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Classical Genetics and Traditional Breeding in Mungbean

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Abstract

Mungbean is a highly self-pollinating diploid species, with chromosome number of $2n = 22$. Varietal improvement in mungbean has benefited greatly from exemplary work done in the past on determination of genetics of key traits. Varietal introductions, pure line selection, recombination breeding and mutagenesis have been employed successfully in developing varieties. Development of high-yielding varieties with synchronous and early maturity (about 60 days), determinate growth habit, large-seed size, resistance to diseases (powdery mildew, Cercospora leaf spot and mungbean yellow mosaic disease) through hybridization and mutagenesis was a game changer in mungbean development. This enabled the expansion of the crop through good adoption by the farming community, particularly in Asia.

4.1 Introduction

This chapter covers information about the cytogenetics and nuclear DNA content in mungbean. The floral biology and the crossing techniques commonly followed are briefly described. The genetics of important agronomic traits and resistance to stresses and the breeding methods employed for varietal development have been discussed.

4.2 Cytogenetics

Mungbean (*Vigna radiata* (L.) Wilczek var. *radiata*) is a diploid with somatic chromosome number of $2n = 22$. Numerous karyotyping studies were conducted to estimate the dimensions of the mungbean chromosome (Table 4.1). Bhatnagar (1974) put forward $4L^{sm} + 4M^{sm} + 3M^{m}$ [L = long (2.7–3.5 µm), M = medium (1.9–2.6 µm, sm = sub median centromere and m = median centromere)] as karyotype formula for mungbean.

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Table 4.1 Morphology and dimensions of mungbean chromosome

Chromosome length (µm)		Number of chromosomes with			Reference
Total	Range	Median	Submedian		
		Centromere	Centromere	Satellite	
23.00	1.4–3.30	6	5		Krishnan and De (1965)
28.81	1.9–3.50	3	8		Bhatnagar et al. (1974)
11.97	0.8–1.39				Joseph and Bouwkamp (1978)
		5	6	2	Bhattacharya (1979)
24.80	1.37–3.35	6	5		Sahai and Rana (1980)
37.40	1.0–2.8	6	5		Sarbhoy (1980)
15.95	1.24–2.04	3	8	3	Sharma and Gupta (1982)
24.90	1.6–3.5	5	6	2	Lavania and Lavania 1983

Source Kumar et al. (2006)

4.3 Nuclear DNA Content

The nuclear DNA (2C DNA) content of the mungbean chromosome was estimated at 0.96 pg and 1.42 pg by Murray et al. (1979) and Johnston et al. (1999) respectively. It was assessed that the haploid genome has approximately 470 Mbps by Murray et al. (1979) and 579 Mbps by Arumuganathan and Earle (1991). Kang et al. 2014 constructed 421 Mb (80%) of the total estimated *V. radiata* var. *radiata* genome and identified 22,427 high-confidence protein-coding genes and 160 *Vigna* gene clusters.

4.4 Floral Biology

Mungbean is a highly self-pollinated crop (cleistogamous) with 4–5% outcrossing (Van Rheenen 1964). It produces green to dark yellowish papilionaceous flowers in terminal racemes or axillary clusters on long peduncles. The flower is a hermaphrodite having a gynoecium covered with a diadelphous androecium (9 + 1), two keels, two wings and one standard petal. Flower opening occurs between 6:00 and 8:00 AM and continues up to 11:00 AM. The standard crossing technique involves emasculation in the evening and pollination in the following morning (Boling et al. 1961; Singh and Malhotra 1975; Park and Yang 1978; Cupka and Edwards 1986; Khattak et al. 1998). However, crossing technique by emasculation and pollination at the same time in the morning can also be done (Tomooka et al. 2002).

4.5 Genetics of Traits

Classical genetic studies of mungbean commenced in the 1930s (Bose 1939). Fery (1980) published a set of rules proposed for the genus *Vigna* and a detailed literature review of the genetics of mungbean. The most comprehensive review on classical genetics of mungbean was made nearly 20 years ago by Poehlman (1991).

4.5.1 Plant Type and Growth Habit

Mungbean genotypes can be erect, semi erect, semispreading or twining. Sen and Ghosh (1959) and Khattak et al. (1999) reported twining habit under the control of a single dominant gene. Pathak and Singh (1963) reported single recessive gene for twining habit, while single dominant gene for semi-spreading habit. Further, single dominant gene for indeterminate growth habit was reported by Talukdar and Talukdar (2003), Isemura et al. (2012) and Li et al. (2018). The gene controlling determinacy is named *st-det5.9.1* by Isemura et al. (2012) and *VrDet1* by

Li et al. (2018). The causal mutation(s) in the promoter region of the *VrDet1* gene cause the difference between the indeterminacy and determinacy (Li et al. 2018). For days to maturity, epistatic gene action is reported (Rao et al. 1984; Malik and Singh 1983; Wilson et al. 1985).

4.5.2 Pigmentation

Pigmentation in mungbean can be observed on hypocotyls, epicotyls, stem, leaf rachis, petiole and peduncle. Purple hypocotyls are dominant over purple spotted and green hypocotyls, and purple spotted over green hypocotyls. Single dominant gene ‘*A*’ for purple hypocotyl colour was reported (Bose 1939). Sen and Ghosh (1958) designated ‘*P*’ gene for purple hypocotyls colour. Anthocyanin pigmentation in peduncle, petiole, stem, hypocotyls and epicotyls was reported to be governed by single dominant gene (Pathak and Singh 1963; Van Rheenen 1965; Verma and Krishi 1969; Misra et al. 1970; Virk and Verma 1977). Also, a single dominant gene ‘*Ppp1*’ with pleiotropic effect controlling this trait was reported by Dwivedi and Singh (1986). Van Rheenen (1965) proposed symbol ‘*R*’ for red colour of top of leaflet stalk, stem and hypocotyls. Appa Rao and Jana (1973) reported single recessive gene for peduncle, petiole, stem, hypocotyls and epicotyls anthocyanin pigmentation. Anthocyanin in hypocotyls was reported to be controlled by two supplementary genes viz. ‘*Sh*’ and ‘*Ph*’ with recessive epistatic interaction (Mukherjee and Pradhan 2002).

4.5.3 Stem Traits

The inheritance of stem fasciation in mungbean was reported to be controlled by single recessive gene ‘*fs1*’ having a pleiotropic effect on the number of floral organs (Dwivedi and Singh 1990). Malik and Singh (1983) reported epistatic effects for higher branches per plant. Both additive and non-additive effects with preponderance of additive effects have been reported for plant height (Bhargava et al. 1966; Yohe and Poehlman 1975; Lal et al. 1982; Malik and Singh 1983; Reddy and Sreeramulu 1982; Rao et al. 1984; Wilson et al. 1985).

4.5.4 Leaf Traits

Large, ovate, entire and lobed trifoliate leaves have been observed in mungbean. Pentafoliate leaf shape is known to be governed by a single gene (Chhabra 1990). Soehendi et al. (2006) reported that hybridization between large-heptafoliate leaves and small-pentafoliate leaves mungbean mutants resulting in F_1 plants with normal trifoliate leaves and F_2 plants segregated in a 9 : 3 : 3 : 1 ratio of large-trifoliate : large-heptafoliate : small-pentafoliate : small-heptafoliate leaves. They proposed symbols *N1*, *n1* and *N2*, *n2* for genes controlling leaflet number. Genotypes *N1_N2_*, *n1n1N2_*, *N1_n2n2* and *n1n1n2n2* were suggested for the above leaf traits, respectively (Soehendi et al. 2006). Gene symbol *A_ B_*, *A_bb*, *aaB_* and *aabb* were suggested for dark green, green, greenish yellow and pale green seed coats, respectively. The results suggested that the genes controlling leaflet size and leaflet number are unlinked. Recently, mungbean mutant showing unifoliate leaf has been identified (Jiao et al. 2019). Unifoliate leaf is recessive to the normal trifoliate leaf and is controlled by a single gene, designated *un* (Jiao et al. 2019). Several researchers (Singh and Mehta 1953; Pohle 1972; Ramamoorthi et al. 1994; Talukdar and Talukdar 2003; Singh 1980; Chhabra 1990) have reported that lobed trifoliate leaf is dominant over the entire leaf. However, there are also reports of two dominant genes, ‘*Tlb1*’ and ‘*Tlb2*’ with duplicate gene action for trilobed leaves (Sareen 1982). Narrow lanceolate leaf is reported to be controlled by two recessive genes, ‘*nl1*’ and ‘*nl2*’ (Dwivedi and Singh 1986).

4.5.5 Inflorescence/Flower Traits

Simple and compound inflorescence have been reported in mungbean. Sen and Ghosh (1959) reported simple inflorescence under control of two dominant genes (*Í1’* and *Í2’*), while double recessive homozygous genotypes result in compound inflorescence. Singh and Singh (1971) reported that single cluster per node is governed by dominant gene '*C*' and its recessive counterpart '*c*' governs three clusters per node. Monogenic recessive inheritance of induced sterility was reported by Saini et al. (1974). Four colours of standard petal have been recorded in mungbean. Light yellowish olive colour was dominant to olive yellow colour and was designated by gene '*O*' (Bose 1939). Murty and Patel (1973) proposed gene symbols *Pg*, *Pb* and *Pn* for allelic series conditioning pale green yellow, bright yellow and naphthalene yellow flower colour. Additive gene action (Yohe and Poehlman 1975; Luthra et al. 1979; Reddy and Sreeramulu 1982; Rao et al. 1984; Malik and Singh 1983; Wilson et al. 1985) and partial dominance (Luthra et al. 1979) have been reported for days to 50% flowering.

4.5.6 Pod Traits

Verma and Krishi (1969) reported that pod shattering is dominant to non-shattering and is governed by a single gene. Singh et al. (1975) reported that resistance to pod shattering in interspecific cross as quantitative trait. Quantitative genetic analysis revealed that pod shattering is conditioned by two loci (Isemura et al. 2012). Swollen pod-tip was reported dominant (gene '*Tp*') over tapering pod-tip (Sen and Ghosh 1958). Khadilkar (1963) reported that pod-pubescence is dominant which is also governed by independent duplicate genes. However, a single dominant gene is reported controlling plant pubescence trait (Murty and Patel 1973). Additive gene effects (Singh and Jain 1971; Singh and Singh 1971; Lal et al. 1982; Luthra et al. 1979; Reddy and Sreeramulu 1982; Wilson et al. 1985) and partial dominance (Malhotra et al. 1980) have been reported for inheritance of pod length. Mungbean mutant possessing twin podded was generated by inducted mutation using gamma ray (Dheeranupattana 1985). The twin podded mutant also showed larger seed size than the wild type. The twin podded is controlled by two genes with dominant and recessive epistasis (Dheeranupattana 1985).

4.5.7 Seed Traits

Two types of seed coat lustre are present in mungbean, dull versus shiny. Dull seed coat is dominant to shiny seed coat and is conditioned by a single gene, designated *D* (Rheenen 1965). Diversity for seed-coat colour (yellow, green, amber, brown, yellow mosaic green mosaic, tan and black) has been recorded in mungbean. Black, black-spotted and dull-green seed-coat colours were found to be dominant over green, non-spotted and shiny green colour, respectively. Khattak et al. (1999) and Lambrides et al. (2004) reported monogenic inheritance for seed-coat colour. Bose (1939) reported that two independent dominant genes control the seed-coat colour where gene '*A*' conditions the green colour, while gene '*B*' conditions the dark green colour. Gene symbol *A_ B_*, *A_bb*, *aaB_* and *aabb* were suggested for dark green, green, greenish yellow and pale green seed coats, respectively. Chen et al. (2001) suggested that the inheritance of black and green seed colours was controlled by a single gene (*B*), black being dominant over green. Sen and Ghosh (1958) suggested that three gene pairs '*BL*', '*bf*' and '*G*' condition blue sap colour, buff sap colour and green chloroplast which together define seed-coat colour. Rheenan (1965) reported dominant allele 'A' and 'Sp' for green and spotted seed coat. Four gene models ('*B*', '*M*', '*Br*' and '*G*') were proposed by Murty and Patel (1973) for defining genotypes for different seed-coat colour. Further, five major genes with non-allelic interactions were reported by Chhabra et al. (1990). Thakare et al. (1980) identified a green cotyledon mutant in mungbean from cultivar S8 and found that green cotyledon is governed by single recessive gene '*gc*'.

Seed hardness in mungbean is reported to be a dominant character which is governed by single gene pair (Singh et al. 1983, 2005; Lawn et al. 1988), designated Hd_1 Hd_1 (Singh et al. 1983).

QTL analysis revealed that four loci control hardseededness (Humphry et al. 2005; Isemura et al. 2012). The major locus on LG1 explained up to 34% of the trait variation (Isemura et al. 2012). Additive gene effects (Bhargava et al. 1966; Singh and Jain 1971; Singh and Singh 1971; Yohe and Poehlman 1975; Reddy and Sreeramulu 1982; Malik and Singh 1983; Rao et al. 1984; Imrie et al. 1985; Wilson et al. 1985) and dominance gene action (Singh and Singh 1971; Singh and Jain 1971 and Rao et al. 1984) for seed weight have been reported. Apart from these, four QTLs for seed weight were identified by Alam et al. (2014b).

4.5.8 Photoperiod Response

Verma (1971) reported that photo insensitiveness was dominant over the photo sensitiveness and was governed by single gene. Tiwari and Ramanujam (1976) observed dominance of earliness and photo insensitivity in F_1 generation. However, in F_2 generation, digenetic control was observed. Swindell and Poehlman (1978) reported dominant or partially dominant gene for sensitivity to photoperiod. Islam et al. (1998) reported two recessive genes for photoperiod sensitivity.

4.5.9 Yield Traits

Seed yield is important trait with complex inheritance. Seed yield is associated with many component traits that make direct and indirect contribution to the ultimate response. Both additive (Yohe and Poehlman 1975; Luthra et al. 1979; Reddy and Seeramulu 1982; Malik and Singh 1983; Rao et al. 1984; Payasi 2015) and non-additive genes (Singh and Jain 1971; Singh and Singh 1971 Lal et al. 1982) and epistatic interaction (Murty and Patel 1973; Singh and Singh 1971) have been reported for seed yield in mungbean. Further, partial dominance (Singh and Jain 1971; Singh and Singh 1971; Rao et al. 1984) and overdominance (Malik and Singh 1983; Luthra et al. 1979) have also been reported for seed yield. From the studies reported, it is quite evident that seed yield is complex trait and mode of inheritance varies with parent genotype.

Seed weight is a key trait contributing to seed yield and affects consumer preference and processing. Seed weight is principally under the control of several genes with additive effects (Yohe and Poehlman 1975; Imrie et al. 1985; Wilson et al. 1985; Malik et al. 1986; Alam et al. 2014), although genes with dominant or overdominant effect are also reported for the trait (Malik and Singh 1983; Rao et al. 1984; Luthra et al. 1979).

Pods per plant is a key agronomic trait which is found determined by additive gene action (Bhargava et al. 1966; Singh and Jain 1971; Yohe and Poehlman 1975; Malhotra et al. 1980, Reddy and Sreeramulu 1982; Rao et al. 1984), partial dominance to overdominance (Singh and Jain 1971; Singh and Singh 1971 and Luthra et al. 1979). Further, non-additive effects were more pronounced than the additive effects for the expression of this trait (Singh and Singh 1971; Alam et al. 2014).

Seeds per pod is an important yield component and additive gene action regulating this trait has been reported by several researchers (Yohe and Poehlman 1975; Luthra et al. 1979; Lal et al. 1982; Reddy and Sreeramulu 1982; Malhotra 1983; Alam et al. 2014). Also partial dominance to overdominance (Singh and Jain 1971; Singh and Singh 1971; Luthra et al. 1979) and epistasis (Malik and Singh 1983) regulation for this trait have been reported.

Pods per cluster is important determinant for yield per plant. Additive effects (Bhargava et al. 1966; Malhotra et al. 1980; Reddy and Sreeramulu 1982; Malik and Singh 1983; Wilson et al. 1985) and partial to overdominance (Singh and Singh 1971) are mainly reported for this trait.

4.5.9.1 Biotic and Abiotic Stress Resistance

Although several insects and diseases attack and cause yield reduction in mungbean, common insects and diseases that have been extensively studied in mungbean, viz. bruchids (*Callosobruchus* spp.), powdery mildew disease caused by fungus *Erysiphe polygoni*, Cercospora leaf spot disease caused by fungus *Cercospora canescens* and MYMD caused by MYMV and MYMIV. Resistance to these insect pests and diseases are each controlled by single or a few genes.

Bruchid resistance in mungbean is controlled by a single dominant locus, *Br*, with few modifying genes (Kitamura et al. 1988; Somta et al. 2007). The *Br* locus also confers resistance to pod sucking bug (***Riptortus pedestris*** Fab.) (Ishimoto and Kitamura 1993). Powdery mildew resistance is controlled by either single or two dominant genes (AVRDC 1979; Reddy et al. 1994; Khajudparn et al. 2007). Three dominant genes for the resistance were named *Pm*1, *Pm*2 and *Pm*3. Combination of dominant alleles at *Pm*1 and *Pm*2 resulting in immune resistance (Reddy et al. 1994; Reddy 2009), while dominant allele at *Pm*3 alone conferring immune resistance (Reddy 2009). Cercospora leaf spot is governed by a single dominant gene (AVRDC 1974; Thakur et al. 1977; Chankaew et al. 2011). The gene symbol *F* was proposed for the Cercospora leaf spot resistance (Thakur et al. 1977). MYMD resistance is controlled by single dominant gene (Lekhi et al. 2018) or single recessive gene (Malik et al. 1986; Khattak et al. 2000; Thakur et al. 1977). Bacterial leaf spot caused by *Xanthomonas phaseoli* is conditioned by a single dominant gene (Thakur et al. 1977). The gene symbol *Bls* was proposed for the resistance (Fery 1980). The gene is inherited independently of the genes for resistance to Cercospora leaf spot and MYMD.

In case of the abiotic stress, genetics of the resistance has been studied for calcareous soil (iron deficiency chrolosis) only. Nopparat et al. (1997) reported that the resistance is controlled by the two genes with inhibitory action, although a single dominant gene action is also possible. However, Srinives et al. (2010) reported that resistance is conditioned by a single dominant gene, designated *IR*, with a few modifying genes.

4.6 Breeding Methods

Ranali and Cubero (1997) discussed the basis of genetic improvement in legumes and the application of breeding methods, including introduction, hybridization, early generation selection and mutation, along with molecular markers that offer opportunity to enhance precision.

4.6.1 Introduction

Introduction is a primary approach in crop improvement, in which introduced germplasm is directly released as variety. In last two decades, lot of mungbean germplasm was introduced into several countries of Asia and Africa from World Vegetable Centre. The introduced germplasm/breeding line possessed earliness, bold seed size and long pod with up to 18 seeds per pod. In India, the germplasm was utilized for broadening the genetic base of mungbean. Introductions have been successful in the development of Pusa 105, Pusa 9531, Pant Moong 5, Pusa Vishal and SML 668. In Thailand and China, the breeding lines from the World Vegetable Centre, such as VC1973A and VC2778A, were selected and released as mega varieties. Those breeding lines/varieties have contributed to the great expansion of mungbean cultivation in Thailand and China (Srinives 1996). At present, in China, the breeding lines are used to cross with local germplasm to develop superior varieties. In Pakistan, the breeding lines were crossed with local germplasm with resistance to yellow mosaic disease, resulting in popular varieties: NIAB Mung 92 (NM92) and NIAB Mung 94 (NM94) that revolutionized mungbean cultivation in this country (Ali et al. 1997). In semi-arid areas of eastern Kenya, mungbean introductions from the World Vegetable Centre were tested for adaptability and seed yield. AVMU 0801, AVMU 1003 and AVMU 8501 were identified as farmer preferred lines through farmer participatory evaluation and finally released as varieties (Karimi et al. 2019).

4.6.2 Pure Line Breeding

Pure line selection is the step preceding introduction of a line, in which the selection of better plant types is made from an already existing genetically heterogeneous population or landrace. These superior plant types are identified as the result of natural selection pressure, which helps to evolve new plant types with strong genetic potential. These variants are fixed by breeders through a continuous cycle of selfing and selection (Gupta and Kumar 2006; Tickoo et al. 2006). In India, many mungbean varieties are developed from pure line selections (Srinives 1996).

4.6.3 Recombination Breeding

Hybridization is the most common method used by plant breeders for combining desirable traits. Better recombinants can be obtained through intraspecific or interspecific hybridization. Landraces, exotic collections and primitive forms are key sources of rare alleles for useful traits in plant breeding. At the World Vegetable Centre, superior breeding lines were developed by hybridizing between high yielding, large seeded, synchronous maturing and photo-insensitive germplasm from the Philippines and disease-resistant germplasm from India (Fernandez and Shanmugasundaram 1988). Several of such the breeding lines are used as parents in crossing to generate new recombinants with better-desired traits. The prior knowledge of parental performance, combining ability and genetics of trait to be incorporated is essential for the breeding of high-yielding genotypes. The knowledge of yield contributing traits helps plant breeder in selection of appropriate breeding material in segregating generations. After hybridization in mungbean breeding material can be advanced following pedigree, bulk, recurrent, backcross or single-seed methods of selection. Interspecific hybridization often results in pre-breeding material which is subsequently utilized by the breeders for varietal improvement. Dahiya and Singh (1986) compared efficiency of selection methods including single-seed descent (SSD), mass selection and selective intermating in mungbean in which progeny developing after two cycles of selection were evaluated for yield and seven agronomic and yield-related traits. Number of high-yielding lines, mean yield of top 10% lines and mean of the highest yielding line were used to determine the relative efficacy of each selection method. They found that selection after two cycles of selective intermating was the best method for developing high-yielding lines and that SSD was the least efficient method. Later, Gill et al. (1995) compared efficiency of four selection methods, viz., honeycomb (HC), pedigree selection (PS), SSD and bulk selection (BS) in mungbean based on the basis of the mean of the lines, the range, the number of superior lines over the best check and the proportion of the top 10% lines in all the crosses and generations. They found that (i) HC is the most efficient method for yield per plant and yield-related traits, (ii) PS, SSD and BS were not different and (iii) HC and SSD methods were suitable for generating superior lines with high seed yield and pods per plant.

For breaking undesirable linkage and accumulating desirable traits, recurrent selection and population improvement have been suggested. Burton (1997) suggested use of early generation testing. This method helps in discarding inferior progenies and reducing population load. In this method, F_2, F_3 and even F_4 families are subjected to early generation selection depending upon the target trait and inferior families are rejected. Interspecific hybridization involving mungbean and black gram (*Vigna mungo* (L.) Hepper) has led to the development of four mungbean varieties (Pant M 4, HUM 1, Meha, PM 6) with improved plant types. Important traits like sympodial bearing, non-shattering, stable MYMD resistance, etc., can be transferred to mungbean from urdbean. Interspecific hybridization between mungbean and rice bean (*Vigna umbellata* (Thunb.) Ohwi and Ohashi) have resulting in mungbean lines with resistance to bruchids (seed weevils) (Mariyammal et al. 2019) and MYMD (Mathivathana et al. 2019).

4.6.4 Mutagenesis

Induced mutations are useful for traits lacking variability in primary gene pool. Mutations may occur spontaneously or can be induced artificially. Effectiveness and efficiency of mutagen are important. Effectiveness of mutagen is associated with mutation per unit dose of mutagens and efficiency is related to changes like sterility, injury and lethality (Goud 1967). Mutation can be induced in seed as well as in the vegetative portion of the plant. The effect and efficiency of mutagen are measured by its effect on genotype which varies with dosage and nature of mutagen. Khan et al. (2006) reported that ethlyl methane sulphonate (EMS) exhibits high mutagenic efficiency in comparison to other chemical mutagens. Gunasekaran et al. (1998) compared efficiency of gamma rays and ethidium bromide in generating variation for different agronomic traits. They reported that gamma rays were more effective in causing genetic changes breaking linkages. Variation for high protein content and yield in mungbean was induced by Chakraborty et al. (1998) using gamma irradiation. Variation for yield and related agronomic traits was induced in mungbean by different researchers (Tah and Saxena 2009; Ahmed et al. 2015; Dewanjee and Sakar 2017; Wani et al. 2017; Das and Baisakhi 2018). Srinives et al. (2000) and Tah (2006) obtained leaf mutants, pod mutants and semi-dwarf plants utilizing gamma irradiation.

Singh and Kole (2006) used EMS and studied genetic variability for agronomic traits. They obtained branchless and multifoliate mutants. Improvement in resistance to powdery mildew, Cercospora leaf spot and cowpea weevil through gamma radiation-induced mutation was reported by Wongpiyasatid et al. (1999). Mutation breeding has been used to develop improved cultivars in mungbean either through mutation breeding directly or by involving mutants as a parent in crossing programmes (Ahloowalia et al. 2004; Gopalakrishna and Reddy 2009). Till date, 38 varieties have been developed using mutation breeding. In India, 16 varieties have been developed through mutation breeding. Most cultivars are early maturing, high yielding and tolerant/resistant to YMV (Ahloowalia et al. 2004). In addition to these popular varieties, Pusa Vishal and SML 668 have been developed through selection in mutant lines NM92 and NM94, respectively. These varieties are early maturing, bold seeded, high yielding and tolerant to MYMD. Mutant varieties NM92 and NM98 are popular in Pakistan and in other countries like Bangladesh and Myanmar. In Thailand, mutation breeding is a main method in developing high-yielding varieties. Mutant variety Chai Nat 72 is popular in the country for its higher yield, larger seed size and better resistance to alkaline soil than the wild type variety. All the currently popular varieties in the country were developed by mutation breeding.

4.7 Conclusion

Traditional breeding has contributed in a great way in developing varieties which have been well adopted by farmers. The chapters on breeding for biotic stresses and abiotic stresses in this book covers more detailed information, with examples. Greater use of mungbean germplasm held in genebanks and also of related species would help in broadening the genetic base of mungbean varieties. This will be critical as the area under the crop expands and new pests and diseases emerge.

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