

Genetic Improvement in Mungbean [*Vigna radiata* (L). Wilzeck] for Yield, Nutrition and Resistance to Stresses - A Review

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ABSTRACT: Mungbean is an important legume crop of south East Asian countries and is primarily cultivated for dry seed for consumption. In the past range of genetic variability for economic important character has been extensively exploited in breeding programme. Genes for resistance to mungbean yellow mosaic viruses (MYMV), powdery mildew and cercospora leaf spot has been transferred by inter-varietal hybridization, or created by induced mutation (physical and chemical mutagens). Interspecific hybridization of mungbean with related *Vigna* species may provide additional gene pool for enrichment of mungbean cultivars for specific characters. Abiotic stresses such as drought, heat, water logging and salinity causes significant amount of loss in economic yield of mungbean. There is utmost need to understand complex nature of abiotic stresses tolerance and development of high throughput screening techniques for precise identification and selection of tolerance genotypes. Reasonable genetic diversity for protein, iron and zinc has been observed in diverse source of germplasm of mungbean and it could be targeted for development of nutrient rich cultivars. Construction of saturated RFLP linkage map has opened scope of mungbean for molecular mapping of several economic important genes and it will augment traditional breeding programme. The development of high-throughput marker such as SSRs and SNPs in related legume crop will accelerate mungbean genomic research in future. Presently it is need of integration of conventional breeding methods with modern innovative breeding technologies in order to achieve the sustaining yield in changing climatic conditions.

Keywords: Mungbean, Stresses, Resistance, Genetic variability, Yield, Nutrition

GENETIC IMPROVEMENT IN MUNGBEAN

Mungbean (*Vigna radiata* L.) also known as green gram is a short duration pulse crop and is primarily cultivated in India, Pakistan, Bangladesh, Sri Lanka and other south East Asian countries. Based on archaeological and scientific evidences now it confirmed that its origin lies in India and Indo-Burma region (Vavilov, 1951). Indian condition, mungbean is used as dal and green pods may be used as vegetables. The major consumption is as food legumes by most of the vegetarians. The states accounting for major area under mungbean cultivation are Orissa, Andhra Pradesh, Madhya Pradesh, Maharashtra, and Rajasthan. Mungbean is cultivated in all the seasons in India, i.e. *kharif*, *zaid* and *rabi*. Generally *zaid* and *rabi* crops are cultivated in irrigated conditions and *kharif* is taken under the rainfed conditions. Due to short duration nature it is an excellent crop to fit in intercropping system with different major crop or it

may be taken as green manure crop to enrich the soil and other biota. Mungbean belongs to family leguminosae and botanically nominated as *Vigna radiata* (L.) and it primarily differs from genus *Phaseolus* (Singh, 1982). The primary centre of genetic diversity was found to be central Asian region, where putative form of wild and its cultivated species are found. *Vigna radiata* var *sublobata* that occur wild in India is considered to be the putative progenitor of mungbean. Very least attention have been paid in mungbean improvement as compare to cereals but in recent era some progress have been made in mungbean improvement by developing the short duration variety, resistance varieties to biotic and abiotic stresses and nutritional aspects. Keeping all these things in view, the present review attempt has been made to cover the various aspects of genetic improvement in relevance with economic important characters of mungbean.

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BREEDING OBJECTIVE AND BREEDING METHODS

The prime breeding objective in mungbean to achieve high and stable yield. Specific breeding objectives are development of mungbean lines having resistance to disease (cercospora leaf spot, MYMV, powdery mildew) and insect pests (Bruchid, pod borer, bean fly and other regional pest), development of short duration variety, better plant type, resistance to shattering, synchronous maturity, high seed quality etc. Mungbean is a typical autogamous crop (self pollinated) and breeding methods are mostly similar applicable to other self pollinated crops. Major breeding procedures includes, introduction, pureline selection, selection followed by hybridization (pedigree, bulk and SSD method Back cross, multiple cross), induced mutation, interspecific hybridization up to some extent polyploidy.

GENETIC VARIABILITY AND VARIETAL IMPROVEMENT IN MUNGBEAN

Genetic variability is raw material for genetic improvement of any crop species. In mungbean wide range of variability of different economic important characters were thoroughly studied by several workers (Vimarni *et al.* 1983). Variability within species and between species of related *Vigna* genus has been utilized for development of high economic important trait specific varieties in India. The major collection of *Vigna radiata* is maintained at AVRDC, Taiwan, Philippines, USDA Georgia and IARI (Poehlman, 1991). AVRDC Taiwan is the prime centre at international level for maintaining of large scale form of mungbean genetic resources as base collection. At this centre, germplasm accession is catalogued for various morphological, agronomically and for other biochemical characters. At initial breeding programme in India several important varieties have been developed through selection from local materials or land races. Type-1, Shining mung-1, Khargone-1, Co-1, Co-2, Gujrat-1 and others were developed through selection. Type-44 was first mungbean variety developed by hybridization (Type-1 x Type 49). Currently more than hundred varieties have been developed in mungbean using the classical breeding techniques.

BREEDING FOR DISEASE AND INSECT PEST IN MUNGBEAN

Mungbean is attacked by several pathogens (fungal, bacteria, viruses and nematodes). The several economically important diseases reported for

mungbean are mungbean yellow mosaic virus (MYMV), cercospora leaf spot, powdery mildew and bacterial leaf spot. MYMV is considered to be the most devastating disease cause huge loss in terms of economic yield by affecting reduction in plant height, fresh shoot weight and seed weight up to 38.2 28.5, and 25.7%, respectively (Chand and Verma, 1983). Resistance source for MYMV have been found in Indian lines MB-57, MB-58 and Pant Mung-2. Resistance genes could be trapped from related species, wild species by interspecific hybridization. Wild species, *Vigna radiata* var. *Sublobata* (progenitor of mungbean) is a good source of resistance as it has been considerable variation in respect of MYMV resistance. Genetics of resistance is studied by several workers and now it is confirmed susceptibility is dominant over resistance. Tolerance to MYMV is generally governed by single recessive genes and resistance by two recessive genes in varietal crosses, whereas in interspecific crosses resistance is governed with pairs of genes with dominant and recessive epistasis (Singh and Sharma, 1983). Breeding methods for MYMV resistance includes, selection from landraces, intraspecific hybridization (most common), interspecific hybridization and mutation breeding. Cercospora leaf spot is one of the important diseases that cause serious losses to mungbean crop yield (23% yield) (Quebral and Cagampang, 1970). Resistance source for cercospora leaf spot have been explored from diverse sources and resistance lines (M-98, 98-cmg-003, C2/94-4-42, NM-1, NM-2, 98 cmg-018, BRM-188, CO-3, Basanti, PDM-11, BARI Mung-2 and VC3960-88) scored with disease score "1" were found highly resistant and it could be also used as potential donor for future breeding programme (Iqbal *et al.*, 2004). Powdery mildew caused by *Sphaerotheca phaseoli* and it causes heavy yield losses ranging from 20-40% particularly in cool dry months (Soria and Quebral, 1973). Resistance to powdery mildew is governed by single dominant gene (AVRDC, 1979) but there are several reports that showed it governed by additive gene action, recessive polygenes. Breeding for insect resistance in mungbean has been given least focused in past but currently some attention have been made in bruchid resistance. Bruchid beetles are the most devastating stored insect pest of grain legumes and cause significant loss to mungbean. Few sources of resistance have been identified in cultivated gene pool were identified, selected and well characterized. Resistance to bruchid is governed by single dominant gene in *Vigna radiata* var. *Sublobata* (Kitamura *et al.* 1988).

BREEDING FOR ABIOTIC STRESSES RESISTANCE IN MUNGBEAN (DROUGHT, WATER LOGGING, HEAT AND SALINITY)

Abiotic stress affect plant cellular metabolism and disrupt major enzymatic pathway involving in physiological and biochemical processes (Arora *et al.* 2002 and Srivalli *et al.* 2003). Abiotic stresses such as drought, water logging, high temperature and salinity causes a significant loss in yield and quality of mungbean. Drought stress is more prevalent in spring and summer mungbean. Drought especially at flowering period may lead to flower drop and cause a significant amount of loss. Genotypic variation for root length has been reported for mungbean and it could be exploited for developing drought tolerant mungbean variety. For avoiding the drought stresses in summer/spring mungbean, there is need to develop variety having short duration nature, determinate growth habit, high harvest index, reduced photoperiod sensitivity, fast initial growth habit and longer pods (Singh and Singh, 2011). Several water-logging tolerant lines have been identified at AVRDC, Taiwan, such lines are, V-1968, V-2984, V-3092, V3372 (Tickoo *et al.* 2006). Terminal heat stresses cause a direct impact on crop growth particularly at reproductive stages and cause a negative impact on flower retention, pollen viability, pod setting and vigour of pods. For heat stress resistance breeding, there is need to select mungbean genotypes which retain maximum number of flowers and maximum pods under adverse condition. Salinity stress cause significant amount of yield in mungbean. Salt stress affect seed germination, shoot growth, root growth, root length, biomass and seedling vigour. Salt tolerance is complex genetically and physiological phenomena and affected by soil, plant and environmental factors or by its inter-relationship. Sherawat *et al.* (2013) has screened the wild relatives of mungbean for salinity tolerance and found 80-100 % yield loss has taken place due to salt stress. Wild species, *Vigna luteola* (accession) and *Vigna trilobata* (accession) showed healthy response and less reduction in yield under salt stress depicted their greater resistance and these could be exploited in breeding programme for development of salt tolerant varieties.

INTERSPECIFIC HYBRIDIZATION OF MUNGBEAN WITH RELATED VIGNA SPP.

Generally intraspecific hybridization in practiced in mungbean breeding and interspecific hybridization will increase gene pool and broaden genetic base

(Singh, 1990). Several attempts have been made to cross mungbean (*Vigna radiata*) with blackgram (*Vigna mungo*), wild progenitor, *Vigna radiata* var., *sublobata*, ricebean *Vigna umbellata*) and *Vigna trilobata* in view of enhancing genepool for desirable characters. Blackgram posses several desirable economic important characters such as resistance to MYMB, cercospora leaf spot, synchronous maturity and other. Mungbean X Blackgram produces fertile F₁ when mungbean is used as female parent and blackgram as male. Few commercial varieties have already been released in India using this technology. Pant Mung-4 was developed from a cross of Type-44 x UPU-2, HUM-1 developed from cross of PHUM1 x Pant U-30 and IPM99-125 developed from Pant Mung-2 x AMP-36 are being in cultivation in large scale in India. Several genetic resources for desirable characters have registered at NBPGR, New Delhi, resulted from cross of mungbean x blackgram cross (BDYR-1 x DPU88-31) at Pantnagar. *Vigna radiata* var., *sublobata*, putative progenitor is easily crossable with mungbean using later as female parent. Putative progenitor has considerable variation for MYMV resistance and this could be a potential source for developing the cultivar of MYMV resistance. Interspecific cross between mungbean x ricebean could be possible by immunosuppressant, E-aminocaproic acid (EACA 100ppm), or by using *Vigna radiata* var *sublobata* as bridge species.

ENRICHMENT OF MICRONUTRIENTS AND PROTEIN IN MUNGBEAN THROUGH BIO-FORTIFICATION

Mungbean is rich source of nutrient and consider being healthy food. Sprouted seeds of mungbean is equivalent to fresh fruit in respect of nutrient content as it contains vitamins A, B, C, E and minerals such as iron, calcium and phosphorous. On fresh dry weight basis it contains 22-28% protein, 1.0-1.5% fat, 3.5-4.5% fibre, 4.5-5.5% ash and 60-65% carbohydrate. It is also a rich source of essential amino acid isoleucine, leucine, lysine, phenylalanine (Lambrides and Godwin, 2007). Bio-fortification is process of increasing available nutrient and bio-availability through plant breeding and biotechnology. Breeding for improved mineral content is quite complicated because the effects of individual loci are small and difficult to identify The wide genetic variability of mineral concentrations (e.g. 0.03-0.06 g Fe kg⁻¹, 0.02-0.04 g Zn kg⁻¹) has been observed in mungbean indicate possibilities to improve its micro-nutrient content through bio-fortification (Maldonado *et al.*

2003). Genotypes, like, IC103179 and 'Kopergaon' with high protein yield along with low content of trypsin inhibitor were screened from Indian germplasm and exploited in hybridization programme (Chattopadhyay, 2009). There is need of collaborative research on nutrient diversity (utilizing conventional and molecular breeding), nutrient digestibility, food processing properties, and bioavailability in order to achieve nutritional security of South East Asian countries.

INDUCED MUTATION FOR MUNGBEAN BREEDING

Mungbean is a self pollinated legume crop and it has limited variability for crop improvement. Induced mutation through physical and chemical mutagens may generate additional variability for its improvement in respect of economic important traits. The mutagenic agents used most frequently are Co60 gamma radiation, X-rays, neutron and chemical mutagens like EMS and DMSO. Irradiation dose of 30-40 KR was found to be very effective for production of desirable mutant. In mungbean desirable mutant have been exploited for character such as early maturity, synchronous maturity, more branches/plant, more pods/cluster, MYMV resistance, higher seed weight and higher protein content (Singh and Chaturvedi, 1981). In India, several mutant varieties have been released for specific characters such as CO-4, Pant Moong-2, MUM-2 and TARM-1. Mutant variety MUM-2 is a high yielding and it showed resistant to MYMV, cercospora leaf spot, leaf crinkle, bacterial blight and macrophomina blight (Gupta, 1996). Mungbean varieties, NIAB Mung19-19 and 121-25 mature earlier (65-70 days) than parental type.

CYTOGENETIC, GENOME RESEARCH AND DNA MARKER OF MUNGBEAN

Somatic chromosome no. of mungbean is $2n=2x=22$. A pachytene chromosome analysis revealed chromosome varied in length from 28.1-73.3 microm with two bivalent associated with nucleolus at pachytene (Krishnan and De, 1965). The nuclear chromosome varied in length and position of secondary constrictions at pachytene. Mungbean has long metacentric and sub-metacentric chromosomes and considered to be more primitive than blackgram (De and Krishnan, 1966). Cytological analysis has been analyzed in interspecific cross of *Vigna radiata*, *V. umbellata* and their interspecific F_1 were examined cytologically. Mungbean has small genome sizes estimated to be 0.60 pg/1C (579 Mbp) that is similar

to those of the other *Vigna* spp. Mungbean is considered one of the most recalcitrant crops in genomic research. Comparative genome mapping between mungbean and several other legumes including azuki bean, common bean, cowpea, soybean, lablab and *Medicago trunculata* revealed various levels of macrosynteny depending on species with the greatest upon common bean (Somta and Srinives, 2007). DNA markers are indispensable for genomic study in any species. Restriction fragment length polymorphism (RFLP) has been used to construct molecular genetics map for most of the major crop plants and it provide useful for selecting of valuable genes. Young *et al.* (1992) has constructed a saturated linkage map of RFLP of mungbean by help of AVRDC, Taiwan. Recently micro-satellite markers have been developed in mungbean and will add more value in molecular studies for economic important characters in future.

PROBLEM AND FUTURE PROSPECT IN MUNGBEAN BREEDING

Mungbean is being grown on marginal and sub marginal land and very least attention have been given to mungbean breeding in comparison of cereals. Yield has not been achieved up to genetic potential level of promising varieties and yields much fluctuating season to season, location to location due to susceptibility of the major disease, insect pest and other abiotic stressess. Traditional breeding method need to be augmented with innovative breeding methods such as marker assisted selection, tissue culture and biotechnology for enhancing the yield in changing climatic conditions. There is utmost important to develop a breeding programme involving, plant breeder, agronomist, physiologist, pathologist, entomologist, nutritional and biotechnologist for sustaining the yield potential and fulfilling the demand of evergrowing population of future generations.

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