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COMBINING ABILITY STUDIES IN CROSSES INVOLVING TALL AND DWARF TYPES IN CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

Five tall chickpea genotypes, four of Russian and one of Indian origin, were mated to nine dwarf genotypes in line × tester design. None of the tall genotypes used as testers showed consistently good combining ability for all the characters studied. However, P 1387 among the lines was a good combiner for all the characters. Majority of the best specific cross combinations for different characters emanated from crosses involving parents with high × low or low × high gca effects. Nonadditive effects were predominant for most characters, although appreciable additive effects were noticed for pod number, seed weight, and biological yield. It is suggested that for chickpea improvement, a breeding method that can combine both fixable and nonfixable types of gene action would be more suitable.

Key words: Gene action, chickpea, combining ability.

For increasing productivity in chickpea, restructuring of plant type is being stressed [1, 2]. The tall Russian lines may be useful for generating desirable variability through hybridization in quest of an improved plant type in chickpea. The present study on combining ability and gene action in crosses of tall and dwarf genotypes in chickpea has been undertaken with this objective.

MATERIALS AND METHODS

Fourteen genotypes were selected on the basis of their geographical and morphological diversity with special reference to plant height. Of the 14 genotypes, 5 were used as males (testers), each crossed with each of the nine genotypes used as females (lines). All the five testers were tall: four (P 9847, P 9656, K 1480 and NEC 136) from the U.S.S.R., and one (NEC 249) from India. Out of the nine dwarf lines, seven (BG 203, P 1387, P 517, K 4, P 10, P 179 and P 370) were from India, one (P 852) from the U.S.S.R., and one (P 840) from Morocco.

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The 45 F_1 and their parents were sown in randomized complete block design with three replications. The parents were randomized among themselves [3]. Each treatment in a replication was sown in a single 1.5 m long row at 60 × 15 cm spacing.

Observations were recorded on five random plants per treatment, excluding the border plants, for nine quantitative characters (Table 1). The statistical analysis was based on plot means. The total variation among F_1 hybrids was partitioned further into variances due to lines, testers and their interaction effects, which were used in estimating additive and nonadditive variances [4]. The analysis of combining ability variance, their effects and the test of significance were carried out by the method given by D. Singh (personal communication).

RESULTS AND DISCUSSION

The ANOVA indicated the presence of significant differences among the entries for all the characters (Table 1). Among the parents, the mean squares due to lines were significant for all the characters but testers showed significant differences only for plant height, pod number, seed weight, biological yield and harvest index. The lines differed from the testers significantly for all the characters. Though hybrids showed highly significant differences for all characters, the parents differed from their hybrids significantly for plant height, primary branches, secondary branches, and seed yield.

Table 1. Analysis of variance (MS) of parents and F_1 hybrids for nine characters in chickpea

Source	d.f.	Plant height	Primary branches	Secondary branches	Pod number	Seeds/ pod	Seed weight	Biological yield	Seed yield	Harvest index
Replications	2	39.6	4.2**	51.8**	2223.2**	0.01	18.6**	126.5	57.4**	91.9*
Entries	58	258.0**	5.5**	56.9**	3538.8**	0.06**	27.7**	930.3**	112.8**	127.3**
Parents vs crosses	1	366.3**	15.3**	137.1**	371.0	0.01	0.3	437.6**	31.1	2.1
Lines vs testers	1	2719.2**	20.7**	636.9**	15618.3**	0.36**	6.7*	778.6**	593.5**	978.1**
Among lines	8	272.9**	10.6**	58.4**	2013.4**	0.10**	65.9**	437.8**	59.0**	49.2*
Among testers	4	148.7**	1.3	13.9	1566.0**	0.03	22.3**	269.2**	25.5	147.7**
Crosses	44	206.9**	4.3**	45.5**	3792.9**	0.05**	22.4**	1094.5**	121.4**	123.2**
Error	116	18.2	0.8	9.1	269.2	0.01	1.6	49.3	10.5	19.3

*, **Significant at 5% and 1% levels, respectively.

Further partitioning of variation among the crosses showed that mean squares due to lines, testers and line × tester interactions were significant for all the characters except seed yield in case of testers (Table 2). The estimates of gca and sca variances indicated that, except seed weight, nonadditive genetic components account for most of the genetic variation for all the characters, though appreciable additive effects were recorded for pod number and biological yield. For seed weight, both additive and nonadditive components were significant, though the former was predominant. Gupta and Ramanujam [5, 6] and Gowda and Bahl [7] also observed similar trend in their materials. These observations suggest that a breeding method that can exploit both additive and nonadditive genetic effects would be useful in chickpea breeding. Recurrent selection and diallel selective mating [8], which provide better opportunity for selection, recombination and accumulation of desired genes, should help increase fixable as well as nonfixable types of gene effects. In fact, a judicious approach of integrating the classical approaches of pedigree and bulk method with recurrent selection or diallel selective mating may be more practical under many such situations.

Table 2. Analysis of variance (MS) of line × tester crosses for nine characters in chickpea

Source	d.f.	Plant height	Primary branches	Secondary branches	Pod number	Seeds per pod	Seed weight	Biological yield	Seed yield	Harvest index
					Mean squares					
Crosses	44	206.9**	4.3**	45.5**	3792.9**	0.05**	22.4**	1094.5**	121.4**	123.2**
Lines	8	261.9**	4.0**	74.7**	7931.2**	0.08**	71.7**	1959.9**	259.3**	82.2**
Testers	4	128.1**	4.6**	70.7**	1703.3*	0.05**	50.9**	1299.5**	24.1	199.5**
Lines × testers	32	203.0**	4.4**	35.0**	3019.6**	0.04**	6.5*	852.6**	99.1**	123.9**
Error	88	16.7	0.7	9.9	305.4	0.01	1.8	50.8	12.5	19.6
					Estimates of variance components					
Lines		3.9	@	2.7	327.4	0.01	4.3	73.8	10.7	@
Testers		@	0.1	1.3	@	0.01	1.7	16.6	@	2.8
gca		@	@	1.8	85.6	0.01	2.6	37.0	2.0	0.8
sca		62.1**	1.2**	8.4**	904.7**	0.01**	1.6**	267.3**	28.9**	34.8**
gca : sca		@	@	0.2	0.1	0.08	1.7	0.1	0.1	0.1

*, **Significant at 5% and 1% levels, respectively.

@ Estimates negative.

The estimates of gca effects for the parental lines are given in Table 3. Among all the lines and testers, P 1387 was an outstanding line, as it showed significant positive gca effects for all the characters including seed yield. BG 203, the second best combiner for seed yield, was also a good combiner for pod number and seeds per pod. None of the tall types, used as testers, proved to be good combiner for seed yield. The genotypes showing good gca for particular components may be useful only in component breeding. The comparison of the per se performance of the parent lines with their gca effect did not reveal a clear association between them, indicating that the choice of the parents on the basis of per se performance alone may not be effective.

Table 3. Estimates of gca effects for nine characters in chickpea

Parent	Plant height	Primary branches	Secondary branches	Pod number	Seeds per pod	Seed weight	Biological yield	Seed yield	Harvest index
Lines:									
BG 203	1.4	−0.1	1.2	21.6**	0.1**	−2.4**	3.3	2.0*	1.7
P 1387	7.8	0.9**	3.6**	27.0**	0.01**	1.3**	25.9**	9.3**	2.9**
P 952	−1.4	−0.9**	−0.7	7.1	0.04**	−1.4**	1.1	0.3	0.4
P 517	−7.3	−0.3	1.2	2.9	0.07**	−1.6**	−5.0**	−1.0	1.3
K 4	0.5	0.5*	1.6*	−5.8	−0.07**	2.0**	2.2	0.2	1.8
P 10	−3.9**	−0.1	0.6	−12.7**	−0.05**	−1.2**	−13.9**	−3.1**	1.6
P 840	−0.4	−1.0**	−2.8**	0.9	−0.02*	−0.9**	−3.0	−1.0	0.7
P 179	1.4	−0.5*	−3.7**	−45.9**	−0.12**	4.5**	−11.4**	−6.0**	−4.5**
P 370	1.9	0.3	−0.8	−5.1	−0.02*	−0.4	1.0	−0.7	−2.1*
SE (gi) ±	0.9	0.2	0.8	4.3	0.01	0.3	1.7	0.9	1.1
SE (gi−gj)	1.5	0.3	1.2	6.4	0.02	0.5	2.6	1.3	1.6
Testers:									
P 9847	0.4	0.1	−0.8	−4.5	−0.07	0.4	−1.4	−1.4	−1.3
P 9656	−1.4*	−0.1	0.5	3.6	0.01*	−0.8**	−2.0	−0.1	−0.2
NEC 249	1.0	−0.1	0.1	11.9**	0.04**	−1.3**	−2.4	0.6	2.4**
K 1480	2.8**	0.7	2.4**	−8.5**	0.03**	2.2**	12.0**	1.1	−3.8**
NEC 136	−2.8**	−0.5	−2.0**	−2.5	−0.01*	−0.5*	−6.2**	−0.3	2.8**
SE (gi) ±	0.7	0.2	0.5	3.0	0.01	0.2	1.2	0.6	0.8
SE (gi-gj)	1.1	0.2	0.9	4.8	0.01	0.4	1.0	0.9	1.2

*, **Significant at 5% and 1% levels, respectively.

The number of crosses showing significant positive sca effects for seed yield and its components were 14 for pod number, 15 for seeds per pod, 6 for seed weight, 14 for biological yield, 13 for seed yield and 10 for harvest index. Generally, the crosses showing significant positive sca effects for seed yield also showed high positive sca effects for pod number, indicating thereby direct dependence of seed yield on pod number. This confirms our earlier results in chickpea [7].

Among the 22 crosses showing high mean (top five ranks) and significant gca effects for the six characters studied, 13 were of high × low, 3 of low × low, and 6 of high × high gca parents (Table 4). The crosses involving one good combiner and the other medium or poor combiner can yield desirable transgressive segregants

Table 4. The related combining ability information on the best five crosses based on per se performance

Character	Cross	Mean	sca effect	gca status of parent		Character	Cross	Mean	sca effect	gca status of parents	
				P_1	P_2					P_1	P_2
Pod number	P 1387 × NEC 136	155.8	23.5	High	Low	Biological yield (g)	P 1387 × K 1480	119.5	29.3**	High	High
	BG 203 × P 9656	155.3	32.4**	High	Low		P 1387 × NEC 136	80.6	8.5*	High	Low
	P 517 × NEC 249	150.2	37.7**	Low	High		P 179 × K 1480	77.4	24.5**	Low	High
	P 1347 × NEC 249	149.3	2.6	Low	Low		P 952 × K 1480	74.8	9.4**	Low	High
	P 1387 × P 9656	142,3	3.9	Low	Low		K 4 × NEC 136	70.8	22.4**	Low	Low
Seeds per pod	P 517 × K 1480	1.67	0.34**	High	High	Seed yield (g)	P 1387 × NEC 136	31.2	5.6**	High	Low
	P 370 × P 9656	1.47	0.08**	Low	Low		P 1387 × K 1480	30.8	3.9**	High	Low
	BG 203 × NEC 249	1.43	0.06**	High	High		P 1387 × NEC 249	26.2	−0.2	Low	Low
	P 840 × NEC 136	1.40	0.21**	Low	Low		P 1387 × P 9656	24.0	−1.7	Low	Low
	P 952 × NEC 249	1.39	0.08**	High	High		BG 203 × P 9656	23.5	5.2**	High	Low
						Harvest index (%)	P 517 × P 9847	46.5	15.1**	Low	Low
Seed weight (g)	P 179 × K 1480	22.1	1.5*	High	High		P 840 × NEC 249	40.9	6.3**	Low	High
	P 179 × P 9847	20.2	1.3*	High	Low		P 952 × NEC 136	40.6	6.0**	Low	High
	P 1387 × K 1480	19.4	1.8**	High	High		BG 203 × NEC 136	39.7	3.8	Low	Low
	P 179 × NEC 136	17.7	−0.2	Low	Low		P 1387 × P 9656	39.6	5.4*	High	Low
	K 4 × P 9847	17.6	1.1	Low	Low		P 517 × NEC 249	39.6	4.5*	Low	High

*, **Significant at 1% and 5% probability levels, respectively.

if the additive effects of one parent and complementary epistatic effects (if present in the cross) act in the same direction and maximise the desirable plant attributes. Two of the crosses, P 1387 × NEC 136 and BG 203 × P 9656, showed such combination of gca effects and high mean values for grain yield and its components. These crosses can be profitably exploited for isolating transgressive segregants for seed yield.

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