

Genetic Divergence and Association Analysis for Yield and Yield Related Traits Among F_4 and F_5 Recombinant Inbred Lines (Rils) of Green Gram [*Vigna radiata* (L.) Wilckeze]

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ABSTRACT

Genetic divergence and association analysis are important tools in quantifying the degree of divergence and knowing the individual contribution of the components traits on total divergence. In the study, the F_4 recombinant inbred line (RIL) population of two crosses Chinamung \times BL 849 and Chinamung LM 1668 of green gram are analyzed for genetic variability, heritability, genetic advance, correlation and path analysis with respect of various important plant traits in identifying high yielding RIL for further stabilization which can be released as a variety. The genotypes differed significantly for all the characters under study in both the crosses except days to fifty per cent flowering, primary branches, and threshing percentage in cross Chinamung BL 849. Seed yield per plant showed highest positive association with pod yield, primary branches, plant height, clusters per plant and threshing percentage. While seed yield per plant showed significant negative correlation with days to 50 per cent flowering in the cross Chinamung \times LM 1668. Maximum direct effect on seed yield per plant was shown by pod yield per plant and threshing percentage whereas maximum indirect effect was shown by clusters per plant, primary branches per plant and plant height in both the crosses. The present study suggests that traits like clusters per plant, pod yield and seed yield are influenced by additive gene action and are therefore, heritable which means selection for such traits will be rewarding for any breeding programmes.

Keywords: Genetic divergence, Recombinant inbred lines, Green gram

GREEN GRAM [*Vigna radiata* (L.) Wilczek] is the third important pulse crop of the country. In combination with cereals forms a complete meal which provides a perfect balance of essential amino acid with high biological value. The crop is grown in both *kharif* and *rabi* season. Though production and marketing of pulse crops occupy immense importance not only for Indian economy, but also for providing balance food to the people of country. There is reduction in area and production of crop because of various biotic, abiotic and management constraints. Yield is the most important factor for determining improvement of a crop. For improvement of crop adequate variability provides a great deal (Ogunniyan and Olakojo, 2014). Estimates of genetic parameters give an indication that how total variation of a character is affected by various type of gene effects (Dagefa *et al.*, 2014). Quantitative traits are highly affected by environment. Hence, it is difficult to infer the variability present is

heritable or influenced by environment (Patel *et al.*, 2014). So, heritability should be high for the traits under selection. The results become more reliable and meaningful if coupled with genetic advance (Ogunniyan and Olakojo, 2014). For quantitative traits, indirect selection among different traits is more effective which is possible by correlation studies. Correlation coefficient analysis provides the degree and relationship among important traits of interest and provides base for the selection (Hemavathy *et al.*, 2015). But it has limitation, as it measures only mutual relationship between two traits but fails to imply the cause and effect of relationship. To overcome the problem, path coefficient analysis has been found reliable. It measures the direct and indirect effects of association and the relative importance of each casual factor. Thus, correlation and path analysis studies give us an idea about the contribution of different plant traits to seed yield (Makeen *et al.*, 2007). Thus, the present

investigation was conducted to assess the genetic variability, heritability, genetic advance, correlation and path analysis with respect of various important plant traits in recombinant inbred lines of green gram, which will help in identifying high yielding recombinant inbred line for further stabilization and can be released as a variety.

MATERIALS AND METHODS

The experimental material comprised of two F_4 recombinant inbred line (RIL) populations of green gram, one from a cross between parent 'Chinamung' and 'BL-849' with 260 lines and second from a cross between parent 'Chinamung' and 'LM-1668' with 249 lines. The F_4 population was sown in *kharif* 2015 which further forwarded to F_5 generation. The parents differ for traits as shown in Table 1. The present experimental work was carried out in *kharif* 2015 at K block, University of Agricultural Sciences, GKVK, Bengaluru. Geographically, the experimental site is located at 13° 00'N latitude and 77° 35'E longitude. The site is at an altitude of 899 m above mean sea level.

TABLE 1

The characteristic features of parents and check varieties (*) of green gram

Parents	Yield	Seed type
Chinamung (Female)	High	Bold shining
BL-849 (Male)	Moderate	Medium size
LM-1668 (Male)	Moderate	Bold
*Pusa Baisakhi	High	Bold
*KKM-3	High	Medium

Experimental details

The experiment material discussed above was sown in augmented Design with two checks *viz.*, Pusa Baisakhi, KKM-3 and parents *viz.*, Chinamung, BL-849 and LM-1668. Each genotype was grown with a spacing of 30 cm × 10 cm. All the recombinant inbred lines of both the crosses Chinamung BL-849 and Chinamung LM-1668 were evaluated for yield and yield attributing traits *viz.*, days to 50 per cent flowering, plant height (cm), primary branches per

plant, clusters per plant, pod yield per plant (g), seed yield per plant (g) and threshing percentage. Seeds from randomly selected single plant of every recombinant inbred lines were taken and forwarded to next generation of RILs. The observations were recorded in respect of quantitative traits for F_4 generation and the mean was subjected to statistical analysis using WINDOSTAT 8.5 for augmented design, genetic variability parameters, correlation and path analysis and SPSS for descriptive statistics.

RESULTS AND DISCUSSION

In the present investigation, the ANOVA for morphological traits has been given in the Table 2. The RILs exhibited significant differences for all the traits under study in both the crosses except for traits like days to fifty per cent flowering and primary branches per plant in cross Chinamung BL-849. The significant differences show the presence of sufficient variability for the material under study. The higher estimates of GCV were observed for clusters per plant (23.63, 26.24), pod yield (54.85g, 46.12g) and seed yield (56.78g, 47.27g) in both the crosses. While, for PCV higher estimates were observed for plant height (23.71cm, 21.36cm), primary branches (25.10, 25.24), clusters per plant (32.38, 34.56), pod yield (61.77g, 59.07g) and seed yield (63.04g, 62.49g) in both the crosses. The heritability in broad sense was recorded to be high for traits like pod yield (78.85 %) and seed yield (81.13 %) in cross Chinamung × BL-849 and primary branches (61.78 %), pod yield (60.96 %) and threshing percentage (74.63%) was found to be high in cross Chinamung × LM-1668. For genetic advance as per cent of mean, the higher estimates were observed for all the traits under study except days to fifty percent flowering and threshing percentage. Higher values of GCV and PCV for traits clusters per plant, pod yield and seed yield show better chances of selection for these traits. But PCV presents environmental effect on traits. GCV represents the range of genetic variability but not sufficient to determine the heritable portion of variation so need heritable estimates (Raturi *et al.*, 2015.). The traits *viz.*, clusters per plant, pod yield and seed yield were recorded with high heritability, GCV, PCV

TABLE 2

Estimates of analysis of variance, descriptive and genetic variability parameters for yield and yield related traits in 260 F₄ RILs of the cross Chinamung × BL 849 and 249 F₄ RILs of the cross Chinamung × LM 1668 in green gram

Characters	MSS		Mean		GCV		PCV		h ² _{bs}		GAM	
	C ₁	C ₂	C ₁	C ₂	C ₁	C ₂						
Days to 50 percent flowering	2.69	2.49 *	42.16	40.00	2.01	2.76	3.85	3.87	27.27	50.96	2.16	4.06
Plant height (cm)	43.69 *	43.25 *	27.37	30.13	16.98	16.20	23.71	21.36	51.28	57.54	25.05	25.32
Primary Branches	0.66	0.76 *	3.19	3.37	17.42	19.84	25.10	25.24	48.16	61.78	24.90	32.12
Clusters per plant	0.81 *	1.21 *	2.78	3.11	23.63	26.24	32.38	34.56	53.27	57.63	35.53	41.03
Pod yield (g)	4.32 **	6.63 *	4.11	4.26	54.85	46.12	61.77	59.07	78.85	60.96	100.34	74.18
Seed yield (g)	1.93 **	3.09 *	2.72	2.75	56.78	47.27	63.04	62.49	81.13	57.21	105.35	73.66
Threshing percent	58.23	62.51 **	65.92	63.25	11.78	10.50	16.97	12.16	25.16	74.63	6.10	18.69

* Significant @ P=0.05, ** Significant @ P=0.01

accompanied with high GAM which indicates that these traits are influenced by additive gene effect and also greater portion is heritable.

The phenotypic correlation coefficient values were calculated by using software WINDOSTAT 8.5. Seed yield per plant showed highest positive association with pod yield per plant (0.98) followed by clusters per plant (0.42), threshing percentage (0.26), primary branches per plant (0.24) and plant height (0.18) in the cross Chinamung × BL-849. In the cross Chinamung × LM-1668 seed yield per plant also showed highest positive significant association with pod yield per plant (0.98) followed by clusters per plant (0.53), plant height (0.42), primary branches per plant (0.31) and threshing percentage (0.37) in F₄ RILs. While seed yield per plant showed significant negative correlation with days to 50 percent flowering (-0.15) in the cross Chinamung × LM-1668 (Table 3).

Path coefficient analysis was carried out at phenotypic level taking seed yield per plant as the dependable character. Maximum direct effect on seed yield per plant was shown by pod yield per plant (0.9670) followed by threshing percentage (0.1880). Clusters per plant (-0.0151) showed direct effect in negative direction on seed yield per plant. Maximum indirect

effect was shown by clusters per plant (0.4292) through pod yield per plant on seed yield per plant followed by primary branches per plant (0.2265) through pod yield per plant and plant height (0.1828) through pod yield per plant on seed yield per plant in the cross Chinamung × BL-849 (Table 5). Whereas in the cross Chinamung × LM-1668, maximum direct effect on seed yield per plant was shown by pod yield per plant (0.9726) followed by threshing percentage (0.1009) followed by clusters per plant (-0.0293) in a negative direction on seed yield per plant (Table 4). Maximum indirect effect was shown by clusters per plant (0.5311) through pod yield per plant on seed yield per plant followed by plant height (0.4068) through pod yield per plant and primary branches per plant (0.3161) through pod yield per plant on seed yield per plant. Days to 50 per cent flowering (-0.1394) through pod yield per plant had high indirect effect in a negative direction on seed yield per plant. Correlation alone often gives misleading information as it measures only mutual relationship between two traits but not the cause and effect of relationship. To overcome the problem, it is important to devise a method which takes into account the cause and effect of relationship. Therefore, path coefficient analysis measures the direct and indirect effects of association and the

TABLE 3

Estimates of phenotypic correlation coefficients for seed yield and its contributing characters in 260 F4 RIL population of the cross Chinamung × BL-849 and 249 F4 RIL population of the cross Chinamung × LM-1668 in green gram

Trait	Cross	Plant Height (cm)	Days to 50 per cent Flowering	Clusters / Plant	Primary Branches / Plant	Pod Yield / Plant (g)	Threshing percentage	Seed Yield / Plant (g)
Plant	C ₁	1.00	0.18 **	0.50 **	0.57 **	0.19 **	-0.05	0.18 **
	C ₂	1.00	-0.11	0.56 **	0.38 **	0.42 **	0.25 **	0.42 **
Days to 50 per cent Flowering	C ₁		1.00	0.07	0.29 **	-0.01	-0.04	-0.01
	C ₂		1.00	-0.13 *	0.07	-0.14 *	-0.14 *	-0.15 *
Clusters / Plant	C ₁			1.00	0.39 **	0.44 **	-0.03	0.42 **
	C ₂			1.00	0.58 **	0.55 **	0.24 **	0.53 **
Primary Branches / Plant	C ₁				1.00	0.23 **	0.04	0.24 **
	C ₂				1.00	0.32 **	0.13 *	0.31 **
Pod Yield / Plant (g)	C ₁					1.00	0.0757	0.98 **
	C ₂					1.00	0.28 **	0.98 **
Threshing percentage	C ₁						1.00	0.26 **
	C ₂						1.00	0.37 **

* Significant @ P=0.05, ** Significant @ P=0.01

TABLE 4

Estimates of direct effects (bold) and indirect effects of different characters on seed yield per plant in 260 F4 RIL population of cross Chinamung × BL 849 in green gram

Trait	Plant Height (cm)	Days to 50 per cent Flowering	Clusters / Plant	Primary Branches / Plant	Pod Yield / Plant	Threshing percentage	Seed Yield / Plant (r)
Plant Height (cm)	0.0009	0.0001	-0.0164	-0.0001	0.4068	0.0255	0.4169 **
Days to 50 per cent Flowering	-0.0001	-0.0006	0.0037	0.0000	-0.1394	-0.0138	-0.1502 *
Clusters / Plant	0.0005	0.0001	-0.0293	-0.0001	0.5311	0.0241	0.5263 **
Primary Branches / Plant	0.0003	0.0000	-0.0171	-0.0002	0.3161	0.0127	0.3118 **
Pod Yield / Plant (g)	0.0004	0.0001	-0.0160	-0.0001	0.9726	0.0286	0.9855 **
Threshing percentage	0.0002	0.0001	-0.0070	0.0000	0.2754	0.1009	0.3696 **

Residual effect = 0.0895, * Significant @ P=0.05, ** Significant @ P=0.01

TABLE 5

Estimates of direct effects (diagonal and bold) and indirect effects of different characters on seed yield per plant in 249 F₄ RIL population of the cross Chinamung × LM 1668 in green gram

Trait	Plant Height (cm)	Days to 50 per cent Flowering	Clusters / Plant	Primary Branches / Plant	Pod Yield / Plant	Threshing percentage	Seed Yield / Plant (r)
Plant Height (cm)	0.0066	0.0003	-0.0076	0.0053	0.1828	-0.0088	0.1787 **
Clusters / Plant	0.0033	0.0001	-0.0151	0.0036	0.4292	-0.0055	0.4157 **
Primary Branches / Plant	0.0038	0.0006	-0.0059	0.0093	0.2265	0.0068	0.2412 **
Pod Yield / Plant (g)	0.0013	0.0000	-0.0067	0.0022	0.9670	0.0142	0.9779 **
Threshing percentage	-0.0003	-0.0001	0.0004	0.0003	0.0732	0.1880	0.2616 **

Residual Effect = 0.1387, * Significant @ P=0.05, ** Significant @ P=0.01

relative importance of each causal factor as discussed in materials and methods. The residual effects were 0.0895 and 0.1387 in the crosses Chinamung × BL 849 and Chinamung × LM 1668 respectively, which means contribution of component characters was quite high.

Thus, from the study we can conclude that the traits like clusters per plant, seed yield and pod yield are influenced by additive gene action and are heritable which means selection for such traits will be rewarding for any breeding programmes.

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(Received : November, 2018 Accepted : January, 2019)