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VARIABILITY STUDIES ON BLACKGRAM (*VIGNA MUNGO* (L.) HEPPER) GENOTYPES FOR MUNGBEAN YELLOW MOSAIC VIRUS (MYMV) RESISTANCE

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Abstract

The current investigation undertaken with two hundred and twelve blackgram genotypes for resistance against Mungbean Yellow Mosaic Virus (MYMV) resistance to assess variability and genetic analysis. The experiment was carried out under MYMV hotspot of Tamil Nadu during *Karif*, 2018 by infector row method (Suceptible and Resistant Check). PCV were higher than GCV for all the traits its indicating there is an influence of environment on expression of these traits. The traits *viz.* percentage of disease infection, single plant seed yield, number of pods per plant, number of clusters per plant, number of pods per cluster, plant height and number of branches per plant had recorded high PCV, GCV, high heritability along with high genetic advance as percent of mean indicated these traits were less influenced by environment and posses high genetic variability. Hence these genotypes can be used to further crop improvement programmes to breed trangressive segregants for every characters further selection.

Key words: PCV, GCV, Heriability (h^2), Genetic Advance, MYMV, Blackgram, Variability Studies.

Introduction

Blackgram (*Vigna mungo* (L.) Hepper 2n = 2x = 22), popularly also known as urdbean is a legume self-pollinating annual diploid crop domesticated from *Vigna mungo* var. *silvestris* (Lukoki *et al*., 1980). Approximately a genome size of blackgram is 574Mbp (Arumuganathan and Earle, 1991). India is the major contributor of blackgram production in the world. During 2017 to 2018 an average productivity is 6.55 q/ha and the production of 3.56 MT per annum and grown in 5.44 Mha area (Anonymous, 2019). In India it is widely cultivated in various climatic zones and different soil types. Whereas significant yield improvements have been made, realizing the yield potential is still a huge challenge posed by many biotic and abiotic stresses with non availability of better plant types for varied growing environment. Among several constraints MYMV is a serious disease occupies foremost position. It is caused by *White fly* (*Bemisia tabaci*) transmitted in a persistent manner and circulative manner. It a geminivirus belonging to genus of begomovirus and family geminiviridae. In India there are different biotypes of YMV such as Mungbean yellow mosaic virus (MYMV)- which is caused in South India and Mungbean yellow mosaic India virus (MYMIV)- which is caused in North India. In year 1955, MYMV is first reported and is spreading quickly towards newer areas. The virus primarily cause yellow patches to extend, then progressively turns the entire leaf become yellow. Infected plants flower sparsely and the pods contain shrivelled seeds. Screening blackgram germplasm against MYMV for identification of resistant genotypes is very much essential. With these background information, the present study was envisaged to screen the blackgram germplasm accessions and identify the resistant to MYMV genotypes with superior plant type and high seed yield through field screening under hotspot condition.

Genetic improvement, either through conventional or molecular technique, has been hampered in the inadequate genomic resources together with narrow genetic diversity in the elite gene pool. There is a need to accelerate evolution of crop improvement programmes through

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finding the wide genetic variability available among genotypes of a crop. India is the centre of origin of *Vigna mungo* (Vavilov, 1926). There is a wide genetic variability available among genotypes of blackgram, providing a wide scope for future blackgram crop improvement programmes in India. The main constraints to achieving superior yield of a crop are lack of genetic variability, genotypes with adaptation to local conditions. The creation of variability is not easy through hybridization due to its highly self pollination, small inflorescence, inflorescence are high sensitive and flower droop. Therefore genetic variability is the essential requirement for making improvement in crop breeding the variability among the available existing germplasm accessions is the prime need to develop a appropriate better plant type for specific production system.

Materials and Methods

Experimental Materials

The experimental materials consist of two hundred and twelve blackgram genotypes collected from three research institutions NPRC-Vamban, IIPR-Kanpure, NBPGR-New Delhi and other local agriculture institutions of Tamil Nadu.

Experimental Site and Design of Experiment

The two hundred and twelve genotypes were grown in RBD with 3 replications each replication raised in 3 rows with 1.5 m length and 30×10 cm (30 line to line; 10 plant to plant) spacing in three replications during *karif*., 2018 at Tirunelveli (Dt.) of T.N. The experimental field raised with infector row method to allowing white fly population and providing disease infection to record percentage of disease infection and there was no insecticidal spray for disease control.

Data collection and Statistical Analysis

The data were recorded for eleven morphological traits *viz*., days to 50% flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, hundred seed weight (g), percentage of disease infection and single plant seed yield (g). Disease incidence was recorded periodically and the percentage disease incidence was worked out as per Bashir *et al.*, (2005).

• Co-efficient of Variation

The phenotypic coefficient of variation and genotypic coefficient of variation (GCV) were computed by using the formula of formula of Burton, (1953).

$$\text{Genotypic co efficient of variance (GCV)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$$

$$\text{Phenotypic co efficient of variance (PCV)} = \frac{\sqrt{\text{phenotypic variance}}}{\text{Grand mean}} \times 100$$

• Heritability in broad sense (h^2_{bs})

Heritability in broad sense was calculated according to Lush, (1940) and expressed in percentage.

$$h2 = \frac{\text{Genotypic Variance}(\sigma 2g)}{\text{Phenotypic Variance}(\sigma 2g)} \times 100$$

• Genetic Advance (GA)

Genetic advance was worked based on the formula given by Johnson *et al*., (1955)

$$GA = \frac{V_g}{V_{ph}} X \sqrt{V_{ph}} \times 100$$

• Genetic Advance as percent of Mean (GAM)

$$GA \text{ as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

Results

Variability studies

Table 1: Magnitude of Variability and estimates of Heritability and Genetic Advance for various characters of blackgram genotypes.

S.No.	Characters	DFF	PH	NBPP	NCPP	NPPC	NPPP	PL	NSPP	100 SW	PDI	SPSY
1.	ECV	5.02	5.68	5.08	5.20	4.98	5.23	4.90	4.81	4.93	5.93	5.27
2.	GCV	8.09	30.32	26.25	38.16	29.22	39.49	8.36	9.51	12.06	78.33	44.91
3.	PCV	9.52	30.85	26.73	38.51	29.64	39.84	9.69	10.66	13.03	78.56	45.21
4.	h² (Broad Sense)	72.3	96.6	96.4	98.2	97.2	98.3	74.4	79.7	85.7	99.4	98.6
5.	Gen. Adv as % of Mean 5%	14.17	61.39	53.08	77.88	59.34	80.65	14.86	17.49	22.99	160.91	91.88
6.	Gen. Adv as % of Mean 1%	18.162	78.678	68.028	99.812	76.046	103.352	19.041	22.413	29.458	206.209	117.744
7.	Genetic Advancement 5%	5.533	28.257	1.865	14.998	2.209	44.354	0.701	1.199	0.948	53.459	11.108
8.	Genetic Advancement 1%	7.090	36.213	2.390	19.221	2.831	56.842	0.899	1.537	1.215	68.510	14.235
9.	General Mean	39.039	46.027	3.513	19.257	3.722	54.998	4.719	6.857	4.124	33.224	12.090
10.	Exp. Mean next Generation	44.572	74.284	5.378	34.256	5.931	99.352	5.421	8.056	5.072	86.683	23.197

***ECV**-Environmental coefficient of variation; **GCV**- Genotypic coefficient of variation; **PCV**- Phenotypic coefficient of variation **h2**-Heritability; **DFF**-Days to 50 % Flowering; **PH**-Plant Height (cm); **NBPP**-Number of Branches per Plant; **NCPP**-Number of Clusters per Plant; **NPPC**-Number of Pods per Cluster; **NPPP**- Number of Pods per Plant; **PL**- Pod Length (cm); **NSPP**-Number of Seeds per Pod; **100 SW**- Hundred Seed Weight (g); **PDI**- Percentage of Disease Infection and **SPSY**- Single Plant Seed Yield(g).*

The phenotypic co-efficient of variation, genotypic coefficient of variation, heritability and genetic advance as percent of mean were estimated for all the eleven characters and presented in table 1 and fig. 1 to 3.

Genotypic coefficient of variation (GCV)

GCV ranged from 8.09 percent (days to 50% flowering) to 78.33 percent (percentage of disease infection). High GCV was observed for percentage of disease infection (78.33), single plant seed yield (44.90), number of pods per plant (39.49), number of clusters per plant (38.15), plant height (30.32), number of pods per cluster (29.22) and number of branches per plant (26.24). Hundred seed weight (12.05) exhibited moderate GCV. Number of seeds per pod (9.51), pod length (8.36) and days to 50% flowering (8.09) recorded low GCV (Table 1 and Fig. 2).

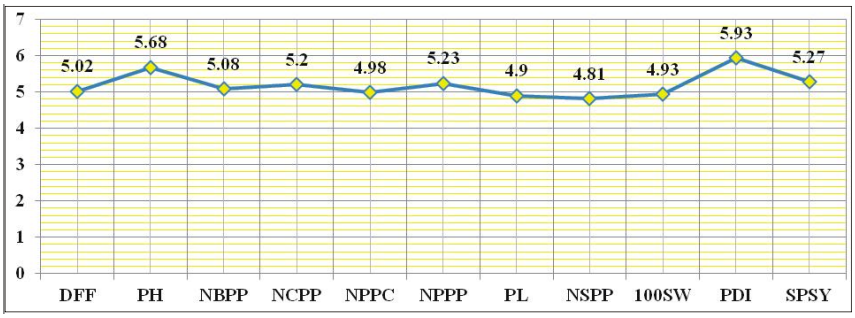

Fig. 1: Environmental coefficient of variation; (Magnitude of Variability, estimates of Heritability and Genetic Advance for various traits of blackgram genotypes).

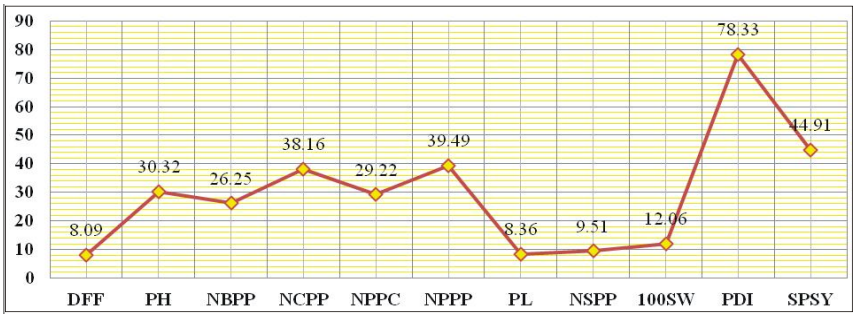

Fig. 2: Genotypic coefficient of variation; (Magnitude of Variability, estimates of Heritability and Genetic Advance for various traits of blackgram genotypes).

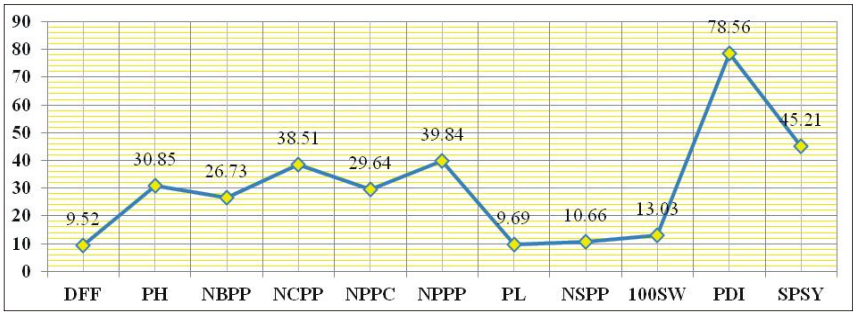

Fig. 3: Phenotypic coefficient of variation; (Magnitude of Variability, estimates of Heritability and Genetic Advance for various traits of blackgram genotypes).

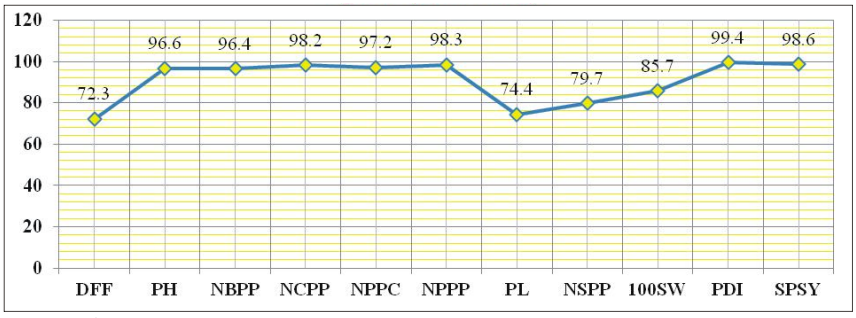

Fig. 4: h^2 (Broad Sense); (Magnitude of Variability, estimates of Heritability and Genetic Advance for various traits of blackgram genotypes).

Phenotypic coefficient of variation (PCV)

The PCV ranged from 9.52 percent (days to 50% flowering) to 78.55 percent (percentage of disease infection). High PCV was observed for percentage of disease infection (78.55), single plant seed yield (45.21), number of pods per plant (39.83), number of clusters per plant (38.50), plant height (30.84), number of pods per cluster (29.64) and number of branches per plant (26.73). Moderate PCV was noticed in hundred seed weight (13.02) and number of seeds per pod (10.65). Pod length (9.69) and days to 50% flowering (9.52) exhibited low PCV (Table 1 and Fig. 3).

Genetic analysis.

Estimates of heritability and genetic advance as percent of mean for eleven characters of blackgram genotypes are presented in the table 1 and fig. 4 to 6.

Heritability (h^2)

The heritability ranged from 72.30 percent days to 50% flowering to 99.40 percent (percentage of disease infection). High heritability was observed for all eleven traits *viz.*, percentage of disease infection (99.40 percent), single plant seed yield (98.60 percent), number of pods per plant (98.30 percent), number of clusters per plant (98.20 percent), number of pods per cluster (97.20 percent), plant height (96.60 percent), number of branches per plant (96.40 percent), hundred seed weight (85.70 percent), number of seeds per pod (79.70 percent), pod length (74.40

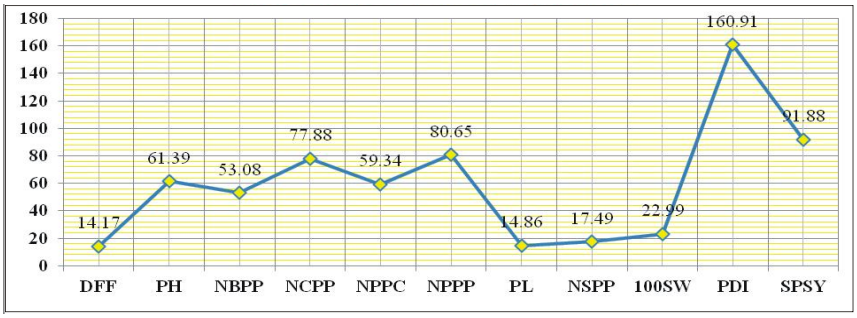

Fig. 5: Genenetic advance as % of mean 5%; (Magnitude of Variability, estimates of Heritability and Genetic Advance for various traits of blackgram genotypes).

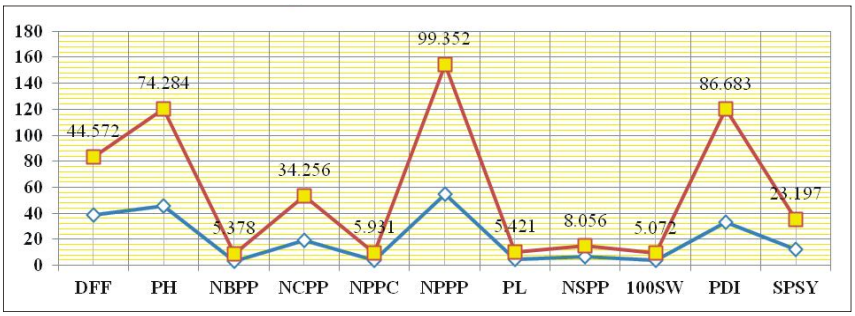

Fig. 6: Expected mean next generation General mean; (Magnitude of Variability, estimates of Heritability and Genetic Advance for various traits of blackgram genotypes).

percent) and days to 50% flowering (72.30 percent) (Table 1 and Fig. 4).

Genetic advance as percent of mean (GAM)

A perusal of genetic advance for all the quantitative traits under study ranged from 14.17 percent (days to 50% flowering) to 160.91 percent (percentage of disease infection). High genetic advance was observed for the traits *viz.*, percentage of disease infection (160.91 percent), single plant seed yield (91.88 percent), number of pods per plant (80.65 percent), number of clusters per plant (77.88 percent) and plant height (61.39 percent). Moderate genetic advance was noticed for number of pods per cluster (59.34 percent) and number of branches per plant (53.08 percent). Hundred seed weight (22.99 percent), number of seeds per pod (17.49 percent), pod length (14.86 percent) and days to 50% flowering (14.17 percent) exhibited low Genetic advance as percent of mean (Table 1 and Fig. 5).

Discussions

The competency of selection mainly depends on the degree of genetic variability there in a population. For any thriving crop improvement programme, the information about the variability parameters such as Genotypic Coefficient of Variation, Phenotypic Coefficient of Variation, Heritability and Genetic Advance as percent of Mean of breeding materials are the principle need. Higher level of genotypic and phenotypic variability is necessary for selection of desirable genotypes, as higher the diversity wider the choice for selection

The estimation of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the eleven traits studied indicating there is an influence of environment on expression of these traits. These findings similar type of results reported by earlier workers (Gowsalya *et al*. 2016; Dharmendra Kumar Rolaniya *et al*., 2018; Manish Patidar *et al*., 2018)

Heritability is a superior index of transmission of traits from parents to their progeny and assist us as a tool for selecting elite genotypes from the diverse hereditary population. The High heritability was observed in the traits *viz.*, percentage of disease infection, single plant seed yield, number of pods per plant, number of clusters per plant, number of pods per cluster plant height, number of branches per plant indicating predominance of additive gene action in the expression of these characters and they can be develop through distinct plant selection. High heritability coupled with high genetic advance as percent of the mean was recorded for percentage of disease infection, single plant seed yield, number of pods per plant, number of clusters per plant, number of pods per cluster plant height, number of branches per plant its indicating the occurrence of additive gene action in controlling gene expression. Similar outcome were reported by Manish Patidar *et al*., 2018 in blackgram.

Conclusion

Based on the results there was sufficient genetic variability among the genotypes studied for all the character. Percentage of disease infection, single plant seed yield, number of pods per plant, number of clusters per plant, number of pods per cluster plant height, number of branches per plant indicated high heritability along with high genetic advance as percent of mean. Hence, these traits were fewer influenced by environment and posses high genetic variability. Thus, these genotypes can be supplementary studied over years across regions to select for direct release as a varieties besides, can be used to further crop improvement programs to breed trangressive segregants for every characters further selection.

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