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Research Note

Genetic variability and correlation studies in black-gram [*Vigna mungo* (L.) Hepper]

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Abstract
The present investigation was carried out to estimate the genetic variability and genotypic correlation among one hundred and twenty black-gram genotypes for nine quantitative characters. High PCV and GCV were recorded for the traits *viz.,* single plant yield, number of clusters per plant, number of pods per plant and number of primary branches per plant. High heritability coupled with high GAM was recorded for the traits *viz.,* plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield. From the association analysis, single plant yield had negative and significant association with days to 50% flowering and it also exhibited significant and positive correlation with the traits *viz.,* number of pods per plant, number of clusters per plant, number of primary branches per plant and hundred seed weight. Hence, simultaneous selection of the above traits would be more rewarding to bring improvement in black-gram.

Keywords
Black-gram, Genetic variability, Genetic association

Pulses are the major source of dietary protein in the vegetarian diet. Black-gram [*Vigna mungo* (L.) Hepper] known as urd-bean in India is a short duration, self pollinating, diploid (2n=2x=22) grain legume crop belonging to the family Leguminosae with a small genome size of 0.56g/PC (574Mbp) (Gupta and Gopalakrishna, 2009). Black-gram seeds contain 65 per cent carbohydrates and 25 per cent protein and are consumed as food and the sprouts are used as vegetable and also the seeds possess rich source of minerals and vitamins (Ghafoor *et al.* 2001). During 2010-11, India produced 1.75 million tons of black-gram with the average productivity of 535 Kg/ ha from 3.26 million hectares (Gupta *et al.* 2013). The major constraints in black-gram genetic improvement are lack of exploitable genetic variability, absence of suitable ideo type for different cropping systems, poor harvest index and susceptibility to biotic and abiotic stresses and non-availability of quality seeds of improved varieties. It is mainly due to the repeated usage of few parents with high degree of relatedness in crossing programmes (Jayamani and Sathya, 2013). Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits (Johnson *et al.* 1955). The association between yield and other yield attributes would be useful for selecting the better genotypes. Association analysis measures the mutual relationship between various plant characters and determines component characters on which selection can be based on improvement in the economically important characters (Hemalatha *et al.* 2017). Hence, the present study was planned to investigate genetic variability and correlation coefficients to identify superior black-gram genotypes for future exploitation in breeding programmes.

The present investigation aimed with the study of genetic diversity using one hundred and twenty germplasm lines collected from different sources *viz.,* National Bureau of Plant Genetic and Resources (NBPGR), New Delhi, National Pulses Research Centre, Vamban, Agricultural College and Research Institute, Madurai and Agricultural College and Research Institute, Killikulam. The field experiment was conducted at Department of Plant Breeding and Genetics at Agricultural College and Research Institute, Killikulam during the year 2017-18. A set of one hundred and twenty genotypes of black-gram were evaluated in Randomized Block Design (RBD) with two replications. Each genotype was raised in a single row of 3 metre length with a spacing of 30 x 10 cm. Observations were recorded on five randomly selected plants in each replication for nine quantitative characters *viz.,* days to 50 % flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per plant, hundred seed weight (g), pod length (cm) and single plant yield (g). The various genetic parameters *viz.,* Genotypic

Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV), heritability (h^2) and Genetic Advance as percentage of Mean (GAM) were calculated by adopting the formulae given by (Johnson *et al.* 1955). Genotypic correlation co-efficient was calculated by using the formulae given by Al-Jibouri *et al.* (1958).

Analysis of variance revealed that significant differences were existed for the genotypes studied and it is represented in Table1. The variability on genetic parameters for nine biometrical characters is presented in Table 2**.** The results revealed that the PCV values were found higher than GCV. However, good correspondence was observed between GCV and PCV for all the biometrical traits. Higher magnitude of GCV was recorded for the trait number of clusters per plant followed by single plant yield, number of pods per plant and number of primary branches per plant. Similar findings were reported by Ramya *et al.* (2014) and Sushmitharaj *et al*. (2018) for the traits for number of clusters per plant and number of pods per plant. Hence, direct selection based on these traits would be effective for the improvement of this crop.

Estimates of heritability and GAM for the studied traits of black-gram are furnished in Table 2. Heritability value was high for all the traits. High GAM was observed for the trait number of clusters per plant followed by single plant yield, number of pods per plant, number of primary branches per plant and plant height. Among the characters, the traits *viz.*, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, hundred seed weight and single plant yield recorded high heritability along with high GAM which indicated selection is highly efficient for these traits due to the presence of additive gene action. Similar findings were reported by Baisakh *et al.* (2014) in black-gram. High heritability with moderate genetic advance was observed for the traits *viz.*, number of seeds per plant and days to fifty per cent flowering. Panigrahi *et al.* (2014) also reported high heritability with moderate genetic advance for the trait days to 50 per cent flowering in black-gram.

Correlation coefficients were computed to assess the magnitude of association existed between seed yield and other contributing traits and are furnished in Table 3. Association pattern of single plant yield exhibited significant and positive correlation with number of pods per plant, number of clusters per plant, number of primary branches per plant and hundred seed weight where as significantly negative genotypic correlation with days to 50% flowering. Similar findings were reported by Punia *et al.* (2014) and Kumar *et al.* (2015).

From the inter correlation studies, the trait of days to 50 per cent flowering had significant and negative correlation with the traits *viz.*, single plant yield, number of clusters per plant, number of pods per plant and number of seeds per pod. Similar findings were reported by Kaveri *et al.* (2007).

The trait number of primary branches per plant revealed positive and significant correlation with the traits *viz.*, number of pods per plant, number of seeds per pod, hundred seed weight and single plant yield and this was in agreement with the findings of Mehra *et al.* (2016).

The trait number of clusters per plant had significant and positive association with number of pods per plant and single plant yield. Similar findings were reported by Konda *et al.* (2008). From the above facts, it was clear that the yield component traits *viz.*, days to 50% flowering, number of clusters per plant, number of pods per plant, hundred seed weight and single plant yield were highly correlated among themselves. Hence simultaneous selection for the above traits will be more rewarding to bring improvement in black-gram.

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Table 1. Analysis of variance of RBD for different characters in black-gram

Source of Variation	d.f.	Mean Sum Squares								
		Days to 50% flowering	Plant height	No .of primary branches /plant	No. of clusters/plant	No. of pods/plant	No. of seeds/ pod	100 seed weight	Pod length	Single plant yield
Replication	1	1.50	26.19	2.24	3.63	17.92	0.009	0.20	0.01	10.27
Genotypes	119	11.78*	83.59*	1.52*	135.13*	306.41*	0.49*	0.38*	0.26*	81.65*
Error	119	1.88	2.09	0.07	1.12	3.50	0.13	0.03	0.01	1.27
S.E.		1.37	1.44	0.28	1.06	1.87	0.37	0.17	0.14	1.12
C.D (5%)		2.71	2.86	0.55	2.10	3.70	0.73	0.35	0.27	2.23

* Significant at 5% level

Table 2. Magnitude of genetic variance for yield components in black-gram

Sl. No	Traits	PCV (%)	GCV (%)	heritability h^2 (%)	GAM
1	**Days to 50% flowering**	7.43	6.33	72.40	11.10
2	**Plant height**	12.53	12.21	95.10	24.54
3	**Number of primary branches per plant**	24.65	23.41	90.20	45.82
4	**Number of clusters/plant**	43.43	43.07	98.30	87.99
5	**Number of pods/plant**	30.67	30.30	97.70	61.76
6	**Number of seeds/ pod**	9.07	6.70	56.10	10.48
7	**100 seed weight**	9.45	8.71	89.80	16.45
8	**Pod length**	8.06	7.49	86.60	14.34
9	**Single plant yield**	35.60	35.05	96.90	71.10

Table 3. Correlation among yield and yield influencing traits in black-gram

Traits	Days to 50% flowering	Plant height	No. of primary branches /plant	No. of clusters/ plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight	Pod length	Single plant yield
Days to 50% flowering	**1.000**	0.110	-0.089	-0.244*	-0.290*	-0.203*	0.163	0.107	-0.255*
Plant height		**1.000**	0.138	-0.022	0.042	0.044	0.121	0.145	0.124
No of primary branches /plant			**1.000**	0.157	0.207*	0.200*	0.323*	0.155	0.267*
No. of clusters/ plant				**1.000**	0.812*	-0.009	0.027	-0.030	0.375*
No. of pods/plant					**1.000**	-0.108	0.058	-0.009	0.394*
No. of seeds/ pod						**1.000**	-0.064	0.127	0.012
100 seed weight							**1.000**	0.144	0.260*
Pod length								**1.000**	-0.125
single plant yield									**1.000**

* Significant at 5% level.