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M SakilaAgricultural College & Research
Institute Eachangkottai,
Thanjavur, Tamil Nadu, India**M Pandiyan**Agricultural College & Research
Institute Eachangkottai,
Thanjavur, Tamil Nadu, India

Realization of facts and profiteering of black gram through different breeding methods

M Sakila and M Pandiyan

Abstract

Blackgram or Urdbean (*Vigna mungo* (L.) Hepper) is a highly self-pollinated crop with cleistogamy up to 42%. Urdbean is grown all over the South East Asia (Puneglov, 1968). In India it is mostly grown as a kharif crop. In the past, remarkable progress has been made towards the development of high yielding, stress resistant and input responsive varieties by utilizing the available germplasm. The impact of these varieties has been well realized in their crop productivity. The present review highlights the past, present and future importance of improving high yield in black gram through different breeding strategies *viz.*, selection, hybridization, mutation and other molecular breeding approaches. But alien gene transfer for several traits such as photo and thermo sensitive, erect plant types stand still. Heterotic studies in blackgram, the important genetic mechanism operates to bring superiority in F₁ hybrid than their parents (Isha Parveen *et al.*, 2013). Heterosis has been of immense economic value in agriculture and has important implications regarding the fitness and fecundity of individuals in natural populations. Considering blackgram (*Vigna mungo* L.), a pulse crop which is self-pollinated, little work has been done on heterosis (Shawn Kaeppler 2012). This genetic tool is the basic mechanism in developing blackgram cultivars with high yielding potentials. The increase in blackgram production volume comes mainly from the increase in blackgram cultivated area. A possible breakthrough for this production limitation is to exploit hybrid vigor of the F₁ for possible production of hybrid varieties. The magnitude of hybrid vigor is normally presented in terms of heterosis (superiority of the F₁ hybrid over its parental mean) and heterobeltiosis (superiority of the F₁ hybrid over its better parent (Soehend and Srinives 2005)). The results on heterosis so far in blackgram were encouraging and still there a scope to utilize this genetic phenomenon to develop new cultivars superior than existing. Hence this review illustrates the facts and proof for different research on black gram and the future prospects. (Isha Parveen *et al.* 2013).

Keywords: Blackgram, genetics, improvement, yield

Introduction

Blackgram (*Vigna mungo*) is an important short-duration pulse crop grown in many parts of India. Blackgram grain contains 24% protein, 60% carbohydrates, 1.3% fat and is the richest source of phosphoric acid among pulses (5-6% richer than others). It is used as a nutritive fodder specially for milch cattle. It is also used as green manuring crop. Being deep rooted crop, helps in binding soil particles and thus prevents soil erosion. It fixes atmospheric N (42 kg/ha/year) to the soil through symbiosis and improves fertility of soil.

India is the largest producer as well as consumer of black gram. Nearly 70% of world's blackgram production comes from India. It produces about 1.5 to 1.9 million tons of urad annually from about 3.5 million hectares of area, with an average productivity of 500kg per hectare. Blackgram accounts for about 13 % total pulses area and 10 % total pulses production in India. In India about 2-3 million tonnes of pulses are imported annually to meet the domestic consumption requirement. Thus, there is need to increase production and productivity of pulses in the country by producing high yielding and widely adopted varieties through various breeding methods.

The combination of dal-chawal (pulse-rice) or dal-roti (pulse-wheat bread) is an important ingredient in the average Indian diet. The biological value improves greatly, when wheat or rice is combined with black gram because of the complementary relationship of the essential amino acids such as arginine, leucine, lysine, isoleucine, valine and phenylalanine etc. In addition, being an important source of human food and animal feed, it also plays an important role in sustaining soil fertility by improving soil physical properties and fixing atmospheric nitrogen. Being a drought resistant crop, it is suitable for dry land farming and predominantly used as an intercrop with other crops.

Correspondence**M Sakila**Agricultural College & Research
Institute Eachangkottai,
Thanjavur, Tamil Nadu, India

Several breeding methods were employed to enhance the genetic base which includes the improvement of yield and resistance to biotic and abiotic stresses. Among the various methods the Diallel and the mutation breeding methods are important.

Areas for improvement in black gram ideotype

Black gram improvement has to be broadened in the following aspects viz., location specific, Urdbean Kharif (North India), rabi (South India), optimum season and duration with their specific ideotypes Optimum maturity (65-75 days), Determinate and bushy plant type, Upright plant growth habit, Optimum plant height (70-80 cm), High number of clusters/plant and pods/cluster, Sympodial bearing, Synchronous maturity, More number of seeds/pod (7-9), Sympodial branching, Tolerance to terminal heat stress, Longer pods with > 7 seeds/pod, Podding above plant canopy, Multi podding and

Bold seeds while Rice-fallow blackgram improvement with Prolific root system, Narrow leaf, Early seedling vigour, Photo-thermo-insensitivity, synchronous maturity and Terminal drought tolerance

Inventive ideotypes for biotic stresses and abiotic stresses

The following traits must be considered for constructing suitable ideotype for various stresses.

I. Ideotypes for biotic stresses

Architectural traits, such as small foliar size, high stem firmness, slow canopy closure, and a small leaf area index, are unfavourable to pathogen development (Andrivon *et al.*, 2013). Ideotypes defined by the pyramiding of multiple QTLs or genes for partial disease resistance and for favourable canopy architecture should be built and tested in integrated protection strategies (Hesham *et al.*; 2015) [23].

On the other hand, some people argue that there are useful and effective sources of resistance available for *Ascochyta* blight control on chickpea crops, but under environmental conditions (extended cool and wet periods) favorable to disease development and spread, the resistance often breaks down.

II. Ideotypes for abiotic stresses

Considering the intrusion of sea water and terminal drought near coastal districts, architecturing blackgram through conventional and molecular breeding is need of the hour following which the review are available Stoddard *et al.*, (2006) studied lower cell membrane injury, high seedling growth Osmotic regulation and high WUE drought tolerant cultivated and wild germplasm which is suitable for drought.. Erskine *et al.* (2011) illustrated early maturing, early growth vigor, rapid root growth for drought escaping germplasm. Charlson *et al.*, (2009) identified *G. max* QTLs identification for multiple traits suggested that several had pleiotropic or location-linked associations.

The review paper narrates the different type of breeding methods achieved for yield improvement in black gram.

Breeding methods in blackgram

Selection

Nearly, 40 % of the cultivars released so far were selections from landraces. Therefore, selection has been the predominant method which has been evidenced through the following studies.

Dahiya and Singh (1986) [15] has been suggested in some cases where seed yield was the main selection criterion. Van Oeveren (1993) [80] studied the Efficiency of Single Seed Descent and Early Selection in the Breeding of Self-fertilizing Crops. While pedigree and single pod descent (SPD) methods were found efficient in maintaining mean performance, the SPD and bulk population method was found better in maintaining variability ((Arya *et al.*, 1995) [9].

The procedure of single seed descent (SSD) can produce superior inbred lines in a more consistent, cheaper and faster way. Early line selection (ELS; without cross selection) is always better than ES. In some cases ELS can, when heritability is intermediate, give a breeder a somewhat higher chance than SSD on obtaining the best possible genotype. This will require additional costs.

Satyawan Arya *et al.* (2000) studied the efficiency of pedigree selection, bulk population (BP) and single pod descent (SPD) methods. The variation was higher in the progenies developed through bulk population (BP) and single pod descent (SPD) methods in all the crosses. Pedigree selection method was most efficient method as it gave the highest number of high yielding progenies (18.6%) followed by bulk (16%) and single pod descent (9.3%) methods.

Shobha Immadi *et al.*, (2005) studied the efficiency of selection methods in irradiated single vs. multiple cross progenies for transgressive segregants in blackgram. Single pod descent method proved to be superior compared to random bulk and IPS methods.

Praveen kataraki *et al.* (2005) compared the breeding methods for their relative efficiency in terms of maintaining higher variability and also in obtaining transgressive segregants for yield and its components. The SPD method proved to be superior to bulk and IPS methods in exhibiting higher variability and also in producing higher frequency of transgressive segregants for yield and its components, whereas the IPS method produced lower number of transgressive segregants.

Shobha immadi *et al.*, (2005) [24] studied phenotypic correlation of seed yield and its component traits in four selected irradiated F₃M₃ population, two three way and one double cross populations of blackgram advanced through bulk, individual plant selection (IPS) and single pod descent (SPD) method. Among the three methods of selection, single pod descent method showed a stronger magnitude as compared to bulk and IPS methods.

Lal and Waldia (1980) studied additive genetic variance through diallel mating for all the characters, except grain yield in which dominance variance was found to be high. Parents 'Pant U30', 'UPU-2' and 'H 76-12' were found to be good general combiners for yield and its components. The parents with high mean values for all traits except yield may be chosen for effective improvement. The best specific combinations for yield and its components were 'H 76-12 × UPU-2' and 'H 76-12 × G8'. High × high g.c.a. parents resulted crosses with high s.c.a. effects. The crosses 'H 70-3 × H 76-12', 'Pant U 26 × Pant U 30' and 'H 76-12 × G8' may provide potential breeding material.

Geethanjali (2015) concluded that direct selection for yield improvement through traits such as number of branches per plant, number of pods per plant, number of seeds per pod, days to 50% flowering and 100 seed weight would be rewarding.

Comparison of different selection methods

Authors	Year	Methods used	Best method observed
Van Oeveren	1993	Single Seed Descent and Early Selection.	Single pod descent method (SPD)
Dahiya and Singh	1986	Single seed descent, selective intermating and mass selection.	Selective intermating
Haddad and Muehlbauer	1980	Random bulk population and single-seed-descent methods.	Single pod descent method (SPD)
Dahiya and Singh	1986	Pedigree and single pod descent (SPD) method and bulk population method.	Pedigree and single pod descent (SPD)
Praveen kataraki <i>et al.</i>	2005	Single pod descent (SPD), bulk and individual plant selection (IPS) methods	Single pod descent (SPD),
Immadi and Shobhakajjidoni	2005	Individual plant selection (IPS) and single pod descent method (SPD).	Single pod descent method (SPD)
Shobha immadi <i>et al.</i> ,	2005	Bulk, individual plant selection (IPS) and single pod descent (SPD) method	Single pod descent method (SPD)
Satyawan Arya <i>et al.</i> ,	2000	Pedigree selection, bulk population (BP) and single pod descent (SPD) methods	Pedigree selection method
Bhosale and Hallale	2011	Gamma rays doses at 10, 20, 30, 40, and 50KR.	30KR

Heterosis Breeding

In self-pollinated plant species, it is rather easy to produce hybrid seed if male sterile lines are available and can be used as the female parent (Soehend and Srinives 2005) [64]. With the success in the use of hybrid rice varieties which are also a self pollinates species, the possibility of using hybrid blackgram should be explored (Isha Parveen *et al.*, 2013 [26]. Generally, legume pollen is heavier than that of cereals and thus could not be effectively transferred by wind (Isha Parveen *et al.*, 2013) [26]. These are interesting topics for blackgram breeders to investigate in the future. However, the significance of heterosis and heterobeltiosis in blackgram has rarely been studied. Keeping this in view, the literatures/complete review on heterosis in blackgram, which could be useful in understanding the importance of heterosis in blackgram. Sivan pillai (1980) [63], concluded that genetic improvement of the traits (pod number, seed yield and methionine content) can be achieved more effectively through combination breeding involving genetically diverse and high combining parents.

Dasgupta and Das (1987) conducted studies on an 8 × 8 half-diallel analysis of blackgram for two locations revealed that both additive and nonadditive genetic variances were important for seed yield and its two major components, i.e., pods and seeds/plant due to increased heterotic response of these two F1 (Mash 1-1 × lu 272 and Mash 1-1 × lu 241) which may principally due to accumulation of favourable and fixable additive genes in nature. Sood and Gartan (1991) analysed Combining ability on a 9 × 9 diallel cross in black gram and revealed that high per se performance of parents does not necessarily reflect their good general combining ability. The hybrids UH 45 × UH 27, HPU 392 × UH 22, UH 27 × Pant U 19, HPU 384 × UH 45, and HPU 392 × UH 2 were identified as potential cross combinations on the basis of heterosis and specific combining ability.

Shanmugasundaram *et al.* (1994) done combining ability analysis using 20 F₁S and 20 F₂ families obtained from a 5 X 5 diallel mating design for yield and its components to which. *gcawere* significant and *scaeffects* were not significant for both the generations. Majority of the observed variance was attributed to additive gene effects.

Abdul *t.al.* (2012) [2] evaluated blackgram germplasm comprising 484 accessions for qualitative and quantitative traits. The germplasm under investigation displayed a wide range of diversity for most of the traits along with some accessions with unique characters which could help to identify landraces with suitable traits to be used in

hybridization programme for breeding to broaden genetic base.

Abdul ghafoor and Zahoor Ahmad (2005) [33] suggested that the genetic base of cultivated black gram should be broadened by involving diverse parents in the breeding programme. Expansion of the genetic base for black gram breeding might be accomplished by systematic use of germplasm that differs in protein profiles and has better quantitative traits (Abdul ghafoor and Zahoor ahmad (2005) [33]. Radheshyam Patidar (2005) [49], studied the combining ability of newly developed genotypes for seed yield and its contributing traits in blackgram and found the crosses IU 8-6 × Pant U 30, IU 8-6 × RBU 38 and JU 3 × RBU 38 were good specific combiner for seed yield and some of its attributing characters in blackgram. Radheshyam Patidar (2005) [49] concluded that high heterotic crosses for seed yield per plant were IU 8-6 × PDU 1, IU 8-6 × JU 3 and PDU 1 × TPU 4 in winter season and OBG 27 × Pant U 30, JU 3 × Pant U 30 and PDU 1 × JU 3 in summer season. The heterosis in seed yield was mainly associated with heterosis in yield components namely. plant height and clusters per plant.

Singh and Singh (2006) [62], studied heritability (narrow sense) and genetic advance in percentage of mean for ten characters based on genetic components derived. The highest heritability ranged from 30 to 52% indicated that there is considerable involvement of non-additive gene action. Therefore, biparental mating and thereafter progeny selection may be used full to achieve anticipated genetic advance for desired segregants.

Karthikeyan *et al.*, (2007) [5] conducted combining ability analysis of 28 F₁'s of a diallel cross (excluding reciprocals) and their parents showed both additive and non-additive components of variation for the inheritance of grain yield/plant and 100 seed weight. Six cross combinations *viz.*, 2 KU 53/TU 94-2, 99 V 48/KU 300, 99 V 48/P 165, KU 300/LBG 645, PV 94-2/LBG 623 and TU 94-2/P 165 recorded high specific combining ability and they could be exploited for further breeding programmes.

Bhagirath ram *et al.* (2009) analyzed a diallel set of 10 parents and their 45 f₁ and 45 f₂ hybrids. As the environmental effect on the expression of the character was very high, different crosses emerged in different environments for seed yield/plant. Thus, the crosses (VBN 3 × UH 84-14 and RBU 38 × UH 84-14 in E1 and NUL 7 × UH 84-14, IU 8-6 × UH 84-14 and IU 8-6 × VBN 4 in E3) can be included in the breeding programme for improvement in yield in specific environment.

Bhagirath Ram (2009) ^[12] found that additive and non-additive gene effects were to be important in the expression of seed yield and quality traits, *i.e.*, protein content, water absorption and *dal* recovery when studies conducted at three locations through a 10×10 diallel cross of blackgram. On the basis of *per se* performance and *gca* effects, the parents GU 1 and RBU 38 emerged as good general combiners for seed yield per plant, protein content, water (absorption g/g seeds) and *dal* recovery.

Supriyochakraborty *et al.* (2010) carried out Line x tester analysis in black gram [*Vigna mungo* (L.) Hepper] to estimate the *gca* (general combining ability) effects of parents (3 lines and 3 testers) and the *sca* (specific combining ability) effects of 9 crosses for seed yield and other eleven quantitative traits. Two crosses namely 'PDB 88-31'/DPU 915' and 'PLU 277'/KAU7' had high *per se* performance along with positive significant *sca* effect for seed yield/plant. Due to presence of high magnitude of non-additive gene action, heterosis breeding could also be attempted to develop low cost hybrid variety using genetic male sterility system in black gram.

Jadhav Sunil Mohan (2013) ^[27], reported that the crosses (T-9 x MASH-114, GU-1 x MASH-114, GU-1 x NPU-1025, UTTRA x MASH-114 and MASH-11 x NPU-1011) possess high *per se* performance also showing high heterotic effect as well as high *sca* effects. These crosses should be selected and used for further blackgram breeding programme.

Isha Parveen and M. Reddi Sekhar (2013) ^[26] observed that the characters (number of seeds per pod, number of pods per plant and harvest index *via* plant height and 100 seed weight) may be given due emphasis in formulating selection indices in order to augment the identified superior genotypes in urdbean. Bhagirath ram *et al.* (2013) ^[12] disclosed the environmental effect on the expression of the character was very high, different crosses emerged in different environments for seed yield/plant. Thus, the crosses (VBN 3 × UH 84-14 and RBU 38 × UH 84-14 in E1 and NUL 7 × UH 84-14, IU 8-6 × UH 84-14 and IU 8-6 × VBN 4 in E3) can be included in the breeding programme for improvement in yield in specific environment.

Isha Parveen *et al.* (2013) ^[26] concluded that heterosis so far in blackgram were encouraging and still there a scope to utilize this genetic phenomenon to develop new cultivars superior than existing.

Kachave *et al.* (2015) ^[28] selected seven genetically diverse varieties of blackgram namely TAU-1, AKU-9904, NUL-7, LBG-402, BDU-1, Pant U-31 and Mesh-1008 and made diallel cross to study combining ability in 21 F₁s and their 7 parents. The crosses, LBG-402 x BDU-1, BDU-1 x Pant-U 31, AKU-9904 x Pant-U 31 and AKU-9904 x NUL-7 evinced high SCA effects for most of the traits, those can be further exploited for isolating superior genotypes.

Panigrahi *et al.*, (2015) ^[39] studied for ten characters to determine the nature of gene action in parents and hybrid population using a diallel set of 8 parents and their 28 F₁. Among crosses the superior hybrids were LBG-17 × Keonjhar Local, OBG-31 × Keonjhar Local, PU-35 × OBG-31, PU-30 × LBG-17, B-3-8-8 × OBG-17, B-3-8-8 × PU-30, B-3-8-8 × OBG-31, B-3-8-8 × Keonjhar Local, TU-94-2 × LBG-17, OBG-17 × LBG-17

Prasad and Murugan (2015) ^[43] conducted hybridization in Line × Tester mating design was with 11 MYMV susceptible lines and three resistant testers in blackgram (*Vigna mungo* (L.) Hepper) to understand the nature of gene action, combining ability of the parents (*gca*) and to assess the

potential for the exploitation of heterosis (*sca*) in hybrids. The crosses involving the parents, LBG 645× PU 31 and ADT 3× PU 31 recorded significant *gca* and non-significant *sca* effect for most of the characters inferring that these crosses would produce superior recombinants for seed yield.

Nakul yaduvanshi (2016) ^[34] estimated the general and specific combining ability for major yield traits. The estimates of *gca* effects revealed that the one line TPU-4 recorded positive and significant *gca* for seed yield per plant. The estimates of *sca* effects revealed that, out of 12, 5 cross combinations exhibited significant and positive *sca* effects for seed yield per plant. The cross with highest *sca* effects for seed yield per plant was JU-2×AKU-96-3.

Balouria (2016) ^[10] suggested that breeding procedures like biparental matings and or diallel selective matings followed by pedigree method or reciprocal recurrent selections can be utilized for breaking undesirable linkages followed by the isolation of superior transgressive segregants from KU-553 x Him Mash-1, DU-1 x Palampur-93 and KUG-216 x Palampur-93.

Thamodharan *et al.* (2016) ^[75] concluded that exploitation of hybrid vigour may be achievable in the crosses (MDU 1/ VBN (Bg) 6, MDU 1/ PU 31, MDU 1/ Mash-114 and MDU 1/ Uttara) which might be helpful in the improvement of this crop. Anbu Selvam and Elangaimannan, (2010) ^[5] studied combining ability, nature of gene action and potential for the exploitation of heterosis in black gram in a 8 x 8 diallel analysis in black gram using nine quantitative characters and adjudged that the two crosses ADT 3/ LBG 645 and 2 KU 53/ LBG 645 as superior for recombination breeding based on *sca* effects. Vijay Kumar *et al.* (2016) ^[38] assessed heterosis and identified the lines *viz.*, IC 587753 and IC 519805 as good general combiners for seed yield and can serve as parental lines in crop improvement programs.

Mutation Breeding

Mutation breeding has a greater role in pulses where where large part of natural variability has been eliminated in the process of adaptation to environmental stresses. In recent years, lot of works has been undertaken on induced mutagenesis through physical and chemical mutagens. Selecting a mutagen and its optimum dose for a genotype is an important step in mutation breeding. (Sonu Goyal and Samiullah Khan, 2010) ^[79].

The earlier report of Appa Rao and Jana (1976) ^[8] revealed four new leaf mutants, crinkled-leaf, waxy-leaf, narrow-leaf and unifoliate in black gram, following treatments with X-rays and/or ethyl methanesulfonate (EMS). The crinkled-leaf and waxy-leaf mutants had normal fertility and vitality, whereas the narrow-leaf mutant was partially sterile and the unifoliate (an extreme dwarf) completely sterile. All the mutants except unifoliate behaved as monogenic recessive to the normal.

Arulbalachandran and Mullainathan (2009) observed chlorophyll mutants in the different dose of gamma rays which were chlorine albino, xantha and viridis. They concluded that EMS provided more number of chlorophyll and morphological mutants followed by gamma rays.

Arulbalachandran and Mullainathan (2009) made an investigation to improve the quantity and quality (methionine) of protein of black gram (*Vigna mungo* L.) through the mutation using physical gamma rays and chemical EMS in M₁ and M_{2,3,4} generation. The results showed some level of improvement in protein content in 0.1% EMS and 60 kR of gamma rays.

Arulbalachandran *et al.* (2009) made an attempt to improve some of the quantitative traits of black gram by using gamma ray irradiation. Anbu Selvam *et al.*, (2010) [5] studied the extent of variability existed in the rice fallow blackgram varieties namely VBN3 and ADT 3 after induction of mutation through chemical mutagens namely EMS and colchicine. The yield attributing traits like number of branches per plant, number of pods per cluster, 100 seed weight and seed yield per plant recorded high heritability coupled with high genetic advance as per cent of mean in M2 generation.

Bhosale and Hallale (2011) [13] studied Gamma Radiation Induced Mutations in Black gram (*Vigna mungo* (L.) Hepper). Seeds of black gram variety TPU-4 was exposed to gamma rays doses at 10, 20, 30, 40, and 50KR. Higher chlorophyll mutation rate was observed with gamma rays dose of 30KR. Gandhi *et al.* (2012) [52] evaluated morphological and biochemical features of blackgram (*Vigna mungo* (L.) Hepper) in M₅ generation. The various dose/concentration of gamma rays (20, 40, 60 kr) and EMS (10, 15, 20 mm) were treated to black gram seed materials. All the mutagenic treatments were effective in inducing genetic variability in black gram.

Sharma *et al.* (2005) [59] used the urdbearcultivars PDU-1 and T-9 were mutagenised with gamma-rays and EMS to determine their mutagen sensitivity, LD₅₀, mutagenic effectiveness and efficiency. The average effectiveness and efficiency (pooled overdoses and genotypes) of EMS was 2.0–2.5 and 1.5–2.0 times higher than the gamma-rays, respectively. The lower doses of mutagens were more effective and efficient than the higher doses.

Mutation for quantitative traits

The role of mutation breeding in increasing the genetic variability for quantitative traits in various crop plants have been proved beyond doubt. An increase in mean values for pods as well as yield per plant in M2 and M3 generations was observed in the variety T-9 (Kundu and Singh, 1982) [32]. The highest level of variability was observed in pod length after gamma irradiation and in number of pods per plant after EMS treatment in the urdbearcultivars ADT-3 and Vamban 1 (Vanniarajan *et al.*, 1989) [81]. Pods per plant exhibited high variability in M₃ and M₄ generations of urdbearcultivars Vamban 1 and ADT 3 treated with 20-90 kR gamma rays (Hepziba and Subramanian, 1994) [22]. Parveen (2006) [40] have been reported the improvement in number of branches and pods due to the effect of mutagens in various pulses.

Mutants used in hybridization programme

The large seed mutants, UM 196 and UM 201 were used in hybridization with the elite cultivar T-9 for developing high yielding varieties TAU 1, TAU 2 and TPU 4 (Pawar and Manjaya, 1996) [41]. So far, seven varieties have been developed through induced mutation and released for cultivation in India. Four of these varieties are the derivatives of mutants used in cross breeding. Punniyamorthy (2007) [48] Mutation breeding has made significant contribution in increasing the production of urdbearcultivars in India. The variety TAU 1, developed at Bhabha Atomic Research Centre (BARC), Mumbai has become the most popular variety in Maharashtra occupying an area over 95% of the total area under urdbearcultivars cultivation in Maharashtra.

Future prospects of mutation breeding

The future mutation breeding programmes should be aimed at

improving the root characters, nodulation in legumes, host pathogen interactions, photo-insensitivity and apomixis in crop plants. The future mutation breeding programmes should be aimed at improving the root characters, nodulation in legumes, host pathogen interactions and photo-insensitivity.

Inter-specific hybridization

Wide hybridization is an important tool to transfer desirable traits from wild or cultivated related species into cultivated ones. However, the transfer of specific genes is frequently associated with transfer of large alien chromosome segments having undesirable traits. Introgression of unexplored genes from the wild relatives could be rewarding for broadening the genetic base of various grain legumes including black gram especially for improving yield-enhancing traits and resistance to diseases. However, the distantly related wild species possess several undesirable traits, and success of desirable introgression is diluted significantly as a result of linkage drag and partial sterility. In this situation, extensive back cross-breeding is warranted that takes a heavy toll in terms of resources and time; hence, breeders are reluctant to use distantly related wild species and rather look for closely related species that possess minimum undesirable traits. (Inderjit Singh *et al.* 2013) [25] Fortunately, ricebean (*Vigna umbellata*), a cultivated *Vigna* species, is a closely related species to black gram. Both the species, black gram and ricebean, are diploid and having same number of somatic chromosomes. (i.e. 2n = 22). Ricebean is not a major cultivated legume; however, it is locally important in parts for South and South-East Asia. It has high test weight and high number of pods that leads to high productivity. Besides, it possesses high level of resistance to MYMV CLS and BLS. It is also a source of bruchid resistance (Tomooka *et al.* 2000) [76]. So far, limited efforts have been made to introgress desirable traits from *V. umbellata* into *Vigna mungo*

Resistance Breeding

Sen and Ghosh (1960) [56] made hybridization between three varieties of the species *Phaseolus Aureus* and a variety of *Phaseolus mungo*, although the seeds obtained were small and shrunken and seedlings of the hybrid progeny weak and semi-sterile. BC₁ plants were more vigorous, but also showed 50-70% pollen sterility.

Ahn and Chang soon (1976) [4] made crosses with three lines of mung bean (*V. radiata*) and two lines each of adzuki bean (*V. angularis*), black gram (*V. mungo*) and rice bean (*V. umbellata*) were made in order to determine the barriers to hybridization between species, and to assess the possibility of overcoming these barriers.

Muhammad bashir *et al.* (2005) [33] evaluated genetic resistance in mungbean and blackgram (mash), 32 accessions (16 each of mungbean and blackgram) and found only one genotype (VH- 9440039-3) was found highly resistant. Evaluated black gram genotypes for resistance to powdery mildew caused by *Erysiphe polygoni* and observed the three genotypes viz., LBG-17, LBG-685 and LBG-685×VT (F2-F3) were found to be resistant.

Guru (2014) [20] screened 64 blackgram [*Vigna mungo* (L.) Hepper] genotypes against powdery mildew during late kharif-2014 season under natural epiphytotic condition and concluded that 15 showed moderate resistance, remaining all genotypes showed moderate resistance to moderately susceptible reaction to the powdery mildew disease.

Bruchid Resistance

Bruchids can cause serious damage to urdbean, mungbean and several other leguminous crops and the attempts made in bruchid resistance development.

Duraimurugan Ponnusamy *et al.* (2014) conducted 'no choice' test seemed to be most reliable and potentially useful for screening of bruchid resistance in greengram and blackgram. Souframanien *et al.* (2010) ^[67] generated Recombinant Inbred Lines by crossing *V. mungo var. mungo* (cv. TU 94-2 bruchid susceptible) and *V. mungo var. silvestris* (bruchid resistant). Selection from the cross has led to the development of new blackgram genotypes TU 26, TU 40, TU 72 with resistance to bruchids.

YMV Resistance

YMV causes major yield losses and the source for the resistance YMV available in wild species and the several attempts were studied in the introgression of resistance genes to cultivated varieties and among interspecific crosses.

Pandiyan *et al.* (2010) ^[38] observed the cross *V. umbellata x V. radiata* showed better performance for the characters viz., number of branches and number of clusters in reciprocal direction. In advanced generation of *Vigna radiata x Vigna umbellata* cross combination has expressed virus resistance for nine seasons. The same line was tested by agro inoculation for confirmation of resistance and was resulted found effective resistance. This line can be used MYMV donar.

Sanjeev Gupta *et al.*, (2013) ^[25] studied the inheritance of MYMIV resistance gene in blackgram using F₁, F₂ and F_{2:3} derived from cross DPU 88-31(resistant) × AKU 9904 (susceptible). The validation of the CEDG 180 marker in nine resistant and seven susceptible genotypes has suggested its use in marker assisted breeding for developing MYMIV resistant genotypes in blackgram.

Panigrahi *et al.*, (2015) ^[39] conducted studies in blackgram using the molecular marker and F₂ population derived from the cross Keonjhar Local (susceptible) × OBG-31(resistant). Amplification of CYR1 marker from the genomic DNA of phenotypic resistant individuals from segregating F₂ populations and F₃ families revealed a tight linkage between this marker with the YMV resistance Subedi *et al.*, (2016) ^[69] screened the blackgram genotypes for resistance against Mungbean Yellow Mosaic Disease and concluded that the genotypes BLG0035-1, BLG 0003-2-1, BLG 0068-1, BLG 0092-2 & BLG 0069-1 of black gram produced good yield and showed resistance to MYMV.

Shamin and Pandey (2016) ^[45] study helpful for the resistant lines of YMV cultivation in North India.

Suguna *et al.* (2017) ^[70] investigated the inheritance of YMV in 12 hybrids. Among the hybrids, VBN 4 × VBN 2, VBN 2 × VBN 4 and VBN 2 × LBG 17 showed complete resistance against YMV, hence the crosses were recommended for further breeding programme to identify high yielding YMV resistant lines.

Molecular Breeding

For the development of Yellow Mosaic Virus resistance in blackgram the molecular breeding plays an important role.

Pal *et al.*, (1991) studied the inheritance of resistance to Yellow Mosaic Virus (YMV) in crosses of mungbean, blackgram and their interspecific crosses with *Vigna sub-lobata*. Resistance to YMV was recessive in the three *Vigna* species. The segregation ratios in F₂ and back crosses indicated that the resistance was digenic recessive in the crosses of mungbean and in interspecific crosses of mungbean with

blackgram and *Vigna sublobata* but YMV resistance was monogenic recessive in blackgram crosses.

The Marker Assisted Selection would be more efficient provided there is tight linkage between the marker and the trait of interest and assuming selection for the marker is more convenient (faster, cheaper, reproducible, early expression). Selection based on the marker will be able to penetrate plant breeding of all grain legumes in the future. This approach would be of particular interest in the selection for disease resistance (disease diagnosis, pathogen identification, and screening methods), a basic prerequisite for improving and stabilizing the yield of grain legumes. Abdul ghafoor *et al.*, (2005) evaluated 105 genotypes of blackgram from diverse origin for agronomic traits for 2 years and seed proteins were analyzed using Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis (SDS-PAGE) through vertical slab type unit and concluded that expansion of genetic base for blackgram breeding might be accomplished by systematic use of germplasm that differ from common banding pattern and known to be associated with variation in quantitative traits.

Chaitieng (2006) ^[14], suggested that the azuki bean SSR markers can be widely used for Asian *Vigna* species and the black gram genetic linkage map will assist in improvement of this crop. Souframanien and Gopalakrishna (2006) ^[68] generated a recombinant inbred line (RIL) mapping population (F₈) by crossing *Vigna mungo* (cv. TU 94-2) with *Vigna mungo var. silvestris* and screened for mungbean yellow mosaic virus (MYMV) resistance. The ISSR811₁₃₅₇ marker was validated using diverse blackgram genotypes differing in their MYMV reaction. The marker will be useful for the development of MYMV-resistant genotypes in blackgram.

Souframanien and Gopalakrishna (2006) ^[68] Screened for the SCAR marker in the RIL population distinguished the MYMV resistant and susceptible plants, agreeing well with the phenotypic data. The ISSR811 marker was validated using diverse blackgram genotypes differing in their MYMV reaction. The marker will be useful for the development of MYMV-resistant genotypes in blackgram.

Tuba Anjum *et al.*, (2010) ^[77] selected the parents for MYMIV mapping population are DPU 88-31 as resistant source and AKU 9904 as susceptible one. For establishment of powdery mildew mapping population RBU 38 was used as resistant and DPU 88-31 as the susceptible one. Parental polymorphism was assessed using 363 SSR and 24 RGH markers. Efforts are being made to identify the markers tightly linked to the genes responsible for resistance which will be useful for marker assisted breeding for developing MYMIV and powdery mildew resistant cultivars in black gram.

Soumitra Maiti *et al.* (2010) ^[66] demonstrated that the two MYMIV-resistance marker loci, YR4 and CYR1, were identified and of these two CYR1 is completely linked with MYMIV-resistant germplasms and co-segregating with MYMIV-resistant F₂, F₃ progenies of urdbean. This method of genotyping would save time and labour during the introgression of MYMIV-resistance through molecular breeding.

Soumitra Maiti (2010) ^[66] studied that genotyping with markers together in a multiplex-PCR-reaction would save time and labour during the introgression of MYMIV-resistance through molecular breeding, as methods of phenotyping against begomoviruses are tedious, labour and time intensive.

Priya Srivastava *et al.* (2011) ^[45] investigated the genetic diversity and relationships among 8 black gram (*Vigna mungo*) varieties using random amplified polymorphic deoxyribonucleic acid (RAPD) markers. The similarity coefficient was maximum between PLU-289 and PLU-456 (0.76) indicated the less divergence between them. Lower similarity was observed between LBG-20 and PLU-289 (0.4337) indicating more divergence.

Abdul ghafoor *et al.* (2012) ^[2] studied thirty seven pure-lines of blackgram using Randomly Amplified Polymorphic DNA (RAPD) markers to investigate diversity and that only a portion of genetic diversity has been exploited for blackgram improvement that should broaden involving diverse parents.

Kumari Basamma *et al.* (2014) ^[31] suggested that the MYMV resistance in blackgram is governed by a single dominant gene. Out of 610 SSR and RGA markers screened 24 were found to be polymorphic between two parents (agronomically superior parent TAU-1 and the resistant parent BDU-4). Based on phenotyping in F₂ and F₃ generations nine high yielding disease resistant lines have been identified. Nirmala sehwat *et al.*, (2014) ^[36] concluded that the hybrids developed by interspecific hybridization of ricebean and urdbean, exhibited a high level of resistance against YMD similar to the donor parents. The morphological characterization and the SSR-PCR analysis efficiently proved the genetic purity of the hybrids

Peeta Gopi *et al.* (2016) ^[42] concluded that the genotypes LBG-17, LBG-402, LBG- 645, LBG 685, are highly susceptible to YMV but agronomical and quality wise were superior and hence improvement of these varieties for YMV resistance is undertaken by developing DNA markers for YMV resistance, resistance for screening molecular aided selection in blackgram improvement.

Vishalakshi *et al.* (2017) concluded that PU31 as a useful variety for the development of markers linked to MYMV, UCLV, wilt and powdery mildew resistance by marker-assisted back cross breeding and facilitates the production of crosses with multiple disease resistance.

Variability in black gram traits

Sufficient genetic variability among the genotypes for all the traits under study. Seed yield per plant and seeds per plant showed heritability along with high genetic advance. Hence, these characters were less influenced by environments and possess high genetic variability. Seeds per plant, pods per plant, biological yield per plant, plant height and 100 seed weight had highly significant and positive correlation with seed yield and also had positive association among themselves. Hence selection of these characters Reena Mehra *et al.*

The variability available in blackgram is limited and available for few characters are concise and the authors who studied the variability are Natarajan (1997) ^[35], concluded that high heritability coupled with genetic advance was also observed for these characters Clusters per plant and pods per plant were highly correlated with seed yield per plant The same two characters also showed high direct effects on seed yield per plant. Kanimozhi *et al.*, (2009) ^[29] studied the genetic diversity using twelve ISSR primers and suggested that suggests that the research institutes have to enlarge the genetic base for variety development genetic diversity is low among the varieties released from the respective institute. According to Vijay Kumar *et al.*, (2015) ^[82] the highest heritability and genetic advance were recorded for days to 50% flowering and clusters per plant respectively. High

genetic advance as percent of mean coupled with moderate to high heritability was observed for number of clusters per plant, pods per plant, seeds per plant, pod weight, seed yield per plant and fodder biomass.

According to Priyanka *et al.* (2016) ^[46] Except for days to maturity a significant variation was noted for all the traits. The genotypes were highly variable for cluster plant-1, pods plant-1, seeds pod-1 and seed yield plant-1. In general phenotypic coefficient of variability was greater than their corresponding genotypic coefficient of variability. Broad-sense heritability was higher for all the traits except for days to 50 per cent flowering and branches plant-1. High heritability coupled with high GAM was observed for the characters pods cluster-1, pod length, test weight, seeds pod-1 and seed yield plant-1 indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of grain yield.

High heritability along with high Genetic advance as % mean was observed by Duddukur Rajasekhar *et al.*, (2017) ^[17] for harvest index and seed yield per plant represents simple selection is effective to improve these characters. Sunayana *et al.*, (2017) ^[71] noticed that highest GCV and PCV were observed various characters. Highest genetic advance as per cent of mean was recorded for necrosis, membrane stability index, plant height, number of branches per plant, biomass, total pod weight per plant, total chlorophyll content, number of pods per plant, seed dry weight per plant, harvest index and canopy temperature difference. High heritability was recorded for photochemical efficiency followed by days to maturity, membrane stability index, plant height, seed dry weight per plant, total chlorophyll content, total pod weight per plant, biomass, number of seeds per pod, days to first flowering, 100 seed weight, days to first pod, flower retention, number of branches per plant. Hence Estimates of correlations revealed that seed yield had positive and significant correlation with flower retention, number of pods per plant, number of seeds per pod, biomass, pod weight per plant, seed weight per plant, harvest index, canopy temperature difference, photochemical efficiency, membrane stability index, total chlorophyll.

Vinod Kumar Reddy *et al.*, (2017) ^[84] reported maximum genotypic and phenotypic variance was recorded for biological yield/plant, plant height and harvest index.

From the YMV resistance studies, Sushmitharaj *et al.*, (2018) ^[73] were analysed twenty five genotypes showed resistant (R) reaction. A perusal of genetic parameters revealed that GCV, PCV, heritability and Genetic Advance as per cent of Mean (GAM) were high for the traits *viz.*, number of clusters per plant, number of pods per plant, hundred seed weight and single plant yield.. Hence, simultaneous selection for the above traits would be more rewarding to bring improvement in black gram.

Inheritance in black gram.

Singh (1980) studied the inheritance of resistance to mungbean yellow mosaic virus (MYMV) in blackgram (*Vigna mungo* (L.) Hepper). The highly resistant donors Pant U-84 and UPU-2 and a highly susceptible line, UL-2, their F₁'s, F₂'s and backcrosses were grown with spreader located every 5 to 6 rows. The resistance was found to be digenic and recessive in all the crosses and free from cytoplasmic effect.

Transgressive segregants in black gram

Dasgupta and Das (1987), conducted studies on an 8 × 8 half-diallel analysis of blackgram for two locations revealed that both additive and nonadditive genetic variances were

important for seed yield and its two major components, i.e., pods and seeds/plant. Increased heterotic response of these two F_1 (Mash 1-1 \times lu 272 and Mash 1-1 \times lu 241) may principally due to accumulation of favourable additive genes which are fixable in nature.

Constraints

The major constraints in achieving higher yield of this crop are lack of genetic variability, poor harvest index, suitable varieties and genotypes with adaptation to local condition.

Yield is considered as an end product of a set of plant processes which are related to each other. It is very complex trait which controlled by poly genes and interlinked with other yield components, hence it is very difficult often to improve yield directly. It can be achieved by improving closely related traits.

The systematic collection of black gram has displayed inadequate variability for biotic and abiotic genes. It is possible that genes for high productivity could have been lost due to overriding role of natural selection and the genetic base of the present day collection remains poor (Delannay *et al.*, 1983) due to lac of variability owing to its autogamous nature.

The creation of variability is difficult through hybridization due to its high self-pollination and flower droop (Deepalakshmi and Anandakumar, 2004). Besides the major constraints in achieving higher yield of blackgram is absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease (Souframanien and Gopalakrishnan, 2004). In order to improve yield and other polygenetic characters, mutation breeding can be effectively utilized (Deepalakshmi and Anandakumar, 2004).

Therefore genetic variability is the basic requirement for making progress in crop breeding in order to improve yield and other polygenetic characters, mutation breeding can be effectively utilized (Deepalakshmi and Anandakumar, 2004). Therefore, genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004).

In India black gram is grown both in winter and summer as monocrop and inter crop, respectively. That is why no single plant type is appropriate for all production system. So the variability among the existing germplasm or the accessions is the primary need to develop appropriate plant type for specific production system.

Breeding for high yielding black gram varieties should be conducted across the constraints such as narrow genetic base, growth habit, quality, pest and disease resistance.

Future Prospects

The response of zinc (Zn) deficiency on reproductive yield and recovery through foliar application of Zn was determined in black gram evidenced through many literatures as the specific variety and the gene for pollen producing capacity, pollen viability, stigma-receptivity and pollen-stigma interaction has to be identified at a molecular level.

Cytogenetic studies has to be enhanced in inter-specific crosses in distantly related species for identifying the causes for partial or full sterility. The YMV resistant gene has to be incorporated into *Vigna mungo* from rice bean. Back cross breeding should be promoted in large number of F_1 hybrids with resistant donor to get more number of recombinants possessing resistance.

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