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Exploring the Genetic Variability of Blackgram [*Vigna mungo* (L.) Hepper] Genotypes Over Environments

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ABSTRACT

Background: The present investigation was carried out in 50 diverse blackgram genotypes during *rabi* 2021-22 in three different locations *viz*., Agricultural College and Research Institute, Madurai (E1), National Pulses Research Institute, Vamban (E2) and a farmer's field at Vizhudhudayan, Ariyalur district (E3) for exploring the genetic variability of the blackgram genotypes over environments.
Methods: The data on 10 quantitative traits *viz*., days to 50% flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, pod length (cm), hundred seed weight (g) and seed yield per plant (g) were subjected to genetic variability analysis.
Result: The traits *viz*., plant height (cm), number of branches per plant, number of clusters per plant, total number of pods per plant, hundred seed weight (g) and seed yield per plant (g) revealed a high phenotypic and genotypic coefficient of variation, heritability and genetic advance as percent of mean. Hence, these traits may be given much importance during selection due to their additive gene action. These results might render yield enhancement in future breeding programs.

Key words: Genetic advance, Genotypic coefficient of variation, Heritability, Phenotypic coefficient of variation, Variability.

INTRODUCTION

Among pulses, blackgram (*Vigna mungo* L.) is an important short-duration legume crop that is extensively grown in India. Blackgram covers 4.63 million ha of area with production and productivity of 2.77 million tonnes and 599 kg/ha respectively (Indiastat-2021-22). It provides us with a high-quality, readily digestible source of protein and can restore soil fertility through symbiotic nitrogen fixation. The main obstacles to increasing this crop's output are its low harvest index, lack of genetic variability and the use of genotypes and varieties that are suited to the environment in the area (Hadimani *et al*., 2016; Gangadhar *et al*., 2023). The outcome of several interconnected plant activities is regarded as yield. Since it is a very complicated trait regulated by multiple genes and interconnected with other yield components, directly increasing yield can be exceptionally difficult. Enhancing traits that are closely linked can help attain it. Thus, genetic variation is a fundamental prerequisite for crop breeding programs (Appalaswamy and Reddy, 2004). The success of the breeding program is mostly determined by the degree of genetic variation that may be achieved in the population (Narayanan *et al.,* 2021). The wide range of genetic variability assists in choosing the best genotype easier. Phenotypic and genotypic variation are the causes of the observed population variances. Phenotypic variance is the term used to describe the physically evident diversity within a population. This variation in phenotype is the result of the interplay between environment and genotype. Genetic variation is an innate trait that is unaffected by external factors. Variability is necessary for the effective selection of any trait during a breeding program. Planning future breeding programs requires an understanding of genetic variability for economically significant traits, as well as their heritability and genetic advancement, to improve any crop species (Singh *et al*., 2007). Thus, the present investigation was carried out to estimate the genetic variability among 50 blackgram genotypes in three different environments and hence study the effect of environment on variability analysis.

MATERIALS AND METHODS

The experimental material comprised of 50 blackgram genotypes raised in randomized complete block design

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during *rabi* 2021-22 in three different environments *viz*., Agricultural College and Research Institute, Madurai (E1), National Pulses Research Institute, Vamban (E2) and a farmer's field at Vizhudhudayan, Ariyalur district (E3). The details of the environments under study are presented in Table 1. The recommended package of practices was followed according to the crop production guide. Ten quantitative traits *viz*., days to 50% flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, pod length (cm), hundred seed weight (g) and seed yield per plant (g) were recorded. The phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated based on Burton (1952). Heritability (h^2) and genetic advance as a percent of the mean (GAM) were worked out by methods advocated by Johnson *et al*. (1955).

RESULTS AND DISCUSSION

In the investigation of the extent of genetic variability among the genotypes, the genetic parameters PCV, GCV, heritability (h^2) and genetic advance as a percent of the mean (GAM) are much noteworthy. The amount of variation in the base population determines the potential of the experimental material (Chauhan *et al.,* 2020). The PCV and GCV of ten quantitative traits over three environments are presented in Table 2. The PCV of all the traits over the environments was observed to be higher than the GCV indicating the environmental influence on the traits under study. This outcome is in accordance with the Ramya *et al*. (2014), Deepshika *et al*. (2014), Priyanka *et al.* (2016), Narayanan *et al.* (2021) and Gangadhar *et al.* (2023).

The graphical representation of PCV and GCV are presented. The trait; days to 50% flowering recorded the lowest PCV in all three environments. The highest PCV was observed in hundred seed weight (40.64%) in E1; number of branches per plant (50.03%) in E2 and seed yield per plant (33.78%) in E3. The traits *viz*., plant height, number of branches per plant, number of clusters per plant, total number of pods per plant, hundred seed weight (g) and seed yield per plant (g) were found to have high PCV in all the three environments suggesting that they have higher environmental influence. These results were in corroboration with Partap *et al*. (2019) for plant height and number of branches per plant Charitha and Lal (2021) and Yergude *et al*. (2021) for number of clusters per plant, total number of pods per plant, hundred seed weight (g) and Gomathi *et al*. (2023) for seed yield per plant (g).

In case of GCV; the trait, days to 50% flowering exhibited lowest in all three environments except for E2 in which the number of pods per cluster recorded the lowest GCV (8.62%). Hundred seed weight (38.24%) showed highest GCV in E1; number of branches per plant in E2 (45.52%) and E3 (36.10%). The traits *viz*., plant height, number of branches per plant, number of clusters per plant, the total number of pods per plant, hundred seed weight (g) and seed yield per plant (g) were found to have high GCV over environments. Similar results were reported by Jeberson *et al.* (2019) for plant height and number of branches per plant, total number of pods per plant, hundred seed weight (g) and seed yield per plant (g); Anuradha *et al.* (2020) for plant height and number of branches per plant, total number of pods per plant and seed yield per plant. The trait; pod length was observed to have moderate PCV and GCV over all environments. This outcome is in agreement with Charitha and Lal (2021) and Teja and Lal (2021).

Regarding heritability (h^2), days to 50% flowering reported the highest heritability in all three environments (Table 3). The lowest h^2 was expressed by the number of

Table 1: Details of the environments under study.

Code	Environment	Agro ecological zone	Rainfall (mm)	Soil type	Latitude	Longitude
E1	Madurai	Southern zone	855	Clay loam	9°58′N	78°12′E
E2	Vamban	Southern zone	881	Red laterite	10°22′N	78°54′E
E3	Vizhudhudayan	North Eastern zone	1050	Red loam	11°24′N	79°20′E

Table 2: Phenotypic and genotypic coefficient of variation for 50 diverse blackgram genotypes over 3 environments.

Characters	Madurai (E1)		Vamban (E2)		Vizhudhudayan (E3)	
	PCV (%)	GCV (%)	PCV (%)	GCV (%)	PCV (%)	GCV (%)
Days to 50% flowering	8.27	8.24	9.05	8.97	7.59	7.54
Plant height (cm)	36.92	34.67	26.74	21.46	27.14	22.06
Number of branches	30.38	24.19	50.03	45.52	41.18	36.10
Number of clusters per plant	36.31	31.11	25.47	20.73	26.45	22.49
Number of pods per cluster	22.26	16.06	17.59	8.62	19.05	15.94
Total number of pods per plant	33.03	27.95	29.18	25.59	29.78	25.17
Pod length (cm)	14.06	12.08	15.58	12.93	13.88	12.85
Number of seeds per pod	24.72	22.65	19.27	18.55	15.57	14.73
Hundred seed weight (g)	40.64	38.24	30.09	28.10	25.31	23.28
Seed yield per plant (g)	26.53	22.62	34.22	27.58	33.78	28.24

Table 3: Heritability and genetic advance as % of mean for 50 diverse blackgram genotypes over 3 environments.

Characters	Madurai (E1)		Vamban (E2)		Vizhudhudayan (E3)	
	h^2 (%)	GAM (%)	h^2 (%)	GAM (%)	h^2 (%)	GAM (%)
Days to 50% flowering	99.44	16.93	98.15	18.30	98.65	15.42
Plant height (cm)	88.23	67.09	64.40	35.48	66.06	36.94
Number of branches	63.40	39.67	82.79	85.32	76.86	65.20
Number of clusters per plant	73.41	54.91	66.24	34.75	72.29	39.39
Number of pods per cluster	52.10	23.89	24.01	8.70	70.07	27.49
Total number of pods per plant	71.57	48.70	76.94	46.25	71.44	43.82
Pod length (cm)	73.83	21.39	68.88	22.11	85.66	24.49
Number of seeds per pod	83.97	42.76	92.59	36.76	89.44	28.69
Hundred seed weight (g)	88.52	74.11	87.20	54.05	84.60	44.11
Seed yield per plant (g)	72.70	39.73	64.95	45.78	69.90	48.64

pods per cluster in E1 (52.10%) and E2 (24.01%) whereas by plant height in E3 (66.06%). All the traits under study exhibited high heritability over all environments except for the number of pods per cluster in E2 (52.10%) and E2 (24.01%). In the case of genetic advance as a per cent of the mean (GAM), the lowest was recorded by the trait, days to 50% flowering in E1 (16.93%) and E3 (15.42%); whereas in E2, it was observed in the number of pods per cluster (8.70). This is in accordance with Yergude *et al*. (2021) for days to 50% flowering. The highest GAM was obtained by hundred seed weight in E1 (74.11%); the number of branches in E2 (85.32%) and E3 (65.20%). All of the traits except days to 50% flowering in E1 and E2; the number of pods per cluster in E2 exhibited high GAM (Table 3). Toppo *et al*. (2019) and Teja and Lal (2021) also observed low GAM for days to 50% flowering and Anuradha *et al.* (2020) for the number of pods per cluster. All studies subjected to multi-environmental data provide much more reliable and efficient conclusions than single environmental data. Hence, in this study genetic variability studies are performed for three different environments and the characters, plant height (cm), number of branches per plant, number of clusters per plant, total number of pods per plant, hundred seed weight (g) and seed yield per plant (g) exposed high PCV, GCV, heritability and genetic advance in all three environments denoting that they are less influenced by environment and can be used for selection in crop improvement.

CONCLUSION

The outcome of the study denotes that, the environment poses a great influence in genetic variability analysis. However, the traits; plant height (cm), number of branches per plant, number of clusters per plant, the total number of pods per plant, hundred seed weight (g) and seed yield per plant (g) showed high PCV, GCV, h^2 and GAM in all the three environments. The variability of these traits was found to be reproducible in all three environments. Results pertaining to more locations are highly reliable than a single environment data. Hence these traits should be given a great emphasis as selection indices in future crop improvement programmes for enhancing crop yield.

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Conflicts of interest and financial disclosures

The authors declare that they have no conflict of interest.

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