

Gene Action for Some Quantitative Traits in Mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Diallel analysis was performed using ten mungbean genotypes and their 45 F₁ hybrids. The experiment was laid down in Randomized Block Design (RBD) with three replications during *kharif* 2012 at Centre of Excellence for Research on Pulses, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar, Gujarat. The estimates of D, H₁ and H₂ which measure the variance due to additive and dominance gene effects were significant for all the seven characters like Seed yield per plant days to flowering, days to maturity, Plant height, Pods per plant, 100-seed weight and Protein contents where Hayman's diallel analysis was fully or partially valid. Narrow sense heritability was low for seed yield and most of the yield component characters. Looking to the role of additive as well as non-additive gene effects in the inheritance of most of the traits in the population under study, biparental mating and diallel selective mating system was found appropriate for creation of more variability and improvement in seed yield per plant. As per Hayman's graphical analysis, the parental line GM 2 had maximum dominant genes for earliness. Similarly, the parental line COGG 192 was found having maximum recessive genes for increasing 100-seed weight.

Key words Gene action, diallel, additive, non additive and Hayman's graphical analysis.

Mungbean [*Vigna radiata* (L.) Wilczek.] commonly known as greengram is the most important pulse crop in India. This is an important seed legume which have prime role in meeting the quantitative and qualitative requirement of food and protein in India and other Asian countries. The diploid chromosome number of mungbean is 2n = 22 (Karpechenko, 1925 and Krishnan and De, 1965). Mungbean is self-pollinated crop. Improved varieties have been developed in Taiwan and India. Genetic improvement in this crop has been made primarily through conventional techniques such as

selection from local material and pedigree method of breeding. According to Vavilov (1926), the mungbean have been originated in Hindustan region of Asia *i.e.*, Indian sub-continent. Genus *Vigna* belongs to tribe Phaseoleae of the family Fabaceae (Leguminosae) and it contains 104 accepted species (ILDIS, 2013). *Vigna radiata* (L.) R. Wilczek. is having two synonyms *i.e.*, *Phaseolus aureus* Roxb. and *Phaseolus radiatus* L. and the species also prescribed having two botanical varieties as *Vigna radiata* var. *radiata* (L.) R. Wilczek. and *Vigna radiata* var. *sublobata* (Roxb.) Verdc. The seed contains, protein (22.88 to 24.65 %), carbohydrates (62.6 %), crude fibre (4.30 to 4.80 %) and lipids (1.53 to 2.63 %). Like other pulses, the protein of mungbean is rich in lysine, an essential amino acid that is absent in cereal grains (Saleem et al., 1998). Seed yield is an important trait as it measures the economic productivity in mungbean, but its inheritance is extremely complex. The classical breeding systems that make use of additive genetic variance will be effective for improving the mungbean seed yield, but very little basic information is available on all types of gene effects controlling the seed yield and its components in mungbean (Khattak *et al.*, 1999). To exploit the existing genetic variability in mungbean breeding material for seed yield as efficiently as possible, the breeder would need basic information regarding the inheritance of grain yield and its closely related components for devising an efficient selection programme. It also provides an insight into the nature and magnitude of fixable and non-fixable genetic variances and thus helps to accomplish proper breeding method.

MATERIAL AND METHOD

The experimental material consisting of ten genotypes (GM 2, GM 3, GM 4, K 851, Meha, Pusa Vishal, Vamban 2, Hum-1, SML-668 and COGG-192) were obtained from the Centre of Excellence for Research on Pulses, Sardarkrushinagar. The crossing in diallel fashion excluding reciprocals among the ten genotypes was

Table 1. Estimation of genetic component of variance and other parameters for various characters in green gram.

Parents	Days to flowering	Days to maturity	Plant height	Branches per plant	Pods per plant	Pod length	Seeds per pod	Seed Yield per plant	100-seed weight	Protein content
b (W _r , V _r) 1	0.39	0.80	0.27	-0.01	0.172	0.18	0.03	0.32	0.59	0.18
t _{b-0}	-2.36*	-5.26**	-0.88	5.42**	-0.81	-3.60	-1.25	-3.17*	-3.15*	-0.63
t _{1-b}	3.71**	1.28	2.33*	5.26**	3.06*	5.76	7.85**	6.74**	2.23	2.93*
t ²	3.67	0.30	0.06	30.11**	2.136	7.97**	7.84**	0.001	1.04	0.36
D	4.59*	4.21*	82.46*	-	36.56**	-	-	3.25*	0.80*	0.58*
H ₁	9.15*	5.53*	26.53*	-	167.9**	-	-	15.57*	2.58*	2.73*
H ₂	7.25*	3.88*	19.94*	-	149.9**	-	-	14.89*	2.03*	1.86*
F	3.05	4.48*	77.16	-	36.0	-	-	2.51	1.03*	1.17*
h ²	1.11	6.36*	4.19	-	5.00	-	-	6.06*	0.00	0.45
E	0.27	0.47*	5.77	-	2.56	-	-	2.45*	0.03	0.01
(H ₁ /D) ^{0.5}	1.41	1.15	1.80	-	2.143	-	-	2.19	1.79	2.15
H ₂ /4H ₁	0.19	0.18	0.18	-	0.22	-	-	0.24	0.19	0.17
KD/KR	1.61	2.74	1.70	-	1.59	-	-	1.43	2.09	2.73
h ² /H ₂	0.15	0.32	0.02	-	0.034	-	-	0.10	0.01	0.24
r (P, W _r + V _r)	0.64*	0.88*	0.21*	-	0.033	-	-	0.75*	0.74*	0.21
Heritability	0.45	0.32	0.42	-	0.188	-	-	0.10	0.24	0.23

carried out during summer 2012. The standard agronomical practices were followed to raise the parental plants under favourable field conditions for satisfactory emasculation, crossing and normal pod development. The selfed seed for each of the ten parental lines was also produced simultaneously. Finally, the experimental material comprised of ten parental lines and their 45 hybrids. The plots of 55 genotypes comprising of 10 parents and their 45 F1 were planted in a randomized block design with three replications in second week of July, 2012. The plot size for each genotype was 2.00 m x 0.45 m keeping 45 cm row to row and 10 cm plant to plant distance. All agronomical and plant protection practices were followed throughout the crop duration.

RESULT AND DISCUSSION

The diallel analysis given by Jinks and Hayman (1953) and Hayman (1954) was employed to understand the gene effects with respect to various characters in mungbean.

Unit slope of regression line and non-significant t² values indicated the validity of the

additive-dominance model for days to maturity and 100-seed weight. The t² values were non-significant, but regression coefficient 'b' deviated significantly from unity for seed

yield per plant, days to flowering, plant height, pods per plant and protein content which indicated partial validity of the assumptions underlying the model. Therefore, numerical genetic component analysis was carried out for these five characters only (Table 1).

The regression co-efficient deviated significantly from unity and t² values (Table 1) were significant for branches per plant, pod length and seed per pod which indicated that, one or more assumptions underlying the Jinks-Hayman diallel analysis were not met and therefore the analysis was not considered valid for these three traits.

Days to maturity

The t² value for days to maturity was non-significant (Table. 1) and regression co-efficient (b = 0.80) for this character revealed validity of the graphical analysis.

Table 2. Comparison of diallel analyses of various characters in mungbean.

Characters	χ^2_{GCA}	$[H_1/D]^{1/2}$	Status of Hayman's analysis
	χ^2_{SCA}		
Seed yield per plant	Over dominance (0.11)	Over dominance (2.19)	Partially valid
Days to flowering	Over dominance (0.41)	Over dominance (1.41)	Partially valid
Days to maturity	Over dominance (0.46)	Over dominance (1.15)	Valid
Plant height	Over dominance (0.32)	Over dominance (1.80)	Partially valid
Branches per plant	Over dominance (0.04)	Over dominance (1.34)	Invalid
Pods per plant	Over dominance (0.12)	Over dominance (2.14)	Partially valid
Pod length	Over dominance (0.35)	Over dominance (2.95)	Invalid
Seeds per pod	Over Dominance (0.26)	Over dominance (1.27)	Invalid
100-seed weight	Over dominance (0.15)	Over dominance (1.79)	Valid
Protein contents	Over dominance (0.01)	over dominance (2.15)	Partially valid

In numerical analysis, components D, H_1 , H_2 and h^2 were significant indicating importance of both additive and dominance effects (Table .1). The parameter F was positive and significantly high which revealed higher proportion of dominant genes in parents. The value of E significant (0.47) indicating effect of environment in the expression of the trait.

The ratio $(H_1/D)^{0.5}$ (1.15) indicated over dominance. The ratio KD/KR (2.74) indicated presence of higher proportion of dominant genes. The parameter h^2/H_2 was (0.32) which suggested that at least one gene group was operating in the inheritance of this trait. The value of $H_2/4 H_1$ was 0.17, which indicated unequal distribution of positive and negative alleles among the parents. The 'r' value (0.88) between Y_r and $(W_r + V_r)$ was significant and positive indicating role of recessive genes in increasing early maturity. The narrow sense heritability was found low (0.32) for this trait.

In Graphical analysis was performed for this trait to obtain genetic information about the parents.

The regression line (Fig. 1) intercepted W_r axis below the origin which revealed over dominance. Widely scattered array points of parents on the graph indicated considerable gene differences among the parental lines. The parent SML 668 occupied its position far away from point of origin represented higher proportion of recessive genes for early maturity whereas the parent GM 3 occupied nearest position from the origin indicating maximum dominant genes for affecting late Maturity.

100-seed weight

The test of validity for Jinks and Hayman diallel analysis revealed that all the assumptions were fulfilled.

The components D, H_1 , H_2 and F were positive and significantly different from zero. The degree of dominance (1.79) indicated over dominance. The ratio KD/KR (2.09) indicated presence of higher proportion of dominant genes. The parameter h^2/H_2 (0.01) suggested that, at least one gene group was operating in the inheritance of this trait. The

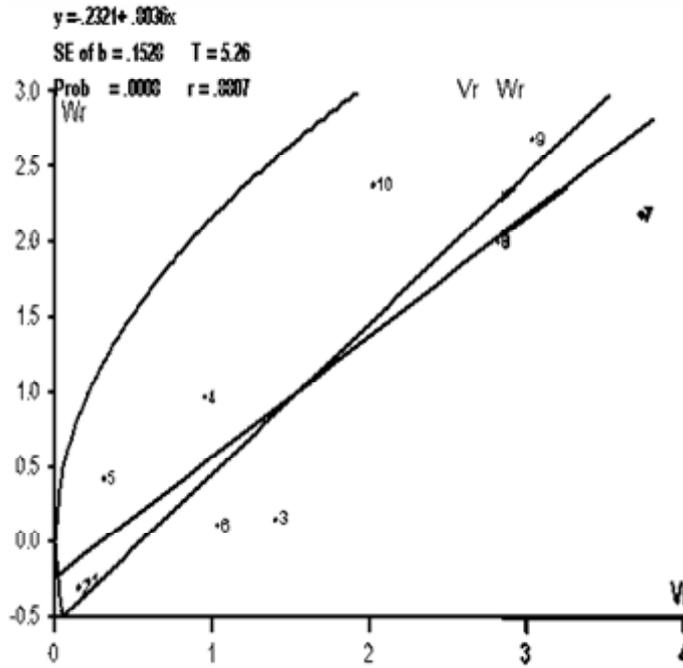


Fig. 1 Vr - Vr graph for days to maturity

1. GM 2, 2. GM 3, 3. GM 4, 4. K 851, 5. Meha, 6. Pusa Vishal, 7. Vamban -2, 8. Hum -1, 9. SML 668, 10. COGG -192

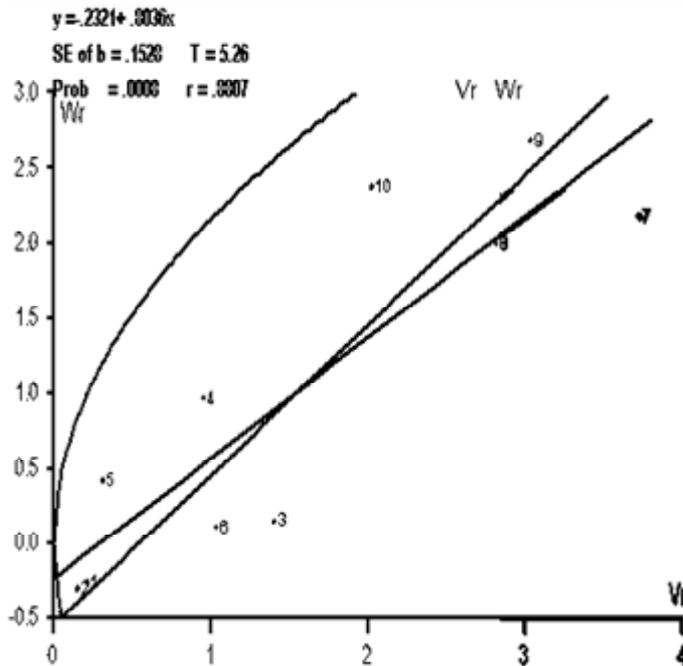


Fig. 2. Vr- Vr graph for 100 seed weight

value of $H_2/4H_1$ was (0.19) and failed to demonstrate equal distribution of positive and negative alleles among the parents. The significant F (1.03) indicated unequal proportion of dominant and recessive genes in the parents. The narrow sense heritability was found low (0.24) the 'r' value (0.74) between Y_r and $(W_r + V_r)$ was significant and positive indicating

the role of dominant genes in increasing 100-seed weight.

In Graphical analysis was performed for this trait to obtain genetic information about the parents. The regression line (Fig. 2) which intercepted W_r axis below the origin revealed over dominance. The widely scattered array points of parents on the

graph indicated considerable gene difference among the parental lines. The parental line COGG-192 was found to have maximum recessive genes for increasing 100-seed weight.

In graphical analysis, the regression line intercepted W_r axes below the origin, which indicated over-dominance for days to maturity and 100-seed weight. The parental line GM 2 was situated near the origin, hence, it had maximum dominant genes for earliness. Similarly, the parental line COGG-192 was found having maximum recessive genes for increasing 100-seed weight as it was situated far from the origin at the end of the regression line. The t^2 values were non-significant, but regression co-efficient 'b' deviated significantly from unity for seed yield per plant, days to flowering, plant height, pods per plant and protein content, which indicated partial validity of the assumptions underlying the Jinks and Hayman's model. Therefore, only numerical genetic component analysis was carried out for these five characters (Table. 1.).

For branches per plant, pod length and seeds per pod, the t^2 values were significant and the regression co-efficient also deviated significantly from unity which indicated non-fulfillment of assumptions of the analysis. Non-fulfillment of assumptions of Jinks and Hayman's model for branches per plant, pod length and seeds per pod, thus, indicated presence of non-allelic gene interactions and/or linkage disequilibrium in their inheritance.

The estimates of D , H_1 and H_2 , which measure the variance due to additive and dominance gene effects, were significant for all seven characters where this diallel analysis was fully or partially valid (Table.1.). These clearly indicated involvement of both additive and dominance gene action for the characters seed yield per plant, pods per plant, 100-seed weight, plant height, protein content, days to flowering and days to maturity. This was reflected clearly in low to moderate heritability for most of these characters. In mungbean, varying magnitude

of additive and non-additive gene effects have been reported for different traits by Singh *et al.* (1993).

The information obtained from Griffing's and Hayman's diallel analyses pertaining to the nature of gene action controlling different characters is summarized in Table 2. A perusal of the table leads to draw the conclusion that, both analyses gave more or less the same picture with regard to the magnitude of additive and non-additive genetic effects for respective characters. Both the diallel analyses revealed over dominance for seed yield and other characters. This situation can be interpreted as presence of epistasis (non-allelic interaction) in the inheritance of seed yield and the component traits.

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Received on 12-06-2016

Accepted on 17-06-2016