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Genetic variability, correlation, path coefficient analysis for yield and yield components in F₄ progenies of KKM 1 x VBN 6 in black gram (*Vignamungo* L. Hepper)

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Abstract

The present research work was performed to quantify the genetic variability parameters, correlation and path coefficient studies for nine quantitative characters in F₄ black gram population. The magnitude of phenotypic coefficient of variance was higher than the observed genotypic coefficient of variance and it was revealed that the environment played a main role in the expression of traits. High genotypic and phenotypic coefficient of variation accompanied with high heritability and high genetic advance was recorded for number of pods per plant and single plant yield which indicated that these traits were governed by additive gene action. Single plant yield showed strong positive correlation with number of clusters per plant, number of pods per plant, number of seeds per pod, pod length and 100 seed weight both at phenotypic and genotypic levels. Number of pods per plant exhibited high and positive direct effect on single plant yield followed by number of seeds per pod and 100 seed weight. Number of pods per plants was highest indirect effect on single plant yield through number of seeds per pod, pod length and 100 seed weight. Hence, selection of these traits indicated scope for improving the single plant yield through selection in black gram.

Keywords: Black gram, genetic variability, correlation, path coefficient analysis

Introduction

Pulses are the most important vegetarian diet crop in many Asian countries like India, Pakistan and West Bengal. Pulses are also known as power house of nutrients (Perfect combination of all nutrients) because they possess high protein (25-26%), carbohydrate (60%), fat (1.5%), high fibre content and large of amount minerals and vitamins. Legumes are well adapted to the agronomic cropping systems, nutritionally important crop with high economic value and they fix atmospheric nitrogen into soil to improve soil fertility. Among the pulses, black gram is self-pollinated, short duration, fast growing warm weather crop and mostly growing in rice fallows in rainfed conditions. Major constraints of higher productivity in black gram are lack of suitable crop types, absence of variability, narrow genetic base (higher degree of relatedness) and highly prone to biotic and abiotic stress (Souframanien *et al.*, 2004) [21]. Genetic variability is an essential tool for the improvement of yield and other complex polygenic characters (Swamy *et al.*, 2004) [23]. Hybridization creates wider genetic variability among available genotypes of black gram, and which is heritable and guide to selection and develops desired plant types. Success of selection depends upon the magnitude and nature of genetic variability present in the population (Johnson *et al.* 1995) [11]. Heritability indicates the expression of particular trait (Priyanka *et al.*, 2016) also it is used to measure the breeding value. Genetic advance will provide information for genetic gain of selection. High heritability with high genetic advance is responsible for effective selection of economically important traits or gene combinations within population (Akbar *et al.*, 2003) [1] and it is the sign of additive gene effects (Aytaç *et al.*, 2009) [3]. Correlation coefficient will give clear cut idea about the direction and magnitude of association and interaction between yield and yield components (Vyas *et al.*, 2018) [25] which serves the selection of most suitable character combinations for black gram yield improvement (Kumar *et al.*, 2003) [13]. Path coefficient analysis designed to quantify the inter-relationship between yield components and their direct and indirect influence on seed yield (Sushmitharaj *et al.*, 2018) [22] and in other words, to measure the direct and indirect effects of various yield components also it helps to combine the desirable traits in single variety. For crop improvement, the understanding of genetic

variability for particular economic traits and their heritability coupled with genetic advance is helpful to develop high yielding genotypes in black gram breeding programs (Rao *et al.*, 2006) [17]. The present research work was performed to quantify the genetic variability parameters, correlation analysis and path coefficient analysis in F₄ black gram population (KKM 1 x VBN 6) with an aim to assess the significant variability of agro-morphological traits can be used for future exploitation.

Materials and Methods

In present study, the experimental materials consists of 90 F₄ plants derived from the cross between KKM 1 x VBN 6 along with one check variety (Co 5) were raised and evaluated under randomised block design (RBD) with two replications. Each replication consists of two rows of each F₄ lines with plot size of 4m x 3m and row to row spacing was 30 cm and plant to plant spacing was 10 cm. The experiments were

conducted in Agricultural College and Research Institute, Killikulam during *Rabi* 2020. Well adopted standard agronomic practices were followed to raise healthy and uniform crops. Five random competitive plants in each entry from each plot were used for biometrical observations. The data recorded on a plot basis for nine quantitative traits *viz.*, days to fifty per cent flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length(cm), 100 seed weight(g) and single plant yield(g). The data were subjected to standard statistical methods used to worked out parameters of genetic variability *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) (Burton,1952) [5], heritability (Burton *et al.*, 1953) [6], genetic advance (Johnson *et al.*, 1955) [11] and path analysis (Dewey *et al.*,1959) [9] respectively.

Parents details

Parents	Cross combination	Source	Special features
KKM 1 (Female)	COBG 643 x VBN 3	Agricultural College and Research Institute, Killikulam.	1. Moderately resistant to Yellow Mosaic Virus, powdery mildew, pod borer 2. Resistant to root knot nematode 3. Rice fallow pulses
VBN 6 (Male)	VBN 1 x <i>Vignamungo var. silvestris</i>	National Pulse Research Centre, Vamban.	1. Resistant to Yellow Mosaic Virus 2. Synchronized pod maturity

Results and Discussion

There was significant genetic variation observed for nine quantitative traits recorded in 90 F₄ plants (Table 1). High level of variations indicated for high level diversity and enhanced to improvement of economically desirable traits.

GCV ranged from 5.87 per cent (days to 50% flowering) to 46.23 per cent (single plant yield) and PCV ranged from 6.18 per cent (days to 50% flowering) to 46.29 per cent (single plant yield). Number of pods per plant (25.63 and 27.30) and single plant yield (46.23 and 46.29) showed high GCV and PCV values, respectively. Similar results were reported by Gomathi *et al.*, (2020) and Kuralarasan *et al.*, (2021). Number of primary branches per plant (14.59 and 19.52), number of clusters per plant (14.37 and 19.51), plant height (14.30 and 15.11), number of seeds per pod (10.93 and 13.92) exhibited moderate GCV and PCV respectively. Similar findings were recorded by Priyanka *et al.*, (2016). 100 seed weight (10.16 and 9.00) showed moderate PCV with low GCV. Similar results were recorded by Shalini *et al.*, (2017) [19] and Kiran *et al.*, (2021) [12]. However, low PCV and GCV were exhibited for days to 50% flowering (6.18 and 5.87) and the result is in agreement with Malarkodi *et al.*, (2020), and also pod length (7.21 and 5.97). Similar result was observed by Rehman *et al.*, (2021). PCV was slightly higher than GCV indicated the influence of environment on expression of nine biometric traits. Relatively high genotypic coefficient of variation coupled with heritability could be a better chance for improvement of all yield related traits.

High heritability together high genetic advance suggests that more effective prediction of genetic gain under the selection (Arora, 1991) [2]. Heritability ranged from 54.25 per cent for number of clusters per plant to 99.73 per cent for single plant yield. High heritability coupled with high genetic advance per mean was observed for the traits *viz.*, plant height (89.55 and 27.88), number of pods per plant (88.13 and 49.56) and single plant yield per plant (99.73 and 95.1). These findings are in accordance with Chippy *et al.*, (2021) [7] and (Kuralarasan *et al.*,(2021). High heritability with substantial amount of genetic advance exhibited for the characters are governed by

additive gene action and it revealed that improvement of particular traits by progeny selection, pure line selection and mass selection is highly effective.

High heritability combined with moderate genetic advance per mean recorded for the traits *viz.*, days to 50% flowering (90.40 and 11.51), number of seeds per pod (61.73 and 17.70) pod length (68.47 and 10.17) and 100 seed weight (78.52 and 16.53). Similar result was reported by Kuralarasan *et al.*,(2018) [21]. Moderate heritability with high genetic advance percent mean was exhibited for number of primary branches (55.87 and 22.46) and number of clusters per plant (54.25 and 21.80) and these results were in agreement with Sarvani *et al.*, (2020) and Kiran *et al.*,(2021) [12]. High heritability with low genetic advance revealed that the presence of non- additive gene action and selection is not effective for improving these traits.

Correlation studies indicated the association between several plant growth characters. The genotypic correlation coefficients between seed yield and its component characters and inter correlation among different traits are presented in Table 2. Estimation of correlation coefficient reveals interrelationship between yield and its related traits and this knowledge is used for genetic improvement of seed yield through high selection efficiency. Correlation tends to reveal only the nature and degree of relationship between yield related characters and does not show its direct and indirect effects however path coefficient analysis provides information about direct and indirect effects of independent variables on the dependent variable. In the present study, correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant association with number of clusters per plant (0.559),number of pods per plant (0.892), number of seeds per pod (0.682), pod length (0.546) and 100 seed weight (0.709). Similar results were reported by Mohanlal *et al.*, (2018) [16]. Days to 50% flowering positively correlated with plant height and it was in agreement with Chippy *et al.*, (2021) [7]. 100 seed weight was positive and significant association with number of pods per plant (0.468), number of seeds pod (0.433) and pod length (0.349). Similar

result findings were observed for number of pods per plant, number of seed pod by Baisakh *et al.* (2014) [4] and pod length was reported by Sathees *et al.* (2019) [18]. Pod length was significant positively correlated with number of pods per plant (0.300), number of seeds per pod (0.832). It was in accordance with earlier findings of Abbas *et al.*, (2021). Number of seeds per pod was positively associated with number of pods per plant (0.399) and similarity in findings was reported by Mohanlal *et al.*, (2018) [16]. Number of pods per plants was positively correlated with number of cluster per plant (0.704) and this result was on par with the finding of Tank *et al.*, (2019) [24]. Days to 50% flowering was non-significant and negatively correlated with number of cluster per plant (-0.063), number of pods plant (-0.076), number of seeds per pod (-0.119), pod length (-0.164), 100 seed weight (-0.042) and single plant yield (-0.089). Similar results were found for number of cluster per plant and number of pods plant by Shanthi *et al.*, (2019) [20], number of seeds per pod by Sathees *et al.*, (2019) [18] and single plant yield (-0.0898) by Dheeraj *et al.*, (2020). Number of pods per plants was significant and positively correlated with number of seeds per pod (0.399), pod length (0.300), 100 seed weight (0.468) and single plant yield (0.892). Similar results were reported for number of seed per pod, 100 seed weight, pod length and single plant yield by Sathees *et al.*, (2019) [18]. Number of seeds per pod significant and positively associated with pod length (0.832) and 100 seed weight (0.433). Similar results reported in number of seeds per pod significant and positively associated with pod length by Gomathi *et al.*, (2020) [10] and 100 seed weight by Abbas *et al.*, (2021). Pod length was significant and positively correlated with 100 seed weight (0.349) and this was earlier reported by Abbas *et al.*, (2021). Correlation matrix chart described the association of different traits in Fig 1 and Fig 2. Path coefficient analysis is a powerful statistical method, it is used for quantify the interrelationship of different yield related traits and their direct (direct influence on seed yield traits) and indirect effects (indirect influences on seed yield

traits) on the yield. Path estimation is based on splitting the observed correlation coefficient into direct (true relationship between them) and indirect effects (yield character interrelationship between another component trait) of yield and its related components. Selection process is based on correlation, may be sometimes misleading to improvement on yield component characters (Codawar, 1980) [8].

In the present investigation, number of pods per plant had high direct effect on seed yield per plant (Table 3). The perusal of results revealed that, number of pods per plant (0.458) exhibited high and positive direct effect on single plant yield followed by number of seeds per pod (0.293), 100 seed weight (0.277), days to 50% flowering (0.024), number of primary branches per plant (0.020), pod length (0.021) showed moderately positive and direct effects on the single plant yield. This was in accordance with the earlier findings of Srividhya *et al.*, (2005) and Punia *et al.*, (2014). Plant height (-0.047), number of cluster per plant (-0.002) showed negative direct effect on single plant yield. Selection based on these traits could be more effective in increasing the seed yield. These results were in identical with Sathees *et al.*, (2019) [18]. Number of pods per plant showed the highest indirect effect on the single plant yield through number of seeds per pod (0.651), pod length, 100 seed weight (0.304) Plant height indicated negligible negative direct effect (-0.047) coupled with negative indirect effects through days to 50% flowering (-0.016), number of primary branches per plant (-0.021), number of seeds per pod (-0.001), pod length (-0.004) and 100 seed weight (-0.005) on single plant yield. On contrary, days to 50% flowering revealed that direct effect (0.024) and negligible indirect negative effects through number of clusters per plant (-0.002), number of pods per plant (-0.002), number of seeds per pod (-0.003), pod length (-0.004) and 100 seed weight (-0.001) on single plant yield. Estimates of residual effects were 0.15 observed in the present investigation which measured the contribution of the characters.

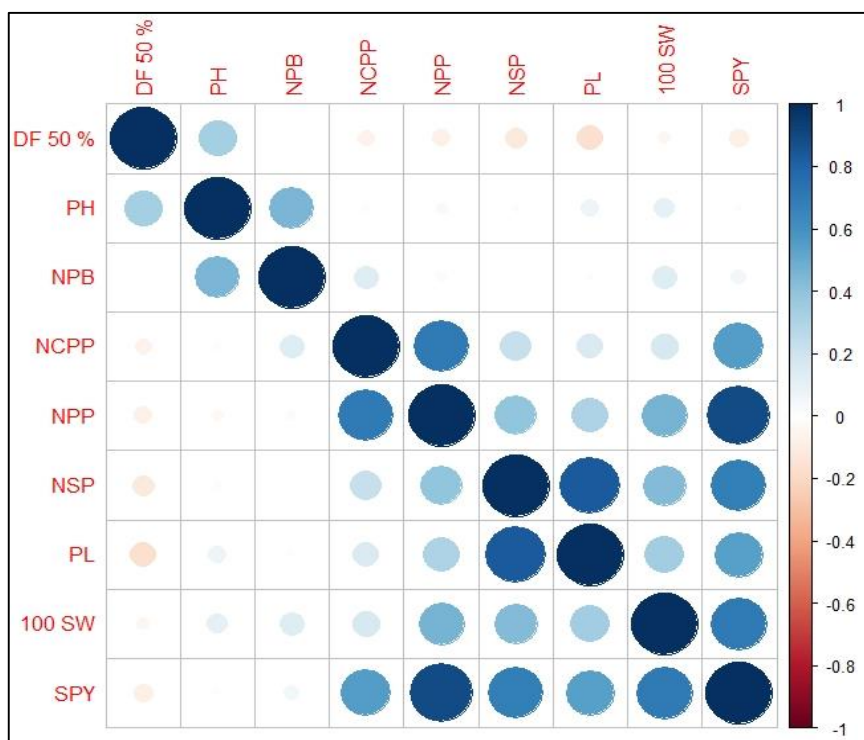


Fig 1: Correlation matrix between different traits in F4 derivatives of black gram

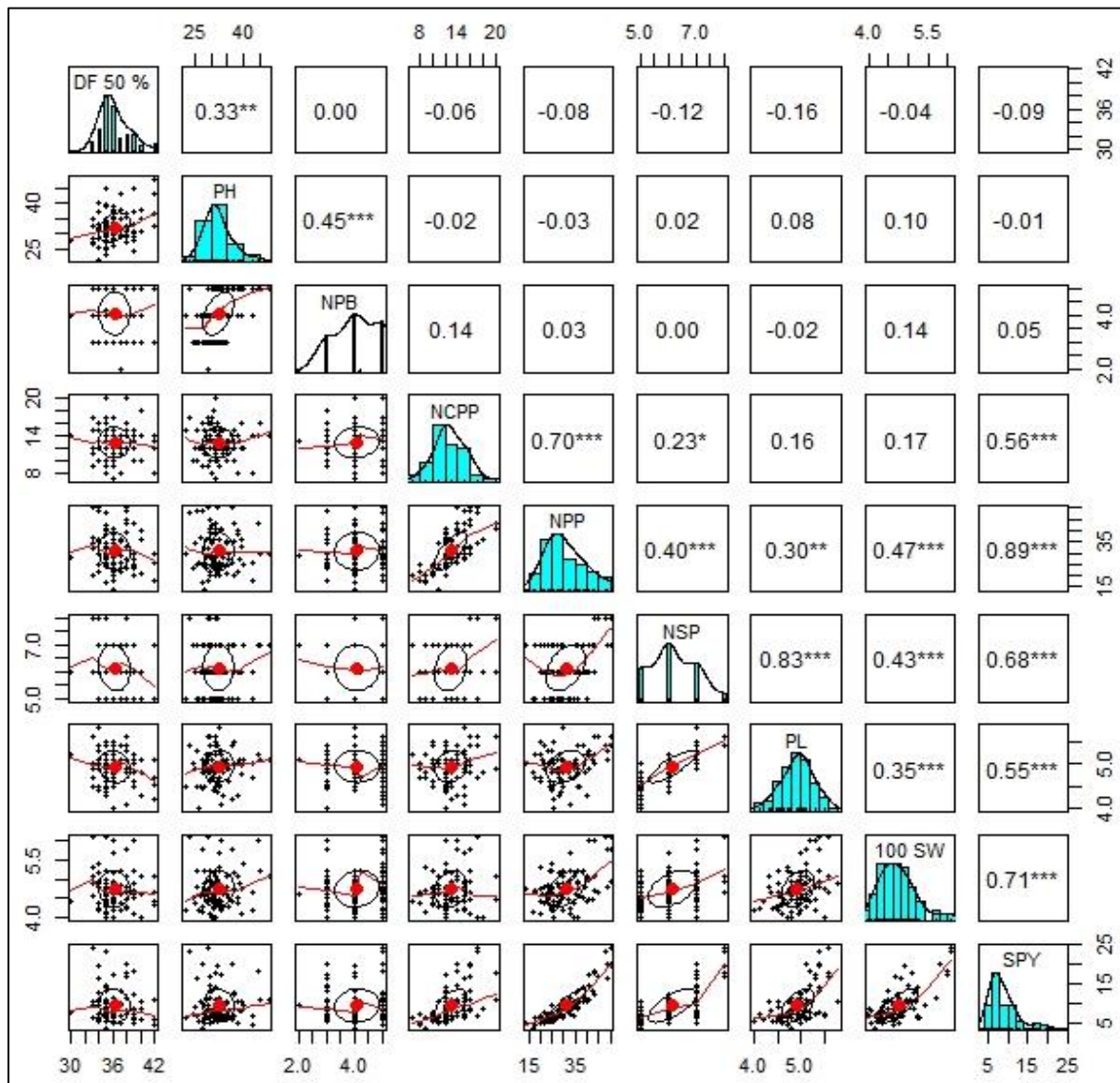


Fig 2: Chart of correlation matrix between different traits in F₄ derivatives of the cross KKM 1x VBN 6

[**significance at 5% level, *** significance at 1% level]
 [DFF-Days to 50 per cent flowering (%), PH-Plant height (cm), NPB-Number of primary branches per plant, NCPP-Number of clusters per plant, NPPP-Number of pods per

plant, NSPP-Number of seeds per pod, HSW-Hundred seed weight (g), PL-Pod length (cm) and SPY-Single plant yield (g)]

Table 1: Summary statistics of genetic variability parameters for nine yield components in F₄ population (KKM1 x VBN 6)

Traits	Range	Mean	CV	PCV (%)	GCV (%)	H (%)	GAM (%)
DFF	30.0 - 42.0	36.18	6.18	6.18	5.87	90.4	11.51
PH	21.60 - 48.00	32.1	15.11	15.11	14.3	89.55	27.88
NPB	2.0 - 4.0	4.08	19.52	19.52	14.59	55.87	22.46
NCPP	7.0 - 20.0	12.9	19.51	19.51	14.37	54.25	21.8
NPP	14.0 - 50.0	30.81	27.3	27.3	25.63	88.13	49.56
NSP	5.0 - 8.0	6.14	13.92	13.92	10.93	61.73	17.7
PL	4.0 - 5.80	4.93	7.21	7.21	5.97	68.47	10.17
HSW	3.98 - 6.10	4.75	10.16	10.16	9.00	78.57	16.43
SPY	3.54 - 24.40	9.31	46.29	46.29	46.23	99.73	95.1

[CV= Coefficient of Variation, PCV= Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H(%) =Heritability, GAM= Genetic advance as per cent of the mean]

Table 2: Summary statistics of correlation coefficients for nine yield components in F₄ population (KKM1 x VBN 6)

Trait	DFF	PH	NPB	NCPP	NPP	NSP	PL	HSW	SPY
DFF	1.000**								
PH	0.335*	1.000**							
NPB	0.003	0.453**	1.000**						
NCPP	-0.063	-0.018	0.139	1.000**					

NPP	-0.076	-0.031	0.028	0.704**	1.000**				
NSP	-0.119	0.018	-0.001	0.226	0.399*	1.000**			
PL	-0.164	0.079	-0.015	0.157	0.300*	0.832**	1.000**		
HSW	-0.042	0.103	0.135	0.169	0.468**	0.433**	0.349*	1.000**	
SPY	-0.089	-0.014	0.052	0.559**	0.892**	0.682**	0.546**	0.709**	1.000**

[*significance at 5% level, ** significance at 1% level]

[DFF-Days to 50 per cent flowering (%), PH-Plant height (cm), NPBP-Number of primary branches per plant, NCPP-Number of clusters per plant, NPPP-Number of pods per plant, NSPP-Number of seeds per pod, HSW-Hundred seed weight (g), PL-Pod length (cm) and SPY-Single plant yield (g)]

Table 3: Direct and indirect effects for nine yield components in F₄ population (KKM1 x VBN 6)

Traits	DDF	PH	NPBP	NCPP	NPPP	NSPP	PL	HSW	SPY
DDF	0.024	-0.016	0.000	0.001	-0.049	-0.035	-0.003	-0.012	-0.089
PH	0.008	-0.047	0.009	0.001	-0.049	0.005	0.002	0.028	-0.014
NPBP	0.000	-0.021	0.020	0.000	-0.020	-0.000	-0.000	0.037	0.052
NCPP	-0.002	0.001	0.003	-0.002	0.018	0.066	0.003	0.047	0.559
NPP	-0.002	0.001	0.001	-0.016	0.458	0.117	0.006	0.129	0.892
NSP	-0.003	-0.001	-0.000	-0.012	0.651	0.293	0.017	0.120	0.682
PL	-0.004	-0.004	-0.000	-0.003	0.195	0.243	0.021	0.097	0.546
HSW	-0.001	-0.005	0.003	-0.003	0.304	0.127	0.007	0.277	0.709

Residual effect = 0.15, direct effects indicated on diagonal

[DFF-Days to 50 per cent flowering (%), PH-Plant height (cm), NPBP-Number of primary branches per plant, NCPP-Number of clusters per plant, NPPP-Number of pods per plant, NSPP-Number of seeds per pod, HSW-Hundred seed weight (g), PL-Pod length (cm) and SPY-Single plant yield (g)]

Conclusion

In general, the results of this study revealed that selection based on number of pods per plant, single plant yield were high heritability and strong genetic advance, showing additive gene action for the expression of these characters and the opportunity for simple selection for trait enhancement. From correlation and path coefficient analysis, it can be concluded that selection for number of pods per plant has a high and positive direct effect on single plant yield, followed by number of seeds per pod, 100 seed weight, days to 50% flowering, number of primary branches per plant, pod length and direct selection based on these traits would be useful for enhancing seed yields.

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