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GENETIC ANALYSIS TO IDENTIFY POTENTIAL PARENTS AND CROSSES FOR YIELD IMPROVEMENT IN CHICKPEA

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ABSTRACT

A seven parent diallel analysis excluding reciprocals revealed the predominance of additive variance for pods/plant and seeds/pod and both additive and nonadditive variance for 100-seed weight and seed yield/plant. The parents A-1 and Phule G-2 were found to be good general combiners for seed yield and 100-seed weight, while Simblapur and P-1631 were good general combiners for seeds/pods and pods/plant, respectively. Four heterotic hybrids, viz., Phule G-2 x P-1631, A-1 x P-3720, A-1 x Parmer 4-141, and A-1 x Phule G-2, were identified as potential crosses and the way in which they should be handled is discussed.

Key words: Chickpea, genetic analysis.

The progress in increasing productivity of grain legumes in general, and chickpea in particular, through breeding is not to the extent as achieved in other crops like cereals. Earlier, lack of sufficient genetic variability was considered to be one of the reasons for the slow progress. But subsequently many reports including that of Singh and Ramanujam [1] revealed the presence of substantial variability in chickpea. Therefore, proper choice of parents for hybridization is very crucial in generating variability. Further, relevant information about the inheritance of different quantitative characters has an important role in deciding proper selection strategies. The present study aims to obtain information on the inheritance of yield and its important attributes and to identify parents and crosses for further use in breeding as per method of Griffing [2].

The material comprised seven adapted genotypes from different agroclimatic regions: A-1 (Karnataka), Phule G-2, Parmer 4-141, Simblapur (all Maharashtra), NPT (IARI, New

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Delhi), P-1631 (Punjab) and P-3720 (Iran). A diallel cross of 7 x 7 parents (excluding reciprocals) was made. Twenty eight entries comprising 7 parents and 21 F₁ hybrids were sown in randomised block design with three replications. Each entry was represented by a single 4.5 m long row. Spacing was maintained at 60 cm between rows and 30 cm between plants. Data on four qualitative traits were recorded on five random plants from each row. Combining ability analysis was carried out following Method II, Model I of Griffing [2].

Analysis of variance for combining ability (Table 1) revealed that gca variance was highly significant for all the characters studied. The sca variance also influenced 100-seed weight and seed yield/plant though gca variance was predominant. Similar results were reported earlier [3].

It is evident (Table 2) that both A-1 and Phule G-2 showed significant gca

 Table 1. Analysis of variance (MS) for combining ability in chickpea

Source	d.f.	Mean squares					
		pods per plant	seeds per pod	100- seed weight	yield per plant		
Gca	6	2087.7**	0.018**	64.3**	59.6**		
Sca	21	243.3	0.002	1.0^{*}	19.5*		
Error	54	328.7	0.002	0.9	10.4		

effects for seed yield/plant and 100-seed weight. A-1 was also a good combiner for seeds/pod, while only P-1631 showed positive significant gca effect for pods/plant. When the parents were assessed for their overall combining ability [4] all of them except NPT and Parmar 4-141 were found to be high combiners.

 Table
 2. Gca effects of parents for yield and yield related characters in chickpea

			1		
Genotype	Pods per plant	Seeds per pod	100-seed weight	Yield per plant	Overall score
A-1	- 11.42*	0.03*	2.10*	2.66*	High
Phule G-2	- 15.65**	- 0.07**	4.93**	3.82**	High
NPT	- 19.35**	- 0.01	- 0.31	- 3.36**	Low
P-1631	20.21**	- 0.02	- 1.90**	0.40	High
Parmer 4-141	8.25	0.02	- 1.32**	- 1.68	Low
Simblapur	7.60	0.07**	2.89**	- 1.95	High
P-3720	10.36	- 0.02	- 0.60	0.09	High
SE <u>+</u>	5. 59	0.01	0.30	0.99	
CD at 5%	10.97	0.03	0.59	1.95	

Table 3 provides information for six crosses with high positive heterosis for yield over the commercial check. Four crosses showed significant heterosis for yield. Heterosis in three of them (Phule G-2 x P-1731, A-1 x P-3720 and A-1 x Parmer 4-141) was mainly due to heterosis for pods/plant. In the fourth crosses, i.e. A-1 x Phule G-2, it was due to 100-seed weight. The other two crosses showed positive but nonsignificant heterosis. In one of these crosses, heterosis for yield could be attributed to heterosis for pods/plant, while in the other it was due to seeds/pod.

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Cross	Heterosis over check variety A-1 for							
	seed yield per plant	pods per plant	seeds per pod	100-seed weight	gca of parents	sca of cross		
Phule G-2 x P-1631	38.3*	59.4**	- 7.6	- 8.8	HxL	L		
A-1 x P-3720	34.4**	50.0*	0.8	- 4.3	HxL	Н		
A-1 x Parmer 4-141	32.6*	64.7**	4.2	- 7.4	HxL	Н		
A-1 x Phule G-2	30.8*	14.3	- 8.4	13.7*	HxH	L		
P-1631 x Simblapur	28.0	86.6**	- 5.0	- 29.3**	НхН	L		
A-1 x Simblapur	22.1	43.1	12.6*	- 16.1**	НхН	L		

Table 3. Promising crosses in chickpea based on heterosis

H---high; L---low.

Two out of four crosses with high positive heterosis for yield (Phule G-2 x P-1631 and A-1 x Phule G-2) involved parents with high gca but they had low sca effects. This implies that mostly additive and additive x additive variation plays a major role in the expression of yield. Direct selection in the segregating generations of these crosses is likely to result in the isolation of superior true breeding lines. These two crosses can also be used to produce a 4-way cross, since heterosis for yield is due to pods/plant in one of them and due to 100-seed weight in the other. A 4-way cross could be more productive in combining genes for these two major yield attributes. The other two heterotic crosses, viz., A-1 x P-3720 and A-1 x Parmer 4-141, involved parents with H x L gca parents and their sca status was high. Nonadditive gene action may be more important in these crosses. Population improvement schemes including intermating, recurrent selection etc. are appropriate for handling such crosses.

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