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Identification of elite genotype through gene action for indirect trait in Mungbean

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Abstract
Diallel analysis was performed using ten mungbean genotypes and their 45 F_1 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. 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.

Keywords: Dialle analysis, recessive, dominant, gene action

Introduction
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 crop is extensively grown under rainfed condition of arid and semi-arid regions of India during monsoon and under irrigated condition during summer season. In India, it is cultivated in the states of Maharashtra, Gujarat, Tamil Nadu, Andhra Pradesh, Bihar and Uttar Pradesh. It is the third important pulse crop of India in terms of area cultivated and production after Chickpea and Pigeonpea. It is the third important pulse crop of India in terms of area cultivated and production after Chickpea and Pigeonpea. The area under greengram in India is around 3.8 million hectares with a production of 1.5 million tonnes. The average productivity of greengram in India is 550 kg/ha (Anonymous, 2008) [1].
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 (Leguminoseae) and it contains 104 accepted species (ILDIS, 2013) [5]. *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. Pulses contribute as a major source of dietary protein for the large portion of vegetarian population of the world. Per capita availability of pulses is only 36 g/person/day in India against the World Health Organization recommendation of 80 g/person/day (Anonymous, 2010) [2]. Pulses also improve the nutrient status of soil through atmospheric nitrogen fixation and adds humus to the soil. The dietary or nutritional value of mungbean has been very popular from the ancient times. 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). In addition, mungbean is lower in phytic acid than Pigeonpea, Soybean and Cereals (Nair *et al*., 2013) [6]. Phytic acid is commonly found in cereal and legume crops and has a negative impact on iron and zinc bio-availability in plant-based diets. In India, mungbean is used as a pulse in the preparation of dhal, a soup eaten with a cereal or other traditional cuisines like bean sprout, mungbean noodles, sweets and dried-fried patties of different kinds. Mungbean has easy digestibility compared to other pulses (Singh *et al*., 2010) [10].
The diploid chromosome number of mungbean is 2n = 22 (Karpechenko, 1925 and Krishnan and De, 1965) [9]. 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. Diallel analysis provides a systemic approach for identification of superior parent and crosses which is the basic material on which the success of a breeding programme depends. The advantage of the diallel analysis is that, it gives better picture of genetic information of the material under investigation in a single generation.

Combining ability analysis furnishes information to identify desirable parents and genetic architecture of the crosses. 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. Genetic information regarding heterosis provides a clue for selecting the most suitable parents for hybridization. The presence of heterosis can only be utilised in highly self-pollinated pulse crops for the development of high yielding pureline varieties (Singh 1971) [9]. The present investigation was therefore, planned on diallel cross analysis involving ten diverse genotypes of mungbean [*Vigna radiata* (L.) Wilczek.]

Material and Methods

Location and climatic condiation

The present investigation was conducted at the Centre of Excellence for Research on Pulses, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar, Gujarat State during the year 2012-13. Geographically, Sardarkrushinagar is situated at 24º - 12'N latitude and 72º - 19'E longitude having an altitude of 154.52 metres above mean sea level. It has typical semi-arid climate with moderate rainfall during June to October. The soil of the experimental plot was sandy loam.

Experimental Material

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 pedigree and source of the genotypes is given in Table.

Table 1: Paedigree of parental lines

Sr. No.	Genotypes	Pedigree	Source
1.	GM 4	GM 3 x Pusa Vishal 9933	SDAU, S.K. Nagar
2.	GM 2	Selection from local Germplasm	SDAU, S.K. Nagar
3.	GM 3	ML 9 x GM 2	SDAU, S.K. Nagar
4	K-851	4453-3 x T-44	CSAU, Kanpur
5.	Meha	Pant Mung 2 x AMP 36	IIPR, Kanpur
6.	Pusa Vishal	Selection from NK 92	IARI (New Delhi)
7.	Vamban-2	VGG 4 x MH 309	TNAU, Vamban
8.	Hum-1	BHUM1 x Pant U-30	BHU, Varanasi
9.	SML 668	Selection from 94	PAU, Ludhiana
10.	COGG-192	MGG-366 x CO GG902	TNAU, Coimbatore

The crossing in diallel fashion excluding reciprocals among the ten genotypes was 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.

Result and Discussion

Days to maturity

The t^2 value for days to flowering was non-significant Table and regression co-efficient (b = 0.80) for this character revealed validity of the graphical analysis.

In numerical analysis, components D, H_1, H_2 and h^2 were significant indicating importance of both additive and dominance effects Table. 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 Yr and (Wr + Vr) 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.

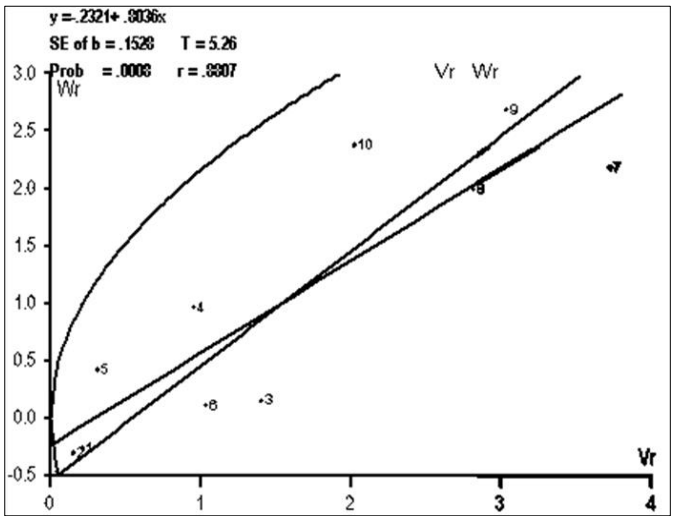

Fig 1: The regression line intercepted Wr axis below the origin which revealed over dominance

Where

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

In Graphical analysis was performed for this trait to obtain genetic information about the parents. The regression line (Fig. 1) intercepted Wr 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.

Table 2: 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 (Wr, Vr) 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, Wr + Vr)	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

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 (Table 4.10) 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 value of $H_2/4$ H_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 Yr and (Wr + Vr) was significant and positive indicating the role of dominant genes in increasing 100-seed weight.

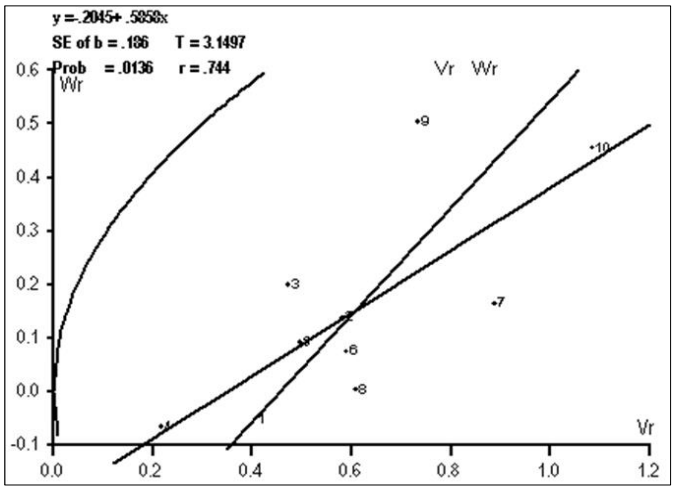

Fig 2: Wr - Vr graph for 100-seed weight

Where

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

In Graphical analysis was performed for this trait to obtain genetic information about the parents. The regression line (Fig. 2) which intercepted Wr 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 Wr 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 information obtained from Griffing's and diallel Hayman's diallel analyses pertaining to the nature of gene action controlling different characters is summarized in Table 5.4.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 epitasis (non-allelic interaction) in the inheritance of seed yield and the component traits.

Hayman (1954) [4] pointed out that his technique provides a test for additive genetic variation in absence of non-additive variation or a test of dominance in absences of epitasis. He noted that a complementary type of epitasis distorts the (Vr, Wr) graph, inflates H_1/D, depresses h^2/H_2 but have little effect on the estimates of gene frequency. A duplicate type of gene interaction depresses h^2/H_2, increases the proportion of dominants, but leaves H_1/D and $H_2/4H_1$ and the Vr - Wr graph almost unaltered. Griffing (1956) [3] has noted that this analysis provides simultaneous test for both general and specific combining ability and is more powerful in presence of non allelic gene interactions. Thus, non-validity of Haymans' analysis with over dominance in combining ability analyses for pod length, seeds per pod and branches per plant in present investigation was most probably due to presence of epitasis, the direction or magnitude of which could not be ascertained through these diallel analyses.

Summary

As per Hayman's graphical analysis, the parental line GM 2 had maximum dominant genes for earliness. Similarly, the parental line COGG-192 was having maximum recessive genes for increasing 100-seed weight.

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