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Diallel analysis for nodulation and yield contributing traits in chickpea

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ABSTRACT

The experiment consisting six genetically diverse chickpea lines and their fifteen F$_1$s made in diallel fashion was conducted for combining ability analysis for nodulation and seed yield components. Genetic analysis revealed that both additive and non-additive genetic components of variation are important for inheritance of all the characters. However, the magnitude of non-additive (sca) variance was considerably higher than additive (gca) variance. The parents 'HC 3' for 100-seed weight, biological yield, seed yield, nodule weight and root weight ; 'HC-1' for harvest index and plant weight ; 'HC-2' for number of nodules and nitrogen content and 'H96-99' for number of pods and leghaemoglobin content were identified as good general combiners. The cross combination 'ICC 4993' × 'HC 3' was the best for seed yield per plant, biological yield, harvest index and plant weight while crosses involving 'H96-99' and 'HC-1' as one of the parent were recorded as better combinations for leghaemoglobin content, nitrogen content and number of nodules. In view of parallel role of both additive and non-additive genetic effects determining the inheritance of different characters, their simultaneous exploitation through adoption of biparental approach/early generation mating is suggested.

Key words: Additive genetic variance, Chickpea, Non-additive genetic variance

Chickpea (*Cicer arietinum* L.) commonly known as gram, is one of the most important leguminous crop of India, playing a crucial role in agricultural production due to its symbiotic potential to fix nitrogen in association with rhizobia. In India it is grown in 8.25 mha area giving an annual production of 7.05 million tonnes. (Chaturvedi 2009). In any crop production system high yielding varieties are must to harvest high yield despite other inputs, for breeding these varieties a defined breeding programme is to be followed.

The choice of breeding method depends on the gene action involved in the inheritance of the characters. Diallel analysis developed by Jinks and Hayman (1953) and Griffing (1956) is one of the most potent technique for the evaluation of the varieties in terms of their genetic makeup as it provides information on the nature and magnitude of genetic parameters and general and specific combining ability of parents and their crosses, respectively. In the present investigation, an attempt has been made to assess the nature of gene effects for nodulation and yield related components for deciding efficient breeding methodology following the diallel analysis.

The interpretation of the results from present diallel analysis are restricted to the specific materials used in the experiments as the parents and cannot be regarded as a random sample from any population. The results have been discussed in view of the most appropriate breeding strategies for the genetic improvement of agronomic characters in chickpea.

MATERIALS AND METHODS

A diallel set of crosses were made excluding reciprocals involving six diverse genotypes (chosen on the base of previously assessed nodulation ability) of chickpea *viz.*, 'ICC 4918', 'ICC 4993' (non-nodulating), 'H96-99', 'HC-1' (medium nodulating), 'HC-2', 'HC-3' (high nodulating). The material comprising twenty one genotypes including 6 parents and their 15 F$_1$'s were sown in a randomized block design with three replications during *rabi* 2004-05 at CCSHAU, Hisar. The row and plant spacing were 30 and 15 cm, respectively. Five random plants were selected from each genotype in each replication and observations were recorded for 13 characters *viz.*, plant height (cm), number of secondary branches, number of pods per plant, 100-seed weight (g), biological yield (g), seed yield (g), number of nodules, nodule weight (g), nitrogen content (%), leghaemoglobin content (mg/g), harvest index (%), root weight (g) and plant weight (g). The nitrogen content was estimated by Kjeldahl's steam distillation method (Bremer 1965) and leghaemoglobin content by Hartree (1955) method. The combining ability analysis was made following Griffing's method (1956).

RESULTS AND DISCUSSION

The analysis of variance revealed significant genotypic differences among the genotypes for all the thirteen characters indicating thereby considerable amount of variability for all the characters thus, justifying the use of the material in the present study (Table 1). Analysis of variance for combining ability (Table 2) revealed significant general combining ability (gca) and specific combining ability (sca) variances for all the characters studied, indicating the importance of both additive as well as non additive genetic components of variation in the inheritance or expression of these attributes. The importance of both types of gene effects has been observed earlier also in chickpea for seed yield and related attributes (Jahagirdar *et al.* 1994, Patil *et al.* 2006, Bhardwaj *et al.* 2009). The magnitude of the non additive (sca) variance was considerably higher

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Table 1. Analysis of variance for thirteen characters in chickpea

Source	D.F.	Plant height (cm)	Secondary branches (no)	Pods (no)	100-seed weight (g)	Biological yield (g)	Seed yield (g)	Nodules (no)	Nodule weight (g)	Nitrogen content (%)	Lb content (mg/g)	Harvest index (%)	Root weight (g)	Plant weight (g)
		Mean Square												
Replications	2	1.254	2.427	70.266	1.196	62.029	5.198	0.062	0.004	1.355	0.0109	1.493	0.016	1.433
Treatments	20	149.82**	308.47**	9489.80**	53.81**	2712.34**	462.73**	5.782**	0.33**	1.041**	2.92**	39.103**	1.23**	40.46**
Error	40	29.04	9.12	248.37	1.78	81.37	16.07	0.054	0.004	0.016	0.01	3.195	0.04	1.86

*, ** Significant at P = 0.05 and 0.01, respectively

Table 2. Analysis of variance for combining ability for thirteen characters in chickpea

Source	D.F.	Plant height (cm)	Secondary branches (no)	Pods (no)	100-seed weight (g)	Biological yield (g)	Seed yield (g)	Nodules (no)	Nodule weight (g)	Nitrogen content (%)	Lb content (mg/g)	Harvest index (%)	Root weight (g)	Plant weight (g)
		Mean Square												
gca effects	5	55.775*	67.66**	1907.06**	44.75**	466.78**	78.29**	4.40**	0.28**	0.72**	2.05**	19.07**	0.73**	21.20**
sca effects	15	47.992	114.54**	3582.00**	9.001**	1049.89**	179.56**	1.10**	0.05**	0.22**	0.61**	11.02**	0.30**	10.91**
Error	40	9.679	3.04	82.79	0.591	27.12	5.355	0.018	0.001	0.005	0.004	1.065	0.013	0.619

*, ** Significant at P = 0.05 and 0.01, respectively

Table 3. Estimates of general combining ability effects and the mean performance (in parenthesis) of parents for thirteen characters in chickpea

Parents	Plant height (cm)	Secondary branches (no)	Pods (no)	100-seed weight (g)	Biological yield (g)	Seed yield (g)	Nodules (no)	Nodule weight (g)	Nitrogen content (%)	Lb content (mg/g)	Harvest index (%)	Root weight (g)	Plant weight (g)
ICC 4918	-2.389** (62.00)	4.431** (17.66)	-3.500 (33.77)	-1.326** (18.10)	-3.983** (33.33)	-3.095** (6.00)	-0.89** (0.00)	-0.196** (0.00)	-0.388** (2.70)	-0.240 (0.00)	-2.357** (18.420)	-0.547** (1.471)	-1.786** (13.962)
ICC 4993	0.0972 (63.333)	0.086 (12.933)	-20.106** (55.667)	0.761** (17.400)	-2.842 (34.400)	-1.266 (7.100)	-0.843** (0.000)	-0.266** (0.000)	-0.353** (2.953)	-0.810** (0.000)	-1.338** (20.753)	0.041** (1.890)	-1.935** (13.176)
H 96-99	4.944** (80.333)	-0.209 (18.667)	24.023** (132.533)	-1.214** (18.200)	6.646** (74.200)	2.109** (22.433)	-0.062 (19.233)	0.014 (1.027)	0.102** (3.268)	0.681 (2.413)	0.322 (30.283)	-0.028 (2.223)	1.277** (16.654)
HC-1	0.653 (73.333)	-2.743** (21.200)	5.673 (77.933)	-1.656** (19.033)	1.208 (64.667)	1.868** (25.367)	0.429** (15.000)	0.137** (0.903)	0.148** (3.466)	0.144 (2.118)	1.799** (41.070)	0.208** (2.129)	1.646** (14.902)
HC-2	-1.764 (52.667)	-3.415** (15.200)	-11.635** (74.733)	-1.068** (18.333)	-11.042** (40.333)	-3.664** (15.067)	0.936** (27.167)	0.112** (0.849)	0.358** (3.317)	-0.063 (2.518)	0.800** (37.623)	-0.013 (1.271)	-0.514** (12.847)
HC-3	-0.472 (65.333)	1.850** (18.667)	5.544 (92.800)	4.503** (32.933)	10.013** (99.667)	4.048** (33.367)	0.429** (23.333)	0.200** (1.065)	0.133** (3.361)	0.288 (2.565)	0.774** (33.547)	0.338** (2.191)	1.311** (14.097)
SE (gi)	1.004	0.562	2.936	0.248	1.680	0.746	0.043	0.012	0.023	0.020	0.333	0.038	0.254
SE (gi-gj)	1.555	0.871	4.549	0.384	2.604	1.157	0.067	0.019	0.036	0.031	0.516	0.059	0.393

*, **Significant at P = 0.05 and 0.01, respectively

than additive (gca) variance for all the characters indicating the preponderance of non additive genetic effects (dominance and epistasis) in controlling the expression of these characters. Earlier studies also showed predominantly non additive genetic control for one or more of these characters (Bajaj *et al.* 1984 and Bhaduoria *et al.* 2002). However, others (Chander *et al.* 2001, Muhammad *et al.* 2003, Bhardwaj *et al.* 2009) reported additive gene effects to be more prominent for these characters in their material. Such disparities in the observations may arise from differences in the genetic constitution of the parental materials studied, variation in the environment, the techniques used in analyzing the data and the precision of the experiment (Singh *et al.* 1992).

The estimates of gca effects (Table 3) showed that none of the parent evinced good gca for all the traits so it was difficult to pick good combiners for all the characters together because the combining ability effects were not consistent for all the yield components, possibly because of negative association among some of the characters (Gowda and Bahl 1978). This shows that genes for different desirable characters would have to be combined from different sources (Kumari 1999). The gca effects indicated that parent ‘H96-99’ was high general combiner for plant height, number of pods and leghaemoglobin content. Parents ‘ICC 4918’ and ‘HC-3’ showed high gca effects for number of secondary branches. The parent ‘HC-3’ was good general combiner for 100-seed weight, biological yield, seed yield, nodule weight and root weight while ‘HC-1’ was good general combiner for harvest index and plant weight. For number of nodules and nitrogen content, 'HC-2' showed high gca effects. An overall perusal of parental lines for general combining ability revealed that the high nodulating variety 'HC-3' was superior over rest of the chickpea parental lines for yield and component traits. The *per se* performance of parents was also highly correlated to the estimates of gca effects thereby, simplifying the selection of the parents based on the *per se* performance. So these parents may be extensively used in hybridization programme.

It is evident that 'HC-3', 'H96-99', 'HC-1' and 'HC-2' were the best parents having high gca effect coupled with good *per se* performance not only for seed yield per plant but also for nodulation and yield components so these parents can be exploited for the development of improved lines of chickpea. The genotypes showing good general combining ability for particular components may be utilized in component breeding for effective improvement in particular components, ultimately seeking improvement in seed yield itself (Singh *et al.* 1983).

The sca effects of hybrids (Table 4) revealed that 8 crosses *viz.*, 'ICC 4918' × 'ICC 4993', 'ICC 4918' × 'H96-99', 'ICC 4918' × 'HC-1', 'ICC 4993' × 'H96-99', 'ICC 4993' × 'HC-2', 'ICC 4993' × 'HC-3', 'H96-99' × 'HC-1' and 'HC-1' × 'HC-2' exhibited positive significant sca effects for seed yield per plant. The cross combinations *viz.*, 'ICC 4993' × 'HC-3' was found to be the best for seed yield per plant, biological yield, harvest index and plant weight; 'ICC 4993' × 'H96-99' for leghaemoglobin content and root weight, 'ICC 4918' × 'ICC 4993' for 100-seed weight and nodule weight; 'ICC 4918' × 'HC-3' for number of secondary branches and number of pods; 'HC-1' × 'HC-2' for plant height; 'ICC 4918' × 'HC-1' for number of nodules and 'ICC 4918' × 'H96-99' for nitrogen content. Preponderance of non additive gene effects for yield and yield components offers a good scope for the exploitation of hybrid vigour and therefore, heterosis breeding may be rewarding for improving chickpea. But the practical production of hybrid gram is not biologically feasible due to small size and cleistogamous nature of the flowers and strong hybridization barriers. In view of such problems, the possibility of deriving purelines performing better than or as well as F_1 hybrids in chickpea have been reported (Singh 1974). This suggest that a large proportion of non additive effects in self pollinated crops seems to be due to additive x additive effects and that selection be deferred to later generations (Singh *et al.* 1992).

It may be inferred from sca effects that most of the superior cross combinations for seed yield and related traits involved either both or atleast one parent with positive and significant gca effects which implies that additive x additive or additive x dominance genetic interactions respectively, are operating in the crosses studied. The high yield potential of cross combinations with high × low gca effects were attributed to interactions between positive alleles from good general combiner and negative alleles from poor combiner (Dubey 1975). These crosses would throw the desirable transgressive segregants if additive genetic system is present in the good combiner and complementary epistatic effects in F_1 acts in the same direction to maximize the desirable plant attributes (Patil *et al.* 1987). Such cross combinations should be fully exploited for the isolation of higher yielding purelines. This is perhaps the most rational breeding policy in pulse crops until hybrid varieties become a reality.

Thus, the sca effect of a cross was reflected through the gca of its parents which demands inclusion of atleast one good combining parent in producing superior hybrids. However, a few of the superior crosses involved both of the parents with poor combining abilities. This suggests that high sca effect of any cross combination does not necessarily depend on the gca effects of the parental lines involved. This

Table 4. Estimates of specific combining ability effects for thirteen characters in chickpea

F_1s	Plant height (cm)	Secondary branches (no)	Pods (no)	100-seed weight (g)	Biological yield (g)	Seed yield (g)	Nodules (no)	Nodule weight (g)	Nitrogen content (%)	Lb content (mg/g)	Harvest index (%)	Root weight (g)	Plant weight (g)
ICC 4918 × ICC 4993	-0.179	10.184**	-35.839**	4.621**	26.020**	6.781**	0.805**	0.813**	0.301**	0.929**	2.134**	-0.386**	-3.939**
ICC 4918 × H96-99	-7.762	9.016**	12.132	-1.038	23.199**	13.672**	0.928**	-0.022**	0.657**	0.397**	4.892**	-0.609**	-0.093
ICC 4918 × HC-1	1.530	-3.984**	90.549**	-0.829	26.970**	14.814**	1.129**	0.250**	-0.063	0.687**	4.034**	-0.008	1.628**
ICC 4918 × HC-2	6.280**	3.241**	2.790	-1.650**	4.987	-2.088	0.345**	0.399**	0.128**	-0.226**	-2.281**	0.462**	0.957
ICC 4918 × HC-3	-3.012	19.199**	112.978**	-3.854**	15.166**	0.733	0.288**	0.004	-0.344**	0.686**	-0.655	-0.228**	-1.926**
ICC 4993 × H96-99	2.821	2.760	47.938**	1.542**	27.858**	10.210**	0.292**	-0.134**	-0.799**	1.176**	2.018**	0.650**	0.358
ICC 4993 × HC-1	-12.887**	-0.173	-12.512	-2.717**	-20.505**	-10.815**	1.050**	0.161**	-0.538**	-0.045	-2.520**	-0.051	-2.221**
ICC 4993 × HC-2	5.863**	2.699	28.996**	0.196	17.545**	5.783**	1.008**	0.038	0.386**	-0.728**	0.992	-0.101	-3.213**
ICC 4993 × HC-3	4.238	14.267**	43.817**	3.358**	47.858**	27.071**	0.531**	0.287**	0.618**	-1.138**	6.292**	0.633**	6.617**
H96-99 × HC-1	-10.470**	4.656**	49.359**	-0.475	16.008**	3.943**	-0.543**	-0.080**	0.554**	-0.073	-1.511	-0.100	3.095**
H96-99 × HC-2	2.613	2.595	-3.466	0.871	8.658	1.742	-0.910**	-0.116**	0.251**	0.087	-1.353	0.069	0.239
H96-99 × HC-3	2.321	-1.937	-10.779	-3.400**	-18.596**	-7.704**	-0.427**	-0.048	-0.518**	-0.255**	-1.126	-0.207**	-0.105
HC-1 × HC-2	8.571**	5.128**	44.350**	0.846	39.829**	13.750**	0.955**	0.005	-0.113	-0.972**	-0.906	0.648**	3.888**
HC-1 × HC-3	-0.387	-3.737**	-40.762**	-2.758**	-7.859	-6.663**	-0.277**	0.004	-0.142**	0.178**	-3.226**	0.445**	2.083**
HC-2 × HC-3	-5.304**	-2.465	-4.521	-2.446**	-16.909**	-5.684**	0.310**	0.022	0.368**	-0.014	-0.525	0.688**	2.073**
SE (S_{ij})	2.694	1.510	7.879	0.666	4.510	2.004	0.116	0.033	0.063	0.055	0.893	0.102	0.681
SE (S_{ij}-S_{jk})	4.1156	2.306	12.036	1.017	6.889	3.061	0.178	0.050	0.096	0.084	1.365	0.156	1.041
SE (S_{ij}-S_{kl})	3.8103	12.135	11.143	0.942	6.378	2.834	0.165	0.047	0.089	0.077	1.264	0.144	0.964

*,**Significant at P=0.05 and 0.01, respectively

superiority of sca effects may be due to complementary type of gene action or involvement of non allelic interaction of fixable and non fixable genetic variance (Sharma and Mani 2001).

Thus, the hybrid combinations 'ICC 4993' × 'HC-3', 'ICC 4918' × 'HC-3', 'ICC 4993' × 'H 96-99' and 'HC-1' × 'HC-2' with high means, with favourable sca estimates and involving atleast one of the parents with high gca would tend to increase concentration of favourable alleles, a situation of great interest for breeding. These could be expected to yield transgressive and stable performing segregants possessing enhanced yielding ability.

The results of the present investigation revealed the importance of both additive and non additive genetic effects for the different characters. Under such a situation where both additive and non additive genetic variances are important factors of inheritance, maximum grain production may be attainable with a system that can exploit both additive and non additive genetic effects simultaneously. Therefore, in such cases, it is advisable to practice biparental mating in F_2 among selected crosses by way of intermating the most desirable segregants alternately with selection to isolate superior genotypes or use of recurrent selection scheme (diallel selective mating system) to enhance the frequency of desirable recombinants with high yield potential (Joshi 1979, Nagaraj *et al.* 2002). This will help in building the population from which desirable purelines could be developed simultaneously. Linkage is another factor that complicates the problem in selection. If linkages are predominantly of the repulsion type, a generation of intercrossing to increase the opportunity of recombination may become important (Singh *et al.* 1992). It can also be concluded from the data that genetically diverse and high combining parents should be used in formulating cross combinations. Selection by progeny testing as well as recurrent selection can then be used to evolve lines which may transgress both the combining parents.

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