

*Full Length Research Paper*

# Genetic analysis of agronomic characters in chickpea using line × tester mating design

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Twenty-one crosses developed from the frame of line × tester analysis along with ten parents were grown in two replicates experiment. Data on days to flowering, days to maturity, plant height, number of pods/plant, number of primary branches, number of secondary branches, number of tertiary branches, number of seeds per pod and seed yield per plant (g), revealed high significant differences exist among lines, testers and crosses for all traits studied. The ratio value of general combining ability variance to specific combining ability variance suggests the preponderance of non-additive type as well as additive gene action for some traits. Genotype Pusa-362 was the best general combiner for days to flowering. Genotype ICCL-87322 was identified as the best general combiner for the number of seeds per plant. Genotype BG329 was identified as the best general combiner for seed yield per plant (g) followed by KPG-59. Genotype PG-92-4 recorded desirable and significant GCA across five traits consistently. Cross PG-92-4 X Pant-186 recorded five significant SCA in the positive direction for secondary branches, number of tertiary branches, number of pods per plant, seed yield per plant and hundred seed weight. This cross is considered the most important compared to other materials under study. The proportional contribution of line × tester interaction was evident for most of the traits followed by the contribution of maternal lines. Days to flowering, days to maturity, primary branches, secondary branches, tertiary branches, pod per plant, seed per pod and seed yield per plant (g) recorded higher SCA variance suggesting non-additive gene action exist in expressing of these traits. The presence of a high SCA effect suggests that heterosis breeding can be exploited. Selection for those characters should be undertaken in later generations when these traits are fixed in homozygous lines.

**Key words:** Chickpea, *Cicer reticulatum*, combining ability, gene action, heritability.

## INTRODUCTION

Chickpea originates in the middle East Anatolia and from there migrated to Europe, North and Central America, India, and North Africa (Pieroni, 2005). India is considered one of the largest producers of chickpea and accounts for 75% of world production (FAOSTAT, 2020). The crop has an average yield of 1.2 tons per hectare

and a potential for up to 2 tons per hectare which needs to be exploited through breeding methods (Vadez et al., 2021). Many varieties have been developed and introduced from ICRSAT-India to Sudan. These included, ICCV 2, ICCV 89509, ICCV 92318 and ICCV91302. They were released under the name of Wad Hamid, Atmor,

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Hwata and Burgeig respectively (Mohamed et al., 2015). In Sudan, chickpea is grown in the Northern part mainly in the River Nile state and the Northern state of Sudan. Chickpea spread South to the central clay plain of Sudan due to its growing importance as a cash crop and its competition with broad beans (*Vicia faba*), for land during winter season. It is now cultivated in the Gazira scheme as a winter crop. It is considered the third largest legume after Broad beans and cowpea. Varieties grown in Sudan are a mixture of introduced varieties and local lines developed through hybridization and selection, often named after their growing areas. The crop is characterized by poor yield due to low-performing local varieties and restricted short winter season (Mohamed et al., 2015). Hybrid vigour and heterosis in chickpea was first reported by Pal (1945), in six crosses. He reported that the number of pods per plant was the only trait which showed marked hybrid vigour. Since then several reports have been published reporting hybrid vigour in chickpea (Bhatt and Singh, 1980; Singh and Ramanujam, 1981; Gadekar and Dodiya, 2013; Gaur et al., 2020). Selection of mating design and material under the study is very crucial in any breeding programme. The choice of mating design is subject to several factors such as time, space, cost and nature of biological limitations such as the form of trait inheritance, type of pollination, type of crossing to be used and type of pollen dissemination (Nduwumuremyi et al., 2013). Line x tester mating design is an extension of top cross method which involves hybridization between lines and wide-based testers. The design uses inbred lines as the base population (Nduwumuremyi et al., 2013; Muthoni and Shimelis, 2020). Line x tester mating design has been used by several researchers in chickpea to identify parents with good combining ability, crosses with marked hybrid vigour and identifying various types of gene actions (Kumar et al., 2018; Jeena and Arora, 2000; Sasane et al., 2022). The objectives of the study were to identify the best-performing parental lines, desirable crosses and the type of gene action for growth, yield and yield-related traits of ten parental lines.

## MATERIALS AND METHODS

The materials comprised 21 F<sub>1</sub>s, seven genetically diverse lines (BG329, BG-384, ICCL-87322, K-850 LM, NDG-8606, PG-92-4, and Pusa-362) and three well adapted and released varieties (Avrodhi, KPG-59 and Pant-186) as testers.

Crosses were made at the G.B. Pant University of Agriculture and Technology in Uttarakhand, India. The resulting hybrids, along with their parents, were assessed under Sudan conditions in the demonstration farm of the faculty of agriculture at Al Zaiem Al Azhari University, Khartoum North, Sudan. The experiment was conducted in a randomized complete block design with two replicates. Each plot was made of one row 60 cm apart, and 10 cm between plants. Irrigation was done every 10 days. A dose of nitrogen in the form of urea was applied at a rate of 30 kg N/ha with the third irrigation. Weeding is done twice in the second and six week from sowing. Data on morphological traits were obtained in two ways, on a plot basis and individual plants. Days to flowering,

and days to maturity were recorded on a plot basis. However, data on plant height, number of pods/plant, number of primary branches, number of secondary branches, number of tertiary branches, number of seeds per pod and yield per plant (g) were recorded on five plants selected randomly from each plot. Hundred-seed weight was recorded using an electronic balance. The analysis of variance to determine the differences among the genotypes (Parents and F<sub>1</sub>'s) was carried out according to Gomez and Gomez (1984). Traits which recorded significant differences were advanced for further analysis to estimate the general combining ability (GCA) variance effects of the parents and the specific combining ability (SCA) variance effect of the hybrids using line x tester mating design as described by Kempthorne (1957).

## RESULTS AND DISCUSSION

The analysis of variance presented in Table 1, revealed high significant differences among lines, testers and crosses for all traits studied. The data were advanced to further analysis to estimate the general and specific combining abilities of the parents and crosses, respectively. Female lines exhibited variation for days to flowering and hundred-seed weight. The testers showed significant differences for days to flowering. The interaction between lines and testers was significant for days to maturity, primary branches, secondary branches, tertiary branches, pod per plant, seed yield/plant (g) and hundred-seed weight (g). The variance due to P vs. C, line x tester and crosses were significant for days to maturity, primary branches, secondary branches, tertiary branches, pods/plant and grain yield/plant(g). According to Table 1, there are no discernible significant differences among the parental lines (testers and lines), however line x tester and P vs. C recorded highly significant differences. This suggests that the above mentioned traits exhibit hybrid vigor. Hundred-seed weights recorded significant variance due to lines, P vs. C, Line x Tester and Crosses. The ratio value of general combining ability variance to specific combining ability variance ( $\sigma^2\text{GCA}/\sigma^2\text{SCA}$ ) was smaller than one for days to flowering, days to maturity, primary branches, secondary branches, tertiary branches, number of pods per plant, number of seed per pod and seed yield/plant (g), suggesting the preponderance of non-additive type of gene action in control of these traits (Gupta et al., 2007; Gautam and Gupta, 2007). The same ratio also suggests that plant height (cm) and hundred seed weight (g) have a value greater than one indicating additive gene action for these traits and eventually less environmental effect and gene interaction. Selection for these traits will produce higher achievements during early generations' selection and will give genotypes with large adaptability. It is very clear that the estimates of SCA variance are higher than GCA variances in most traits and this is in agreement with the findings by Sonali et al. (2020). General combining ability estimates for lines and testers are presented in Table 2. Among parents, Pusa-362 is the best general combiner for days to flowering recording highly significant negative GCA followed by KPG-59

**Table 1.** Analysis of variance and mean squares of combining ability.

Source variation	of	d.f.	Mean squares									
			Days to flower	Days to maturity	Plant Height (cm)	Primary branches	Secondary branches	Tertiary branches	Pod per Plant	Seed per pod	Seed yield/plant (g)	Hundred seed weight(g)
Treatments	30		43.06**	24.68**	50.55*	12.22**	63.16**	25.23**	1,663.19**	0.07*	62.52**	42.89**
crosses	20		41.77**	26.72**	42.28	12.63**	45.51**	29.12**	1,267.20**	0.06	48.46**	32.49**
P vs C	1		14.67	88.76**	19.88	91.65**	333.82**	140.12**	17,129.14**	0.03	718.98**	29.89**
Lines	6		83.74**	37.08	71.46	13.91	25.92	24.11	1,430.34	0.11	46.32	78.06**
Testers	2		100.33**	1.81	47.05	11.09	5.88	39.82	1,430.34	0.01	68.47	28.23
Lines × Testers	12		11.03	25.70**	26.89	12.25**	61.91**	29.84**	997.65*	0.05	46.19**	10.41**
Error	30		7.46	7.32	26.32	1.42	3.05	3.16	395.74	0.03	4.60	2.54
$\sigma^2$ gca			1.201	0.040	0.601	0.015	-0.641	-0.028	10.529	0.001	0.089	0.862
$\sigma^2$ sca			1.782	9.187	0.283	5.415	29.430	13.342	300.956	0.008	20.795	0.008
$\sigma^2$ gca / $\sigma^2$ sca			0.67	0.00	2.12	0.00	-0.02	0.00	0.03	0.13	0.00	107.75

\*Significant at 5% level. \*\*Significant at 1% level.

Source: Author's own work.

respectively. Parent BG-384 recorded highly significant negative GCA for days to maturity while genotype K-850 LM produced highly significant positive GCA. It is difficult to be conclusive in pointing out the best general combiner; as early maturity is a trait of choice when considering the short restricted winter in Sudan although late maturity provides a longer time for seed filling and results in heavier and larger seeds which in turn is associated with high yield and higher hundred-seed weight (Tuba, 2009). Small and larger seed sizes are equally important in Sudan and Middle Eastern culinary hence the decision on these traits should take into consideration the balance required between desirable seed size as well as the limitations of a short restricted winter. Genotype Pusa-362 is identified as the best general combiner for plant height recording the highest significant value for GCA in this trait. Genotype BG-384 is the best general combiner for primary branches recording highly significant

GCA and followed immediately by PG-92-4. Genotype NDG-8606 is the best general combiner for secondary branches followed by PG-92-4. Genotype PG-92-4 is also identified as the best general combiner for tertiary branches and the number of pods per plant. Genotype ICCL-87322 recorded the highest significant GCA for seeds per plant. Genotype BG329 was identified as the best general combiner for seed yield per plant (g) followed by KPG-59. Genotypes K-850 LM, PG-92-4, Pusa-362, BG329 and KPG-59 recorded higher significant GCA for hundred seed weight. None of the parents recorded significant GCA for all traits; however, genotype PG-92-4 consistency recorded desirable and significant GCA across seven traits that include days to flowering, primary branches, secondary branches, tertiary branches, pod per plant, seed yield per plant (g) and hundred seed weight (g); followed by BG-384, K-850 LM, Pusa-362 and KPG-59. The genotype KPG-59 produced three significant GCA values

for days to flowering, seed yield per plant (g) and hundred seed weight (g), two of which are yield-associated traits. Records for specific combining ability effects of hybrids were presented in Table 3. Cross PG-92-4 X Pant-186 recorded five significant SCA in the positive direction, for secondary branches, number of tertiary branches, number of pods per plant, seed yield per plant (g) and hundred-seed weight. This cross is considered the most important cross in the materials under study. Cross NDG-8606 X KPG-59 comes second in importance and recorded three significant SCA in the positive direction for secondary branches, seed yield per plant (g) and hundred seed weight. Both crosses are a form of good combiner x poor combiner indicating the presence of additive x epistatic effect. These two hybrids are recommended for heterosis breeding for yield and yield-associated traits. The proportional contribution of lines, testers and their interaction is presented in Table 4. It is clear that

**Table 2.** Estimates of general combining ability effects of lines and testers.

Parent	Days to flowering	Days to maturity	Plant height (cm)	Primary branches	Secondary branches	Tertiary branches	Pod per plant	Seed per pod	Seed yield per plant (g)	Hundred seed weight (g)
<b>Lines</b>										
BG329	3.66**	0.52	-0.05	-0.51	0.83	-0.90	-0.53	0.00	3.91**	1.72*
BG-384	-2.55*	-4.81**	0.80	2.42 **	-2.69**	-1.18	-7.56	0.11	-0.94	0.21
ICCL-87322	-2.20	-1.48	0.95	-1.38**	-1.89*	-1.53*	-25.35**	0.25**	-1.54	-4.35**
K-850 LM	1.96	2.86*	0.37	-0.66	1.78	3.37**	10.12	-0.09	1.68	3.56**
NDG-8606	1.81	0.86	-6.80 **	0.22	2.26**	-1.83*	6.17	-0.04	-4.55**	-5.72**
PG-92-4	3.56**	1.52	-0.15	1.60**	1.61*	2.20**	23.45**	-0.10	1.98*	2.58**
Pusa-362	-6.25**	0.52	4.85*	-1.68**	-1.89*	-0.13	-6.31	-0.12	-0.54	2.01**
S.E.(gi)lines	1.12	1.10	2.09	0.49	0.71	0.73	8.12	0.07	0.88	0.65
S.E.(gi -gj) line	1.58	1.56	2.96	0.69	1.01	1.03	11.49	0.10	1.24	0.92
<b>Testers</b>										
Avrodhi	0.12	0.05	1.32	-1.02**	-0.73	-1.72**	-10.72	0.02	-1.63**	-0.78
KPG-59	-2.74**	-0.38	0.77	0.59	0.23	0.06	-3.85	-0.02	2.52**	1.64**
Pant-186	2.61**	0.33	-2.09	0.43	0.50	1.65**	14.57*	0.00	-0.88	-0.86
S.E.(gi) testers	0.73	0.72	1.37	0.32	0.47	0.47	5.32	0.05	0.57	0.43
S.E.(gi-gj) tester	1.03	1.02	1.94	0.45	0.66	0.67	7.52	0.07	0.81	0.60

\*Significant at 5% level; \*\*Significant at 1% level.

Source: Author's own work.

**Table 3.** Estimates of crosses specific combining ability.

Genotype	DF	DM	PH (cm)	PB	SB	TB	P/P	S/P	Y/P (g)	HSW (g)
BG329 X Avrodhi	0.98	6.62**	4.10	-0.94	1.78	2.63*	9.29	-0.12	0.57	0.03
BG329 X KPG-59	2.04	-3.95*	0.00	0.94	-0.03	-2.20	13.07	-0.08	-2.93	-1.15
BG329 X Pant-186	-3.01	-2.67	-4.09	0.00	-1.75	-0.44	-22.36	0.20	2.37	1.11
BG-384 X Avrodhi	0.40	-1.05	-4.35	-1.38	1.80	1.57	-4.23	0.16	-0.23	-0.21
BG-384 X KPG-59	-0.40	0.38	6.00	-3.64**	-3.31*	-0.01	-0.55	0.05	-1.03	0.37
BG-384 X Pant-186	0.00	0.67	-1.64	5.02**	1.51	-1.55	4.78	-0.21	1.27	-0.16
ICCL-87322 X Avrodhi	-1.30	-2.38	1.50	0.32	-1.35	0.27	9.10	0.18	2.22	-0.07
ICCL-87322 X KPG-59	-1.75	2.05	-1.65	1.51	2.89*	2.49	12.24	-0.13	2.77	-0.40
ICCL-87322 X Pant-186	3.05	0.33	0.16	-1.83*	-1.54	-2.75*	-21.34	-0.05	-4.98**	0.47
K-850 LM X Avrodhi	-2.32	1.29	0.53	-1.44	-6.72**	-3.43*	-30.21*	-0.24	-3.40*	2.42*
K-850 LM X KPG-59	2.94	-2.29	0.38	1.14	4.47**	2.59*	25.57	0.15	2.60	-1.12
K-850 LM X Pant-186	-0.61	1.00	-0.91	0.30	2.25	0.85	4.64	0.09	0.80	-1.30

**Table 3.** Contd.

NDG-8606 X Avrodhi	0.23	0.29	0.45	3.37**	6.50**	1.22	7.24	0.01	2.83	-1.00
NDG-8606 X KPG-59	-2.26	-2.29	1.30	-1.94*	3.74**	2.09	-8.33	0.05	5.48**	2.73*
NDG-8606 X Pant-186	2.04	2.00	-1.74	-1.43	-10.24**	-3.30*	1.09	-0.06	-8.32**	-1.73
PG-92-4 X Avrodhi	2.58	-1.38	-2.35	-0.36	-3.35*	-4.47**	-4.40	-0.02	-2.35	-3.52**
PG-92-4 X KPG-59	-0.16	5.05*	-2.20	1.53	-4.16**	-3.90**	-33.06*	0.02	-5.30**	-0.41
PG-92-4 X Pant-186	-2.41	-3.67	4.56	-1.17	7.51**	8.36**	37.46*	0.00	7.65**	3.94**
Pusa-362 X Avrodhi	-0.55	-3.38	0.15	0.42	1.35	2.22	13.22	0.04	0.37	2.35*
Pusa-362 X KPG-59	-0.40	1.05	-3.80	0.46	-3.61**	-1.06	-8.95	-0.06	-1.58	-0.02
Pusa-362 X Pant-186	0.95	2.33	3.66	-0.88	2.26	-1.15	-4.27	0.02	1.22	-2.34
S.E. sca effect	1.93	1.91	3.64	0.84	1.23	1.26	14.07	0.13	1.52	1.13

\*Significant at 5% level; \*\*Significant at 1% level; DF=Days to Flowering, DM=Days to Maturity; PH=Plant Height (cm), PB=Primary Branches; SB=Secondary Branches; TB=Tertiary Branches; P/P=Pod per plant; S/P=Seed per pod; Y/P=Seed yield per plant (g); HSW=Hundred seed weight (g).

Source: Author's own work.

**Table 4.** Proportional contribution of lines, testers and their interaction to total variance.

Character	Line (%)	Tester (%)	Line x Tester (%)
Days to flower	60.14	24.02	15.84
Days to maturity	41.63	0.68	57.70
Plant height(cm)	50.71	11.13	38.16
No. primary branches	33.03	8.78	58.19
No. secondary branches	17.09	1.29	81.62
No. tertiary branches	24.89	13.67	61.48
No. pod per plant	33.86	18.90	47.24
No. seed per pod	52.11	1.08	46.81
Seed yield per plant (g)	28.68	14.13	57.19
Hundred seed weight(g)	72.09	8.69	19.22

Source: Author's own work.

lines contributed to days to flowering, days to maturity, number of seeds per pod and hundred seed weight. Testers had low contributions towards all traits. The contribution of the interaction of line x tester was evidence for the

rest of the traits. There is an excellent venue for the exploitation of hybrid vigour and therefore, heterosis breeding may be used for improving chickpea.

In this study genotypes PG-92-4 was considered

the best parent for yield attributes including pod per plant, seed yield per plant (g) and hundred-seed weight (g) followed by genotype KPG 59 and BG329 for seed yield per plant (g) and hundred-seed weight (g). These promising parents could

be utilized in providing yield traits in any future breeding programme. Cross PG-92-4 X Pant-186 is identified as the most important cross in the materials under study. It recorded five significant SCA in the positive direction, for secondary branches, number of tertiary branches, number of pods per plant, seed yield per plant and hundred-seed weight followed by cross NDG-8606 X KPG-59. Both crosses are a form of good combiner x poor combiner indicating the presence of additive x epistatic effect.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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