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## REVIEW ARTICLE

### ORIGIN, DOMESTICATION, TAXONOMY, BOTANICAL DESCRIPTION, GENETICS AND CYTOGENETICS, GENETIC DIVERSITY AND BREEDING OF MUNG BEAN (*Vigna radiata* (L.) R. Wilczek)

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#### ABSTRACT

Mung bean belongs to the Family Faboideae, Subfamily Faboideae, Genus *Vigna* and Species *Vigna radiata* (L.) R. Wilczek. The *Vigna* species grow in warm temperate and tropical regions globally. *Vigna* is most closely related to *Phaseolus*, hence Asia *Vigna* (subgenus *Ceratotropis*) was treated as *Phaseolus* until 1970. Mungbean (*Vigna radiata*) cultivation spread to all hot and warm Asian countries in ancient times, hence considerable diversification is recognized. Mung bean belonging to the subgenus *Ceratotropis* is a diploid species with  $2n = 2x = 22$  chromosomes. The mung bean is commonly named as Mung bean, mung bean, moong bean, mash, golden gram, moong, Chickasaw, Oregon pea, and chop suey bean, chickasaw pea, chiroko or simply mung, celera bean, Jerusalem pea and green gram. These species encompass small herbs to large tropical canopy trees and grow well in the humid tropics, temperate zones, high land, low land and arid zones. This legume has a strategic position in Southeast Asian countries for nutritional security and sustainable crop production. Originating in India as early as 1500 BCE, the mung bean has historically been grown in warmer climates, able to thrive in tropical areas with little rainfall, though ideally a rainy season plant. There is also evidence that the green gram spread to China and Southeast Asia as early as 3000 years ago, known there as nga choi. Having been harvested in regions where many European powers had colonial outposts, green gram was likely exported to Europe for consumption. Worldwide, this crop is of minor importance with restricted geographical distribution, and has cautiously been subjected to detailed and intensive genetic and cytogenetic investigations. The dried grains of mung bean can be split or eaten whole after cooking and made into a soup or dhal. The iron availability in mung bean improves substantially to 7.2–11.3% through cooking practices such as soaking, fermenting and sprouting. Mung bean is also widely relished as sprouts. The germinated grains have higher nutritional value as compared with asparagus or mushroom. Green pods and seeds can be cooked as vegetables. These pulses are frequently fed to children, convalescents and geriatrics or used when “breaking” a long fasting period owing to their ease of digestibility. The haulms are used for fodder and the beans husks and small broken pieces are useful as a feed concentrate. The crops are also grown for hay, green manure and cover crop. Mung bean makes better hay than urad bean as the stems and leaves are less hairy. One hundred gram dry mung bean contains: protein 22 g and carbohydrate 60 g. It is a good source of minerals, provitamin A and vitamin B-complex. The seeds are aphrodisiac, tonic, appetiser, diuretic, good for heart and fatigue and used in paralysis, rheumatism and affections of nervous system. Generally, it is used for its antipyretic, antiscorbutic, diuretic, antidote, antihypertensive and anticancer properties. It has also been recommended for ache, heat, high blood pressure and inflammation. Seeds of this edible legume are used either raw or in cooked form at matured poultice because of its curative potential for polyneuritis. Seeds of mung beans are used to treat alcoholism also. These crops have the ability to fix atmospheric nitrogen (58–109 kg per ha in kg per ha mung bean) in symbiotic association with *Rhizobium* bacteria, which enables them to meet their own nitrogen requirement and also benefit the succeeding crops. Mung bean production is mainly (90%) situated in Asia: India is the largest producer with more than 50% of world production but consumes almost its entire production. China produces large amounts of mung beans, which represents 19% of its legume production. In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding, Uses, Nutritional Value and Health Benefits of mung bean are discussed.

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## INTRODUCTION

Mung bean belongs to the Family Faboideae, Subfamily Faboideae, Genus *Vigna* and Species *Vigna radiata* (L.) R. Wilczek (Wikipedia, 2023b). The *Vigna* species grow in warm temperate and tropical regions globally. *Vigna* is most closely related to *Phaseolus*, hence Asia *Vigna* (subgenus *Ceratropis*) was treated as *Phaseolus* until 1970. Mung bean (*Vigna radiata*) cultivation spread to all hot and warm Asian countries in ancient times, hence considerable diversification is recognized (Norihiko *et al.*, 2011). Mung beans are one of many species moved from the genus *Phaseolus* to *Vigna* in the 1970s. The previous names were *Phaseolus aureus* or *P. radiates* (Döring, 2022). The mung bean is also known as green gram, golden gram and moong. Mung bean belonging to the subgenus *Ceratropis* is a diploid species with  $2n = 2x = 22$  chromosomes. Worldwide, this crop is of minor importance with restricted geographical distribution, and has cautiously been subjected to detailed and intensive genetic and cytogenetic investigations (Mehandi *et al.*, 2019).

The mung bean is commonly named as mash, golden gram and green gram. These species encompass small herbs to large tropical canopy trees and grow well in the humid tropics, temperate zones, high land, low land and arid zones (NAS, 1979). It is also known as green gram, golden gram, moong, Chickasaw, Oregon pea, and chop suey bean and this legume has a strategic position in Southeast Asian countries for nutritional security and sustainable crop production (Mehandi *et al.*, 2019). Mung bean (*Vigna radiata* (L.) Wilczek) is also known as green gram, golden gram, Oregon pea, chickasaw pea, chiroko or simply mung (Akpapunam, 1996; BSMRAU, 2015). Mung bean, mungbean, moong bean, golden gram, green gram, celera bean, Jerusalem pea (Heuzé *et al.*, 2015). Mung bean, (*Vigna radiata*), also called green gram or yellow gram, legume plant of the pea family (Fabaceae), grown for its edible seeds and young sprouts (Petruzzello, 2023). Mungbean (*Vigna radiata* (L.) R. Wilczek var. *radiata*), which is also known as the green gram, or moong, is primarily grown in East Asia, Southeast Asia, and the Indian subcontinent (Mishra *et al.*, 2022). "Moong" called in Hindi in different rural areas of Uttar Pradesh in India. "Bean" is not always appended. They are often sold as "moong". Mung bean (*Vigna radiata* L. Wilczek), is one of the leguminous crops that plays an important role in improving national food security and sustaining livelihoods of small-scale farmers in the developing world (Kwokong, 2022). It is also called as Green Gram, Mung Bean, Mung Dahl in English, Mung in Hindi, Pasha-Pesalu in Telugu, Pacche Hasiru in Kannada and Mug, Mung in Bengali.

Mung bean has its own place due to some very unique features like short crop duration, low input requirement, wide adaptability, and tolerance to various abiotic stresses including heat and drought. Besides, mung bean is also very rich in overall nutrient content which makes it the most preferred crop for various culinary preparation including *dal*, soups, sprouts. In addition to the biotic and abiotic stresses, breeding focus should be on other economic traits like extra-early maturity and photothermal insensitivity in the genotypes, which will help in suitable fitting of the developed varieties in various cropping systems and patterns. Due to its unique health and nutritional properties, along with soil and environment ameliorative ability, mung bean is one of the preferred crops for food, nutrition, and environmental security and sustainability (Mishra *et al.*, 2022). The seeds of mung bean (*Vigna radiata* (L.) R. Wilczek) have gained immense popularity for drug discovery and research besides aiding to resolve the malnutrition problem across the globe. This ancient food source is recognized as one of the most important edible legume, rich in necessary food supplements and consumed as cereal based human diet by most households in Asia (Doyle, 1994).

The mung bean is mainly cultivated in East, Southeast and South Asia. It is used as an ingredient in both savoury and sweet dishes. Mung bean (*Vigna radiata* L. Wilczek) is economically most important crop of *Vigna* group. This crop has also been reported to smother weed flora appreciably (20–45%) when intercropped with tall cereals or pigeonpea and consequently, minimize the cost incurred on weed control. On account of short duration and photo-thermo insensitivity, they are considered excellent crops for crop intensification and diversification (Mehandi *et al.*, 2019). Mung bean are tropical grain legumes widely grown in the sub-tropical countries of South and Southeast Asia. Nevertheless, these crops are cultivated over a wide range of latitudes in the regions where average diurnal temperatures during the growing season are warmer than about 20°C (Mehandi *et al.*, 2019). A seed of mung bean is highly nutritious containing 24–28% protein, 1.0–1.5% fat, 3.5–4.5% fibre, 4.5–5.5% ash and 59–65% carbohydrates on dry weight basis and provide 334–344 kcal energy. Mung bean protein is considered to be easily digestible.

Originating in India as early as 1500 BCE, the mung bean has historically been grown in warmer climates, able to thrive in tropical areas with little rainfall, though ideally a rainy season plant. There is also evidence that the green gram spread to China and Southeast Asia as early as 3000 years ago, known there as nga choi. Having been harvested in regions where many European powers had colonial outposts, green gram was likely exported to Europe for consumption (Tenochtitlan, 2023).

Although whole mung beans are also occasionally used in Indian cuisine, beans without skins are more commonly used. In Karnataka, Maharashtra, Gujarat, Kerala and Tamil Nadu, whole mung beans are commonly boiled to make a dry preparation often served with congee. Hulled mung beans can also be used in a similar fashion as whole beans for the purpose of making sweet soups. Mung beans in some regional cuisines of India are stripped of their outer coats to make mung *dal*. In Bangladesh and West Bengal the stripped and split bean is used to make a soup-like dal known as *mug dal*. In the South Indian states of Karnataka, Tamil Nadu, Telangana and Andhra Pradesh, and also in Maharashtra, steamed whole beans are seasoned with spices and fresh grated coconut. In South India, especially Andhra Pradesh, batter made from ground whole moong beans (including skin) is used to make a variety of dosa called pesarattu or pesara dosa (Wikipedia, 2023b). The dried grains of mung bean can be split or eaten whole after cooking and made into a soup or dhal. The iron availability in mung bean improves substantially to 7.2–11.3% through cooking practices such as soaking, fermenting and sprouting. Mung bean is also widely relished as sprouts. The germinated grains have higher nutritional value as compared with asparagus or mushroom. Green pods and seeds can be cooked as vegetables. These pulses are frequently fed to children, convalescents and geriatrics or used when "breaking" a long fasting period owing to their ease of digestibility. The haulms are used for fodder and the beans husks and small broken pieces are useful as a feed concentrate. The crops are also grown for hay, green manure and cover crop. Mung bean makes better hay than urad bean as the stems and leaves are less hairy (Mehandi *et al.*, 2019). Mung bean starch, which is extracted from ground mung beans, is used to make transparent cellophane noodles (also known as bean thread noodles, bean threads, glass noodles, fensi, tung hoon). Cellophane noodles become soft and slippery when they are soaked in hot water. A variation of cellophane noodles, called mung bean sheets or green bean sheets, are also available. In Korea, a jelly called nokdumuk (also called cheongpomuk) is made from mung bean starch; a similar jelly, colored yellow with the addition of gardenia coloring, is called hwangpomuk. In northern China, mung bean jelly is called liangfen, which is a very popular food during summer. The Hokkiens add sugar to mung bean jelly to make it a dessert called Liók-tāu hún-kóe. Mung batter is used to make crepes named pesarattu in Andhra Pradesh, India and pancakes named bindaetteok in Korea (Döring, 2022). Whole cooked mung beans are generally prepared from dried beans by boiling until they are soft. Mung beans are light yellow in colour when their skins are removed. Mung bean paste can be made by hulling, cooking, and pulverizing the beans to a dry paste (Wikipedia, 2023b). The mung bean is likely native to the Indian subcontinent and is widely cultivated in Asia for use in a variety of

sweet and savory dishes, particularly in India, China, Korea, and Thailand. It is also grown in relatively dry tropical and subtropical areas, including the Caribbean and parts of Africa (Petruzzello, 2023). Like other culinary beans, mung beans are high in dietary fibre and protein and are also a source of iron, magnesium, potassium, and a number of essential amino acids (Petruzzello, 2023).

One hundred gram dry mung bean contains: protein 22 g and carbohydrate 60 g. It is a good source of minerals, provitamin A and vitamin B-complex (BSMRAU, 2015). Generally, it is used for its antipyretic, antiscorbutic, diuretic, antidote, antihypertensive and anticancer properties. It has also been recommended for ache, heat, high blood pressure and inflammation. Seeds of this edible legume are used either raw or in cooked form at matured poultice because of its curative potential for polyneuritis. Seeds of mung beans are used to treat alcoholism also (Dahiya *et al.*, 2015). The seeds are aphrodisiac, tonic, appetiser, diuretic, good for heart and fatigue and used in paralysis, rheumatism and affections of nervous system (BSMRAU, 2015). Mung bean has been consumed for more than 2000 years in China as it is well known for its health benefits such as reducing gastrointestinal disorders and heat stroke, and clearing toxins from the body. It is also considered to aid in reducing the cholesterol level in the body, manipulation of tumor cells and regulating blood pressure. Owing to its palatable taste and nutritional quality, mung bean has been used as an iron-rich whole food source for baby food and induces less flatulence hence well tolerated by children. Furthermore, starch in mung bean is highly digestible when compared to those in chickpea (*Cicer arietinum*), pigeon pea (*Cajanus cajan*) and lentils (*Lens culinaris*) (K gokong, 2022).

As a legume plant, mung bean is in symbiotic association with Rhizobia which enables it to fix atmospheric nitrogen (58–109 kg per ha mung bean). It can provide large amounts of biomass (7.16 t biomass/ha) and Nitrogen to the soil (ranging from 30 to 251 kg/ha). The nitrogen fixation ability not only enables it to meet its own nitrogen requirement, but also benefit the succeeding crops. It can be used as a cover crop before or after cereal crops in rotation, which makes a good green manure (Mehandi *et al.*, 2019; Döning, 2022). Holders of the largest germplasm collections are AVRDC, Shanhuai, in Taiwan (6000 accessions), USDA, Georgia and Colorado, in USA (3500), Punjab Agricultural University, Ludhiana, in India (3000), and CAAS, Beijing, China (3000). Several smaller but important collections exist at research institutes in the South-East Asian countries: FCRI (Bangkok) in Thailand, BORIF (Bogor) and MARIF (Malang) in Indonesia, IPB (Los Banos) in the Philippines. Internationally, the emphasis is at present on evaluation and documentation work to improve user's access to the collections (Siemonsma and Lampung, 2016). Mungbean or green gram [*Vigna radiata* (L.) R. Wilczek] is a nutrition-rich, short-duration and warm season grain legume which is cultivated in several countries across Asia, East Africa and Australia. Owing to its nitrogen fixing ability and adaptability to wider climate regimes, it finds a prominent place in several cereal-based cropping systems. Nonetheless, being grown so widely, mung bean suffers from several biotic and abiotic stresses including diseases, insect-pests, high temperature, terminal moisture stress, soil salinity and photo-thermo period sensitivity which affect its productivity as well as grain quality rendering it less remunerative despite huge potential (Mehandi *et al.*, 2019).

In many traditional mung bean growing areas, farmers still grow old landraces, mixtures of homozygous genotypes, very well equipped to adjust to changing environmental conditions, giving stable, but seldom excellent, yields. Even recently, many cultivars have been developed from these landraces by simple pure-line selection: identification of the outstanding genotypes in these mixtures. These well-adapted local selections form an excellent starting point for hybridization programmes. Nowadays, the breeding challenge is to overcome the genetic limitations deriving from centuries-long adaptation of mung bean to marginal environments. The traditional, late, robust plant types have been replaced by new types useful for short seasons and multiple cropping systems with mung bean occupying the land for short periods between major crops. These are short, compact plants with high harvest index, with reduced photoperiod sensitivity, and with a more uniform maturity. Many modern cultivars have already been released in the major producing countries, which also have improved resistance to major pests and diseases. Sources of resistance have been identified in germplasm of mung bean and related species. Black gram (*Vigna mungo*) shows, among the Asiatic *Vigna* species, most promise for interspecific hybridization with mung bean. At present, little attention is given to protein content and quality, because much more impact on total protein production is to be expected from increasing yields (Siemonsma and Lampung, 2016).

Most of the high yielding varieties of mung bean bred and released so far have been developed through single cross pedigree method of selection. The single plant selections made in the early generations restrict carrying forward the bulk of created variability, which gets lost quickly giving way to homozygosity with each succeeding generation. This method has served the mung bean improvement programme well in the past, but lately no productivity advances are materializing due to the inherent genetic limitation of the method. The intermitting of selected F<sub>2</sub> plants and selections in the late generations will help to harness most of the desirable genes (Mehandi *et al.*, 2019).

Mung bean production is mainly (90%) situated in Asia: India is the largest producer with more than 50% of world production but consumes almost its entire production. China produces large amounts of mung beans, which represents 19% of its legume production (Heuzé *et al.*, 2015). Mung bean crops grown for seeds are generally harvested when pods begin to darken. They are mostly hand-picked at weekly intervals. In newer varieties in which the plants mature uniformly, the whole plants are harvested and sun-dried before being threshed. Once pods have dried, the seeds are removed by beating or trampling. The mung bean can be grazed six weeks after planting and two grazings are usually obtained. It can be used to make hay, when it should be cut as it begins to flower and then quickly dried for storage. It is possible to make hay without compromising seed harvest (Heuzé *et al.*, 2015). In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding, Uses, Nutritional Value and Health Benefits of mung bean are discussed.

## ORIGIN AND DOMESTICATION

The crop is said to have originated from India and must have been derived from var. *sublobata* which occurs wild throughout India and Burma. From there it has spread to South and East Asia, East and Central Africa, the West Indies and the United States (Akpapunam, 1996). The centre of species diversity for section *Ceratotropis* is South Asia. The presumed progenitor of mung bean is the wild form *Vigna radiata* var. *sublobata* (Roxb) Verdcourt, which is widely distributed across the Old World tropics from western Africa to northern Australia and Papua New Guinea. Archaeobotanical finds and literary records suggest that mung bean was domesticated in India where wild mung bean is widely distributed. Archaeobotanical evidence points to both south-eastern India between the Godavari and Krishna rivers and western Himalayan foothills as likely places where domestication could have occurred (Chontira Sangi *et al.*, 2007). The *Vigna* species grow in warm temperate and tropical regions globally. *Vigna* is most closely related to *Phaseolus*, hence Asia *Vigna* (subgenus *Ceratotropis*) was treated as *Phaseolus* until 1970. Mungbean (*Vigna radiata*) cultivation spread to all hot and warm Asian countries in ancient times, hence considerable diversification is recognized (Narihiko *et al.*, 2011). The mung bean is thought to have originated from the Indian subcontinent where it was domesticated as early as 1500 BC. Cultivated mung beans were introduced to southern and eastern Asia, Africa, Austronesia, the Americas and the West Indies. It is now widespread throughout the Tropics and is found from sea level up to an altitude of 1850 m in the Himalayas (Heuzé *et al.*, 2015).

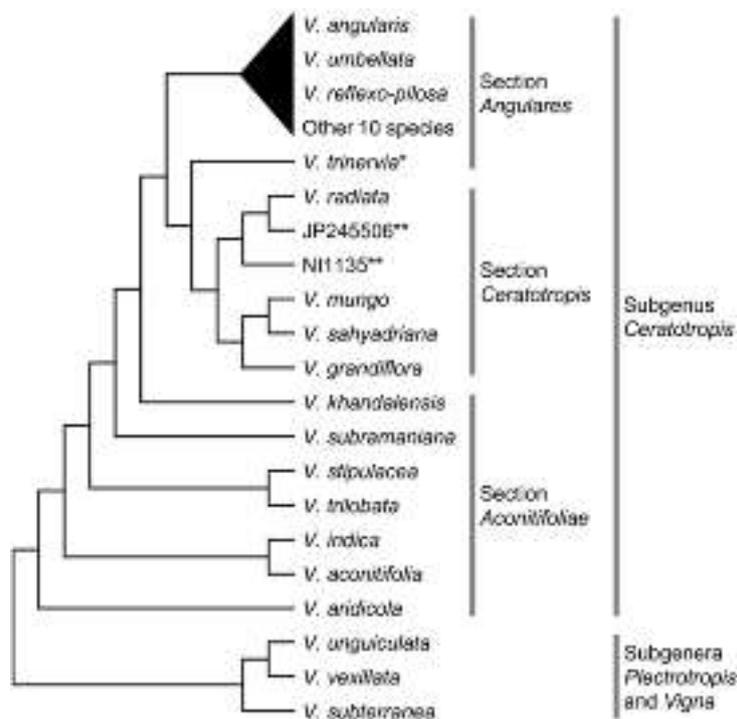
Mung bean originated in India or the Indo-Burmese region where it has been cultivated for several millenar ies. It spread in early times to most other Asian countries, and more recently also to other continents. In spite of its present wide distribution, mung bean never became a major commercial crop outside Asia. In most South-East Asian countries, mung bean ranks among the three most important grain legumes (Siemonsma and Lampang, 2016). Mung bean is distributed in India, Pakistan, Bangladesh, Sri Lanka, Philippines, Taiwan, Thailand, Nepal and Southern Asian countries. In India it is distributed in Maharashtra, UP, MP, Karnataka, Gujarat A.P, Tamil Nadu and Rajasthan (CU, 2017).

Mung bean is of Indian origin as is evidenced by their occurrence at archeological sites in the continent. *Vigna radiata* is native to north eastern India-Myanmar regions of Asia. *Vigna radiata* var. *sublobata* Verdc. is the closest wild relatives of the cultivated mung bean, respectively, and are regarded as their putative progenitors. Based on morphological evidence alone, many researchers have considered var. *sublobata* as progenitor of mung bean. The detailed morpho-chemotaxonomic studies on wide collections of var. *sublobata*, cross ability and chromosome pairing evidence have led to the conclusion that var. *sublobata* is a polymorphic taxon; two distinct morphological groups of it are the wild progenitors of mung bean and can be designated as *V. radiata* var. *sublobata*. The wild collections have characteristics conducive to domestication like annual growth habit, erect plant type, photoperiod insensitivity, more pods with high number of seeds, and smaller leaves. The present day cultivars of mung bean might have originated from new combinations of the already existing variants, changes in growth habit and seed size have been brought about by possible accumulation of recessive mutant genes. Moreover, during domestication the dehiscent nature of pods and seed hardness of the wild progenitors have been selected out (Mehandi *et al.*, 2019). The mung bean was domesticated in India, where its progenitor (*Vigna radiata* subspecies *sublobata*) occurs wild. Carbonized mung beans have been discovered in many archeological sites in India. Areas with early finds include the eastern zone of the Harappan civilisation in modern-day Pakistan and western- and northwestern India, where finds date back about 4,500 years, and South India in the modern state of Karnataka where finds date back more than 4,000 years. Some scholars, therefore, infer two separate domestications in the northwest and south of India. In South India, there is evidence for the evolution of larger-seeded mung beans 3,500 to 3,000 years ago. By about 3500 years ago mung beans were widely cultivated throughout India. Cultivated mung beans later spread from India to China and Southeast Asia. Archaeobotanical research at the site of Khao Sam Kaeo in southern Thailand indicates that mung beans had arrived in Thailand by at least 2,200 years ago (Döning, 2022).

The mung bean is likely native to the Indian subcontinent and is widely cultivated in Asia for use in a variety of sweet and savory dishes, particularly in India, China, Korea, and Thailand. It is also grown in relatively dry tropical and subtropical areas, including the Caribbean and parts of Africa (Petruzzello, 2023). Originating in India as early as 1500 BCE, the mung bean has historically been grown in warmer climates, able to thrive in tropical areas with little rainfall, though ideally a rainy season plant. There is also evidence that the green gram spread to China and Southeast Asia as early as 3000 years ago, known there as nga choi. Having been harvested in regions where many European powers had colonial outposts, green gram was likely exported to Europe for consumption (Tenochtitlan, 2023). The mung bean was domesticated in India, where its progenitor (*Vigna radiata* subspecies *sublobata*) occurs wild. Carbonized mung beans have been discovered in many archeological sites in India. Areas with early finds include the eastern zone of the Harappan civilisation in modern-day Pakistan and western- and northwestern India, where finds date back about 4,500 years, and South India in the modern state of Karnataka where finds date back more than 4,000 years. Some scholars, therefore, infer two separate domestications in the northwest and south of India. In South India, there is evidence for the evolution of larger-seeded mung beans 3,500 to 3,000 years ago. By about 3500 years ago mung beans were widely cultivated throughout India. Cultivated mung beans later spread from India to China and Southeast Asia. Archaeobotanical research at the site of Khao Sam Kaeo in southern Thailand indicates that mung beans had arrived in Thailand by at least 2,200 years ago (Sikdar, 2023; Wikipedia, 2023b).

## TAXONOMY

Mung bean belongs to the Family Fabaceae, Subfamily Faboideae, Genus Vigna and Species Vigna radiata (L.) R. Wilczek (BSMRAU, 2015; Invasive, 2018; Wikipedia, 2023b ; Wikipedia, 2023c; USDA, 2023). Phylogenetic tree of the species in the genus *Vigna* is given in Fig. 1



About 40 different types of Mung are met with in cultivation which can be botanically grouped under 5 varieties (Sikdar, 2023), viz

1. var. *radiatus* (typical variety) leaves drak green, pods spreading, seeds green.
2. var. *aurea* (Roxb) R. Wilczek (Sonamung) Leaves pale, pods reflexed, seeds dull yellow.
3. var. *grandis* (Prain) R. Wilczek Leaves large, pods spreading, flowers with prominent bracts, seeds green.
4. var. *brunea* (Bose) R. Wilczek Leaves bright green, spreading pods, brown seeds.
5. var. *glabra* (Roxb) R. Wilczek Leaves and other parts more or less glabrous.

Another “variety occurs wild in the subtropical region of the Himalaya viz. var. *sublobatus* (Roxb) R. Wilcz. This is regarded as the progenitor of Mung as well as Urud. This self-pollinated and diploid legume crop belongs to the family Leguminosae or Fabaceae. This plant family is widely spread all over the world and resides for the third position for the biggest family of flowering plants. It has approximately 650 genus and 20,000 species (Doyle, 1994). Mungbean belongs to the Asian *Vigna*, subgenus *Ceratotropis*. Taxonomically, subgenus *Ceratotropis* has been divided into the following three sections: *Ceratotropis*, *Angulares* and *Aconitifoliae*. Section *Ceratotropis* also includes the South Asian cultigen black gram [*V. mungo* (L.) Hepper] (Sangiri *et al.*, 2007). Mung bean (*Vigna radiata*) used to be known as *Phaseolus aureus* Roxb. before many *Phaseolus* species were moved to the *Vigna* genus. In spite of its usual vernacular name of mung bean, *Vigna radiata* is a different species from *Vigna mungo*, which is usually called black gram or urdbean. Both species have a similar morphology. The mung bean (*Vigna radiata* (L.) R. Wilczek) is a legume cultivated for its edible seeds and sprouts across Asia. There are 3 subgroups of *Vigna radiata*: one is cultivated (*Vigna radiata* subsp. *radiata*), and two are wild (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*) (Heuzé *et al.*, 2015). Mung bean is morphologically very similar to black gram (*Vigna mungo* (L.) Hepper) and they are sometimes considered variants of the same species. Chemotaxonomy and cytogenetics, however, support the distinction, but the debate still continues. Both species are sometimes considered to be domesticates from the same wild forms (*Vigna sublobata*, based on *Phaseolus sublobatus* Roxb.). Nowadays, the cultivated forms of mung bean are usually grouped as *V. radiata* var. *radiata*, although a classification into cultivar groups would be more appropriate. The wild forms are usually classified into two botanical varieties: var. *sublobata* (Roxb.) Verdc. and var. *setulosa* (Dalzell) Ohwi & Ohashi. Var. *sublobata* is smaller in all parts compared to var. *radiata*, and occurs in India, Sri Lanka, S.-E. Asia, Queensland, Madagascar and East Africa. Var. *setulosa* has large, almost orbicular stipules and dense long hairs on the stem. It occurs in India, China, Japan and Indonesia (Siemonsma and Lampan, 2016). Mung beans are one of many species moved from the genus *Phaseolus* to *Vigna* in the 1970s. The previous names were *Phaseolus aureus* or *P. radiates* (Döring, 2022).

**Synonyms** (Wikipedia, 2023b; Wikipedia, 2023 c)

1. *Azuki radiata* (L.) Ohwi
2. *Phaseolus abyssinicus* Savi
3. *Phaseolus chanetii* (H.Lev.) H.Lev.
4. *Phaseolus hirtus* Retz.
5. *Phaseolus novo-guineense* Baker f
6. *Phaseolus radiatus* L.
7. *Phaseolus setulosus* Dalzell
8. *Phaseolus sublobatus* Roxb.
9. *Phaseolus trinervius* Wight & Am.
10. *Pueraria chanetii* H.Lev.
11. *Rudua aurea* (Roxb.) F.Maek.
12. *Rudua aurea* (Roxb.) Maekawa
13. *Vigna brachycarpa* Kurz
14. *Vigna opistricha* A.Rich.
15. *Vigna perrieriana* R.Vig.
16. *Vigna sublobata* (Roxb.) Babu & S.K.Sharma
17. *Vigna sublobata* (Roxb.) Bairig. & al.

**Synonyms (Heuzé et al., 2015).**

1. *Phaseolus aureus* Roxb.,
2. *Phaseolus radiatus* L.,
3. *Phaseolus setulosus* Dalzell,
4. *Phaseolus sublobatus* Roxb.,
5. *Phaseolus sublobatus* var. *grandiflora* Prain,
6. *Phaseolus trinervius* Wight & Am.,
7. *Vigna radiata* var. *setulosa* (Dalzell) Ohwi & H. Ohashi,
8. *Vigna sublobata* (Roxb.) Bairig. et al.

Mung beans are one of the many species which have been moved from the genus *Phaseolus* to *Vigna* in the 1970s. According to the International Legume Database and Information Service reports several synonyms were found viz.,

*Vigna radiata* var. *glabra* (Roxb) Verdc,  
*Vigna radiata* var. *grandiflora*,  
*Vigna radiata* var. *glabra*,  
*Vigna radiata* var. *setulose* (Dalzell),  
*Vigna radiata* var. *sublobata* (Roxb) have been cited in the literature.

*Vigna radiata* var. *radiata*: Golden gram, Green gram, Moog-bean; plants short, erect, leaflets unlobed, fruits thinner, 6-9 cm long, sparsely covered with shorter brownish hairs, seed light green, longer. *Vigna radiata* var. *sublobata*: Jarusalem pea, wild moog; plants twinning, leaflets generally lobed, fruit thinner, 4-6 cm long, sparsely covered with shorter brownish hairs, seeds light green, shorter (Garg, 2020).

Higher taxonomic ranks and intraspecific varieties of mung bean (*Vigna radiata*) and phylogenetic tree of the species in the genus *Vigna* (Takahashi and Tomooka, 2020) is given in Fig. 2:

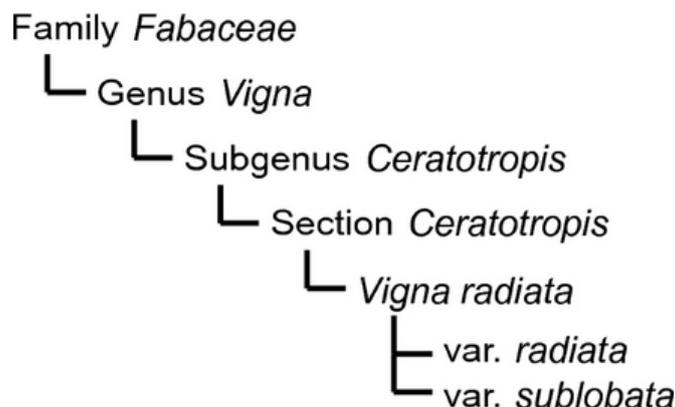


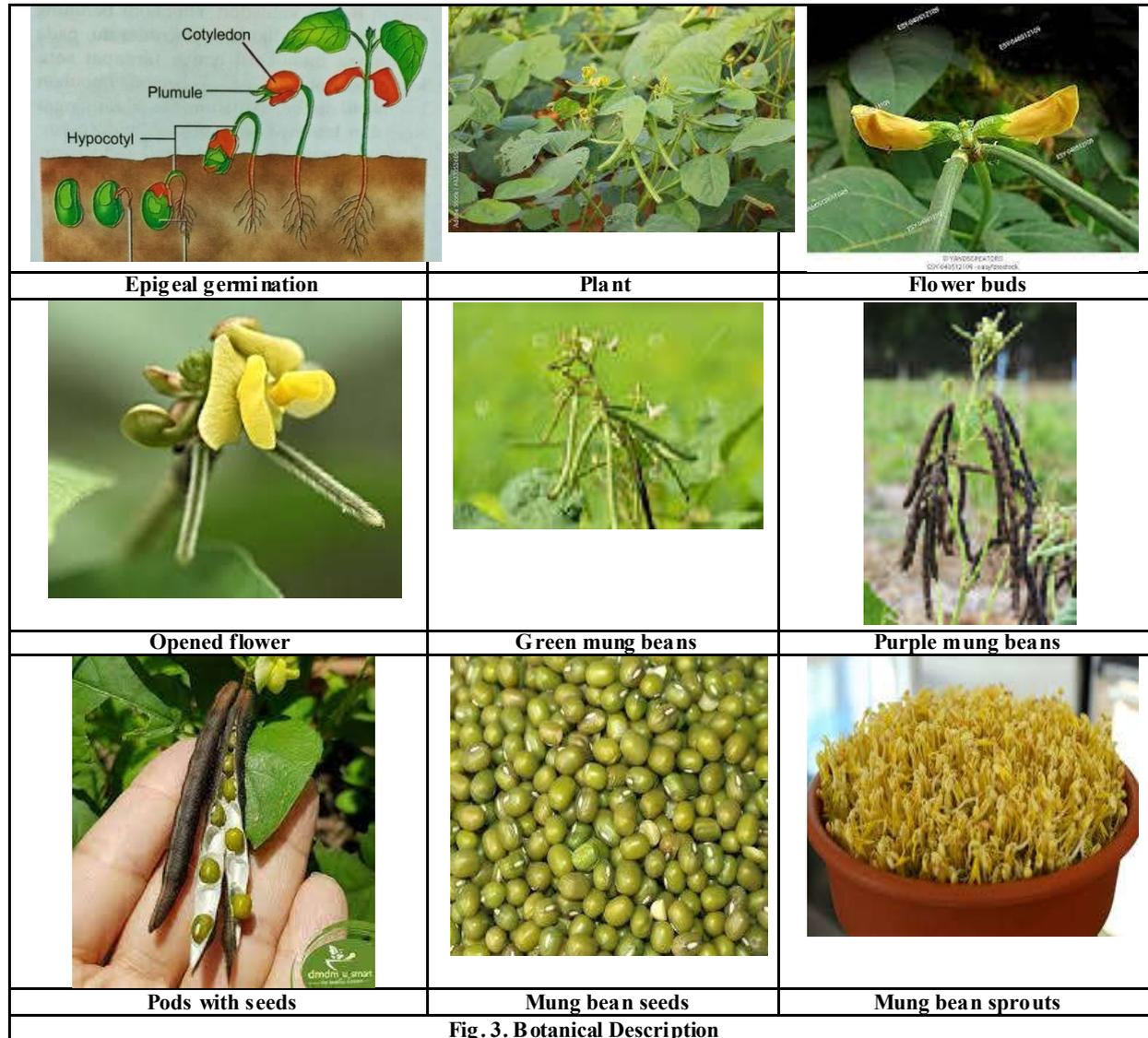
Fig.2. Higher taxonomic ranks and intraspecific varieties of mung bean (*Vigna radiata*)

## BOTANICAL DESCRIPTION

Leaves are trifoliate, entire leaflet, ovate to rhombic, acuminate 5-15 cm in length. Flowers are yellow to yellowish-green clusters of 10-25 flowers on long pedicels. Pods are 5.5-10 cm in length and thin cylindrical with short pubescences. Stems are long, thin, Round, Cylindrical, hairy with a twinning to its upper branches and 50-160 cm long. Seeds are more or less globular, often green in color and sometimes found in black, yellow, green, purple-brown, brown, fine surface, wavy ridges some-times may be almost invisible, flat hilum covered by white rough layer. Roots are small rootlet with parent root (Akpapunam et al., 1996). Green gram is a cultivated annual herb. It has tap root system, the root contain nodule having the  $N_2$ -fixing bacteria *Rhizobium* spp. Stem is erect to sub-erect, highly branching and hairy. Leaf is compound, trifoliate. Inflorescence is a raceme. Flower is zygomorphic, complete, papilionaceous. Calyx contains 5 sepals, gamosepalous. Corolla contains 5 petals, divided into standard, wing and keel; aestivation vexillary. Androecium contains 10 (9+1) stamens, diadelphous. Gynoecium consists of carpel one, style spirally twisted, ovary superior, placentation marginal. Fruit is a pod with densely trichomed (BSMRAU, 2015). The mung bean plant is an annual, erect or semi-erect, reaching a height of 0.15-1.25 m. It is slightly hairy with a well-developed root system. Wild types tend to be prostrate while cultivated types are more erect. The stems are many-branched, sometimes twinning at the tips. The leaves are alternate, trifoliate with elliptical to ovate leaflets, 5-18 cm long x 3-15 cm broad. The flowers (4-30) are papilionaceous, pale yellow or greenish in colour. The pods are long, cylindrical, hairy and pending. They contain 7 to 20 small, ellipsoid or cube-shaped seeds. The seeds are variable in colour: they are usually green, but can also be yellow, olive, brown, purplish brown or black, mottled and/or ridged. Seed colours and presence or absence of a rough layer are used to distinguish different types of mung bean. Cultivated types are generally green or golden and can be shiny or dull depending on the presence of a texture layer. Golden gram, which has yellow seeds, low seed yield and pods that shatter at maturity, is often grown for forage or green manure. Green gram has bright green seeds, is more prolific and ripens more uniformly, with a lower tendency for pods to shatter. In India, two other types of mung beans exist, one with black seeds and one with brown seeds (Heuzé et al., 2015). The mung bean resembles the black gram (*Vigna mungo* (L.)) with two main differences: the corolla of *Vigna mungo* is bright yellow while that of *Vigna radiata* is pale yellow; mung bean pods are pendulous whereas they are erect in black gram. Mung bean is slightly less hairy than black gram. Mung bean is sown on lighter soils than black gram (Heuzé et al., 2015).

An erect or semi-erect, sometimes twining, herbaceous annual, 25-130 cm tall. Branching starts from lower and intermediate nodes (rarely from cotyledons or unifoliate leaves). First two leaves opposite and simple, subsequent leaves alternate and trifoliate; leaflets ovate to deltoid, 5-18 cm x 4-15 cm, usually entire. Flowers are large, 1-2 cm in diameter, greenish to bright yellow, self-fertile, borne in clusters of 5-25 on axillary racemes, 2-20 cm long. Pods spreading and pendent, cylindrical, up to 15 cm long, usually straight, pubescent or glabrous, black or tawny brown, with up to 20 globose to ellipsoid seeds. Seeds green or yellow, occasionally brown or blackish, with dull or glossy lustre (associated with pod wall remnants); hilum flat and white. Germination is epigeal (Siemonsma and Lampang, 2016). Mung bean or Green gram (*Vigna radiata* (L.) Wilczek) has many desirable traits, such as erect growth habit, early maturity, and long pods, with large number of seeds (Singh et al., 2021). The green gram is an annual vine with yellow flowers and fuzzy brown pods. The English word mung originated (and used as is) from the Hindi word ("mūng"), which is derived from the Sanskrit word ("mudga"). Mung bean (*Vigna radiata*) is a plant species of Fabaceae which is also known as green gram. It is sometimes confused with black gram (*Vigna mungo*) for their similar morphology, though they are two different species. The green gram is an annual vine with yellow flowers and fuzzy brown pods. There are three subgroups of *Vigna radiata*, including one cultivated (*Vigna radiata* subsp. *radiata*) and two wild ones (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*). It has a height of about 15-125 cm. Mung bean has a well-developed root system. The lateral roots are many and slender, with root nodules grown. Stems are much branched, sometimes twinning at the tips. Young stems are purple or green, and mature stems are grayish yellow or brown. They can be divided into erect cespitose, semi-trailing and trailing types. Wild types tend to be prostrate while cultivated types are more erect. Leaves are ovoid or broad-ovoid, cotyledons die after emergence, and ternate leaves are produced on two single leaves. The leaves are 6-12 cm long and 5-10 cm wide. Racemes with yellow flowers are borne in the axils and tips of the leaves, with 10-25 flowers per pedicel, self-pollinated. The fruits are elongated cylindrical or flat cylindrical pods, usually 30-50 per plant. The pods are 5-10 cm long and 0.4-0.6 cm wide and contain 12-14 septum-separated seeds, which are either green, yellow, brown or blue and can be cylindrical or spherical in shape. Seed colors and presence or absence of a rough layer are used to distinguish different types of mung bean (Döning, 2022). The mungbean is an annual, semi erect to erect or sometimes twining, deep rooted herb, 30-120 cm tall.

The central stems are more or less erect while side branches are semi erect. The root system consists of a well-developed taproot with deeply placed lateral roots and leaves are alternate and trifoliate, or sometimes with five leaflets. Leaflets are medium to dark green, broadly ovate, sometimes lobbed, rounded at the base and pointed at the apex, 5 to 12 cm long, and 2 to 10 cm wide. Both the stems and leaves are covered with short brownish hairs. The flowers are greenish to bright yellow and are self-fertile and highly self-pollinated. Flowering is indeterminate and may continue over a period of several weeks if the plant stays healthy. Pods mature in about 20 days after flowering. The pods are linear, sometimes curved, round and slender with short pubescence and consist of 8-20 seeds grains per pod. The seeds are small and globe shaped, exhibiting a wide range of variation from yellow, yellow greenish, light green, shiny green, dark green, dull green, brown and purplish black marbled or mottled with black patches. The seed coat often has ridges, making the seed rough to touch. The white yellowish, flat hilum is not concave and germination is epigeal (Kkokong, 2022). Epigeal germination is marked by the up-lifting of the hypocotyl above the ground level. Cotyledon divides quickly to form leaves. This type of germination can be observed in mung bean plants (Fig. 3).



The mung bean is a fast-growing erect or semi-erect annual plant with a sturdy taproot. Like many other members of the pea family, mung bean plants add nitrogen to the soil by means of nitrogen-fixing bacteria housed in nodules on their roots. The compound leaves alternate along the branching stems and have three leaflets that are roughly triangular to ovate. The small pale yellow or greenish flowers grow in dense clusters and are insect-pollinated. The resulting legume fruits, borne in pendulous whorls, are long and straight, and they turn dark at maturity; each pod holds up to 20 small seeds. The most common mung bean cultivar bears green seeds, but yellow, brown, and mottled green variations also occur (Petruzzello, 2023). The green gram is an annual vine with yellow flowers and fuzzy brown pods. There are three subgroups of *Vigna radiata*, including one cultivated (*Vigna radiata subsp. radiata*) and two wild ones (*Vigna radiata subsp. Sublobata* and *Vigna radiata subsp. glabra*). It has a height of about 15–125 cm. Mung bean has a well-developed root system. The lateral roots are many and slender, with root nodules grown. Stems are much branched, sometimes twining at the tips. Young stems are purple or green, and mature stems are grayish yellow or brown. They can be divided into erect cespitose, semi-trailing and trailing types. Wild types tend to be prostrate while cultivated types are more erect. Leaves are ovoid or broad-ovoid, cotyledons die after emergence, and ternate leaves are produced on two single leaves. The leaves are 6–12 cm long and 5–10 cm wide. Racemes with yellow flowers are borne in the axils and tips of the leaves, with 10-25 flowers per pedicel, self-pollinated. The fruits are elongated cylindrical or flat cylindrical pods, usually 30-50 per plant. The pods are 5–10 cm long and 0.4-0.6 cm wide and contain 12-14 septum-separated seeds, which are either green, yellow, brown or blue and can be cylindrical or spherical in shape. Seed colors and presence or absence of a rough layer are used to distinguish different types of mung bean. Germination is typically within 4–5 days, but the actual rate varies according to the amount of moisture introduced during the germination stage. It is epigeal, with the stem and cotyledons emerging from the seedbed. After germination, the seed splits, and a soft, whitish root grows. Mung bean sprouts are harvested during this stage. If not harvested, it develops a root system, then a green stem which contains two leaves shoots up from the soil. After that, seed pods begin to form on

its branches, with 10-15 seeds contained in each pod. The maturation can take up to 60 days. Once matured, it can reach up to 76 cm tall, with multiple branches with seed pods. Most of the seed pods become darker, while some remain green (Wikipedia, 2023b). Mung is a scandent or subscandent shrub or under shrub with long trailing branches, more or less densely pubescent with reddish brown hairs. Leaves are pinnately 3-foliolate, stipulate and stipulate; leaflets ovate-lanceolate, the terminal rhomboid ovate, 5-8 cm long, sparsely setosely hairy; stipules 5-7 nerved, usually ciliate, about 1 cm long. Racemes axillary, few-flowered; bracts and bracteoles present; peduncle short at first, elongating in fruit. Flowers pale yellow 6-7 mm long, bisexual and zygomorphic. Calyx campanulate with linear teeth. Corolla papilionaceous; standard petal orbicular, much the largest and covering the wings and keel; wings obviate-falcate, slightly adnate to the keel; keel incurved, shortly beaked. Stamens 9+1, diadelphous, vexillary stamen free, anthers uniform. Ovary superior, monocarpellary, with many ovules on marginal placenta; style filiform, longitudinally bearded on the inner face; stigma oblique with a short beak. Pod linear, nearly erect, 4-7 cm long, very hairy when young, glabrescent afterwards, septate between the seeds; seeds subquadrate, about 2 mm long, brown or dull greenish grey; cotyledons yellow in some varieties and white in others (Sikdar, 2023).

## GENETICS AND CYTOGENETICS

### Genetics

Information on the genetics of unusual traits in a crop is crucial for its systematic breeding programmes. Several studies have been conducted to know the genetics of qualitative and quantitative traits in addition resistance to major diseases and insect pests in mung bean, the results of which are presented in Table 1 (Mehandi *et al.*, 2019).

Table 1. Genetics of qualitative traits

Qualitative traits	Characteristic	Gene involved
Plant type and growth habit	Erect, semi erect, semi-spreading or twining type	Single dominant gene T
	Twining habit, semi-spreading habit is dominant to erect habit	Single dominant gene
	Erect, semi erect, semi-spreading or twining type	Dwarf mutant
Pigmentation	Indeterminate growth habit which inherited independently from leaf shape	Single dominant gene
	Purple hypocotyl which is dominant over green hypocotyl	Single gene 'A'
	'P' gene for the purple hypocotyl and a multiple allelic series 'C', 'C' and 'c' for purple, purple spotted and green epicotyl	Single dominant gene
	Anthocyanin pigmentation in hypocotyl, epicotyl, stem, petiole and peduncle	Single dominant genes
	A gene 'R' that conditions red colour of the cotyledons, hypocotyls and top of the leaflet stalk	Single dominant genes
	Anthocyanin pigmentation in the hypocotyl, epicotyl, stem, petiole, and peduncle	Single recessive gene
Stem fasciation	Anthocyanin in hypocotyl	Two supplementary genes, designated as 'Sh' and 'Ph' with recessive epistatic interaction
	Purple pigmentation on stem, petiole and veins of leaves	Single dominant gene 'Ppl' with pleiotropic effect
	Stem fasciations on the number of floral organs	Single recessive gene 'fsl' with a pleiotropic effect
	Inheritance of leaf size revealed that large leaflet is dominant over small leaflet	Single dominant gene
Leaf traits	Pentafoliate leaf	One recessive gene
	Pentafoliate leaf	Two recessive genes with duplicate gene action
	Nine foliate leaf mutant	Single recessive gene
	Induced unifoliate and multifoliate leaf mutants	Single recessive genes
	Narrow lanceolate leaf	Two recessive genes, 'nil' and 'n12'
	Lobed trifoliate leaf is dominant over entire leaf	Single dominant gene
	Trilobate leaf	Two dominant genes 'T1b1' and 'T1b2' with duplicate action
Chlorophyll mutants	Chlorophyll mutants have been reported in mungbean with lethal and nonlethal effects. The albino seedling is controlled by monogenic recessive inheritance for the induced xantha, variegata, and greenish yellow chlorina mutants	Single recessive 'al' and 'l' genes
	Independent monogenic recessive inheritance for albina, chlorina, xantha and virescens types of chlorophyll mutants	Single recessive gene
Inflorescence type	Simple inflorescence is governed by two dominant genes ('I1', 'I2') and double recessive homozygous genotype results in the compound inflorescence	Two dominant genes ('I1', 'I2')
	Inheritance of the number of clusters per node shows that a single dominant gene 'C' conditions one cluster per node and its recessive counterpart 'c' determines three clusters per node	Single dominant gene
	Induced sterility	Single dominant gene
	A flower mutant with extended stigma and male sterility	Monogenic recessive inheritance
Flower colour	Four colours of the standard petal namely, red yellow, olive yellow, yellowish olive and light yellowish olive	Single dominant gene
	Light yellowish olive colour is partially dominant to olive yellow	Single partially dominant gene with gene symbols of 'Pg', 'Pb'
Pubescence	Dense plant pubescence	Single dominant gene 'Dp'
	Brown colour of the trait is recessive to colourless and therefore, dominant forms of both the genes are required for colourless pubescence	Two genes 'N' and 'Br'
	Pod pubescence is dominant over non-pubescence	Single dominant gene
Pod colour	A gene responsible for flower colour also conditions the colour of unripe pods	Single dominant gene
	Purple colour on the suture of unripe pod	Single dominant gene
	Inheritance of dry pod colour for light popcorn and almond biscuit colours	Genes 'lp' and 'lab'

	Colour of mature pods	Single dominant gene with black dominant over light brown colour
	Swollen tip is dominant over tapering pod tip	Single dominant gene 'Tp'
Pod shattering	Pod shattering is dominant to non-shattering	A single gene
	Resistance to shattering in the interspecific hybrids between mungbean and urd bean was dominant but nonshattering plants could not be recovered in the segregating generations suggesting that the pod shattering is a quantitatively inherited trait	A single gene
Seed coat colour	Thickness of the texture layer in seeds is under the quantitative genetic control while inheritance of the brown pigment in the texture layer The presence of brown pigment being dominant to its absence	Two complementary genes
	Inheritance of mottling in the seed coat is monogenic. The presence of anthocyanin being dominant to its absence. It indicated that the inheritance of black and green seed colours was controlled by a single gene, 'B' with black being dominant over green	A single gene
	Seed coat colour	A single gene
	Seed coat colour	Two independent dominant genes
	Seed coat colour The dominant alleles, 'A' and 'Sp', condition green and spotted seed coat whereas their recessive counterparts confer yellow and non-spotted colours	Two gene pairs
	Seed colour	Two genes, 'Dgsm1' and 'Dgsm2'
	Each gene conditioning blue sap colour, buff sap colour and green chloroplast respectively which together define the seed coat colour	Three gene pairs, 'Br', br and 'G'
	Seed coat colour	Three-gene model
	Seed coat colour	Three genes with several modifiers giving mottling patterns on yellow (mmbb <sup>g</sup> g), yellow green (mmBB <sup>g</sup> g), green (mmBBGG) and black (MMBBGG) seed coats
	Seed coat colour Black, brown, green mosaic, yellow mosaic, amber, green, and yellow seed coat	Four-gene (W, M, 'Br and G)
	Inheritance of seed coat colour	Five major genes with non-allelic gene interactions
Seed coat surface	Dull rough seed surface is monogenically dominant over glossy smooth surface and the gene symbols assigned for dull seed coat are 'C'	Single dominant gene
	Digenic duplicate interaction (D1 and D2) is involved in the inheritance of seed luster, dullness being dominant over shiny	Two dominant gene
Cotyledon colour	Green cotyledon is conditioned by which is inherited independently of the red colour present in the hypocotyl and petiole	Single recessive gene 'gc'
Hard seediness	Hard seediness	Single dominant gene, 'Hdl'
	Hard seediness	Four QTL
Photoperiod response	The photoperiod insensitiveness is reportedly dominant over photosensitiveness	A single gene

## Cytogenetics

The cytogenetic studies showed that these two cultivated species are closely related with chromosome differentiation having occurred through one major reciprocal translocation. Attempts made to combine the desirable features of these two cultivated species of Asiatic *Vigna* genus have been successful (Singh et al., 2021). It is a self-pollinated crop having diploid  $2n = 2x = 22$  chromosomes with a genome size of 579 Mbp (Siemonsma and Lam pang, 2016; Markam et al., 2018). Chromosome number  $2n=22, 24$  is also reported (BSMRAU, 2015). Cytogenetics and morphological studies have been conducted to compare between the cultivated and wild relatives of the genus *Vigna* in Egypt. Eleven germplasm, representing three species of the genus *Vigna*, were obtained from National Gene Bank (NGB), as well as collected taxa from natural habitats. In general, the plant hairiness, flower color, pod wall thickness, cotyledon color, seed color, eye pattern and color, seed turgidity and seed crowding are the most important morphological attributes to distinguish between two the subgenera, *Vigna* and *Ceratotropis* of the genus *Vigna*. The taxa under study are diploid, twenty-two chromosomes are observed in somatic cells of the eleven studied taxa of *Vigna* (Fig. 4) (Soliman et al., 2008).

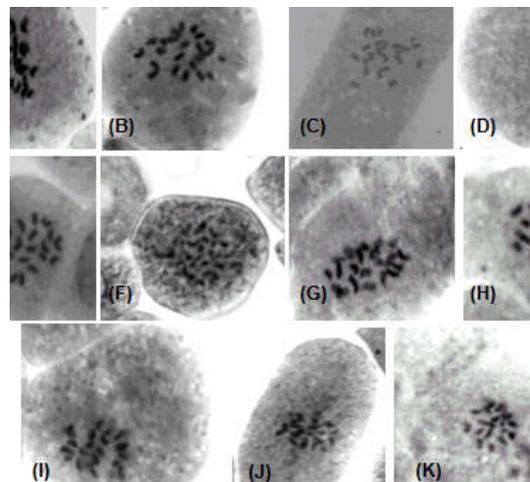


Fig.4 Somatic cell with chromosome number ( $2n=22$ ). (A) (V.u.) Doli-126, (B) (V.u.) Doli- 31, (C) (V.u.) Kafr EL- Sheikh, (D) (V.u.) Kahha-1, (E) (V.u.) Kream-7, (F) (V.u.) Fodder, (G) (V.l.) Rosetta, (H) (V.l.) Basendela, (I) (V.r.) Qumi-1, (J) (V.r.) VC2719 and (K) (V.r.) L303, (X=1000).

## GENETIC DIVERSITY

Genetic diversity has been widely used as a powerful tool in the classification of cultivars and the study of taxonomic status of various crop species for successful breeding programmes. Genetic diversity can be defined as variation of inherited characteristics in a population arising from evolution, mutation, migration, domestication, plant breeding and selection. Genetic diversity plays a vital role in plant breeding through the development of new and high yielding varieties and protecting the productivity of such varieties by integrating genes for disease and insect pest resistance as well as tolerance to abiotic stresses. With respect to climate change, genetic diversity may also assist plant breeders in breeding climate resilient varieties with desirable traits like tolerance to new insect-pest and diseases, extreme heat and cold and various air soil pollutants. The study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships within crop species, and assist in selection of germplasm in an effective way to develop strategies to incorporate in their breeding programmes. A successful breeding programme depends on the complete knowledge and understanding of genetic diversity within and among genetic resources of the available germplasm and enables breeders to choose parental sources that will generate diverse populations for selection particularly those at risk of extinction. Assessment of genetic diversity of cultivated crop plants is very important to select proper genotypes and can also provide valuable information in order to help plant breeders identify promising crosses in a commercial hybrid programme. There are different ways of estimating genetic diversity within species of plants which include morphological characterization techniques, molecular and biochemical techniques. Genetic variability, which is referred to as a heritable difference among cultivars is required within a population to facilitate and sustain an effective long term plant breeding programme. Hence, understanding the genetic variability present in a given crop species for the character under improvement is of importance for the success of any plant breeding programme and broadening the gene pool of crops. The multivariate techniques, such as cluster analysis and principal component analysis may be efficient tools in the quantitative estimation of genetic variation. Introduction of exogenous materials which have a specific genetic background from other regions may play a great role in widening the genetic base, and also, to maximize hybrid vigour. Lack of genetic diversity can potentially limit the ability of cropping systems to resist unknown pests or adverse environmental conditions (Fig. 5, 6, 7, 8) (Kkokong, 2022).



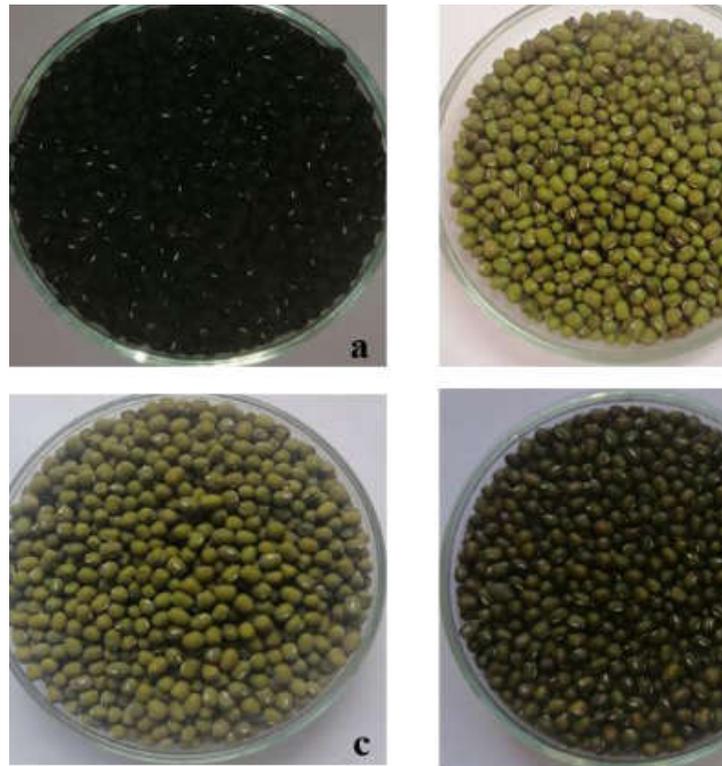
Fig. 5. Variability for seed shape, size and color of mung bean (*Vigna radiata*)



Fig. 6. Variability for seed shape, size and color of mung bean (*Vigna radiata*)



Fig. 7. Variation in pod color, (a) Black, (b) Brown, (c) Tan (d) Olive green



**Fig. 8. Variation in seed color and testa texture, (a) Black and (b) green, (c) Rough and (d) Smooth to rough**

A large representative collection of mung bean (*Vigna radiata* (L.) Wilczek) consisting of 415 cultivated, 189 wild and 11 intermediate accessions was analysed by using 19 SSR primers. These SSR primers showed polymorphism in wild and cultivated mung bean and were selected from those available for the related species azuki bean [*V. angularis* (Willd.) Ohwi & Ohwi]. One or more SSR primer for each linkage group (on the basis of the azuki linkage map) was analysed. In total, 309 alleles were detected and of these, about twice as many were detected in wild (257 alleles) as in cultivated accessions (138 alleles). The results show that Australia and New Guinea represent a distinct centre of diversity for wild mung bean. Cultivated mung bean has greatest diversity in South Asia, which supports the view that South Asia is where this crop was domesticated. SSR marker allelic diversity for cultivated mung bean has distinct regional variation, with high variation in South and West Asia. The present study represents the first comprehensive analysis of wild and cultivated mung bean germplasm diversity by SSR markers, and highlights specific genetic diversity that might be used to broaden the genetic base of currently grown mung bean cultivars (Sangini *et al.*, 2007). The study was carried out to assess the genetic diversity and to analyze the population genetic structure for a total of 692 mung bean accessions preserved at National Agrobiodiversity Center (NAC) of the Rural Development Administration (RDA), Korea. Mung bean accessions were collected from 27 countries in nine different geographic regions, and were genotyped using 15 microsatellite markers, which were developed in our previous study. A total of 66 alleles were detected among 692 accessions at all the loci with an average of 4.4 alleles per locus. All the microsatellite loci were found to be polymorphic. The expected heterozygosity ( $H_E$ ) and polymorphism information content ( $PIC$ ) ranged from 0.081 to 0.588 (mean = 0.345) and from 0.080 to 0.544 (mean = 0.295), respectively. Of the 66 alleles, 17 (25.8%) were common (frequency range between 0.05 and 0.5), 15 (22.7%) were abundant (frequency range > 0.5), and 34 (51.5%) were rare (frequency range < 0.05). Locus GB-VR-7 provided the highest number of rare alleles (eight), followed by GB-VR-91 (six) and GB-VR-113 (four). Country-wide comparative study on genetic diversity showed that accessions from the USA possessed the highest genetic diversity ( $PIC$ ) followed by Nepal, Iran, and Afghanistan. And region-wide showed that accessions from Europe possessed the highest average genetic diversity, followed by accessions from the USA, South Asia, West Asia, and Oceania. Twenty-seven countries were grouped into seven clades by phylogenetic relationship analysis, but clustering pattern did not strictly follow their geographical origin because of extensive germplasm exchange between/among countries and regions. As a result of a model-based analysis (STRUCTURE) of microsatellite data, two distinct genetic groups were identified which shared more than 75% membership with one of the two genetic groups. However the genetic group pattern did not reflect their geographical origin. The Duncan's Multiple Range Test among these two genetic groups and an admixed group, with a mean of 16 phenotypic traits, showed significant difference in 12 quantitative and qualitative traits on the basis of ANOVA. These 15 newly developed SSR markers proved to be useful as DNA markers to detect genetic variation in mung bean germplasm for reasonable management and crossbreeding purposes (Gwag *et al.*, 2010).

Random amplified polymorphic DNA (RAPD) markers were used to study the DNA polymorphism in Indian mung bean cultivars. A total of 60 random primers were used in the study and 33 of them generated reproducible RAPD patterns. Amplification of genomic DNA of most popular 24 Indian mung bean cultivars with these RAPD primers yielded 249 fragments that could be scored, of which 224 were polymorphic, with an average of 7.0 polymorphic fragments per primer. Number of amplified fragments with random primers ranged from 2 (OPI 9) to 17 (OPD 7). Percentage polymorphism ranged from 33% (OPX 5) to a maximum of 100% (OPX 4, OPX 6, OPX 13, OPX 15, OPX 19, OPD 5, OPD 7, OPD 20, OPI 4, OPI 6, OPI 13, OPI 14, OPI 18 and OPF 1), with an average of 90%. The Jaccard's similarity indices based on RAPD profiles were subjected to UPGMA cluster analysis. And genotypes grouped in two major groups. Sixteen out of 24 released cultivars grouped to cluster I. This indicated the narrow genetic base in the Indian mung bean cultivars used in the study. The details of diversity analysis and possible reasons for narrow genetic base in mung bean cultivars are discussed in the present study (Datta *et al.*, 2012). To evaluate genetic diversity of 20 genotypes of mung bean, an experiment was laid out in a Randomized Complete Block Design with two replications during the period from November, 2010 to February, 2011 at the experimental field of Genetics and Molecular Biology, Institute of Biological science, University of Malaya, Kuala Lumpur, Malaysia. Eight morphological characters including plant height, number of fruiting branches per plant, number of pods per plant, number of pod clusters per plant, pod length, number of seeds per pod, 1000-seed weight and total seed yield per plant were measured.

Analysis of variance showed significant differences among genotypes for all traits. A total of four groups were defined through cluster analysis and distinct genetic variations were observed among these groups. Using cluster analysis by unweighted pair group method with arithmetic mean (UPGMA) method, all genotypes were grouped into 3 main groups and 1 minor group. Cluster I consisted of 9 genotypes, cluster II of 7, cluster III of 1 and cluster IV of 3 genotypes. Principal component analysis was done to evaluate diversity and morphological traits which had more effects on diversity and three components explained near 79% of total variation among genotypes. By plot of first two components score for genotypes confirmed the result of cluster analysis (Abna *et al.*, 2012).

We used 30 newly developed simple sequence repeat (SSR) markers designed from the mapped sequence scaffolds of the Korean Sunhwanokdu and Gyonggijaerae 5 mung bean genomes. These markers were used to examine loci in 83 mung bean accessions collected from diverse geographical areas in Indonesia. A total of 107 alleles were detected among the accessions with 29 polymorphic markers. However, the mean of polymorphic information content (0.33) value and diversity index (0.38) value was indicative of low genetic diversity in this germplasm. The mung bean population structure was not clearly differentiated and the number of subpopulations was unclear. Neighbour-joining tree analysis revealed that the genetic cluster did not reflect the geographical origin of the accessions. Interestingly, the most agriculturally improved varieties were genetically similar to some landraces from one of the main mung bean-producing regions. These newly developed SSR markers could be useful for detecting genetic variability as a basis for establishing a conservation strategy for mung bean germplasm with the aim of enhancing Indonesian breeding programmes (Lestari *et al.*, 2014). A set of genotypes comprising 81 local land races, four wild forms and four improved varieties of mung bean were grouped into 15 genetic clusters. The genotypes revealed wide variation in stable morphological characters as well as agronomic traits which provided the necessary base for genetic divergence. The wild forms TCR 192, TCR 213 and TCR 243 were viny with late maturity and had distinctly different leaflet, inflorescence and pod characteristics. Whereas, a wild accession TCR 20 was erect with sturdy stem, vigorous growth, broad ovate leaflets, long pods, profuse podding with high yield potential and resistance to biotic (bruchids, CLS, PM and YMV) and abiotic (drought) stresses. Clustering pattern confirmed more proximity of TCR 20 with cultivated forms and therefore, it may be amenable for hybridization with cultivated land races and improved varieties for transfer of its desirable traits. Balarampur Keonjhar local was quite distinct from other land races owing to its vigorous growth, broad leaves and long pods with very bold seeds, but worst affected by YMV. In contrast, TARM 1 had high field resistance to diseases including YMV. Nipania munga -an elite land race of Kalahandi district of Odisha was highly drought tolerant with dwarf plant type and good initial vigour. These above genotypes being morphologically unique and having unique desirable agro-economic traits, formed small divergent clusters and hence, may serve as valuable material for genetic improvement in mung bean through hybridization (Swapan *et al.*, 2015).

The genetic diversity of mung bean is poorly characterized. In this study, our goal was to develop and use microsatellite simple sequence repeat (SSR) markers for germplasm evaluation. In total, 500 novel expression sequence tag EST-based SSRs (eSSRs) and genomic SSRs (gSSRs) were developed from mung bean transcriptome and genome sequences. Of these, only 58 were useful for diversity evaluation in a panel of 157 cultivated and wild mung bean accessions from different collection sites in East Asia. A total of 2.66 alleles were detected on average per locus which shows that polymorphism is generally low for the species. The average polymorphic information content (PIC) of gSSRs was higher than eSSRs and most of the polymorphic gSSRs were composed of di- and tri-nucleotide repeats (52.4% and 38.1% of all loci, respectively). The genotypes were differentiated into nine subgroups by cluster analysis, and the wild mung bean accessions separated well from the cultivated accessions. Analysis of molecular variance indicated that 22% of variance was observed among populations and 78% was due to differences within populations. Clustering, population structure analyses showed that non-Chinese cultivated and wild mung bean accessions were separated from Chinese accessions, but no geographical distinctions existed between genotypes collected in China. Interestingly, the average PIC value of cultivated mung bean (0.36) was higher than that of wild mung bean (0.25) showing that further collecting and wide crosses are necessary for mung bean improvement (Chen *et al.*, 2015).

Mung bean (*Vigna radiata* L. Wilczek) is one of the famous legume crops. The grain yield of mung bean is affected by various biotic and abiotic factors. The yield can be increased by improving the genetic makeup and incorporating the resistance against the environmental stresses. Common breeding methods are not useful in enhancing production of mung bean because of low genetic variability. The production can be improved by improving the available genotypes through mutation or by using other advanced breeding methods (Javed *et al.*, 2016).

Three mung bean, genotypes from the Kingdom of the Saudi Arabia were evaluated for genetic diversity. There were significant differences in the morphological and molecular characteristics in the tested mung bean (*Vigna radiata* L.), genotypes. The sequence-related amplified polymorphism (SRAP) and amplified fragments length polymorphism (AFLP) markers exhibited a considerable genetic diversity among the tested genotypes. The genotypes differed for plant height, primary branches, pod length, pods per plant, grain per pod and 100-grain weight. All the tested genotypes of mung bean, differed in the number of alleles. Maximum number of alleles per primer combination was 112 in mung bean. Polymorphism percentage of all the tested genotypes of the mung bean was 100%. Existence of genetic diversity of these tested mung bean, genotypes offers opportunities to exploit favourable alleles for use in the breeding program aimed at yield improvement (Alghamdi *et al.*, 2017).

Twentyfive seed samples/accessions of mung bean germplasm were collected with the largest number from South Batinah coastal governorate represented by wilayat Rustaq followed by southern Dhofar governorate, eastern Sharqiyah governorates, Dhahira & Buraimi governorates, interior Al-Dakhliyah governorate and North Batinah coastal governorate. The seed samples of the accessions collected were highly diverse with respect to all the characters associated with seed such as seed length (cm) and width (cm), 100-seed weight (g) and seed color. Seed length varied from 0.35 cm to 0.76 cm; seed width ranged from 0.245 cm to 0.495 cm; 100-seed weight varied from 1.8 g to 7.3 g. The accessions were grouped into 16 genetically diverse clusters based on the Principal Component Analysis, which indicated the major contribution of seed width and 100-seed weight to the total variation existing in indigenous germplasm collected from all the governorates of Oman. With respect to seed color, six accessions numbering OMA 284, OMA 295, OMA 313, OMA 335, OMA 341 and OMA 345 were homogenous (pure) with their characteristic green color. The remaining 19 seed accessions were heterogeneous (mixture) with seeds of various colors such as green, brown and black. Critical analysis of seed colors of these samples indicated the presence of 4 groups of which the largest group had 12 seed accessions with green, black seed color followed by one group of three seed accessions with green, brown and black seed color and two groups of two accessions, each with green, black, brown, and green, brown seeds, respectively (Al-Saady *et al.*, 2018).

The aim of this study was to determine the relationship among mung bean accessions based on quantitative and qualitative traits. A total of 122 local mung bean accessions from Indonesian was obtained from ILETRI germplasm collections which have been cultivated in Jambegede Research Station. Thirteen variables quantitative and five variables qualitative were observed. Data were analyzed using principal component analysis (PCA) and cluster analysis. The results showed that five principal components (PC) contributed 76% of total variation. The most

important characters for PC 1 was number of branches, number of fertile nodes per branches, number of pod cluster, and number of filled pod, PC 2 was days 50% to flowering and maturing days, PC 3 was percentage plant affected to root rot diseases, PC 4 was seed weight per plant and plant height, and PC 5 was 100-seed weight. The dendrogram clustered 122 accessions into four groups. Based on clusters analysis there were four clusters with similarity distance 72.29%. There was no parallelism between geographical distributions in each cluster (Hapsari *et al.*, 2018).

Here we describe observations on the adaptability of mung bean germplasm obtained from the United States Department of Agriculture and their genetic diversity assessment using SSR markers. Several accessions were shown to be mixtures, based on their phenotypes for some characters. Most accessions were able to complete their lifecycles when grown in Beijing, China, making them ideal for crossbreeding without day length control. High diversity was revealed by the SSR markers, with an average of 4.2 alleles per locus and a PIC value of 0.650 per locus. STRUCTURE analysis divided the accessions into six groups. There was no obvious trend of accessions forming groups according to their geographical origin, owing mainly to germplasm exchange and an uneven distribution of accessions (Wang *et al.*, 2018).

Simple Sequence Repeats (SSR) markers were used to assessing of genetic diversity in 24 mung bean genotypes. Total 10 SSR markers (primers) were used, out of 10 markers nine markers shown polymorphism and only one marker shown monomorphic nature for molecular diversity. After analysis a total of 20 alleles were detected in 24 genotypes on all chromosomes. The number of alleles per locus generated by each marker ranged from 1 to 3 alleles with an average number of 2 alleles per locus. Cluster analysis was performed using Jaccard's similarity matrices calculated from SSR markers to generate a dendrogram of 24 parental lines could be grouped into eight clusters. Similarity ranged from 0.30 to 1.00 with an average similarity of 0.65 or 65% for molecular based diversity. Cluster VI had maximum eight genotypes under it followed by cluster VII had six genotypes and cluster IV had three genotypes. Cluster III and V each have two genotypes. Cluster I, II and VIII each have single genotype only. Maximum similarity of 100% was shown among genotypes CO 6 and RM 03-71 in cluster VI; Paury Mung, Malviya Jyoti & Pratiksha and Pusa Vishal & HUM -12 in cluster VII (Markam *et al.*, 2018). Assessment of genetic diversity in available cultivars has important implications in understanding the progress made in any breeding programme. Morphological markers are routinely used for estimating the genetic diversity, but recently many molecular marker techniques have developed into powerful tools to analyze genetic relationships. It is based on the DNA sequence are more varied and reliable. They are unaffected by environment and detectable in all stages of development. Genetic diversity within varieties or germplasm using molecular markers has been studied in several food legume species. In mung bean, different marker systems like RAPD, AFLP and ISSR have been employed (Markam *et al.*, 2018).

A set of twelve cultivars of mung bean were taken as experimental materials in the present study. The young leaves were collected from five individual plants and leaf samples were pooled for each accession. Random amplified polymorphic DNA (RAPD) markers were used to study the DNA polymorphism in twelve Indian mung bean cultivars. A total of 17 random primers were used in the research and 11 of them generated reproducible RAPD patterns. Out of 17 random primers, a total of 11 highly polymorphic primers were used for amplification of genomic DNA isolated from 12 mung bean cultivars in this study. Thus the result is based on the amplification products of 11 polymorphic primers with 12 cultivars of mung bean. Amplification of genomic DNA of 12 Indian mung bean cultivars with 11 RAPD primers yielded 152 fragments that could be scored, of which 108 were polymorphic, thus with average number of bands amplified per primer was 13.8 and with an average of 9.8 polymorphic fragments per primer. Number of amplified fragments with random primers ranged from 8 (OPA 14) to 22 (OPA11). Percentage polymorphism ranged from 23.08% (OPA09) to a maximum of 100% (OPN 05 and OPN 016), with an average of 71.05%. The Jaccard's similarity coefficients matrix based on RAPD profiles were subjected to UPGMA cluster analysis. The RAPD cluster pattern segregated the 12 mung bean cultivars into two major clusters. The cultivar Pusa-0672 formed Cluster 1 (C-1) and cultivars Samrat, BPMR-145, HUM-2, MUM-2, Paury Mung, Pant M-2, Pant M-4, PKV AKM-4, Pusa-9072, RMG-62 and RMG-268 have made Cluster 2. This indicated the narrow genetic base in the Indian mung bean cultivars used in the study (Varma *et al.*, 2019). The study explores the potential of mung bean in the U.S. northern latitudes through the utilization of the USDA germplasm resources. Complete collection of USDA mung bean germplasm was screened under Iowa field conditions in 2017, to shortlist 482 accessions to create an Iowa mung bean panel. The Iowa mung bean panel was further characterized for field adaptability traits in 2018 and 2019 and genotyped using genotype-by-sequencing (GBS) to conduct association mapping of important traits. Genetic markers were identified for both quantitative trait (days to flowering [DTF], plant height [PHT], leaf drop at maturity [LDMS], 100-seed weight [SDWT], and Fusarium wilt score [WS]) and qualitative traits (seed color [SC], seed-coat texture [ST], hypocotyl color [HC], and pod color [PC]). We report *FERONIA*, a known flowering-pathway gene, as the candidate gene for the quantitative trait locus (QTL) with largest effect on DTF. In addition, important epistatic interactions were also uncovered for WS and SDWT. Further, accessions with desirable magnitude of traits were identified as potential parents. Diversity analyses and field phenotypic data indicate potential for mung bean improvement to suit mid-western U.S. cultivation (Sandhu and Singh, 2020).

The main objectives of this research were (1) to study the root traits related with the phenotypic and genetic diversity of 375 mung bean genotypes of the Iowa (IA) diversity panel and (2) to conduct genome-wide association studies of root-related traits using the Automated Root Image Analysis (ARIA) software. We collected over 9,000 digital images at three-time points (days 12, 15, and 18 after germination). A broad sense heritability for days 15 (0.22–0.73) and 18 (0.23–0.87) was higher than that for day 12 (0.24–0.51). We also reported root ideotype classification, *i.e.*, PI425425 (India), PI425045 (Philippines), PI425551 (Korea), PI264686 (Philippines), and PI425085 (Sri Lanka) that emerged as the top five in the topsoil foraging category, while PI425594 (unknown origin), PI425599 (Thailand), PI425610 (Afghanistan), PI425485 (India), and AVMU0201 (Taiwan) were top five in the drought-tolerant and nutrient uptake “steep, cheap, and deep” ideotype. We identified promising genotypes that can help diversify the gene pool of mung bean breeding stocks and will be useful for further field testing. Using association studies, we identified markers showing significant associations with the lateral root angle (LRA) on chromosomes 2, 6, 7, and 11, length distribution (LED) on chromosome 8, and total root length-growth rate (TRL\_GR), volume (VOL), and total dry weight (TDW) on chromosomes 3 and 5. We discussed genes that are potential candidates from these regions. We reported beta-galactosidase 3 associated with the LRA, which has previously been implicated in the adventitious root development *via* transcriptomic studies in mung bean. Results from this work on the phenotypic characterization, root-based ideotype categories, and significant molecular markers associated with important traits will be useful for the marker-assisted selection and mung bean improvement through breeding (Chitani *et al.*, 2021).

Seven mung beans accessions from Eastern Kenya were evaluated using thirteen phenotypic traits. In addition, 10 SSR markers were used to determine their genetic diversity and population structure. This aimed at enhancing germplasm utilization for subsequent mung bean breeding programs. Analysis of variance for most of the phenology traits showed significant variation, with the yield traits recording the highest. The first three principal components (PC) explained 83.4% of the overall phenotypic variation, with the highest (PC1) being due to variation of majority of the traits studied such as pod length, plant height, and seeds per pod. The dendrogram revealed that the improved genotypes had common ancestry with the local landraces. The seven mung beans were also genotyped using 10 microsatellite markers, eight of which showed clear and consistent amplification profiles with scorable polymorphisms in all the studied genotypes. Genetic diversity, allele number, and polymorphic

information content (PIC) were determined using powermarker (version 3.25) and phylogenetic tree constructed using DARWIN version 6.0.12. Analysis of molecular variance (AMOVA) was calculated using GenALEX version 6.5. A total of 23 alleles were detected from the seven genotypes on all the chromosomes studied with an average of 2.875 across the loci. The PIC values ranged from 0.1224 (CEDG056) to 0.5918 (CEDG092) with a mean of 0.3724. Among the markers, CEDG092 was highly informative while the rest were reasonably informative except CEDG056, which was less informative. Gene diversity ranged from 0.1836 (CEDG050) to 0.5102 (CEDG088) with an average of 0.3534. The Jaccard's dissimilarity matrix indicated that genotypes VC614850 and N26 had the highest level of dissimilarity while VC637245 and N26 had lowest dissimilarity index. The phylogenetic tree grouped the genotypes into three clusters as revealed by population structure analysis ( $K = 3$ ), with cluster III having one unique genotype (VC6137B) only. AMOVA indicated that the highest variation (99%) was between individual genotype. In addition, marker traits association analysis revealed 18 significant associations ( $P < 0.05$ ). These findings indicate sufficient variation among the studied genotypes that can be considered for germplasm breeding programs (Mwangi *et al.*, 2021).

The results of this study showed the existence of genetic variation among the eighteen genotypes available in Botswana's mung bean germplasm collection at both morphological and molecular levels. The level of similarity displayed by most of the analysed morphological traits (quantitative and qualitative) indicated a narrow genetic base among the tested genotypes. Majority of the characters showed greater relevance in these genetic variations and relationships among the evaluated genotypes which included growth habit, leaf colour, raceme position, pod colour, testa texture, days to flowering, peduncle length, grain yield ha<sup>-1</sup> and harvest index. Even though variation existed, some morphological characters were unable to distinguish some of the tested mung bean genotypes. The observed variation in the evaluated characters gives a scope for manipulation of local mung bean germplasm to start a good hybridization programme in developing more productive varieties. Overall, genotypes E084, E116 and VC1482E outperformed control genotype (Mmelegi) based on various morphological traits and by virtue of their promising performance, they have a great potential and can be used as parents in future mung bean programmes to provide progenies with high genetic variability. The results of this study also displayed significant variation in root-nodule traits and photosynthetic parameters among the studied mung bean genotypes, hence these traits could be manipulated to provide a powerful genetic approach for yield enhancement in mung bean (Kgakong, 2022).

The investigation was conducted with thirty-six mung bean genotypes under two seasons *i.e.*, Kharif 2019 and zaid 2020 to identify the diverse genotypes for utilization in hybridization through genetic diversity analysis. Thirty-six genotypes were grouped into seven clusters. Cluster I and cluster II were polygenotypic and were the largest clusters each comprising of 18 and 25 genotypes in Kharif and summer respectively. During the Kharif season, Cluster II showed maximum intra-cluster  $D^2$  value. Cluster I showed maximum intra-cluster  $D^2$  value followed by cluster II for the summer season. The number of seeds per pod (43.33%) and biological yield per plant (g) (44.29%) contributed towards maximum genetic divergence. Entries from cluster II and cluster I were found to be superior and highly diverse, thus suitable as parents for hybridization. The potential genotypes based on the  $D^2$  statistics under both seasons were found as SML 1831, PDM-139, TM-37 and Ganga-8 (Tiwari *et al.*, 2022).

We evaluated 166 diverse mung bean genotypes in two seasons using multivariate and multi-traits index approaches to identify superior genotypes. The total Shannon diversity index (SDI) for qualitative traits ranged from moderate for terminal leaflet shape (0.592) to high for seed colour (1.279). The analysis of variances (ANOVA) indicated a highly significant difference across the genotypes for most of the studied traits. Descriptive analyses showed high diversity among genotypes for all morphological traits. Six components with Eigen values larger than one contributed 76.50% of the variability in the principal component analysis (PCA). The first three PCs accounted for the maximum 29.90%, 15.70%, and 11.20% of the total variances, respectively. Yield per plant, pod weight, hundred seed weight, pod length, days to maturity, pods per plant, harvest index, biological yield per plant, and pod per cluster contributed more to PC1 and PC2 and showed a positive association and positive direct effect on seed yield. The genotypes were grouped into seven clusters with the maximum in cluster II (34) and the minimum in cluster VII (10) along with a range of intra-cluster and inter-cluster distances of 5.15 (cluster II) to 3.60 (cluster VII) and 9.53 (between clusters II and VI) to 4.88 (clusters I and VII), suggesting extreme divergence and the possibility for use in hybridization and selection. Cluster III showed the highest yield and yield-related traits. Yield per plant positively and significantly correlated with pod traits and hundred seed weight. Depending on the multi-trait stability index (MTSI), clusters I, III, and VII might be utilized as parents in the hybridization program to generate high-yielding, disease-resistant, and small-seeded mung bean. Based on all multivariate-approaches, G45, G5, G22, G55, G143, G144, G87, G138, G110, G133, and G120 may be considered as the best parents for further breeding programs (Azam *et al.*, 2023).

## BREEDING

### Genetic resources

Holders of the largest germplasm collections are AVRDC, Shanhua, in Taiwan (6000 accessions), USDA, Georgia and Colorado, in USA (3500), Punjab Agricultural University, Ludhiana, in India (3000), and CAAS, Beijing, China (3000). Several smaller but important collections exist at research institutes in the South-East Asian countries: FCRI (Bangkok) in Thailand, BORIF (Bogor) and MARIF (Malang) in Indonesia, IPB (Los Banos) in the Philippines. Internationally, the emphasis is at present on evaluation and documentation work to improve user's access to the collections (Siemonsma and Lampan, 2016).

### Breeding objective (CU, 2017).

1. High yield, medium duration dry land varieties.
2. High yielding, short duration irrigated varieties: Lines having rapid growth rate or dry matter increase associated with high harvest index.
3. Breeding for rice fallows.
4. Breeding for disease resistance, YMV, Leafcrinkle virus, Tarai local Lm214 - resistant.
5. Breeding for quality a) Mung bean has highest digestibility among grain legumes from 83 to 90%. Varieties having bold seeds to use as sprouts is the aim. b) Transfer of high methionine content from black gram to green gram. c) High dal recovery - 80% and more d) Less hard seed.

### Breeding Methods (CU, 2017)

1. Introduction - Pusa baisaki
2. Pure line selection - Col

3. Hybridisation and selection Inter Varietal : Inter specific - To transfer high methionine content from black gram to green gram. *V. radiata* x *V. umbellata* rice bean to transfer resistance to bean fly crossing with *V. radiata* var. *sublobata* resistance to bruchids
5. Mutation breeding Co4 - mutant of Co1
6. Embryo culture : Green gram x Black gram Ideal plant type :
  - 1) 60 - 65 days duration with determinate habit for irrigated conditions
  - 2) 80 days duration with indeterminate type for dry land condition Plants with more pods and seeds, increased branches podding from base of main stem with synchronised maturity non - shattering habit. Varieties: Jawahar – 45, WGG-2, LGG-127.

### Breeding

In many traditional mung bean growing areas, farmers still grow old landraces, mixtures of homozygous genotypes, very well equipped to adjust to changing environmental conditions, giving stable, but seldom excellent, yields. Even recently, many cultivars have been developed from these landraces by simple pure-line selection: identification of the outstanding genotypes in these mixtures. These well-adapted local selections form an excellent starting point for hybridization programmes. Nowadays, the breeding challenge is to overcome the genetic limitations deriving from centuries-long adaptation of mung bean to marginal environments. The traditional, late, robust plant types have been replaced by new types useful for short seasons and multiple cropping systems with mung bean occupying the land for short periods between major crops. These are short, compact plants with high harvest index, with reduced photoperiod sensitivity, and with a more uniform maturity. Many modern cultivars have already been released in the major producing countries, which also have improved resistance to major pests and diseases. Sources of resistance have been identified in germplasm of mung bean and related species. Black gram (*Vigna mungo*) shows, among the Asiatic *Vigna* species, most promise for interspecific hybridization with mung bean. At present, little attention is given to protein content and quality, because much more impact on total protein production is to be expected from increasing yields (Siemonsma and Lampan, 2016).

In order to develop high yielding disease resistant varieties in mung bean, the common breeding methods employed were pure line selection, hybridization followed by pedigree selection, mutation breeding and wide hybridization. While exercising selection, major emphasis has been placed on short duration, photo and thermo-insensitivity, synchronous maturity and resistance to mung bean yellow mosaic virus and powdery mildew. More than 150 varieties have been developed in India employing pure line selection, pedigree method of selection following hybridization, mutation and wide hybridization. The first variety of mung bean was Type 1 developed from local selection of Muzaffarpur (Bihar), which has been extensively used afterward as one of the parents in hybridization programmes for the development of improved varieties like Type 2, K 851, T 44 and Sunaina. Utilization of T 44 in hybridization has resulted in the development of Pusa Baisakhi which, in turn, has given PIMS 4 and Jyoti. Through mutation breeding, about 14 varieties using gamma rays or occasionally ethyl methane sulphonate as mutagens have been developed. Varieties developed through mutation like CO 4, Pant Moong 2, TAP 7, BM 4, MUM 2 and TARM 1 (Mehandi *et al.*, 2019). The main reason that the expected yield advances by the conventional component breeding methods have not materialized in mung bean is that the parents used in crossing programmes are not duly evaluated before their use. Seed yield of parents has a positive significant bearing on the yield of the progenies and in the inheritance of this character, additive variance is of paramount importance than the non additive variance, although many a times the latter also has significant bearing. The choice of the parents besides on their agronomic attributes like yield and its components must also be based on their genetic diversity, phenotypic stability and combining ability. So logically all the would-be parents must be evaluated by their progeny tests across environments and locations before their use in a crossing programme. A progeny test provides genetic composition of the parental plants and helps in selection of superior ones. In self-pollinated crops like mung bean, many minor genes of additive effect control yield and in any breeding programme, the ultimate goal is to accumulate and harness these genes. High yielding varieties from different genetic backgrounds and carrying different genes for yield when crossed and subjected to replicated progeny tests are expected to generate higher frequency of high yielding plants. Yield stability in mung bean is very important owing to significantly variable response of high yielding varieties across locations and years. Work on stability analysis done in mung bean shows that no high yielding varieties are stable across time and space. All the potential parents in a hybridization programme must be evaluated for their mean yield performance and yield stability, F1 performance, F2 mean yield and the variance generated, combining ability and their interaction with the important environmental variables. All these variables give a measure of the comparative potential of different F2 crosses. It is desirable that the progenies of only those parents be advanced beyond F2 generation that show high grain yield, yield stability, a positive general combining ability for grain yield and that are of distant genetic origin. Progenies of parents with low yield and negative general combining ability for yield must not be advanced beyond F2 generation. In an intra-species crossing programme, one parent should be a good agronomic base with higher stability and the other parent a good general combiner for yield and its components. Crosses with this strategic selection of parents are expected to give a wide range of genetic variability. To achieve stability and get a true measure of inherent genetic potential, the parental lines must be tested over a number of locations and get their combining ability estimates (Mehandi *et al.*, 2019).

Most of the high yielding varieties of mung bean bred and released so far have been developed through single cross pedigree method of selection. The single plant selections made in the early generations restrict carrying forward the bulk of created variability, which gets lost quickly giving way to homozygosity with each succeeding generation. This method has served the mung bean improvement programme well in the past, but lately no productivity advances are materializing due to the inherent genetic limitation of the method. The intermitting of selected F<sub>2</sub> plants and selections in the late generations will help to harness most of the desirable genes (Mehandi *et al.*, 2019). Resistance to biotic stresses namely, mung bean yellow mosaic virus (MYMV), powdery mildew (PM), cercospora leaf spot (CLS), root diseases caused by *Pythium* spp. There is variability in the virulence of MYMV in white fly for incubation of different isolate in mung bean plant for genes governing resistance/tolerance to the virus and its vector. Gene transfer across species in *Vigna* group has been found difficult. Biotechnological tools are being presently used to overcome these barriers. In the field, spreader row technique has been found to be most effective in screening the materials. However, parental lines to be used in crossing and promising selections before their release for cultivation may be screened under artificial inoculation (Mehandi *et al.*, 2019).

**Component breeding:** Fifty years of conventional approach of engineering different yield components in mung bean to build up a new plant type with higher productivity levels has thus far given only modest yield gains over the traditional cultivars. This approach has failed to break the present yield barriers as a whole and bring changes of scale. Based upon correlation analysis of various yield components, selections have been based mainly on number of pods per plant, seeds per pod and 100-seed weight and sometimes also on number of pods per bunch and branches per plant or podding per unit area usually called 'Pod Index'. Pods per plant is by far the most important yield component and almost all the workers have found it having positive correlation with seed yield. It is the best selection index for seed yield and could be increased by increasing number of branches per plant or number of bunches per plant or by increasing the number of pods per bunch. Most of the work has shown that branch number per plant is negatively correlated with seed yield, but bunches per plant has mostly been found to be positively

correlated with seed yield. Increasing pods per bunch is physiologically constrained in grain legumes owing to fall of flowers and unripe or partially filled pods. It seems the most feasible path to increase seed yield is through increasing number of bunches per plant. This in essence means a plant with more number of nodes with a shorter internode length, with three to four erect branches emerging from the lower to lower-middle nodes at around 20–30° angle with the main stem, and sympodial bearing of pod in inflorescences coming from the upper nodes of the main stem, each carrying around 8–10 pods. Number of seeds per pod has been shown mostly positively correlated with seed yield but many workers show it to be negatively correlated with yield. However, an optimal level of 14–16 seeds per pod should be a breeder's objective. Seed weight is generally negatively correlated with seed yield but some results have shown it to be positively correlated. The strength of the newly developed second generation varieties like Pusa Vishal and Pusa Ratna lies in the fact that they have more seeds per pod (12–16) with higher 100-seed weight (5.0–5.5 g) without compromising on the pod number per plant. Many researchers advocated cereal mimics with sympodial bearing and suggested increasing pods per plant through the path of increasing the average number of pods per node and building up a soybean like plant type in mung bean [76]. He found the main stem bearing under the control of a single recessive gene and normal conventional bearing to be incompletely dominant. Plant height has been found positively correlated with seed yield. An optimal upright plant height incorporates more functional nodes and thus more number of pods per plant. After pods per plant, this is the second most important character to be used for selection of seed yield. Owing to their high heritability, 100-seed weight and branch number could be excellent selection criteria but for their unfavorable correlations with yield. Also due to the compensatory mechanisms operating within the plant as a whole, this correlation based selection methodology has not brought the desired productivity levels in mungbean. Alternatively, the best option is direct selection for seed yield on a unit area basis (Mehandi *et al.*, 2019).

**Mutation breeding:** Both physical and chemical mutagens have been employed in improvement of mung bean crop India. The main drawbacks of this method are that the frequencies of desirable mutants are very less, necessitating evaluation of very large population and the difficulty in identification and scoring of micro mutations. Tickoo and Chandra using both physical and chemical mutagens could induce significantly higher variability in mung bean for characters like yield per plant, pods per plant, seed number per pod, seed weight, days to flower and harvest index in M<sub>2</sub> generation. Mean values of all the characters had a negative shift in M<sub>2</sub> but after selection changed to positive direction in M<sub>3</sub> but were still associated with significantly higher interfamily and overall variances than the control populations. Such characters may be incorporated into the cultivated varieties by backcross method. Many a times the selected mutants have been released as new varieties as such for cultivation. Some varieties have been released in India including Pant Mung 2, Co 4, Dhauri, TAP 7, BM 4 and MUM 2 and some in Pakistan including NM 51 and NM 54. The latter two large seeded varieties resistant to MYMV have been developed by hybridization and irradiation of the F<sub>1</sub> seeds (Mehandi *et al.*, 2019).

#### Interspecific crosses

The crosses of *V. radiata* as female and *V. mungo* as male were attempted by several workers since 1960. The reciprocal cross of *V. mungo* × *V. radiata* was rarely attempted and was successful through embryo culture. The usefulness of interspecific crosses in genus *Vigna* in the on-going breeding program has been emphasized. The crossed pod of *V. radiata* × *V. mungo* has one seed and rarely two seeds. The F<sub>1</sub> plants have partially filled pods. In the F<sub>2</sub> and F<sub>3</sub> generations, few plants akin to black gram were observed which were sterile and finally dead, and the remaining populations were akin to mung bean with few characters like, yellow mosaic virus and *Cercospora* leaf resistance and more clusters per plant and more pods per cluster. Large number of plants in the segregating generation showed mottling of seeds (green background with dark gray spot on seed coat). Therefore, such crosses have been used to transfer resistance to foliar diseases and synchronous maturity from black gram to mung bean (Singh *et al.*, 2021). However, some of the elite lines from such crosses have added advantage of more clusters per plant and more pods/cluster. At Pantnagar University, the studies on interspecific hybridization of *V. radiata* × *V. mungo* were continued for about three decades. As a result of this work, Pant Mung-4 was developed and released in 1997, and it is the first variety developed directly from an interspecific cross of mung bean (cultivar T-44) and black gram (cultivar UPU-2). Pant Mung-4 has more pods per cluster and more clusters per plant and has multiple resistance to foliar diseases in contrast to T-44, which was highly susceptible to foliar diseases. Resistance to foliar diseases and clustering pattern from black gram were transferred from cv. UPU-2 by using pedigree selection. From the above findings it can be inferred that with routine techniques *V. radiata* × *V. mungo* crosses could be made and superior varieties of mung bean could be developed through recombination breeding. However, rarely progenies, similar to mung bean and black gram through routine procedure have also been selected from interspecific crosses. The cross of *V. radiata* cv. BDYR-1 as female and *V. mungo* cv. DPU 88-31 as male has produced progenies similar to mung bean and urd bean genotypes. From this cross seven elite lines akin to mung bean and six akin to black gram were selected for unique characteristics and registered with NBPGR, India. These elite lines had new combinations of desirable traits, not seen in parental lines or other available released cultivars. These traits included higher seed yield, protein, iron and/or zinc, and disease resistance (Singh, 2021).

**Exploitation of Hybrid vigour:** Twenty one crosses resulting from 7 × 7 diallel excluding reciprocals were studied to know the magnitude of heterosis over mid parent and better parent for seed yield and its components in mung bean. The highest heterosis to the extent of 26.1% over mid parent and 22.8% over better parent for seed yield per plant was observed in the cross BM 4 × TARM 18, which exhibited high heterosis (%) for either one or more yield components. The promising hybrids viz. BM 4 × TARM 18, Vaibhav × TARM 18, AKM 8802 × BM 4 and Kopargaoon × TARM 18 were identified, which have immense potential to exploit the hybrid vigour or to isolate desirable segregants (Dethle and Patil, 2008).

**Varieties:** In India, yields of mung bean ranging from 100 to 200 kg/ha have been reported, whereas averages of 1000 kg/ha and 1125 kg/ha has been reported in Sri Lanka and the United States, respectively (Akpapunam, 1996). A number of varieties were developed mainly through selection from the germplasm. Earlier a variety Virat has been released from ICAR—Indian Institute of Pulses Research, Kanpur, Uttar Pradesh; it is mature by 55 days only and fitted to rice-wheat cropping system (Mehandi *et al.*, 2019). The mung bean varieties now are mainly targeted in resistance to pests and diseases, particularly the bean weevil and mung bean yellow mosaic virus (MYMV). For now, the main varieties include Samrat, IPM2-3, SML 668 and Meha in India; 'Summer Moong' is a short duration mung bean pulse crop grown in northern India. Due to its short duration, it can fit well in between of many cropping systems. It is mainly cultivated in East and Southeast Asia and the Indian subcontinent. It is considered to be the hardiest of all pulse crops and requires a hot climate for germination and growth. Pure lines continued even during the early 40s to mid from these landraces were isolated on the basis of colour of stem, foliage, flower, unripe and ripe pods, seed colour and texture and other morphological features. The types selected were best suited in their respective regions mostly under low management. In mung bean, the first promising variety released was Type 1 for cultivation in Uttar Pradesh in 1948. It is a local selection from Muzaffarpur (Bihar). A large number of varieties were developed afterwards through selection from local materials and were released in different states between 1948 and 1970. Some of the important varieties developed through selection are Co 1 and ADT 1 (Tamil Nadu), Jalgaon (Maharashtra), Khargone 1, Krishna (Madhya Pradesh), and G 65 (Punjab). Jawahar 45 (Hybrid 45) released in 1971 in Madhya Pradesh and Type 44 released in Uttar

Pradesh in 1972 was perhaps the first varieties developed through hybridization (Mehandi *et al.*, 2019). The mung bean varieties now are mainly targeted in resistance to pests and diseases, particularly the mung bean weevil and mung bean yellow mosaic virus (MYMV). For now, the main varieties include Samrat, IPM2-3, SML 668 and Meha in India. Also, with the help of the World Vegetable Centre, the traits of mung bean have been improved a lot (Döning, 2022). Varieties of mung bean released by Central and State are furnished in **Tables 2 and 3**.

**Table 2. Central released varieties of Green Gram/Mungbean in India**

Variety	Year of release	Originating centre	Yield (q/ha)	Days to maturity	Area of Adoption
MH 2-15 (Sattaya)	2007 (CVRC)	Hisar	10.55	67	NWPZ
Pant Mung 6	2007 (CVRC)	GBPUA& T, Pantnagar	10.52	96	NHZ
KM 2241	2008 (CVRC)	CSAU, Kanpur	10-11	65-70	NHZ
IPM 02-3	2009 (CVRC)	IIPR, Kanpur	11	62-68	NWPZ
PKV AKM 4	2009 (CVRC)	PKV, Akola	10	62-66	CZ & SZ
Pusa 0672	2009 (CVRC)	IARI, New Delhi	10	64	NHZ
IPM 02-14	2010 (CVRC)	IIPR, Kanpur	11	60-65	SZ
DGGV 2	2014 (CVRC)	UAS Dharwad	11-14	70-75	Karnataka
MH 421	2014 (CVRC)	CCSHAU, Hissar	10-12	60-61	NWPZ
Pusa 1371	2016 (CVRC)	IARI, New Delhi	9-10	81-91	NHZ
IPM 410-3 (Shikha)	2016 (CVRC)	IIPR, Kanpur	11-12	65-70	NWPZ/CZ
IPM 205-7 (Virat)	2016 (CVRC)	IIPR, Kanpur	10-11	52-56	PB, Har., Raj., UP, Bih., Jha., MP, GJ, TN, Telan., AP, KA
SML 1115	2016 (CVRC)	PAU, Ludhiana	11-12	65-70	NEHZ
GM 6	2018 (CVRC)	SDAU, S.K.Nagar	11-12	70-75	NEHZ
IPM 512-1 (Soorya)	2020 (CVRC)	IIPR, Kanpur	12-13	60-65	NEPZ
MH 1142	2020 (CVRC)	HAU, Hisar	11-12	60-65	NEPZ & NWPZ

**Table 3. State released varieties of Green Gram/Mungbean in India**

Variety	Year of release	Originating centre	Yield (q/ha)	Days to maturity	Area of Adoption
PKV Green gold(AKM9911)	2007 (SVRC)	Dr.PDKV, Akola	10-12	64-72	Vidarbha Region of MS
TM 96 -2	2007 (SVRC)	BARC and ANGRAU, Lam	9	65-70	AP
TJM 3	2007 (SVRC)	BARC and JNKVV	9-10	65-70	MP
PAU 911	2007 (SVRC)	PAU, Ludhiana	12-13	75-80	Punjab
MGG 347	2009 (SVRC)	ARS, Madhira	13-15	65-70	Andhra Pradesh
MGG 207	2009 (SVRC)	ARS, Madhira	12-14	75-80	Andhra Pradesh
VBN (Gg) 3	2009 (SVRC)	NPRC, Vamban, Tamil Nadu	9-10	65-70	Tamil Nadu
Basanti	2010 (SVRC)	CCSHAU, Hisar, Haryana	12-15	64-70	Haryana
Paury Mung	2010 (SVRC)	IGKV, Raipur	12	65-70	CG
KM 2195	2010 (SVRC)	CSAUAT, Kanpur	10-11	60-65	UP
TM 2000-2 Paury Mung	2010 (SVRC)	BARC, and IGKV, Raipur	10-11	88-90	CG
SML 832	2010 (SVRC)	PAU, Ludhiana	11-12	60-65	Punjab
DGGV 2	2012 (SVRC)	UAS, Dharwad	11-14	70-75	Karnataka
Shalimar Mung 2	2013 (SVRC)	Srinagar centre, SKUASTA	10-12	99-100	Kashmir valley
CO. (Gg) 8	2013 (SVRC)	TNAU, Coimbatore	10-12	60-65	Tamilnadu
SGC 16	2014 (SVRC)	RARS, Shilongani, AAU Assam	13-14	60-65	Assam
BGS 9 (Somnath)	2014 (SVRC)	UAS, Raichur	12-13	65-68	Karnataka
MH 318	2016 (SVRC)	CCSHAU, Hisar	14 in Kharif and 10 in Spring/Summer	60-65	Haryana
Utkarsh KM 11- 584	2016 (SVRC)	MS State Seed Corporation	12-13	60-65	Maharashtra
Pant Mung 8 (PM 9-6)	2016 (SVRC)	GBPUAT, Pantnagar	10-11	78-83	Uttarakhand
Yadadri(WGG 42)	2016 (SVRC)	PJTSAU, Hyderabad	10-12	55-60	Telangana
Sri Rama (MGG351)	2016 (SVRC)	PJTSAU, Hyderabad	12-14	60-65	Telangana
RMG 975 (KeshwanandMung 1)	2016 (SVRC)	RARI, Dugapura	8-9	65-70	Rajasthan
MSJ 118 (KeshwanandMung 2)	2016 (SVRC)	RARI, Dugapura	7-8	60-65	Rajasthan
ML 2056	2016 (SVRC)	PAU, Ludhiana	11-12	70-75	Punjab
GBM 1	2016 (SVRC)	NAU, Gujarat	11-12	102-105	Gujarat
KM 2328	2018 (SVRC)	CSAUAT, Kanpur	10-12	60-62	Western Zone of UP
Pusa 1431	2018 (SVRC)	IARI, New Delhi	12-14	56-66	NCR region of Delhi state
SGC 16	2018 (SVRC)	AAU, Jorhat, Assam	12-13	65-70	Assam
GAM 5	2018 (SVRC)	AAU, Anand	18-19	60-65	Gujarat
Gujarat Mung-7(GM-7)	2018 (SVRC)	Navsari	10-11	75-80	Gujarat
Varsha (IPM 2K 14-9)	2018 (SVRC)	IIPR, Kanpur	10-11	65-75	Uttar Pradesh
PKV AKM-4	2018 (SVRC)	IIPR, Kanpur	10-12	65-75	Uttar Pradesh
Tripura Mung 1 (TRCM 131)	2018 (SVRC)	ICAR Research complex for NE region	10-11	55-60	Tripura
VBN 4 (VGG 10-008)	2019 (SVRC)	NPRC, Vamban	10-11	65-70	Tamil Nadu
Pant M 9 (PM 09-11)	2019 (SVRC)	GBPUA & T, Pantnagar	9-10	70-75	Uttarakhand
SML 1827	2019 (SVRC)	PAU, Ludhiana	12-13	60-65	Punjab
KM 2342 (Azad Mung 1)	2020 (SVRC)	CSAU&T, Kanpur	8-10	65-70	U.P.
IPM 312-20 (Vashudha)	2020 (SVRC)	IIPR, Kanpur	10-11	70-75	U.P.
IPM 409-4 (Heera)	2020 (SVRC)	IIPR, Kanpur	8-10	65-70	U.P.

Dry seeds are directly consumed by the human being. Immature green pods are utilized as a source of vegetables in rural areas and cooked as oriental dishes (Tang *et al.*, 2014). Generally, it is used for its antipyretic, antiscorbutic, diuretic, antidote, antihypertensive and anticancer properties. It has also been recommended for ache, heat, high blood pressure and inflammation. Seeds of this edible legume are used either raw or in cooked form at matured poultice because of its curative potential for polyneuritis. Seeds of mung beans are used to treat alcoholism also (Dahiya *et al.*, 2015). It is one of the most highly prized pulses which is boiled and eaten whole or after splitting into soup (*dal*). It is ground and mixed with wheat or rice powder to make bread. The green pod is used as vegetable. The plant is used as green manure and cover crop. The hulls and straw are used as fodder (BSMRAU, 2015). The mung bean is a major edible legume seed in Asia (India, South East-Asia and East Asia) and is also eaten in Southern Europe and in the Southern USA. The mature seeds provide an invaluable source of digestible protein for humans in places where meat is lacking or where people are mostly vegetarian. Mung beans are cooked fresh or dry. They can be eaten whole or made into flour, soups, porridge, snacks, bread, noodles and ice-cream. Split seeds can be transformed into dhal in the same way as black gram or lentils. Mung beans can be processed to make starch noodles (vermicelli, bean thread noodles, cellophane noodles) or soap. The sprouted seeds ("bean sprouts" in English, and incorrectly called "germes de soja" or "pousses de soja" in French) are relished raw or cooked throughout the world. The immature pods and young leaves are eaten as a vegetable. The mung bean plant makes valuable green manure and can be used as a cover crop (Heuzé *et al.*, 2015).

The dried beans are prepared by cooking or milling. They are eaten whole or split (*dhal*). The seeds or the flour may enter in a variety of dishes like soups, porridge, snacks, bread, noodles and even ice-cream. Mungbean starch is extensively used for starch noodles, mung bean protein for fortifying cereal flours. Both fractions can be separated by air-classification. Most popular as a fresh vegetable in oriental cooking are sprouted mungbean seeds. Crop residues are an important fodder. Mung bean is sometimes specifically grown for hay, green manure or cover crop (Siemonsma and Lampang, 2016). The dried grains of mung bean can be split or eaten whole after cooking and made into a soup or *dhal*. The iron availability in mung bean improves substantially to 7.2–11.3% through cooking practices such as soaking, fermenting and sprouting. Mung bean is also widely relished as sprouts. The germinated grains have higher nutritional value as compared with asparagus or mushroom. Green pods and seeds can be cooked as vegetables. These pulses are frequently fed to children, convalescents and geriatrics or used when "breaking" a long fasting period owing to their ease of digestibility. The haulms are used for fodder and the beans husks and small broken pieces are useful as a feed concentrate. The crops are also grown for hay, green manure and cover crop. Mung bean makes better hay than urad bean as the stems and leaves are less hairy (Mehandi *et al.*, 2019).

Although whole mung beans are also occasionally used in Indian cuisine, beans without skins are more commonly used. In Karnataka, Maharashtra, Gujarat, Kerala and Tamil Nadu, whole mung beans (called *pachai payaru* in Tamil, *chenupayar* in Malayalam, *pesalu* in Telugu and *hesaru kaalu* in Kannada) are commonly boiled to make a dry preparation often served with rice gruel (*kanji*). It is called *mung* in Hindi, and *mug* in Bengali. In Odia, it is called *muga dāli* (Döring, 2022). Hulled mung beans can also be used in a similar fashion as whole beans for the purpose of making sweet soups. Summer Moong is a short duration mung bean pulse crop grown in northern India. Due to its short duration, it can fit well in between of many cropping systems. It is mainly cultivated in East and Southeast Asia and the Indian subcontinent. It is considered to be the hardest of all pulse crops and requires a hot climate for germination and growth. Mung beans in some regional cuisines of India are stripped of their outer coats to make *mung dal*. In Bangladesh and West Bengal the stripped and split bean is used to make a soup-like *dal* known as *moo g dal*. In the South Indian states of Karnataka, Tamil Nadu, Telangana and Andhra Pradesh, and also in Maharashtra, steamed whole beans are seasoned with spices and fresh grated coconut in a preparation called "*pesalu*" in Telugu or *usuli* or *guggari* in Kannada or *sundal* in Tamil or "*usal*" in Marathi. In South India, especially Andhra Pradesh, batter made from ground whole moong beans (including skin) is used to make a variety of *dosa* called *pesarattu* or *pesara dosa*. The same is called *Adai Dosai* in Tamil Nadu and *ade dose* in Karnataka (Döring, 2022). These sprouts have been transferred from a similarly-shaped colander in which they had been grown with moisture. They are ready to be cooked. Mung beans are germinated by leaving them in water for four hours of daytime light and spending the rest of the day in the dark. Mung bean sprouts can be grown under artificial light for four hours over the period of a week. They are usually simply called "bean sprouts". However, when bean sprouts are called for in recipes, it generally refers to mung bean or soybean sprouts. Mung bean sprouts are stir-fried as a Chinese vegetable accompaniment to a meal, usually with garlic, ginger, spring onions, or pieces of salted dried fish to add flavour. Uncooked bean sprouts are used in filling for Vietnamese spring rolls, as well as a garnish for *phở*. They are a major ingredient in a variety of Malaysian and Peranakan cuisine, including *char kway teow*, *hokkien mee*, *mee rebus*, and *pasembor*. In Korea, slightly cooked mung bean sprouts, called *sukjunamul*, are often served as a side dish. They are blanched (placed into boiling water for less than a minute), immediately cooled in cold water, and mixed with sesame oil, garlic, salt, and often other ingredients. In the Philippines, mung bean sprouts are made into *lumpia* rolls called *lumpiang togie*. In India, mung bean sprouts are cooked with green chili, garlic, and other spices. In Indonesia the food are often used as fillings like *tahu isi* (stuffed tofu) and complementary ingredient in many dishes such as *rawon* and *soto*. In Japan, the sprouts are called *moyashi* (Döring, 2022). Mung bean starch, which is extracted from ground mung beans, is used to make transparent cellophane noodles (also known as bean thread noodles, bean threads, glass noodles, *fensi*, *tung hoon*). Cellophane noodles become soft and slippery when they are soaked in hot water. A variation of cellophane noodles, called mung bean sheets or green bean sheets, are also available. In Korea, a jelly called *nokdu muk* (also called *cheongpomuk*) is made from mung bean starch; a similar jelly, colored yellow with the addition of gardenia coloring, is called *hwangpomuk*. In northern China, mung bean jelly is called *liangfen*, which is a very popular food during summer. The Hokkiens add sugar to mung bean jelly to make it a dessert called *Liòk-tāu hún-kóe*. Mung batter is used to make crepes named *pesarattu* in Andhra Pradesh, India and pancakes named *bindaetteok* in Korea (Döring, 2022).

Whole cooked mung beans are generally prepared from dried beans by boiling until they are soft. Mung beans are light yellow in colour when their skins are removed. Mung bean paste can be made by hulling, cooking, and pulverizing the beans to a dry paste (Wikipedia, 2023b). Although whole mung beans are also occasionally used in Indian cuisine, beans without skins are more commonly used. In Karnataka, Maharashtra, Gujarat, Kerala and Tamil Nadu, whole mung beans are commonly boiled to make a dry preparation often served with congee. Hulled mung beans can also be used in a similar fashion as whole beans for the purpose of making sweet soups. Mung beans in some regional cuisines of India are stripped of their outer coats to make *mung dal*. In Bangladesh and West Bengal the stripped and split bean is used to make a soup-like *dal* known as *mug dal*. In the South Indian states of Karnataka, Tamil Nadu, Telangana and Andhra Pradesh, and also in Maharashtra, steamed whole beans are seasoned with spices and fresh grated coconut. In South India, especially Andhra Pradesh, batter made from ground whole moong beans (including skin) is used to make a variety of *dosa* called *pesarattu* or *pesara dosa* (Wikipedia, 2023b). The beans themselves are cooked fresh or dry and have a mild, slightly sweet flavour. They are often used in curries, soups, and porridge, and split seeds are made into *dal* throughout the Indian subcontinent. Fermented beans are used as an ingredient in a number of dishes. Dried beans can be processed into a starchy flour used to make bread or transparent mung bean noodles. Mung bean paste is used to make frozen desserts in a number of Asian countries. The seeds germinate easily, and fresh, barely sprouted seeds are sometimes used as a salad topping. More commonly, mung bean sprouts are harvested after a few days of growth and are eaten raw or cooked in stir-fries, sandwiches, or soups. Immature seed pods and young

leaves are also eaten as a vegetable. Agriculturally, mung bean are particularly valuable as a soil-enriching crop and are useful as cover crops and as green manure. Yellow gram, a low-producing cultivar with yellow seeds, is often grown for this purpose. The plants are also used as livestock fodder (Petruzzello, 2023). Having been first domesticated in Manchuria, mung beans have been incorporated into various Asian dishes including zongzi, eaten at the Dragon Boat Festival. A cultural dish specific to China, zongzi is traditionally made from sticky rice and wrapped in bamboo leaves with different recipes often times calling for special fillings, ranging from sweet to savory. In many cases, the choice of filling is geographically specific with diverse regions of China cooking their zongzi differently. Green gram, prepared as a paste, is a typical filling in eastern Asia such as Suzhou, Jiaxing, and Ningbo where the stuffing is a mixture of bean paste and pork. This festive use of mung beans is just one of a great variety of ways that they would have been implemented by people of the early modern times. Used in many different forms, mung beans would likely have been a significant product for consumption. While they can be eaten whole, the beans themselves are also able to be ground into flours for soups, breads, porridges, and noodles. In addition, the bean sprouts are widely used in cooking and the peapod a commonly eaten vegetable, evidence that the crops were employed in a multiplicity of ways. Not only this, but green gram is also a very good source of protein and thus is capable of being substituted for animal meat, possibly in cultures where consumption of certain meats were forbidden or in regions where animal meat is scarce. The various means of preparing mung beans in dishes suggests their value as an individual harvesting the beans could prepare them in multiple ways to suit their needs (Tenochtitlan, 2023). Green grams are used as pulses in many countries, they are added to several dishes. They make healthy salads. Green grams are used extensively in pharmaceutical labs. They are also used to make several cosmetics (Sikdar, 2023).

**Side-effects and allergies of mung bean (Green Gram):** Green beans are not known to trigger any adverse effects on health. However, green beans contain oxalates which are substances found naturally in plants, animals and humans. When these oxalates accumulate in the body fluids, they may crystallize and lead to health complications. Hence people with kidney and gall bladder disorders may have to avoid consuming green beans. Oxalates may also hamper the absorption of calcium in the body. Raw husks contain chemicals that can cause stomach upset, vomiting, and diarrhea. This, however, should not be a problem if your digestive system is healthy and you chew your food properly (Sikdar, 2023).

## NUTRITIONAL VALUE

Table 4 gives the contents of phytochemicals in mung bean (Sosulski and Dabrowski, 1984).

**Table 4. Phytochemicals in seeds of mung beans (*Vigna radiata* (L.) R. Wilczek)**

Polyphenol Class	Compound Name
Flavonoids	2,4,4'-Trihydroxy chalcone, Dihydrobiochanin, Delphinidin 3- $\alpha$ -glucoside, Naringenin, Eriodictyol, Naringin, Neohesperidine, Phloretin, Dihydroquercetin, Naringenin 7-o-glucoside, Eriodictyol 7-o-glucoside, Apigenin 6-C-glucoside, 5,7-Dihydroxy flavanone, Apigenin, Luteolin, Apigenin-7-o-glucosides, Kaempferol, Kaempferol 3-O-rutinoside, Rhamnetin, Kaempferitrin, Daidzein, Formononetin, Genistein, Glycitein, Genistin, 6-O-Acetylgenistin, Pomiferin, 2-Hydroxy genistein, Quercetin, Quercetin 3-o-glucoside, 5,7-Dihydroxy-8,4-dimethoxyisoflavone.
Other Polyphenol	Coumestrol, Scopoletin, Scopolin, Rhododendrin.
Phenolic acids	Protocatechuic acid, Gallic acid, Gentisic acid, Ellagic acid, 4-Hydroxybenzoic acid, Vanillic acid, Ellagic acid glucoside, Syringic acid, Caffeic acid, Feruloyl glucose, Ferulic acid, chlorogenic acid, Sitosterolferulate, p-Coumaric acid.

Mung beans are commonly used as a pulse or food legume in addition to occasional utility as forage or green pods for vegetables. In Asian and western cultures mung sprouts are widely consumed as a fresh salad, vegetable or even as a common food. Dried seeds of mung beans could also be ingested whole or split, cooked, fermented, or processed and ground into flour. It is also used for making alcoholic beverages, porridge, confections, curries, and soups. These seeds conjointly promote digestion and eliminate toxins. Consumption of mung bean seeds and sprouts with other cereals was found to have healthy benefits for people with obesity and polygenic disease. Furthermore, mung beans are composed of wealth of anti-nutrients like tannins, phytic acid, trypsin inhibitors, hemagglutinin which possess anti-oxidant properties. The effects of some domestic traditional processes, such as dehulling, soaking and germination has been reported to reduce the inhibition of as trypsin, tannins and hemagglutinin activity contents - whereas germination was more effective in reducing phytic acid, stachyose and raffinose. Mung beans are recognized as protein rich source containing 20%–25% protein of total dry weight. Among them, globulin (60%) and albumin (25%) are the primary storage proteins. Seed of mung beans also contains numerous enzymes and plentiful microelements and causes less flatulence in human compared to other forms of legumes. Keeping in view the high protein content and easy digestibility, it is advisable to include mung beans with other cereals as a part of diet plan for reducing the disease load. The protein of Mung seeds is wealthy in essential amino acids, like total aromatic amino acids, leucine, isoleucine, and valine. Over the last few decades, chemical characterization authenticated the presence of varied quantities of secondary metabolites like flavonoids (Flavone, isoflavoneisoflavonoids) phenolic acids (cinnamic acid, vanillic acid) (Cao *et al.*, 2011). See Table 5.

**Table 5. Nutritional value of seeds of mung beans (*Vigna radiata* (L.) R. Wilczek)(100 g)**

Basic Composition	(mg/g)	Basic Composition	(mg/g)
Water	9.05g	Vitamin K	9 $\mu$ g
Protein	23.86g	Lipids	
Fat	1.15g	Total monosaturated fatty acids	0.161g
Energy	347kcal	Total saturated fatty acids	0.348g
Carbohydrate	62.62g	Phytosterol	23mg
Total dietary fiber	16.3g	Amino acid	
Total Sugar	6.60g	Tryptophan	0.260g
Ash	3.32g	Threonine	0.782g
Minerals		Isoleucine	1.008g
Iron	6.74mg	Leucine	1.847g
Calcium	132mg	Lysine	1.664g
Magnesium	189mg	Methionine	0.286g
Phosphorus	367mg	Cysteine	0.210
Selenium	8.2mg	Phenylalanine	1.443g
Sodium	15mg	Tyrosine	0.714g
Zinc	2.68mg	Valine	1.237g

Copper	0.941mg	Arginine	1.672g
Iron	6.74mg	Histidine	0.695g
Calcium	132mg	Alanine	1.050g
Magnesium	189mg	Aspartic acid	2.756g
Phosphorus	367mg	Glutamic acid	4.264g
Selenium	8.2mg	Glycine	0.954g
Sodium	15mg	Proline	1.095g
Thiamine	0.621mg	Serine	1.176g
Riboflavin	0.233mg	Isoflavones	
Niacin	2.251mg	Daidzein	0.00mg
Pantothenic acid	1.910mg	Genistein	0.09mg
Ascorbic acid	4.8mg	Glycitein	0.00mg
Vitamin B-6	0.382mg	Total isoflavones	0.09mg
Folate	625µg	Biochanin	0.00mg
Choline	97.9mg	Formononetin	0.21mg
Beta Carotene	68 µg	Coumestrol	0.00mg
Alpha Carotene	0 µg	Flavonols	
Beta-cryptoxanthin	0 µg	Kaempferol	0.1mg
Vitamin A	114iu	Myricetin	0.1mg
Vitamin E	0.61mg	Quercetin	0.1mg

One hundred gram dry mungbean contains: protein 22 g and carbohydrate 60 g. It is a good source of minerals, provitamin A and vitamin B-complex (BSMRAU, 2015). Mung bean seeds are rich in protein (20-30% DM) and starch (over 45% DM) with a low lipid content (less than 2% DM), and variable but generally low amounts of fibre (crude fibre 6.5% DM on average). The amino acid profile of mung beans is similar to that of soybean (Heuzé *et al.*, 2015). See Table 6

**Table 6: Chemical composition and nutritional value of Mung bean (*Vigna radiata*), seeds**

Main analysis	Unit	Avg	SD	Min	Max	Nb
Dry matter	% as fed	90.0	1.4	88.1	93.1	14
Crude protein	% DM	25.8	2.8	19.5	29.4	16
Crude fibre	% DM	6.3	2.6	4.3	12.4	8
NDF	% DM	15.6				1
ADF	% DM	8.5		6.6	10.3	2
Ether extract	% DM	1.9	1.2	0.2	3.7	14
Ash	% DM	4.6	3.0	0.9	14.0	17
Starch (polarimetry)	% DM	47.0	2.1	45.4	49.4	3
Gross energy	MJ/kg DM	18.7	0.6	17.2	19.1	8
Minerals	Unit	Avg	SD	Min	Max	Nb
Calcium	g/kg DM	1.6	1.4	0.8	4.7	7
Phosphorus	g/kg DM	4.5	0.8	3.6	6.2	9
Potassium	g/kg DM	9.6				1
Magnesium	g/kg DM	2.2		1.7	2.6	2
Zinc	mg/kg DM	35		29	41	2
Copper	mg/kg DM	8		0	16	2
Iron	mg/kg DM	537		64	1010	2
Amino acids	Unit	Avg	SD	Min	Max	Nb
Alanine	% protein	3.6	0.2	3.1	3.7	5
Arginine	% protein	5.9	1.2	3.4	7.3	7
Aspartic acid	% protein	9.3	0.9	8.1	10.9	6
Cystine	% protein	0.8	0.2	0.7	1.2	8
Glutamic acid	% protein	13.3	1.6	10.8	15.6	6
Glycine	% protein	2.9	0.5	1.8	3.2	6
Histidine	% protein	2.5	0.2	2.4	2.9	6
Isoleucine	% protein	3.7	0.3	3.5	4.4	6
Leucine	% protein	6.8	0.8	5.9	8.2	6
Lysine	% protein	6.9	1.0	5.8	8.2	9
Methionine	% protein	1.3	0.3	0.7	1.9	10
Phenylalanine	% protein	5.3	1.2	3.1	6.7	7
Proline	% protein	5.2	0.4	4.6	5.5	5
Serine	% protein	4.1	0.7	2.9	4.5	5
Threonine	% protein	2.7	0.5	2.0	3.6	7
Tryptophan	% protein	1.3	0.3	0.9	1.8	6
Tyrosine	% protein	2.4	0.3	1.8	2.8	6
Valine	% protein	4.4	0.6	3.6	5.6	7
Secondary metabolites	Unit	Avg	SD	Min	Max	Nb
Tannins (eq. tannic acid)	g/kg DM	2.3				1
Tannins, condensed (eq. catechin)	g/kg DM	2.3	1.3	0.0	3.4	5

Avg: average or predicted value; SD: standard deviation; Min: minimum value; Max: maximum value; Nb: number of values (samples) used

Mung bean has better digestibility and lower production of flatulence than most other pulses, making it suitable for children and older people. Dry mung bean seeds have, per 100 g edible portion, an energetic value of 1430 kJ, and contain water 10 g, protein 22 g, fat 1 g, carbohydrates 60 g, fibre 4 g and ash 3 g. Variation in protein content (17-26%) is more influenced by environment than by genotype. Mung bean protein is

deficient in methionine and cystine, but has high lysine values, making it an excellent complement to rice. Mung bean seeds are a good source of minerals, provitamin A and vitamin B complex, while bean sprouts are in addition rich in ascorbic acid (vitamin C). Mung bean is low in antinutritional factors. Heating and sprouting denatures growth inhibitors. Seed weight varies between 1.5 and 8.5 g/100 seeds (Siemonsma and Lampang, 2016). Being rich in quality protein, minerals and vitamins, they are inseparable ingredients in the diets of a vast majority of Indian population. When supplemented with cereals, they provide a perfect mix of essential amino acids with high biological value. A seed of mung bean is highly nutritious containing 24–28% protein, 1.0–1.5% fat, 3.5–4.5% fibre, 4.5–5.5% ash and 59–65% carbohydrates on dry weight basis and provide 334–344 kcal energy. Mungbean protein is considered to be easily digestible (Mehandi et al., 2019). Mung bean (*Vigna radiata* L.) is an important pulse consumed all over the world, especially in Asian countries, and has a long history of usage as traditional medicine. It has been known to be an excellent source of protein, dietary fiber, minerals, vitamins, and significant amounts of bioactive compounds, including polyphenols, polysaccharides, and peptides, therefore, becoming a popular functional food in promoting good health (Hou et al., 2019).

Green beans consists of nutritional values which includes Vitamins Folate, Niacin, Pantothenic acid, Riboflavin, Thiamin, Vitamin A, Carotene beta, Vitamin B12, Vitamin B6, Vitamin C, Vitamin D, Vitamin E, Vitamin K. It consists of minerals, which includes Calcium, Copper, Iron, Magnesium, Manganese, Phosphorus, Potassium, Selenium, Sodium, and Zinc (Firdous, 2020). See **Table 7**.

**Table 7. Nutritional facts Per 100 grams**

347 Calories
1.2 g Total Fat
15 mg Sodium
1,246 mg Potassium
63 g Total Carbohydrate
24 g Protein
<i>Vitamins and Minerals</i>
2 % Vitamin A
0.13 Calcium
8 % Vitamin C
37 % Iron
20 % Vitamin B-6
47 % Magnesium

Seeds of Mung bean (*Vigna radiata* (L.) R. Wilczek) have been recognized as a 'Green pearl' of Asian cuisine due to abundance of dietary fibres, protein, minerals, vitamins and wide variety of bioactive agents (Uppalwar et al., 2021). Nutritional value Mung beans are recognized for their high nutritive value. Mung beans contain about 55%-65% carbohydrate (equal to 630 g/kg dry weight) and are rich in protein, fat, vitamins and minerals. It is composed of about 20%-50% protein of total dry weight, among which globulin (60%) and albumin (25%) are the primary storage proteins (see table). Mung bean is considered to be a substantive source of dietary proteins. The proteolytic cleavage of these proteins are even higher during sprouting. Mung bean carbohydrates are easily digestible, which causes less flatulence in human compared to other forms of legumes. Both seeds and sprouts of mung bean produce lower calories compared to other cereals, which makes it more attractive to obese and diabetic individuals (Döring, 2022). According to the United States Department of Agriculture (USDA) Trusted Source, 100 grams (g) of boiled mung beans contain: 7.02 g of protein; 19.15 g carbohydrate, including 2 g sugar; and 7.60 g dietary fiber. Mung beans are also a good source of B vitamins that are necessary for a range of bodily functions and help maintain the brain's health. In particular, mung beans are an excellent source of vitamin B-9, also known as folate, which helps a person's body make DNA. Folate is essential before and during pregnancy, as it helps prevent some birth abnormalities. 100 g of mung beans contain 159 micrograms (mcg) of folate. The recommended daily allowance for folate is 400 mcg for adults and 600 mcg during pregnancy. So, it is unlikely that a person will meet their folate requirement by eating mung beans alone. For women, dietary supplements may be a more practical way of getting the correct amount of folate before and during pregnancy (Mishra et al., 2022).

Like most legumes, mungbeans are relatively high in proteins and they are a good substitute for animal protein in many Asian diets as they contain high amounts of cheap protein. The most important part is the seed as it is used in several food products, both as whole seed and in processed forms (Kogong, 2022). See **Table 8**.

**Table 8. Chemical composition of mungbean seeds per 100g**

Water 9.1
Protein 23.9 g
Fats 1.2 g
Carbohydrates 62.6 g
Dietary fibre 16.3 g
Calcium 132 mg
Magnesium 189 mg
Phosphorus 367 mg
Iron 6.7 mg
Zinc 2.7 mg
Vitamin A 114 IU
Thiamine 0.62 mg
Riboflavin 0.23 g
Niacin 2.3 mg
Vitamin B6 0.38 mg
Folate 0.25 mcg
Ascorbic acid 4.8 mg

Like other culinary beans, mung beans are high in dietary fibre and protein and are also a source of iron, magnesium, potassium, and a number of essential amino acids (Petruzzello, 2023). Green beans consists of nutritional values which includes Vitamins Folate, Niacin, Pantothenic acid,

Riboflavin, Thiamin, Vitamin A, Carotene beta, Vitamin B12, Vitamin B6, Vitamin C, Vitamin D, Vitamin E, Vitamin K. It consists of minerals, which includes Calcium, Copper, Iron, Magnesium, Manganese, Phosphorus, Potassium, Selenium, Sodium, and Zinc (Sikdar, 2023). Nutritional value of mung bean mature seeds, raw is given in Table 9.

**Table 9. Mung bean mature seeds, raw; Nutritional value per 100 g (Wikipedia, 2023b)**

<b>Energy</b>	1,452 kJ (347 kcal)
<b>Carbohydrates</b>	62.62 g
Sugars	6.6 g
Dietary fiber	16.3 g
<b>Fat</b>	1.15 g
<b>Protein</b>	28.86 g
<b>Vitamins</b>	<b>Quantity %DV<sup>†</sup></b>
Thiamine (B1)	54% 0.621 mg
Riboflavin (B2)	19% 0.233 mg
Niacin (B3)	15% 2.251 mg
Pantothenic acid (B5)	38% 1.91 mg
Vitamin B6	29% 0.382 mg
Folate (B9)	156% 625 µg
Vitamin C	6% 4.8 mg
Vitamin E	3% 0.51 mg
Vitamin K	9% 9 µg
<b>Minerals</b>	<b>Quantity %DV<sup>†</sup></b>
Calcium	13% 132 mg
Iron	52% 6.74 mg
Magnesium	53% 189 mg
Manganese	49% 1.035 mg
Phosphorus	52% 367 mg
Potassium	27% 1246 mg
Zinc	28% 2.68 mg

Mung beans are recognized for their high nutritive value. Mung beans contain about 55%–65% carbohydrate (equal to 630 g/kg dry weight) and are rich in protein, fat, vitamins and minerals. It is composed of about 20%–50% protein of total dry weight, among which globulin (60%) and albumin (25%) are the primary storage proteins (see table). Mung bean is considered to be a substantive source of dietary proteins. The proteolytic cleavage of these proteins are even higher during sprouting. Mung bean carbohydrates are easily digestible, which causes less flatulence in humans compared to other forms of legumes. Both seeds and sprouts of mung bean produce lower calories compared to other cereals, which makes it more attractive to obese and diabetic individuals (Wikipedia, 2023b).

## HEALTH BENEFITS

Mung bean plant has high nutritive significances responsible for plentiful health benefits either to prevent or cure human diseases (Thompson, 1969; Wilson, 1983; Carbonaro *et al.*, 2015; Shi *et al.*, 2016; Ramos-Ruiz *et al.*, 2018; Weththasinghe *et al.*, 2018). In addition to the nutritional component, seeds of mung beans are rich in several phytoconstituents such as phenolic acid, polyphenols, flavonoids, organic acid, sterol and triterpenes, aldehyde and lipids. Seed contents have high levels of proteins, amino acid, polyphenols, and oligosaccharides which are considered the main contributors to the anti-inflammatory, antioxidative, antitumor, antimicrobial activities. This plant could be considered as the best source of supplementing human body with nutrients like niacin, thiamine, pantothenic acid, vitamin B6, riboflavin, vitamin K, folate, copper, manganese, iron, magnesium, phosphorus, potassium, vitamin C and dietary fiber. Being a low cholesterol and saturated fat content, soluble fibres of this food source has demonstrated beneficial effects for healthy and hypercholesterolemic patients. Regular intake of this food sources could provide ample amount of lysine for vegetarian population lacking in requisite amount of lysine. It is well known for its detoxification properties ranging from enhancement of human mental function to alleviation of heat stroke and swelling during the summer seasons. Epidemiological studies promulgated that the consumption of this antioxidant rich food has shown potential activities against degenerative diseases including cardiovascular, diabetes, cancer, arthritis and Alzheimer's diseases. The mung bean has also exhibited beneficial effects in the regulation of gastrointestinal upset and to moisturize the skin.

The seeds are aphrodisiac, tonic, appetiser, diuretic, good for heart and fatigue and used in paralysis, rheumatism and affections of nervous system (BSMRAU, 2015). The mung bean has been documented to ameliorate hyperglycemia, hyperlipemia, and hypertension, and prevent cancer and melanogenesis, as well as possess hepatoprotective and immunomodulatory activities. These health benefits derive primarily from the concentration and properties of those active compounds present in the mung bean. Vitexin and isovitexin are identified as the major polyphenols, and peptides containing hydrophobic amino acid residues with small molecular weight show higher bioactivity in the mung bean (Hou *et al.*, 2019). Encouraging outcomes of various studies pertaining to medicinal importance of seeds of mung beans have been reviewed in this paper. Food recipes comprising of seeds of mung beans could be a choice of potential diet for patients with varied ailments like depression, cardiovascular disorders, diabetes, cancer. This potential may be attributed to the wealth of bioactive constituents (Proteins, Polyphenols, Flavonoids, Terpenoids) present in seeds of mung beans providing a defense mechanism against several precursors (Uppalwar *et al.*, 2020).

**Following health benefits of mung bean are reported (Firdous, 2020; Sikdar, 2023):**

**Helps reduce weight and fights obesity:** Mung beans are a filling food. The high fibre and protein levels produce longer satiety times due to the double increase of the satiety hormone cholecystokinin as compared to meals that are devoid of these beans. Therefore consuming mung beans on a regular basis helps decrease food intake, thus lower weight and aid in fighting obesity.

**Lowers blood pressure:** It is a proven fact that mung beans are fat controllers and regulators. Moreover, the presence of large amount of magnesium makes it a very potent BP regulator. It maintains the level of magnesium in the blood. Magnesium eases blood vessels and lowers hypertension. This, in turn, keeps the blood pressure of the body under control.

**Controls cholesterol and heart disease risk:** By preventing oxidation of LDL, mung beans keep the arteries clear and improve blood circulation. Not only does this reduce inflammation, it reverses damage to the blood vessels. By preventing deposition of plaque the risk of heart attack and stroke is reduced as well.

**Help fight cancer:** Mung beans keep free radicals under control. These free radicals can be an outcome of anything like pollution, stress, unhealthy snacking and toxicity in body. They have the ill-fate of interfering with normal cell growth. Abnormal cell growth can even lead to cancer. Mung bean, which is a natural suppressor of free radicals, is a good option to keep cancer at bay.

**Boosts immunity and protects against infections:** The wide variety of phytonutrients in mung beans is not only anti-inflammatory but anti-microbial as well. These help fight harmful bacteria and viruses, maintain healthy gut bacteria and raise immunity levels. They ensure optimal digestive tract health and thus promote optimum nutrient absorption.

**Improves skin health:** Green gram adds shine and radiance to human skin. The presence of copper increases its use in various face packs and face creams. Using mung bean as a scrub is also a good option. It is very easy to make a natural exfoliating face pack using mung beans at home. Undoubtedly, it is one of the best natural scrubs one can use to make their skin radiant!

**Anti-toxic benefits:** Toxicity is a serious problem and can have long lasting side-effects including ulcers and cancer. Consumption of mung beans helps to keep your body free of toxins. It maintains the circulatory health of the body as well. It flushes out toxins from the body easily and keeps the formation of free radicals under check.

**Decreases PMS symptoms:** The various B complex vitamins, especially folate and B6, and magnesium help regulate hormonal fluctuations which cause these PMS symptoms. Mungbean has been consumed for more than 2000 years in China as it is well known for its health benefits such as reducing gastrointestinal disorders and heart stroke, and clearing toxins from the body. It is also considered to aid in reducing the cholesterol level in the body, manipulation of tumor cells and regulating blood pressure. Owing to its palatable taste and nutritional quality, mungbean has been used as an iron-rich whole food source for baby food and induces less flatulence hence well tolerated by children. Furthermore, starch in mungbean is highly digestible when compared to those in chickpea (*Cicer arietinum*), pigeon pea (*Cajanus cajan*) and lentils (*Lens culinaris*) (Kogokong, 2022)

#### Following Health benefits are reported (Mishra *et al.*, 2022):

**Antioxidant effects:** Research shows that several compounds in mung beans demonstrate antioxidant activity.

**Antifungal and antimicrobial activity:** These include some against the *Helicobacter pylori* bacteria that causes stomach ulcers.

**Anti-inflammatory activity:** Test tube studies suggest that mung bean extracts may have potential to improve symptoms of inflammatory conditions, such as allergies.

**Diabetes:** Studies in rats suggest mung bean extracts may help lower blood glucose levels.

**Hypertension:** Studies in rats suggest sprout extracts may help lower blood pressure.

**Cancer:** Test tube studies suggest that compounds in mung beans may have antitumor properties.

Bioactive components of mung bean seeds exhibited a wide array of activities such as anticancer, antihyperlipidemic, antihypertensive, antidiabetic, anti-microbial, antioxidant, treatment of alcoholism reducing obesity, increasing muscular strength, rheumatism, piles, liver and neurological diseases. This curative potential highlighted its various beneficial outcomes in the field of drug research and increasing scientific interest in the identification of bioactive compounds responsible for various pharmacological activities. This legume is gaining importance for its use in the pharmaceutical, food and cosmetic products (Uppalwar *et al.*, 2021).

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