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Combining Ability and Inheritance of Pod and Cluster Number in *Phaseolus mungo* L.

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Summary. A set of six *Phaseolus mungo* lines was studied in a diallel cross over two generations to investigate general and specific combining ability and mode of inheritance for cluster and pod number. General combining ability effects were more important for both characters. *Per se* performance appeared to be a good index to rank the parental lines for general combining ability. Additive gene effects with partial dominance to overdominance for these traits were noted. High cluster and pod number seem to be governed by recessive genes.

The concept of combining ability given by Sprague and Tatum (1942), with the technique developed by Griffing (1956), helps to rank parental lines for desirability in the hybridization programme. Graphical analysis, components of variance and constant parent regression analyses provide information on mode of inheritance and gene action for quantitative traits which are of immense use to the plant breeder in a hybridization programme for selection of superior segregates.

Bond (1966), using field beans, reported that most of the variance for pods per plant and clusters per plant was associated with significant general combining ability effects. Dickson (1967), in a diallel cross of F_2 generation of snap beans, reported that additive genetic variance was predominant for pods per plant. He also noted that recessive genes governed high pod number.

Information on combining ability and pattern of inheritance is lacking in *Phaseolus mungo*. This paper deals with combining ability and mode of inheritance for two yield components — pods per plant and clusters per plant.

Materials and Methods

The material for this investigation comprised six pure breeding lines, namely Mash 1–1 (P_1), Mash 47 (P_2), Mash 26–59 (P_3), Mash 35–5 (P_4), D 6–7 (P_5) and Mash 8–2 (P_6). All possible crosses, excluding reciprocals, between these lines were made in 1967. F_2 generation seed was raised from March to June 1968. Due to unfavourable environmental conditions the seed of F_2 of most of the crosses involving P_6 was not obtained. Hence, the complete diallel of 6×6 of F_1's and of 5×5 of F_2's, hereafter called set I and set II, were studied. 6 parents, 15 F_1's and 10 F_2's were grown from July to November 1968 in randomized block design with three replications. Rows and plants were spaced 90 cm and 30 cm apart. One row of each parent and of the F_1's, and four rows of F_2's, were sown in rows 3 meters long using 10 plants in each row. Non-experimental rows were provided all round the experimental plots to nullify border effects. At maturity observations were recorded for pods and clusters per plant on a randomly selected 5 plants per entry of the parents and F_1 hybrids and 15 plants per entry of F_2 generations from each replication.

Means of parents and F_1's over 5 plants, and F_2's over 15 plants, were used for statistical analysis. Analysis of variance of randomized block design was done separately for both the diallel sets. Combining ability analysis was done by using Method II and Model I of Griffing (1956). The diallel cross technique given by Jinks (1954) and Hayman (1954) was followed for graphical and components of variance analyses. $Vr\,Wr$ (Variance-covariance) and $Wr\,W'$ (Covariance-covariance) graphs were computed for both the diallel sets for both characters. The constant parent regression method suggested by Hull (1945) and developed by Griffing (1950) was used to estimate direction of dominance and type of gene action.

Results

Combining Ability

The analysis of variance showed significant differences among progeny in both the sets for both the characters. Mean values of parents, their F_1's and F_2's are given in Table 1. General combining ability effects were significant for both the sets for clusters per plant and pods per plant, but specific combining ability effects were non-significant (Table 2). Components of general combining ability were much higher than the components of specific combining ability for both the characters over both generations. Components of general combining ability increased in the F_2 generation for both the characters.

The parent P_3 bore maximum clusters per plant followed by P_2 with mean values of 32.1 and 28.0 clusters per plant respectively; P_5 bore minimum clusters with a mean value of 13.3 clusters per plant (Table 1). The parents P_3 and P_5 gave the highest and lowest general combining ability effects respectively (Table 3).

For pods per plant, in both the diallel sets parent P_3 was the best combiner and P_5 the poorest combiner; the rest of the parents gave average combining ability effects (Table 3).

Graphical Analysis

The slope of the regression line in $Vr\,Wr$ graphs for clusters per plant (Fig. 1a and 1c for set I and II respectively) did not differ significantly from ex-

Table 1. *Mean value of six parents, 15 F_1's and 10 F_2's for pods per plant and clusters per plant*

Parent/cross		Clusters per plant (No.)		Pods per plant (No.)	
Parent					
Mash 1-1		26.4		57	
Mash 47		28.0		66	
Mash 26-59		32.1		73	
Mash 35-5		24.7		50	
D 6–7		13.3		29	
Mash 8-2		26.5		59	
Cross		F_1	F_2	F_1	F_2
Mash 1-1	× Mash 47	11.4	19.6	24	47
	× Mash 26-59	22.8	34.9	51	87
	× Mash 35-5	17.5	21.4	39	51
	× D 6-7	10.9	21.2	20	47
	× Mash 8-2	23.6	—	50	—
Mash 47	× Mash 26-59	17.9	23.8	36	55
	× Mash 35-5	22.0	27.9	44	64
	× D 6-7	20.3	15.4	51	35
	× Mash 8-2	17.0	—	36	—
Mash 26-59	× Mash 35-5	23.8	28.8	55	71
	× D 6-7	19.3	18.2	48	49
	× Mash 8-2	24.8	—	56	—
Mash 35-5	× D 6-7	23.4	25.0	50	56
	× Mash 8-2	27.7	—	59	—
D 6-7	× Mash 8-2	11.1	—	24	—
C.D. at 5%		11.07	10.27	27.22	24.00
C.D. at 1%		14.58	13.83	35.84	32.32

Table 2. *Analysis of variance for combining ability*

Source of variation	Diallel set	D.F.	Mean square Clusters per plant	Mean square Pods per plant
General combining ability	I	5	59.156**	287.600*
	II	4	78.319**	378.680**
Specific Combining ability	I	15	28.370	174.200
	II	10	18.870	113.000
Error	I	40	15.980	96.740
	II	28	10.900	68.860

* and ** significant at 5% and 1% respectively.

pected unit slope indicating additive type of gene action to be predominant. The regression line passed through the *W r*-axis below the point of origin in set I, but passed through the origin point in set II, showing the presence of overdominance, and complete dominance, respectively. The array point for parent P_4 being nearest to the point of origin in the graphs of both generations, P_4 possessed the majority of dominant alleles; the array point for P_6 was farthest from point of origin in set I, and that of P_3 was farthest in set II, so that P_6 and P_3 contained most of the recessive alleles. Other parents had a balance of positive and negative alleles. The spreading pattern of array points around and along the

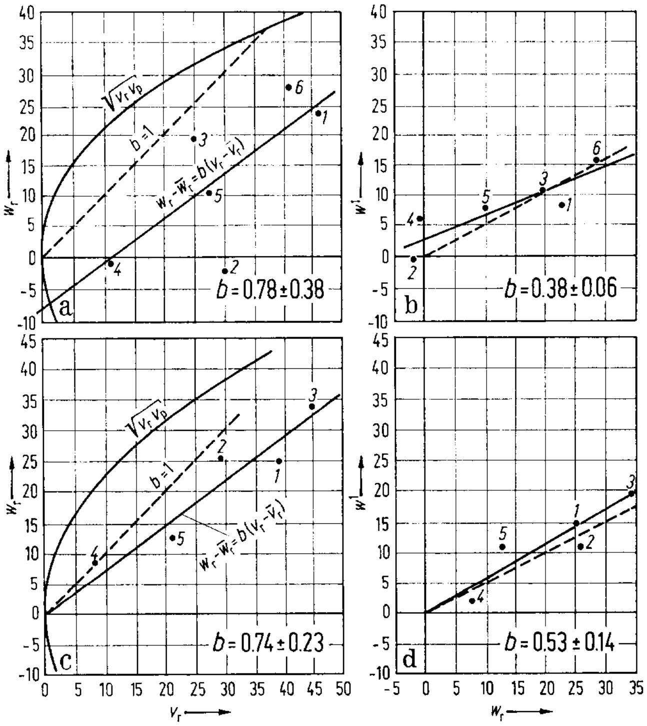

Fig. 1a. *Vr Wr* graph for clusters per plant set I
Fig. 1b. *Wr W'* graph for clusters per plant set I
Fig. 1c. *Vr Wr* graph for clusters per plant set II
Fig. 1d. *Wr W'* graph for clusters per plant set II

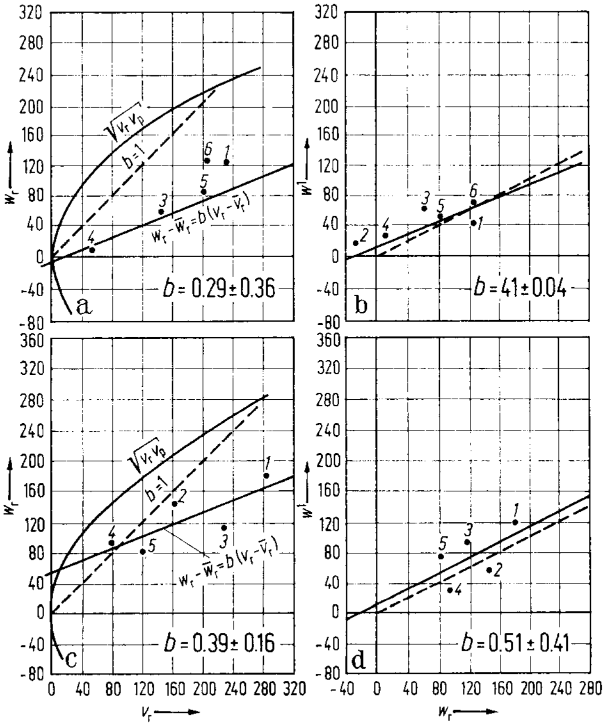

Fig. 2a. *Vr Wr* graph for pods per plant set I
Fig. 2b. *Wr W'* graph for pods per plant set I
Fig. 2c. *Vr Wr* graph for pods per plant set II
Fig. 2d. *Wr W'* graph for pods per plant set II

Table 3. *General combining ability effects of clusters per plant and pods per plant for both sets*

Character	Diallel set	Parent						S.E. gi	C.D. at 5%	C.D. at 1%
		Mash 1-1	Mash 47	Mash 26-59	Mash 35-5	D 6-7	Mash 8-2			
Clusters per plant	I	−1.150	−0.450	3.075	1.950	−4.575	1.125	±1.29	3.92	5.16
	II	0.800	−2.230	3.360	1.170	−5.410	—	±1.11	6.38	8.58
Pods per plant	I	−3.500	−0.500	8.250	2.620	−9.370	2.120	±3.17	9.60	12.64
	II	1.570	−0.300	10.430	1.000	−12.860	—	±2.80	9.06	12.20

Table 4. *Components of variance for clusters per plant and pods per plant*

Character	Set	Component								
		D	H_1	H_2	F	E	$\overline{Vr}/\overline{Wr}$	$\sqrt{H_1/D}$	u	v
Clusters per plant	I	24.11	65.08	56.92	6.52	15.98	2.29	1.64	0.67	0.64
	II	38.65	202.24	185.92	1.44	10.90	1.34	2.30	0.33	0.36
Pods per plant	I	135.92	393.08	336.92	89.52	96.74	2.79	1.70	0.67	0.30
	II	218.64	1264.52	1051.52	−3.28	68.86	1.42	2.40	0.30	0.70

Table 5. *Constant parent regression for clusters per plant and pods per plant*

Character	Diallel set	Regression							Direction of dominance (h_1)
		First order regression						Second order regression (b_2)	
		1	2	3	4	5	6		
Clusters per plant	I	0.784	−0.316	0.284	−0.018	0.220	0.984	0.003	−0.051
	II	0.603	0.545	0.791	0.186	−0.858	—	0.092	−1.725
Pods per plant	I	0.766	−0.677	−0.269	0.058	0.493	0.766	−0.190	0.836
	II	0.768	0.513	0.610	0.357	−1.353	—	0.034	−1.496

regression line indicated the presence of genotype × environment interaction and diversity among parents. *W r W′* graphs (Fig. 1 b and 1 d) confirmed the results of *V r W r* graphs. The slope of the regression line in *V r W r* graphs (Fig. 2a and 2c) for pods per plant ($b = 0.39 \pm 0.36$ and 0.39 ± 0.16 for set I and set II respectively) differed greatly from unit slope indicating genetic interaction. The regression line cut the *W r*-axis below and above the point of origin showing overdominance in the F_1 and partial dominance in the F_2 generation. Most of the array points fell below the line of unit slope in the *V r W r* graph and shifted their positions above the line of half slope in the *W r W′* graph (fig. 2b and 2d), confirming complementary type of gene action. Eliminating each parental array point one by one showed that the exclusion of P_2 eliminated genic interaction, with the slope $b = 0.93 \pm 0.32$ (Fig. 3a). The fall of one array point, P_2, in the fourth quarter (Fig. 2d) showed that P_2 was responsible for overdominance. Because array points or P_4 were nearest to the point of origin in the both graphs of generations, P_4 possessed higher proportions of dominant alleles, whereas parent P_1, whose array points were farthest from the origin point possessed most of the recessive genes.

Component Analysis

Dominant components for clusters per plant were greater than the additive components, whereas the environmental component was relatively high (Table 4). Positive *F* value indicated excess of dominant alleles over recessive alleles. Ratios $\overline{V}r/\overline{W}r$ and $\sqrt{H_1/D}$ showed overdominance for both the sets. Dominant alleles were twice as frequent as recessive alleles in the F_1 generation, while a ratio of 16 dominant: 9 recessive alleles was obtained in the F_2 generation.

Pods per plant showed dominant components 4 to 5 times higher than the additive components while the environmental component was also higher. Dominant alleles were more frequent in the F_1 genera-

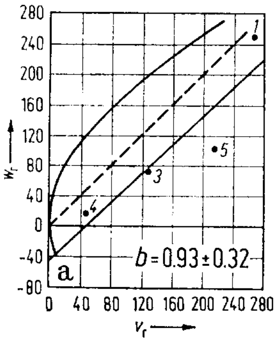

Fig. 3a. *Vr Wr* graph for pod number excluding array 6 and 2 set I

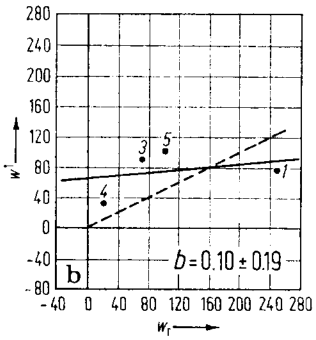

Fig. 3b. *Wr W′* graph for pod number excluding array 5 and 2 set II

tions, while in the F_2 generations directly opposite results were obtained. The estimates of degree of dominance from $\bar{V}r/\bar{W}r$ and $\sqrt{H_1/D}$ indicated overdominance.

Constant Parent Regression

Second degree regression (b_2) was positive for both the sets for clusters per plant but a negative value was obtained for the F_1 generation for pods per plant. This indicated that negative dominance was present in both generations for clusters per plant and in the F_2 for pods per plant, but positive dominance was exhibited in the F_1 generation for pods per plant. The trait, clusters per plant, showed negative partial dominance and negative overdominance with arithmetic gene action in the F_1 and F_2 generations, respectively. For pods per plant, positive partial and negative overdominance were observed in the F_1 and F_2 generations, respectively.

Discussion

General combining ability effects for clusters per plant were more important than specific combining ability effects, indicating the predominance of additive effects. Additive type of gene action was further confirmed from studies of graphical analysis and constant parent regression. This character exhibited overdominance with a high magnitude of environmental effects. Parent P_2 was the only interacting parent. High dominance components in component analysis may be due to the specific effect of this parent. Results reported here are in close agreement with those of Bond (1966) who reported additive effects for cluster number in winter beans. Recessive genes seem to govern the high cluster number.

General combining ability effects for pods per plant were highly significant, indicating additive gene effects. Graphical analysis indicated complementary gene action with overdominance and a high magnitude of environmental effects. P_2 for this character was also responsible for genic interaction. Similar gene effects were also reported by Hana and Hayes (1967) and Dickson (1967). Low pod number was observed to be dominant over high pod number as also reported by Dickson (1967) in snap beans.

It was interesting to note that ranking of the parents with respect to general combining ability was almost the same as on the basis of *per se* performance for both cluster and pod number indicating that when general combining ability effects are predominant, the parents can be ranked for their general combining ability effects on the basis of their actual performance.

It is worth mentioning that parents P_1 and P_3, having high mean cluster and pod number coupled with high general combining ability effects, could be used in a hybridization programme for developing selections high in pod and cluster number. In view of the superior performance of the crosses, $P_4 \times P_6$ for cluster number and $P_1 \times P_3$ for pod number in F_1 and F_2 generations, it is suggested that these crosses may be used to evolve better performing strains for cluster and pod number.

All parents except one exhibited mostly additive gene effects. A simple method of progeny selection may prove useful for the improvement of these characters. Recurrent selection may be used to accumulate desirable genes from different parents. Vigilance on the part of breeders would be desirable while selecting for these characters as recessive genes were found to govern high cluster and pod number.

Zusammenfassung

Für zwei Ertragskomponenten bei *Phaseolus mungo*, die Zahl der Fruchtstände und der Hülsen je Pflanze, wurde die allgemeine und spezifische Kombinationseignung sowie ihre Vererbung untersucht. Die Prüfung erfolgte über zwei Generationen an Diallel-Kreuzungen von 6 *Phaseolus*-Linien.

Für beide Merkmale war die allgemeine Kombinationseignung von größerer Bedeutung. Die Leistungen der Elternlinien in bezug auf die Anzahl der Fruchtstände und Hülsen erwiesen sich als gute Basis für die Einschätzung ihrer allgemeinen Kombinationseignung. Es wurden additive Genwirkungen mit partieller Dominanz bis Superdominanz festgestellt. Hohe Fruchtstands- und Hülsenanzahl scheint auf rezessiven Genen zu beruhen.

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