 114 from *V. mungo* x *V. umbellata* cross and a summer urdbean variety Mash 1008 from *V. radiata* x *V. mungo* cross. Similarly, in mungbean, a summer mungbean variety SML1827 and a kharif mungbean MYMIV resistant variety ML 2015 developed from *V. radiata* x *V. umbellata* crosses were released respectively for Punjab state and for NEPZ, India. Two other mungbean varieties, ML 1808 and ML 1839, developed from *V. radiata* x *V. mungo* crosses, were released respectively for the Punjab state and NEPZ of India at the national level. However, Pant Moong 4, released in 1997, is the first variety developed from interspecific hybridization between *V. radiata* x *Vigna mungo* developed at GBPUA&T, Pantnagar.

Mutation breeding, a powerful tool to generate novel variability and to develop varieties, has resulted in development of some good mungbean varieties (Pant Moong 2, MUM 2, Co 4, LGG 407, LGG 405, BM 4) and urdbean varieties (Prasad, Ujala). Pant Moong 2, a mutant of ML 26, is moderately resistant to MYMV and has shining green seeds. Urdbean variety Vamban 2, a mutant of Type 9, is resistant to MYMV and tolerant to drought. Very recently, in the year 2025, PAU, Ludhiana, has developed a summer mungbean variety, SML 2575, through mutation from variety TMB 37. SML 2575 is a high-yielding and YMD-resistant variety, while the parental variety TMB 37 is highly susceptible to YMD. Under the aegis of AICRP on Kharif Pulses (earlier AICRP-MULLaRP), a comprehensive list of mungbean and urdbean varieties released at the national level for different zones and State level, starting from 1987 to 2026, is given in Table 3.

Table 3. Varieties of mungbean and urdbean released at the national and state level from 1987-2026 in India

National level		
Year	**Mungbean**	**Urdbean**
1987-1996	MUM 2, ML 267, PDM 11, PDM 54, Pusa 105, Vamban 1, Co 5, RMG 62, ADT 3, LGG 450, BM 4, Narendra Mung 1, Phule M 2, AAU 34, ML 613, Pusa 9072, Warangal 2 (WGG 2), AKM 8803LGG 407, TARM 2, Jawahar Mung 721, PDM 84-178, TARM 1, SML 134, TARM 18, Gujarat Mung 3 (Pushkara)	TAU 2, PDU 1 (Basant Bahar), Jawahar Urd 2, Jawahar Urd 3, Pant U 35, LBG 17 (Krishnaya), LBG 402 (Prabhava), LBG 20 (Teja), Vamban 1, ADT 4, ADT 5, TPU 4, Narendra Urd 1 (NDU 88-8), WBU 108, KBG 512, LBG 611, Mash 338, Birsa Urd 1, AKU 4 (Melghat) Udid
1997-2006	Pant Moong 4 (UPM 92-1), HUM 1 (Malviya Jyoti), RMG 268, CO 6, Pusa 9531, Pusa Vishal, HUM 2 (Malaviya Jagriti), Ganga 8, HUM 6 (Malaviya Janpriya), OUM 11-5, HUM 12 (Malaviya Janchetna), Meha (IPM 99-125), TMB 37, COGG 912 (COGG 7), HUM 16 (Malaviya Jankalyani)	TU 94-2, Vamban 2, KU 301, WBG 26, KU 92-1 (Azad U 1), IPU 94-1 (Uttara), RBU 38 (Barkha), Pant U 40, NDU 99-2 (Narendra Urd -2), KU 96-3 (Azad urd 3), Pant U 31, KU 300 (Shekhar Urd 2)

2007-2016	MH 2-15 (Sattaya), Pant Mung-6, KM 2241, IPM 02-3, PKV AKM 4, Pusa 0672, IPM 02-14, MH 421, DGGV-2, IPM 410-3 (Shikha), IPM 205-7 (Virat), SML 1115	WBU 109 (Sulata), IPU 02-43, NUL7, LU 391, KUG 479, VBG 04-008, TU 40, LBG 787 (Tulasi)
2017-2026	Pusa 1371, GM 6, IPM 512-1 (Soorya), MH 1142, SML 2015, ML 1839, LGG 600, MH 1762, MH 1772, LGG 610 (Lam Pesara 610)	VBN 8, Mukundra urd 2 (KPU 405), VBN 9 (VBG 12-111), Kalinga Urd 41(OBG 41), Pant Urd 10 (PU 10-23), KPU 12-1735 (Kota Urd 4), VBN 10 (VBG 12-034), Pant Urd 12 (PU 1541), Kota Urd 5 (KPU 52-87), Mash 1190 (SUG 1190), KPU 18-1 (Kota Urd 6), Mash 878 (KUG 878), Pant Urd 13 (PU 1920), Pant Urd 14 (PU 1921)
State level		
1987-1996	Asha, MGG 295, LGG 410	LBG 402 (Prabhava), Mash 218, APK 1, LBG 22 (Lam –22), K1, PDU-1, UG-218, LBG 648, Pant U19
1997-2006	Shalimar Moong-1, LGG 460 (Lam 460), PBM 1, K1, AKM - 8802, Pratap, Pragya, Samrat (PDM 139), G M- 4, Pant Mung 5, VBN (Gg) 2, VRM (Gg)1, PDM 139, MGG 348, RMG 492, Pusa Ratna (Pusa 9972), Muskan, RMG 344, Suketi,	LBG 623, LBG 685, VBN 3, PKV Udid -15 (AKU - 15), LBG 645, PBG1, PBG 107, KU 309 (Shekhar 3), VBN (Bg) 4, GU-1, Mash1008, P 93, P 93, LBG 709, VBN (Bg) 5
2007-2016	PKV Green gram (AKM-9911), TM-96-2, TJM-3, MH 318, PAU 911, MGG 347, SML 832, MGG-207, Basanti, SGC 16, Pairymung, KM 2195, TM-2000-2, VBN (Gg) 3, DGGV-2 (Mungbean), Shalimar Moong-2, CO (Gg) 8, (Somnath), Yadadri (WGG 42), MSJ 118 (Keshvanand mung 2), Sri Rama (MGG 351), RMG 975 (Kesvanand mung 1), ML 2056, GBM-1, Utkarsh (KM 11-584)	Himachal Mash 1, DU-1, Mash 114, LBG 752 (Tulasi/ Raghava), CO 6 /COBG 653, VBN 6, UH-1, PratapUrd -1 (KPU 07-08), DBGV-5, MDU1, Vallabh Urd 1, Indira Urd Pratham (RU 03-14), PDKV Blackgold (AKU 10-1)
2017-2026	Mung-7 (GM-7), SML 1827, IPM 312-20 (Vasudha), Pant Mung 8 (PM 09-6), KM 2328, PM 707-5 (Phule Chetak), Pusa 1431, SGC 16 (Rupohi), GAM 5, Gujarat Varsha (IPM 2K 14-9), Pusa 1641, Kanika (IPM 302-2), Tripura Mung 1 (TRCM 131), VBN 4 (VGG 10-008), Pant M 9 (PM 09-11), KM 2342 (Azad Mung 1), IPM 409-4 (Heera), MGG 385 (Madhira Pesara-01), ML 1808, SGC 16 (Rupohi), GAM 8 (Hara Moti), Shalimar Mung 3, VBN 5 (VGG 15013), Lam Pesara 574 (LGG 574), GM 9 (SKNM 1705), Lam Pesara 607 (LGG 607), TRCRM-147, HUM 27 (Malviya Jan Kranti), VBN 6 (VGG	Tirupati Minumu-1 (TBG 104), KKM-1, ADT 6, IPU 11-02, Pant Urd 7 (PU 10-16), Pant U 8 (PU 11-14), TRCRU-22, Pant U 9 {PU 11-25), IPU 13-1, Mash 1137, IPU 10-26, GBG 1 (Ghantashala Minumu-1), Tripura Maskalai (TRC Urd 99-2), VBN 11 (VBG 12-062), OBG 33 (Shashi), KPU 524-65 (Kota Urd 3), CO 7 (COBG 10-05), LBG 791, IPU 17-1, Birsa Urd 2 (RUB 12-02), SBC 40 (Shyamal), JAU 4 (Shyamal), Lam Minumu 884, Madhira Minumu-01 (MBG -1070), BDU-12, DBG-16 (DBGV-16), TJU 130 (Trombay Jawahar Urd 130), Phule Vasu (PU-0609-43), Mash 883 (KUG 883), TJU 339 (Trombay Jawahar Urd

	15-030), OUAT Kalinga Greengram 1 (Shreejan), (OBGG 58), Co-9 (COGG 13-19), SGC 20 (AAU SHN Mung 02) (Buroi), LGG 630, GJM 1701, PMS 8, PMD 9, PMD 10, VBN 7 (VGG 18-002), Ankush (WBM-031), Phule Suvarn (Phule M 0702-1), PMS-12 (Pusa Sodicity Mungbean-12), Dweep Mung 1 (ANM-11-12), Dweep Mung 4 (ANM-12-02), Raj Vijay Indore Moong 750 (RVIM 750), Raj Vijay Sehore Mung 1 (RVSM 1), PDKV Phalguni (TAKSM 140), PDKV Varsha (TAKM-141), SML 2575	339), Dristi (IPU 17-2), Narmada (IPU 19-10), SBC 47 (AAU SHN Urd 02) (Pabhoi), Black gram ADT 7 (AD) (TR) BG 14003, Pant Urd 11, LBG 904, SB 42-8 (SHL Urd-03), TBG 129 (Tirupati Minumu 2), Phule Rajan (PU 0819-18), IPU 13-6, VBN 12, OUAT Kalinga Blackgram 1 (Shreeya) (OBG 101), Dweep Urd 1 (ANU-11-29), Vijeta (IPU 18-02), Raj Vijay Sehore Urd 1 (RVSU 1)

*Source: PC Report 2025-26, ICAR- All India Coordinated Research Project on Kharif Pulses

Constraints and Future Perspectives

Mungbean and urdbean are short-duration legume crops, traditionally grown in India for food security and soil health. They are the primary source of protein for the vegetarian population, like in India and other Asian countries. However, as compared to cereals *viz*., wheat and rice, they provide low remuneration to the farmers. Their low yield potential can be attributed to narrow genetic bases, high susceptibility to diseases and insect pests, sensitivity to abiotic stresses/climate change and poor mechanization. The narrow genetic base of these legumes leads to limited genetic diversity of cultivated varieties, thus restricting progress of genetic improvement for economically important traits. Among biotic stresses, Mungbean MYMV, Urdbean leaf crinkle virus (ULCV), powdery mildew, Cercospora leaf spot, whitefly, thrips, Maruca and pod borers are major threats, while sensitivity to extreme temperatures (both high and low) at flowering or early growth (depending upon growing season), waterlogging, drought, and salinity adversely affect the yield potential. Due to an indeterminate growth habit and non-synchronous maturity, most of the varieties are not amenable to mechanical harvesting, thus making manual harvesting necessary and expensive. Prolonged rains at maturity may cause pre-harvest sprouting which reduce seed quality and market value of the produce. Weak seed production system of many pulses including mungbean and urdbean is also responsible for poor availability of high-quality seeds of improved varieties to the farmers resulting in low productivity.

Traditional plant breeding has played a great role in improving the yield potential of these crops, will continue to be at the forefront in future also. However, advanced techniques like genomics, transcriptomics and metabolomics can be used to identify genes associated with resistance to diseases (e.g., YMD) and pests (e.g., Borers, Bruchids). Marker-assisted selection may improve efficiency of conventional breeding by accelerating the development of climate-smart and resistant varieties. Genome editing offers the potential for precise genetic modifications to improve specific traits such as increased resistance to viral diseases and better nutritional quality. Development of varieties with determinate growth, erect plant type and synchronous maturity should be a top priority to increase production efficiency and acceptability by farmers. Wild *Vigna* species provide a pool of novel genes for resistance to salinity, drought, and temperature extremes, which can be introgressed into elite cultivars through pre-breeding efforts supplemented with molecular breeding tools to enhance yield potential. Thus, a combination of traditional breeding, biotechnological, molecular techniques, pre-breeding, strengthening the seed production system and

research-extension linkages may transform mungbean and urdbean from "orphan" legumes to a highly profitable and sustainable cropping system.

References

Ahmed, S. (2009). Effect of soil salinity on the yield and yield components of mungbean. *Pakistan Journal of Botany, 41*(1), 263–268.

Ahmed, S., Nawata, E., & Sakuratani, T. (2002). Effects of waterlogging at vegetative and reproductive growth stages on photosynthesis, leaf water potential, and yield in mungbean. *Plant Production Science, 5*(2), 117–123. https://doi.org/10.1626/pps.5.117

AppaRao, S., & Jana, M. K. (1973). Inheritance of anthocyanin coloration in *Phaseolus* mutants. *Proceedings of the Indian Science Congress Association, 60*, 302.

Arora, L., & Narula, A. (2017). Gene editing and crop improvement using CRISPR/Cas9 system. *Frontiers in Plant Science, 8*, Article 1932. https://doi.org/10.3389/fpls.2017.01932

Aski, M. S., Rai, N., Reddy, V. R. P., Gayacharan, Dikshit, H. K., Mishra, G. P., Singh, D., Kumar, A., Pandey, R., Singh, M. P., Pratap, A., Nair, R. M., & Schafleitner, R. (2021). Assessment of root phenotypes in mungbean mini-core collection (MMC) from the World Vegetable Center (AVRDC), Taiwan. *PLOS ONE, 16*(3), e0247810. https://doi.org/10.1371/journal.pone.0247810

AVRDC. (1979). *AVRDC progress report for 1978*. Asian Vegetable Research and Development Center.

AVRDC. (1981a). *Progress report, 1979* (pp. 42–55). Asian Vegetable Research and Development Center.

AVRDC. (1981b). *Progress report, 1980* (pp. 40–50). Asian Vegetable Research and Development Center.

Baroowa, B., Gogoi, N., & Farooq, M. (2016). Changes in physiological, biochemical and antioxidant enzyme activities of green gram (*Vigna radiata* L.) genotypes under drought. *Acta Physiologiae Plantarum, 38*(9), Article 219. https://doi.org/10.1007/s11738-016-2233-0

Basak, J., Kundagrami, S., Ghose, T. K., & Pal, A. (2004). Development of a SCAR marker linked to a MYMV resistance gene in mungbean. *Genome, 47*, 1152–1156.

Bashir, M., Ahmad, Z., & Mansoor, S. (2005). Studies on inheritance of resistance to urdbean leaf crinkle disease in blackgram. *Pakistan Journal of Botany, 37*, 51–58.

Basu, P. S., Pratap, A., Gupta, S., Sharma, K., Tomar, R., & Singh, N. P. (2019). Physiological traits for shortening crop duration and improving productivity of greengram (*Vigna radiata* L. Wilczek) under high temperature. *Frontiers in Plant Science, 10*, Article 1508. https://doi.org/10.3389/fpls.2019.01508

Bhanu, A. N., Singh, M. N., & Srivastava, K. (2018). Crossability studies of interspecific hybridization among *Vigna* species. *Biomedical Journal of Scientific & Technical Research, 2*(5).

Bhattacharjee, S. (2024). Breeding for biotic stress in urdbean through genomics-enabled strategies. In A. K. Parihar, A. Bohra, A. Lamichaney, R. Mishra, & R. K. Varshney (Eds.), *Genomics-aided breeding strategies for biotic stress in grain legumes.*

Bindra, S. (2016). *Introgression of urdbean anthracnose resistance and yield components involving Vigna mungo × V. umbellata hybridization* (Doctoral dissertation). Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya.

Bindumadhava, H., Sharma, L., Nair, R. M., Nayyar, H., Riley, J. J., & Easdown, W. (2018). High-temperature-tolerant mungbean (*Vigna radiata* L.) lines produce better yields when exposed to higher CO_2 levels. *Journal of Crop Improvement, 32*(3), 418–430. https://doi.org/10.1080/15427528.2018.1439132

Bisht, I. S., Bhat, K. V., Lakhanpaul, S., Biswas, B. K., Ram, B., & Tanwar, S. P. S. (2004). The potential of enhanced germplasm for mungbean (*Vigna radiata* (L.) Wilczek) improvement. *Plant Genetic Resources: Characterization and Utilization, 2*(2), 73–80. https://doi.org/10.1079/PGR200433

Bose, R. D. (1939). Studies in Indian pulses. IX. Contribution to genetics of mung (*Phaseolus radiatus* Linn. syn. *P. aureus* Roxb.). *Indian Journal of Agricultural Sciences, 9*, 607–624.
Cao, D., Li, H., Yi, J., Zhang, J., Che, H., Cao, J., Yang, L., Zhu, C., & Jiang, W. (2011). Antioxidant properties of the mungbean flavonoids on alleviating heat stress. *PLOS ONE, 6*(6), e21071. https://doi.org/10.1371/journal.pone.0021071

Chaitieng, B., Kaga, A., Tomooka, N., Isemura, T., Kuroda, Y., & Vaughan, D. (2006). Development of a black gram (*Vigna mungo* (L.) Hepper) linkage map and its comparison with an azuki bean (*Vigna angularis* (Willd.) Ohwi & Ohashi) linkage map. *Theoretical and Applied Genetics, 113*, 1261–1269.

Chandel, K. P. S., & Lester, R. N. (1991). Origin and evolution of Asiatic *Vigna* species. In *Golden Jubilee Celebration Symposium on Grain Legumes* (pp. 25–45). Indian Society of Genetics and Plant Breeding.

Chandel, K. P. S., Lester, R. N., & Starling, R. J. (1984). The wild ancestors of urd and mungbeans [*Vigna mungo* (L.) Hepper and *Vigna radiata* (L.) Wilczek]. *Botanical Journal of the Linnean Society, 89*(1), 85–96.

Chandra, N., & Tickoo, J. L. (1998). Genetic analyses of protein content in mungbean (*Vigna radiata* L. Wilczek). *Indian Journal of Genetics and Plant Breeding, 58*(4), 475–478.

Chaudhary, S., Jha, U. C., Paul, P. J., Prasad, P. V. V., Sharma, K. D., Kumar, S., Gupta, D. S., Sharma, P., Singh, S., Siddique, K. H. M., & Nayyar, H. (2022). Assessing the heat sensitivity of urdbean (*Vigna mungo* L. Hepper) genotypes involving physiological, reproductive and yield traits under field and controlled environment. *Frontiers in Plant Science, 13*, Article 1042999. https://doi.org/10.3389/fpls.2022.1042999

Chauhan, Y. S., & Williams, R. (2018). Physiological and agronomic strategies to increase mungbean yield in climatically variable environments of northern Australia. *Agronomy, 8*(6), Article 83. https://doi.org/10.3390/agronomy8060083

Chauhan, Y., Douglas, C., Rachaputi, R., Agius, P., Martin, W., King, K., & Skerman, A. (2010). Physiology of mungbean and development of the mungbean crop model. In *Proceedings of the 1st Australian Summer Grains Conference*. Australia.

Chen, H., & Liu, X. (2001). Inheritance of seed color and lustre in mungbean (*Vigna radiata*). *Agricultural Science and Technology Hunan, 2*, 8–12.

Chen, H., Wang, L., Wang, S., Liu, C., & Blair, M. W. (2015). Transcriptome sequencing of mung bean (*Vigna radiata* L.) and identification of EST-SSR markers. *PLOS ONE, 10*(4), e0120273. https://doi.org/10.1371/journal.pone.0120273

Chen, J., Somta, P., Chen, X., Cui, X., Yuan, X., & Srinives, P. (2016). Gene mapping of a mutant mungbean (*Vigna radiata* L.) using new molecular markers suggests a gene encoding a YUC4-like protein regulates the chasmogamous flower trait. *Frontiers in Plant Science, 7*, Article 830. https://doi.org/10.3389/fpls.2016.00830

Chen, K., & Gao, C. (2014). Targeted genome modification technologies and their applications in crop improvement. *Plant Cell Reports, 33*, 575–583. https://doi.org/10.1007/s00299-013-1539-6

Chhabra, A. K. (2006). *A practical manual on floral biology of crop plants*. Department of Plant Breeding, CCS Haryana Agricultural University.

Christy, B. P., Delahunty, A. J., Norton, S. L., Wallace, A. J., Riffkin, P. A., O'Leary, G. L., & Nuttall, J. G. (2022). New legume species as opportunistic summer crops for southern Australia—Part 1: Environmental suitability. In *Proceedings of the 20th Agronomy Australia Conference.* Australia.

Dana, S. (1998). Collection of wild *Vigna* in seven states in India. *Green Journal, 1*, 9.

Dana, S., & Karmarkar, P. G. (1990). Species relation in *Vigna* subgenus *Ceratotropis* and its implications in breeding. *Plant Breeding Reviews, 8*, 19–42.

Dasgupta, T., Banik, A., & Das, S. (1998). Combining ability in mungbean. *Indian Journal of Pulses Research, 11*, 28–32.

de Candolle, A. (1884). *Origine des plantes cultivées*. Nabu Press.

Du, B., et al. (2025). Genetic dissection of yield and yield-related traits in mungbean based on QTL meta-analysis. *Frontiers in Genetics*.

Durga, K. K., & Kumar, S. S. (1997). Screening for pre-harvest sprouting in pulses. *Legume Research, 20*, 193–197.

Dutta, P., & Bera, A. K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research, 31*, 145–148.

Dutta, P., Bandopadhyay, P., & Bera, A. K. (2016). Identification of leaf-based physiological markers for drought susceptibility during early seedling development of mungbean. *American Journal of Plant Sciences, 7*, 1921–1936. https://doi.org/10.4236/ajps.2016.714176

Dwivedi, S., & Singh, D. P. (1990). Inheritance of fasciation in mungbean (*Vigna radiata* L. Wilczek). *Indian Journal of Genetics, 50*, 80–82.

Evans, A. M., Luse, R. A., & Rachie, K. O. (1976). Species hybridization in the genus *Vigna*. In *Proceedings of the IITA Collaborators' Meeting on Grain Legume Improvement* (pp. 31–34). International Institute of Tropical Agriculture.

Fakir, M. S. A., Mondal, M. M. A., Ismail, M. R., & Ashrafuzzaman, M. (2011). Flowering pattern and reproductive efficiency in mungbean. *International Journal of Agriculture & Biology, 13*(6), 966–970.

Fatokun, C. A., Danesh, D., & Young, N. D. (1993). Molecular taxonomic relationships in the genus *Vigna* based on RFLP analysis. *Theoretical and Applied Genetics, 86*(1), 97–104.

Fatokun, C. A., Danesh, D., Menancio-Hautea, D. I., & Young, N. D. (1992). A linkage map of cowpea [*Vigna unguiculata* (L.) Walp.] based on DNA markers (2n = 22). In S. J. O'Brien (Ed.), *Genome maps* (pp. 6256–6258). Cold Spring Harbor Laboratory.

Fujita, K., & Okamoto, I. (2006). *Agricultural policies and development of Myanmar's agricultural sector: An overview*. Institute of Developing Economies (IDE-JETRO).

Garrity, D. P., & Pernito, R. (1996). Mungbean response to surface drainage when grown as a pre-rice crop on waterlog-prone rice lands. *Agricultural Water Management, 29*(3), 299–314. https://doi.org/10.1016/0378-3774(95)01221-0

Gayacharan, Archak, S., Gupta, K., Gupta, V., Tyagi, V., & Singh, K. (2019). Mungbean genetic resources and utilization. In R. M. Nair & R. Schafleitner (Eds.), *The mungbean genome*. Springer.

Gayacharan, Parida, S. K., Mondal, N., Yadav, R., Vishwakarma, H., & Rana, J. C. (2023). Mining legume germplasm for genetic gains: An Indian perspective. *Frontiers in Genetics, 14*, Article 996828. https://doi.org/10.3389/fgene.2023.996828

Gentry, J. (2010). *Mungbean management guide* (2nd ed.). Department of Employment, Economic Development and Innovation.

Goyal, S., & Khan, S. (2010). Induced mutagenesis in urdbean (*Vigna mungo* L. Hepper): A review. *International Journal of Botany, 6*, 194–206. https://doi.org/10.3923/ijb.2010.194.206

Gupta, D. S., Kumar, J., Parihar, A. K., & Gupta, S. (2020). Breeding for high-yielding and disease-resistant urdbean cultivars. In S. S. Gosal & S. H. Wani (Eds.), *Accelerated plant breeding* (Vol. 3). Springer. https://doi.org/10.1007/978-3-030-47306-8_6

Gupta, D. S., Kumar, J., Parihar, A. K., Chandra, A., Sujayanand, G. K., & Gupta, S. (2022). Urdbean breeding. In D. K. Yadava, H. K. Dikshit, G. P. Mishra, & S. Tripathi (Eds.), *Fundamentals of field crop breeding*. Springer. https://doi.org/10.1007/978-981-16-9257-4_23

Gupta, S. R., Singh, R. A., Gupta, S., & Dikshit, H. K. (2001). Variability and its characterization in Indian collections of blackgram (*Vigna mungo* (L.) Hepper). *Plant Genetic Resources Newsletter*, 20–24.

Gupta, S., & Kumar, S. (2006). Urd bean breeding. In M. Ali & S. Kumar (Eds.), *Advances in mungbean and urdbean* (pp. 149–168). Indian Institute of Pulses Research.

Gupta, S., Das, A., Pratap, A., & Gupta, D. S. (2021). Urdbean. In *Beans and peas* (pp. 33–54). Elsevier. https://doi.org/10.1016/B978-0-12-821450-3.00014-7

Gupta, S., Gupta, D. S., & Singh, B. B. (2008). Genetic variability and inheritance of protein content in blackgram (*Vigna mungo*). *Indian Journal of Pulses Research, 21*, 45–49.

Gupta, S., Souframanien, J., & Gopalakrishna, T. (2008). Construction of a genetic linkage map of black gram. *Genome, 51*, 628–637.

Gupta, V. P., & Singh, R. B. (1984). Inheritance of leaf morphology traits in blackgram (*Vigna mungo*). *Indian Journal of Genetics and Plant Breeding, 44*, 349–354.

Ha, Y. H., Cho, A., Kim, T. H., & Gil, H. Y. (2025). De novo assembly and characterization of *Aria alnifolia* chloroplast and mitochondrial genomes reveal homologous conformational changes mediated by repeat regions and gene transfer. *BMC Genomics, 26*(1), Article 730.

Haeften, V. S., Dudley, C., Kang, Y., Smith, D., Nair, R. M., Douglas, C. A., Potgieter, A., Robinson, H., Hickey, L. T., & Smith, M. R. (2023). Building a better mungbean: Breeding for reproductive resilience in a changing climate. *Food and Energy Security, 12*(6), e467. https://doi.org/10.1002/fes3.467

Hanif, A., & Wahid, A. (2018). Seed yield loss in mungbean is associated with heat stress-induced oxidative damage and loss of photosynthetic capacity in proximal trifoliate leaf. *Pakistan Journal of Agricultural Sciences, 55*(4), 777–786.

Hanumantha Rao, B., Nair, R. M., & Nayyar, H. (2016). Salinity and high temperature tolerance in mungbean (*Vigna radiata* L. Wilczek) from a physiological perspective. *Frontiers in Plant Science, 7*, Article 957. https://doi.org/10.3389/fpls.2016.00957

Harlan, J. R., & de Wet, J. M. J. (1971). Toward a rational classification of cultivated plants. *Taxon, 20*, 509–517.

Hawkes, J. G. (1983). *The diversity of crop plants*. Harvard University Press.

Heuzé, V., Tran, G., Bastianelli, D., & Lebas, F. (2015). *Mungbean (Vigna radiata)*. Feedipedia (INRAE, CIRAD, AFZ & FAO). https://www.feedipedia.org/node/235

Heuzé, V., Tran, G., Boval, M., Bastianelli, D., Lebas, F., & Lessire, M. (2016). *Black gram (Vigna mungo)*. Feedipedia (INRAE, CIRAD, AFZ & FAO). https://www.feedipedia.org/node/236

Hou, D., Yousaf, L., Xue, Y., Hu, J., Wu, J., Hu, X., & Shen, Q. (2019). Mungbean (*Vigna radiata* L.): Bioactive polyphenols, polysaccharides, peptides, and health benefits. *Nutrients, 11*(6), Article 1238. https://doi.org/10.3390/nu11061238

Hu, H., Feng, N., Shen, X., Zhao, L., & Zheng, D. (2022). Transcriptomic analysis of *Vigna radiata* in response to chilling stress and uniconazole application. *BMC Genomics, 23*(1), Article 205. https://doi.org/10.1186/s12864-022-08377-0

Humphry, M. E., Lambrides, C. J., Chapman, S. C., Aitken, E. A. B., Imrie, B. C., Lawn, R. J., McIntyre, C. L., & Liu, C. J. (2005). Relationships between hard-seededness and seed weight in mungbean (*Vigna radiata*) assessed by QTL analysis. *Plant Breeding, 124*, 292–298.

ICAR–Indian Institute of Pulses Research. (2023). *Annual report: AICRP on kharif pulses (2022–23)*. Indian Council of Agricultural Research.

ICAR–Indian Institute of Pulses Research. (2024). *Annual report 2023–24*. https://www.icar-iipr.org.in

ICAR–Indian Institute of Pulses Research. (n.d.). *Gene bank: Germplasm holdings*. https://www.icar-iipr.org.in/gene/

ICAR–Indian Institute of Pulses Research. (2023). *Urdbean*. https://www.icar-iipr.org.in/urdbean/

Iqbal, J., Shabbir, G., Shah, K. N., Fayyaz-ul-Hassan, & Qayyum, A. (2021). Deciphering genotype × environment interaction to identify stable heat-tolerant mungbean genotypes by GGE biplot analysis. *Journal of Soil Science and Plant Nutrition, 21*(3), 2551–2561. https://doi.org/10.1007/s42729-021-00531-3

Irfan, M., Bhat, M. A., Rashid, U., et al. (2025). Genetic diversity assessment and morpho-agronomic characterization of mungbean (*Vigna radiata* (L.) Walp.) germplasm using multivariate analysis. *BMC Plant Biology, 25*, Article 1514. https://doi.org/10.1186/s12870-025-07561-z

Ishimoto, M., & Kitamura, K. (1993). Inhibitory effects of adzuki bean weevil-resistant mungbean seeds on growth of the bean bug. *Japanese Journal of Breeding, 43*, 75–80.

Islam, M. R., Hamid, A., Karim, M. A., Haque, M. M., Khaliq, Q. A., & Ahmed, J. U. (2008). Gas exchange and yield responses of mungbean (*Vigna radiata* L. Wilczek) genotypes differing in flooding tolerance. *Acta Physiologiae Plantarum, 30*(5), 697–707. https://doi.org/10.1007/s11738-008-0164-y

Jansen, P. C. M. (2006). *Vigna mungo* (L.) Hepper. In M. Brink & G. Belay (Eds.), *Plant resources of tropical Africa 1: Cereals and pulses*. PROTA Foundation.

Kaewwongwal, A., Kongjaimun, A., Somta, P., Chankaew, S., Yimram, T., & Srinives, P. (2015). Genetic diversity of the black gram [*Vigna mungo* (L.) Hepper] gene pool as revealed by SSR markers. *Breeding Science, 65*, 127–137. https://doi.org/10.1270/jsbbs.65.127

Kajale, M. D. (1974). Ancient grains from India. *Bulletin of the Deccan College Research Institute, 34*, 55–74.

Kanade, R. S. (2006). *Post harvest profile of black gram*. Directorate of Marketing and Inspection, Ministry of Agriculture, Government of India.

Kang, J. Y., Kim, S. K., & Kim, M. Y. (2014). Genome sequence of mungbean and insights into evolution within *Vigna* species. *Nature Communications, 5*, Article 5443. https://doi.org/10.1038/ncomms6443

Katiyar, P. K., Dixit, G. P., & Singh, B. B. (2010). Varietal characterization of urdbean. *Journal of Food Legumes, 23*(2), 106–109.

Katiyar, P. K., Singh, A., Singh, A. K., Tripathi, A., Lamichaney, A., Yadav, P., & Singh, N. P. (2017). Ancestral relationship of blackgram cultivars developed in India. *Journal of Food Legumes, 30*(4), 293–296.

Keatinge, J. D. H., Easdown, W. J., Yang, R. Y., Chadha, M. L., & Shanmugasundaram, S. (2011). Overcoming chronic malnutrition in a future warming world: The key importance of mungbean and vegetable soybean. *Euphytica, 180*, 129–141.

Khajudparn, P., Wongkaew, S., & Thipyapong, P. (2007). Identification of genes for resistance to powdery mildew in mungbean. *African Crop Science Conference Proceedings, 8*, 743–745.

Khattak, G. S. S., Haq, M. A., Ashraf, M., & Tahir, G. R. (2002). Triple test cross for some morphological traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Euphytica, 126*, 413–420.

Khattak, G. S. S., Haq, M. A., Rana, S. A., Srinives, P., & Ashraf, M. (1999). Inheritance of resistance to mungbean yellow mosaic virus (MYMV) in mungbean (*Vigna radiata* (L.) Wilczek). *Thai Journal of Agricultural Science, 32*, 49–54.

Kumar, R., Yadav, S., & Singh, P. (2023). CRISPR/Cas9 for mungbean improvement. *Plant Biotechnology Journal, 21*(5), 789–797.

Lambrides, C. J., Godwin, I. D., Lawn, R. J., & Imrie, B. C. (2004). Segregation distortion for seed testa colour in mungbean (*Vigna radiata* L. Wilczek). *Journal of Heredity, 95*, 532–535.

Lee, Y. B. (1980). *Inheritance study on resistance to Cercospora leaf spot in mungbean*. Asian Vegetable Research and Development Center.

Lukoki, L., Maréchal, R., & Otoul, E. (1980). Les ancêtres sauvages des haricots cultivés: *Vigna radiata* (L.) Wilczek et *Vigna mungo* (L.) Hepper. *Bulletin du Jardin Botanique National de Belgique, 50*, 385–391. https://doi.org/10.2307/3667837

Mahalingam, A., Satya, V. K., Manivannan, N., Narayanan, S. L., & Sathya, P. (2018). Inheritance of mungbean yellow mosaic virus disease resistance in greengram [*Vigna radiata* (L.) Wilczek]. *International Journal of Current Microbiology and Applied Sciences, 7*(1), 880–885. https://doi.org/10.20546/ijcmas.2018.701.107

Mahto, R. K., Ambika, S. C., Chandana, B. S., Singh, R. K., Verma, S., Gahlaut, V., et al. (2022). Chickpea biofortification via genome editing to enhance stress tolerance. *Frontiers in Genetics, 13*, Article 900324. https://doi.org/10.3389/fgene.2022.900324

Maiti, S., Basak, J., Kundagrami, S., Kundu, A., & Pal, A. (2011). Molecular marker-assisted genotyping of MYMV-resistant germplasms in mungbean and urdbean. *Molecular Biotechnology, 47*(2), 95–104. https://doi.org/10.1007/s12033-010-9314-1

Makeen, K., Abrahim, G., Jan, A., & Singh, A. K. (2007). Genetic variability and correlations studies on yield and its components in blackgram (*Vigna mungo* L. Hepper). *Journal of Agronomy, 6*, 216–222.

Manasa, L. S., Panigrahy, M., Panigrahi, K. C., Mishra, G., Panda, S. K., & Rout, G. R. (2023). Cold tolerance mechanisms in mungbean (*Vigna radiata* L.) genotypes during germination. *Agriculture, 13*(2), Article 315. https://doi.org/10.3390/agriculture13020315

Maréchal, R., Mascherpa, J. M., & Stainier, F. (1978). *Étude taxonomique d'un groupe complexe d'espèces des genres Phaseolus et Vigna (Papilionaceae)*. *Boissiera, 28*, 1–273.

Mehandi, S., Quatadah, S. M., Mishra, S. P., Singh, I. P., Praveen, N., & Dwivedi, N. (2019). Legume crops characterization and breeding for improved food security. In M. A. El-Esawi (Ed.), *Legume crops:*

Characterization and breeding for improved food security. IntechOpen. https://doi.org/10.5772/intechopen.84483

Mehta, T. R., & Sahai, J. M. (1955). A review of breeding work on mung (*Phaseolus aureus* Roxb.) in Uttar Pradesh. *Agriculture and Animal Husbandry, 6*, 56–57.

Menancio-Hautea, D., Fatokun, C. A., Kumar, L., Danesh, D., & Young, N. D. (1993). Comparative genome analysis of mungbean (*Vigna radiata* L. Wilczek) and cowpea (*Vigna unguiculata* L. Walp.) using RFLP mapping data. *Theoretical and Applied Genetics, 86*(7), 797–810. https://doi.org/10.1007/BF00226715

Mishra, G. P., Aski, M. S., Dikshit, H. K., Kohli, M., Gupta, S., Yadav, P. S., Tripathi, K., Kumar, P., Roy, J., & Nair, R. M. (2024). Mungbean (*Vigna radiata* (L.) R. Wilczek) breeding. In G. P. Dixit, H. K. Dikshit, G. P. Mishra, & M. S. Aski (Eds.), *Fundamentals of legume breeding*. Springer. https://doi.org/10.1007/978-981-96-7838-9_5

Mishra, R. C., Sahu, R. C., & Tripathy, D. (1970). A note on heterosis in greengram (*Phaseolus aureus* Roxb.). *Current Science, 39*, 190–191.

Mishra, S. P., & Asthana, A. N. (1996). Inheritance of yellow mosaic virus resistance in mungbean (*Vigna radiata* (L.) Wilczek). In A. N. Asthana & D. H. Kim (Eds.), *Recent advances in mungbean research* (pp. 214–219). Indian Society of Pulses Research.

Mishra, S. P., Asthana, A. N., & Yadav, L. (1988). Inheritance of Cercospora leaf spot resistance in mungbean (*Vigna radiata* (L.) Wilczek). *Plant Breeding, 100*, 228–229. https://doi.org/10.1111/j.1439-0523.1988.tb00245.x

Misra, A. N., Murmu, B., Singh, P., & Misra, M. (1996). Growth and proline accumulation in mungbean seedlings as affected by sodium chloride. *Biologia Plantarum, 38*(4), 531–536. https://doi.org/10.1007/BF02896668

Mohan, S., Sheeba, A., Murugan, E., & Ibrahim, S. M. (2014). Screening of mungbean germplasm for resistance to mungbean yellow mosaic virus under natural conditions. *Indian Journal of Science and Technology, 7*(7), 891.

Mukherjee, A., & Pradhan, K. (2002). Genetics of lobation in trifoliate leaf of mungbean. *Perspectives in Cytology and Genetics, 11*, 88.

Munns, R., & Tester, M. (2008). Mechanisms of salinity tolerance. *Annual Review of Plant Biology, 59*(1), 651–681. https://doi.org/10.1146/annurev.arplant.59.032607.092911

Murty, B. K., & Patel, G. J. (1973). Inheritance of some morphological characters in mungbean. *Bansilal Amritlal College of Agriculture Magazine, 25*, 1–9.

Nair, R. M., Chaudhari, S., & Somta, P. (2024). Genetics and breeding of mungbean. *Frontiers in Plant Science, 14*.

Nair, R. M., Chaudhari, S., Devi, N., Shivanna, A., Gowda, A., Boddepalli, V. N., Pradhan, H., Schafleitner, R., Jegadeesan, S., & Somta, P. (2024). Genetics, genomics, and breeding of black gram

(*Vigna mungo* (L.) Hepper). *Frontiers in Plant Science, 14*, Article 1273363. https://doi.org/10.3389/fpls.2023.1273363

Nair, R. M., Pandey, A. K., War, A. R., Hanumantha Rao, B., Shwe, T., Alam, A. K. M. M., Pratap, A., Malik, S. R., Karimi, R., Mbeyagala, E. K., Douglas, C. A., Rane, J., & Schafleitner, R. (2019). Biotic and abiotic constraints in mungbean production-Progress in genetic improvement. *Frontiers in Plant Science, 10*, Article 1340. https://doi.org/10.3389/fpls.2019.01340

Nair, R. M., Schafleitner, R., & Lee, S. H. (Eds.). (2020). *The mungbean genome*. Springer. https://doi.org/10.1007/978-3-030-20008-4

Nair, R. M., Schafleitner, R., Kenyon, L., Srinivasan, R., Easdown, W., Ebert, A., & Hanson, P. (2019). Genetic improvement of mungbean. *SABRAO Journal of Breeding and Genetics, 51*(1), 1–20.

Nandini, R., S. B., M., Ambika, Rajagopal, A., & S., H. H. (2025). Resistance gene analogue-assisted screening for MYMV in mungbean genotypes. *Indian Journal of Genetics and Plant Breeding, 85*(4), 765–772.

Negi, K. S., & Muneem, K. C. (1998). Preliminary evaluation of black gram (*Vigna mungo* (L.) Hepper) germplasm of North-West Himalaya. *Indian Journal of Hill Farming, 11*, 19–23.

Nene, Y. L. (1973). *A survey of viral diseases of pulse crops in Uttar Pradesh* (Research Bulletin). G. B. Pant University of Agriculture and Technology.

Pan, J., Sharif, R., Xu, X., & Chen, X. (2021). Mechanisms of waterlogging tolerance in plants: Research progress and prospects. *Frontiers in Plant Science, 11*, Article 627331. https://doi.org/10.3389/fpls.2020.627331

Pandiyan, M., Senthil, N., Balaji, T., Veeramani, P., Savitha, B. K., Senthivel, V., et al. (2017). Studies on performance of drought-tolerant genotypes under drought and normal conditions through morpho-physiological and biochemical attributes of black gram (*Vigna mungo* L.) and green gram (*Vigna radiata* L.). *International Journal of Current Advanced Research, 5*(2), 489–496. https://doi.org/10.21474/IJAR01/3176

Pokle, Y. S. (1972). Spontaneous mutation in mung (*Phaseolus aureus* Roxb.). *Science and Culture, 38*, 142.

Prakash, M., Elangaimannan, R., Sunilkumar, B., & Narayanan, G. S. (2017). Evaluation of blackgram genotypes for drought tolerance based on root dynamics and gas exchange parameters. *Legume Research, 41*(3), 384–391.

Pratap, A., Chaturvedi, S. K., Tomar, R., Rajan, N., Malviya, N., Thudi, M., Saabale, P. R., Prajapati, U., Varshney, R. K., & Singh, N. P. (2017). Marker-assisted introgression of resistance to *Fusarium* wilt race 2 in Pusa 256, an elite cultivar of desi chickpea. *Molecular Genetics and Genomics, 292*(6), 1237–1245.

Pratap, A., Gupta, D. S., Singh, B. B., & Kumar, S. (2013). Development of super early genotypes in greengram (*Vigna radiata* L. Wilczek). *Legume Research, 36*, 105–110.

Pratap, A., Gupta, S., Tomar, R., Malviya, N., Maurya, R., Pandey, V. R., Mehandi, S., & Singh, N. P. (2016). Cross-genera amplification of informative microsatellite markers from common bean and scarlet runner bean for assessment of genetic diversity in mungbean (*Vigna radiata*). *Plant Breeding, 135*(4), 499–505.

Priya, M., Sharma, L., Kaur, R., Bindumadhava, H., Nair, R. M., Siddique, K. H. M., & Nayyar, H. (2019). GABA (γ-aminobutyric acid) as a thermoprotectant to improve the reproductive function of heat-stressed mungbean plants. *Scientific Reports, 9*(1), Article 7788. https://doi.org/10.1038/s41598-019-44340-4

Rana, J. C., Gautam, N. K., Gayacharan, C., Singh, M., Yadav, R., Tripathi, K., et al. (2016). Genetic resources of pulse crops in India: An overview. *Indian Journal of Genetics and Plant Breeding, 76*, 420–436. https://doi.org/10.5958/0975-6906.2016.00061.4

Sadeghipour, O. (2009). The influence of water stress on biomass and harvest index in three mungbean (*Vigna radiata* (L.) R. Wilczek) cultivars. *Asian Journal of Plant Sciences, 8*(3), 245–249.

Saha, P., Chatterjee, P., & Biswas, A. K. (2010). NaCl pretreatment alleviates salt stress by enhancement of antioxidant defense system and osmolyte accumulation in mungbean (*Vigna radiata* L. Wilczek). *Indian Journal of Experimental Biology, 48*(6), 593–600.

Saini, R., & Jaiwal, P. K. (2005). Efficient transformation of *Vigna mungo*. *Plant Cell Reports, 24*, 164–171.

Saini, R., Jaiwal, S., & Jaiwal, P. K. (2003). Stable genetic transformation of *Vigna mungo*. *Plant Cell Reports, 21*(9), 851–859.

Sandhu, T. S., Brar, J. S., Sandhu, S. S., & Verma, M. M. (1985). Inheritance of resistance to mungbean yellow mosaic virus in greengram. *Journal of Research, Punjab Agricultural University, 22*, 607–611.

Santos, I. S. (1969). Induction of mutations in mungbean (*Phaseolus aureus* Roxb.) and genetic studies of some of the mutants. In E. Doyle (Ed.), *Induced mutations in plants* (pp. 169–179). International Atomic Energy Agency.

Sareen, P. K. (1985). Genetic analysis of the trilobate leaf mutants in mungbean (*Vigna radiata* var. *aureus* (L.) Wilczek). *Current Science, 54*, 930–931.

Sarkar, S., & Bhattacharya, S. (2014). Inheritance of bruchid resistance and morphological traits in greengram. *Indian Journal of Genetics and Plant Breeding, 74*(1), 98–102.

Schafleitner, R., Nair, R. M., Rathore, A., Wang, Y. W., Lin, C. Y., Chu, S. H., Lin, P. Y., Chang, J. C., & Ebert, A. W. (2015). The AVRDC–The World Vegetable Center mungbean (*Vigna radiata*) core and mini core collections. *BMC Genomics, 16*, Article 344. https://doi.org/10.1186/s12864-015-1556-7

Sehgal, A., Sita, K., Kadambot, H. M. S., Kumar, R., Sailaja, B., Varshney, R. K., et al. (2018). Drought or/and heat-stress effects on seed filling in food crops: Impacts on functional biochemistry, seed yields, and nutritional quality. *Frontiers in Plant Science, 9*, Article 1705. https://doi.org/10.3389/fpls.2018.01705

Sehrawat, N., Bhat, K. V., Kaga, A., Tomooka, N., Yadav, M., & Jaiwal, P. K. (2014). Development of new gene-specific markers associated with salt tolerance for mungbean (*Vigna radiata* L. Wilczek). *Spanish Journal of Agricultural Research, 12*(3), 732–741. https://doi.org/10.5424/sjar/2014123-4843

Sen Gupta, D., Katiyar, P. K., Kumar, J., Kumar, A., Gupta, S., & Singh, N. P. (2020). Development of extra early urdbean genotypes using intra-specific hybridization. *Journal of Food Legumes, 33*(1), 56–57.

Setter, T. L., Waters, I., Sharma, S. K., Singh, K. N., Kulshreshtha, N., Yaduvanshi, N. P. S., et al. (2009). Review of wheat improvement for waterlogging tolerance in Australia and India: The importance of anaerobiosis and element toxicities associated with different soils. *Annals of Botany, 103*(2), 221–235.

Shanmugasundaram, S., Keatinge, J. D. H., & Hughes, J. (2010). The mungbean transformation. *Agricultural Development, 8*, 381.

Sharma, L., Priya, M., Bindumadhava, H., Nair, R. M., & Nayyar, H. (2016). Influence of high temperature stress on growth, phenology, and yield performance of mungbean (*Vigna radiata* L. Wilczek) under managed growth conditions. *Scientia Horticulturae, 213*, 379–386. https://doi.org/10.1016/j.scienta.2016.11.005

Sharma, S., Mittal, R. K., Chaudhary, H. K., & Sood, V. K. (2022). Introgression of disease resistance in urdbean (*Vigna mungo*) by involving its related species. *Indian Journal of Agricultural Sciences, 92*(11), 1348–1352. https://doi.org/10.56093/ijas.v92i11.124619

Shukla, G. P., & Pandya, B. P. (1985). Resistance to yellow mosaic in greengram. *SABRAO Journal of Plant Breeding, 17*, 165–171.

Siemonsma, J. S., & Lampang, A. N. (2016). *Vigna radiata* (PROSEA). *Plant Resources of South-East Asia*. https://uses.plantnet-project.org/en/Vigna_radiata_(PROSEA)

Singh, A. K., & Singh, B. B. (1988). Inheritance of resistance to powdery mildew in blackgram. *Indian Phytopathology, 41*, 602–604.

Singh, A., & Patel, P. N. (1977). Studies on resistance in crops to bacterial diseases in India. Part VIII. Investigations on inheritance of reactions to bacterial leaf spot and yellow mosaic diseases and linkage, if any, with other characters in mungbean. *Indian Phytopathology, 30*, 202–206.

Singh, B. B., & Singh, D. P. (1995). Inheritance of a small leaf mutant in mungbean. *Indian Journal of Genetics and Plant Breeding, 55*, 69–70.

Singh, C., Kumar, R., Sehgal, H., Bhati, S., Singhal, T., Gayacharan, et al. (2023). Genomics and gene editing in chickpea. *Frontiers in Genetics, 14*.

Singh, D. P. (1980). Note on the inheritance of lobed leaf in greengram. *Indian Journal of Genetics and Plant Breeding, 40*, 608–609.

Singh, D. P. (1982). *Genetics and breeding of blackgram and greengram* (Research Bulletin No. 109). G. B. Pant University of Agriculture and Technology.

Singh, D. P. (1983). A high-yielding mungbean variety through mutation breeding. *Mutation Breeding Newsletter, 22*, 1–2.

Singh, D. P. (2014). *Genetics and breeding of pulse crops* (3rd ed.). Kalyani Publishers.

Singh, D. P., Singh, B. B., & Pratap, A. (2016). Genetic improvement of mungbean and urdbean and their role in enhancing pulse production in India. *Indian Journal of Genetics and Plant Breeding, 76*(4), 550–567.

Singh, H. B., Joshi, B. S., Chandel, K. P. S., Pant, K. C., & Saxena, R. K. (1974). Genetic diversity in some Asiatic *Phaseolus* species and its conservation. *Indian Journal of Genetics and Plant Breeding, 34*, 52–57.

Singh, M., Singh, D. P., & Rani, S. (2008). Inheritance of resistance to Cercospora leaf spot (CLS) in mungbean. *International Journal of Tropical Agriculture, 17*(3–4), 187–189.

Singh, N., Singh, H., & Nagarajan, P. (2013). Development of SSR markers in mungbean (*Vigna radiata* (L.) Wilczek) using *in silico* methods. *Journal of Crop and Weed, 9*(1), 69–74.

Singh, P., Pandey, B., Pratap, A., Gyaneshwari, U., Nair, R. M., Mishra, A. K., & Singh, C. M. (2022). Genetic and genomics resources of cross-species *Vigna* gene pools for improving biotic stress resistance in mungbean (*Vigna radiata* L. Wilczek). *Agronomy, 12*(12), Article 3000. https://doi.org/10.3390/agronomy12123000

Singh, S. K., Singh, C. M., & Kumar, R. (2015). Inheritance and screening for Cercospora leaf spot resistance in blackgram. *Legume Research, 38*, 516–520. https://doi.org/10.18805/lr.v38i4.1787

Singh, S., & Bains, T. S. (2006). Wide hybridization in *Vigna*. In M. Ali & S. Kumar (Eds.), *Advances in mungbean and urdbean* (pp. 169–186). Indian Institute of Pulses Research.

Singh, T. P., & Singh, K. B. (1970). Inheritance of clusters per node in mungbean (*Phaseolus aureus* Roxb.). *Current Science, 39*, 265.

Singh, V., & Bell, M. (2021). Genotypic variability in architectural development of mungbean (*Vigna radiata* L.) root systems and physiological relationships with shoot growth dynamics. *Frontiers in Plant Science, 12*, Article 725915. https://doi.org/10.3389/fpls.2021.725915

Sinha, M. K., Aski, M. S., Mishra, G. P., Kumar, M. B. A., Yadav, P. S., Tokas, J. P., et al. (2023). GWAS for micronutrients in mungbean. *Frontiers in Nutrition, 10*, Article 1099004.

Smartt, J. (1981). Gene pools in *Phaseolus* and *Vigna* cultigens. *Euphytica, 30*, 445–459.

Solanki, R. K., Gill, R. K., Verma, P., & Singh, S. (2011). Mutation breeding in pulses: An overview. In *Breeding of pulse crops* (pp. 85–103). Kalyani Publishers.

Somta, C., Somta, P., Tomooka, N., Ooi, P. C., Vaughan, D. A., & Srinives, P. (2008). Characterization of new sources of mungbean (*Vigna radiata* (L.) Wilczek) resistance to bruchids, *Callosobruchus* spp. (Coleoptera: Bruchidae). *Journal of Stored Products Research, 44*(4), 316–321. https://doi.org/10.1016/j.jspr.2008.01.002

Somta, P., Ammaranan, C., Ooi, P. A. C., & Srinives, P. (2007). Inheritance of seed resistance to bruchids in cultivated mungbean and related *Vigna* species. *Euphytica, 155*, 47–55.

Somta, P., Chen, J., Yundaeng, C., Yuan, X., Yimram, T., Tomooka, N., et al. (2019). SNP-based linkage map in black gram. *Scientific Reports, 9*, 1–9.

Sorajjapinun, W., Rewthongchum, S., Koizumi, M., & Srinives, P. (2005). Quantitative inheritance of resistance to powdery mildew disease in mungbean (*Vigna radiata* (L.) Wilczek). *SABRAO Journal of Breeding and Genetics, 37*, 91–96.

Souframanien, J., & Gopalakrishna, T. (2006). Molecular marker-assisted characterization of powdery mildew resistance in blackgram and related *Vigna* species. *Journal of Food Legumes, 19*, 53–56.

Souframanien, J., Raizada, A., Dhanasekar, P., & Suprasanna, P. (2021). Draft genome of black gram. *Scientific Reports, 11*, Article 11247.

Swindell, R. E., & Poehlman, J. M. (1978). Inheritance of photoperiod response in mungbean (*Vigna radiata* (L.) Wilczek). *Euphytica, 27*, 325–333. https://doi.org/10.1007/BF00043167

Takahashi, Y., & Tomooka, N. (2020). Taxonomy of mungbean and its relatives. In R. M. Nair, R. Schafleitner, & S. H. Lee (Eds.), *The mungbean genome* (pp. 27–41). Springer.

Talakayala, A., Mekala, G. K., Reddy, M. K., Ankanagari, S., & Garladinne, M. (2022). CRISPR/Cas9-mediated resistance to MYMV. *Frontiers in Sustainable Food Systems, 6*, Article 911574. https://doi.org/10.3389/fsufs.2022.911574

Talukdar, D., & Talukdar, T. (2003). Inheritance of growth habit and leaf shape in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Genetics and Plant Breeding, 63*(2), 165–166.

Tamilzharasi, M., Vanniarajan, C., & Souframanien, J. (2019). MYMV resistance in mungbean. *Legume Research, 43*(5), 728–734.

Tardieu, F., Simonneau, T., & Muller, B. (2018). The physiological basis of drought tolerance. *Journal of Experimental Botany, 69*(1), 1–14. https://doi.org/10.1093/jxb/erx330

Thakare, R. G., Gadgil, J. D., & Mitra, R. (1988). Origin and evolution of seed protein genes in *Vigna mungo* and *Vigna radiata*. In *Mungbean: Proceedings of the Second International Symposium* (pp. 47–52). Asian Vegetable Research and Development Centre.

Thakur, R. P., Patel, P. N., & Verma, J. P. (1977a). Studies on resistance in crops to bacterial diseases in India. XI. Genetic make-up of mungbean differentials of the races of bacterial leaf spot pathogen, *Xanthomonas* spp. *Indian Phytopathology, 30*, 217–221.

Thakur, R. P., Patel, P. N., & Verma, J. P. (1977b). Genetic relationships between reactions to bacterial leaf spot, yellow mosaic, and Cercospora leaf spot diseases in mungbean (*Vigna radiata*). *Euphytica, 26*, 765–774. https://doi.org/10.1007/BF00021708

Thakur, R. P., Patel, P. N., & Verma, J. P. (1977c). Independent assortment of pigmentation and resistance to Cercospora leaf spot in mungbean. *Indian Phytopathology, 30*, 264–265.

Thakur, R. P., Patel, P. N., & Verma, J. P. (1980). Inheritance of resistance to Cercospora leaf spot in mungbean. *Indian Phytopathology, 33*, 377–379.

Thamodhran, G., Geetha, S., & Ramalingam, A. (2016). Genetic study in urdbean (*Vigna mungo* (L.) Hepper) for inheritance of mungbean yellow mosaic virus resistance. *International Journal of Agriculture, Environment and Biotechnology, 9*(1), 33–37. https://doi.org/10.5958/2230-732X.2016.00005.5

Tickoo, J. L., Lal, S. K., Chandra, N., & Dikshit, H. K. (2006). Mungbean breeding. In M. Ali & S. Kumar (Eds.), *Advances in mungbean and urdbean* (pp. 110–148). Indian Institute of Pulses Research.

Tomooka, N. (1992). Genetic diversity and landrace differentiation of mungbean, *Vigna radiata* (L.) Wilczek, and evaluation of its wild relatives (subgenus Ceratotropis) as breeding materials. *Tropical Agriculture Research Center*.

Tomooka, N., Kashiwaba, K., Vaughan, D. A., Ishimoto, M., & Egawa, Y. (2000). The effectiveness of evaluating wild species: Searching for sources of resistance to bruchid beetles in the genus *Vigna* subgenus *Ceratotropis*. *Euphytica, 115*, 27–41. https://doi.org/10.1023/A:1003906715119

Tomooka, N., Lairungreang, C., Nakeeraks, P., Egawa, Y., & Thavarasook, C. (1991). Center of genetic diversity, dissemination pathways and landrace differentiation in mungbean. *Theoretical and Applied Genetics, 81*, 853–863.

Uprety, D., & Bhatia, A. (1989). Effect of water stress on photosynthesis, productivity, and water status of mungbean (*Vigna radiata* L. Wilczek). *Journal of Agronomy and Crop Science, 163*(2), 115–123. https://doi.org/10.1111/j.1439-037X.1989.tb00741.x

van Rheenen, H. A. (1965). The inheritance of some characters in the mungbean, *Phaseolus aureus* Roxb. *Genetica, 36*, 412–419. https://doi.org/10.1007/BF01507406

Vavilov, N. I. (1926). *Studies on the origin of cultivated plants*. Institute of Applied Botany and Plant Breeding.

Verma, S. K., Singh, C. K., Taunk, J., Gayacharan, Joshi, D. C., Kalia, S., Dey, N., & Singh, A. K. (2022). Vignette of *Vigna* domestication: From archives to genomics. *Frontiers in Genetics, 13*, Article 960200. https://doi.org/10.3389/fgene.2022.960200

Verma, S. N. P., & Krishi, J. N. (1969). Inheritance of some qualitative characters in greengram (*Phaseolus aureus* Roxb.). *Indian Journal of Heredity, 1*, 105–106.

Wahid, A., Hameed, M., & Rasul, E. (2004). Salt-induced injury symptoms, changes in nutrient and pigment composition and yield characteristics of mungbean. *International Journal of Agriculture & Biology, 6*(6), 1143–1152.

Yadav, A. K., & Prasad, P. V. V. (2022). Impacts, tolerance, adaptation, and mitigation of heat stress on wheat under changing climates. *International Journal of Molecular Sciences, 23*(5), Article 2838. https://doi.org/10.3390/ijms23052838

Yadav, I. C., Chand, J. N., & Saharan, G. S. (1981). Inheritance of resistance in mungbean to bacterial leaf spot. In J. C. Lozano (Ed.), *Proceedings of the Fifth International Conference on Plant Pathogenic Bacteria* (pp. 580–583).

Yohe, J. M., & Poehlman, J. M. (1975). Regression, correlations, and combining ability in mungbean (*Vigna radiata* (L.) Wilczek). *Tropical Agriculture, 52*, 343–352.

Young, N. D., Danesh, D., Menancio-Hautea, D., & Kumar, L. (1993). Mapping oligogenic resistance to powdery mildew in mungbean with RFLPs. *Theoretical and Applied Genetics, 87*, 243–249. https://doi.org/10.1007/BF00223772

Zeven, A. C., & Zhukovsky, P. M. (1975). *Dictionary of cultivated plants and their centres of diversity*. PUDOC.