Int.J.Curr.Microbiol.App.Sci (2019) *8*(6): 1640-1651

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 8 Number 06 (2019)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2019.806.196

L X T Analysis of Yield Characters in Chickpea (*Cicer arietinum* L.) under Rice Based Cropping System

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Keywords

L x T analysis, Chickpea, Rice based Cropping System

Article Info

Accepted:
12 May 2019
Available Online:
10 June 2019

A B S T R A C T

Line x Tester analysis mean sum of square due to genotypes was highly significant for all the traits in E_1, E_2 and E_3. Analysis of variance for combining ability revealed that the variance due to gca were highly significant for all the characters in all the environments except for days to maturity in E_1, plant height and primary branches plant^{-1} in E_1, E_2 and E_3, secondary branches, seed yield and harvest index in E_2 and E_3, pods plant^{-1} in E_1 and E_2, biological yield plant^{-1} in E_2 and protein content in E_1. Similarly variance due to sca were highly significant for all the characters in all the environments except days to maturity in E_1, plat height, primary branches plant^{-1} and secondary branches plant^{-1} in E_3, seed yield plant^{-1} in E_2 indicated the importance of both additive and non-additive gene effect in their expression. Per se performance seed yield plant^{-1} is the ultimate and most important traits presented in table. In the present investigations, the degree of heterosis for seed yield varied considerably. Out of 21 crossed 2 crosses (JG 130 x JG 97 and JG 315 x JG 97) exhibited significant positive mid and better parents heterosis in all three environments. However, the highest mean value was sown JG 130 x JG 97(71.30 g plant^{-1}) in E_1, 66.55 g plant^{-1} in E_2 and 40.55 g plant^{-1} in E_3 for high seed yield should be utilized for future hybridization programme

Introduction

Chickpea [*Cicer arietinum* (L.) $2n = 2x = 16$] belongs to genus *Cicer*, tribe Cicereae, family Fabaceae, and subfamily Papilionaceae. It is commonly called gram, bengal gram or garbanzo bean, is the most important cool season food grain legume in the world after common bean (*Phaseolus vulgaris* L.) and pea (*Pisum sativum* L.). Chickpea is the world's third most important food legume crop grown as rainfed in cool and dry climate in semi-arid regions. During the last few decades, due to increasing demand of the food for world's growing population depend to a large extent on the conservation and use of world's remaining plant genetic resources. Chickpea covers about 11.7 million ha area and 9.3 million tones production in over 45 countries of the world. India is the largest chickpea producer accounting a share of about 67% in global chickpea production with about 9.93 million ha area, 9.53million tones production and productivity of 960 kg/ha.

Distribution of chickpea in six states *viz*., Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Karnataka and Andhra Pradesh together contribute 90.2% of the production and 90.8 % of the area of the country. Chhattisgarh covers 0.276million ha area with production 0.213million tones and productivity of 771kg ha^{-1}. (Project Coordinators Report, 2014-15). Yield is a complex polygenic trait and is influenced by large number of quantitative and qualitative traits. There may not be genes for yield *per se*, in spite there could be genes, which govern the inheritance of yield characters. Information regarding association between yield and yield characters are required in any breeding programme.

Materials and Methods

The experimental material comprised *viz.* seven lines *viz.*, Vaibhav, Indira Chana-1, JG 315, JG 11, JG 14, JG 16, JG 130 of agronomic base and three testers JG 97, ICCV 96029 and ICCV 96030 for early maturity were crossed as per Line x Tester mating design fashion (Kempthorn, 1957) to develop 21 F_1 during 2014-15. These F_1along with their parents were evaluated two replication in one row plot during 2015-16. Under following three rice based cropping system *viz.* E_1: Cropping System I: after harvest of early rice variety (Danteshwari) CS-I, E_2: Cropping System II: after harvest of medium rice variety (Mahamaya). CS-II, $E_{3:}$ Cropping System III: after harvest of late rice variety (Dubraj) CS-III. The row to row and plant to plant spacing 30 x 10 cm maintained at Research cum Instructional farm, Department of Plant Breeding and Genetics, Indira Gandhi Agricultural University, Raipur The recommended packages of practices were adopted to raise the normal crops. Observations on metric traits where recorded on single plant basis on five randomly selected competitive plant of each genotypes from each replication in each cropping system were as observation on days to 50% flowering, days to maturity, plant height (cm), number of primary branches $plant^{-1}$, pods $plant^{-1}$, Biological yield $plant^{-1}$ (g), harvest index (%), 100 seed weight (g), Seed yield $plant^{-1}$ (g), seed volume (ml $seed^{-1}$), hydration capacity $seed^{-1}$ (g), hydration index, swelling index and protein content (%) were recorded on plot basis as per the chickpea descriptor developed by ICRISAT-IBPGR- ICARDA (1993). Jinks (1983) outlined the importance of heterosis breeding in self-pollinated crops to extract pure breeding lines equalling or outperforming the best F1s. Therefore, the present investigation was made to generate information on heterosis for yield and physiological attributes in chickpea. Rojas and Sprague (1952) concluded that the information on the SCA would often be lower in predictive value than the information on the gca. Kempthorne (1957) proposed this concept in line × tester analysis.

Results and Discussion

Analysis of variance

The analysis of variance for line x tester analysis for the traits under study has been presented in Table 1). The mean sums of square due the genotypes significant of the mean square for parents *vs.* hybrid are taken to indicate presence of heterosis. Although this method is statistically valid, conclusion regarding heterosis may not be reliable and useful. It is a comparison of mean of the parents as a group with the mean of crosses as group. Significant could result even when mean of crosses as a group is smaller than mean of parental line as a group. The highly significant variance due to parent *vs* crosses recorded for all the characters in all three environments except days to 50 % flowering in E_1, days to 50 % flowering, harvest index and seed yield $plant^{-1}$in $E_{2,}$ days to 50 %

flowering, plant height and secondary branches plant^{-1}in E_3.Mean square due to line and tester were found to be significant for all the traits in all the environments except days to maturity in all the Environments. Primary branches plant^{-1}in E_1 and E_3, secondary branches plant^{-1} and yield plant^{-1}in $E_2$and protein content in E_3. Hence, its indicated that line does not appear to behave consistently over different tester in the respective environments.

Analysis of variance for combining ability

Analysis of variance for combining ability (Table 2) revealed that the variance due to gca were highly significant for all the characters in all the environment except for days to maturity in E_1, plant height and primary branches plant^{-1} in E_1, E_2 and E_3, secondary branches, seed yield and harvest index in E_2 and E_3, pods plant^{-1} in E_1 andE_2, biological yield plant^{-1} in E_2 and protein content in E_1. Similarly variance due to sca were highly significant for all the characters in all the environments except days to maturity in E_1, plant height, primary branches plant^{-1}and secondary branches plant^{-1} in E_3, seed yield plant^{-1} in E_2indicating importance of both additive and non-additive gene effect in their expression. Result of the analysis revealed that the variance due to gca was lower than sca variance for all most all the characters in all the environments except protein content in E_2, primary branches plant^{-1} and secondary branches plant^{-1} in E_3, suggesting the predominance of non-additive gene action controlling these characters. Dominance genetic variance was larger than additive genetic variance for the characters, these result are supported by ratio of variance to general to specific combining ability (σ^2gca/ σ^2sca) which was smaller than unity and by the degree of dominance (σ^2D/ σ^2A) which take values greater than unity. Therefore, it applied that the inheritance of these traits was controlling by a preponderance of non-additive gene effect. Such types of gene action clearly indicated that selection of superior plant for these characters should be postponed to latter generation where these characters can be improved by making selection among the recombinants which the segregating population. As the ratio of gca: sca variance more than unit recorded for protein content in E_2, primary branches plant^{-1} and secondary branches plant^{-1} in E_3 further supported by finding degree of dominance and heritability indicated the role of additive genetic variance in their expression. Hence, direct selection for the characters would be advantageous in isolating chickpea genotypes of more protein content and more primary branches and secondary branches. These finding are in general agreement with the finding of Verma and Waldiya (2010), Monpara and Dhamelia (2013).

High estimate of heritability in narrow sense were observed for secondary branches plant^{-1} in E_1,E_2 and E_3, days to 50 % flowering in E_1, primary branches plant^{-1} in E_2 and E_3, harvest index in E_2 and E_3,swelling index in E_1 $E_2$and $E_3$and protein content in E_2.This supported the involvement of both additive and non-additive gene effects. Rest of the character showed moderates to low narrow sense heritability over the environments. Similar finding were reported by Khan *et al.*, (2006), Gupta *et al.*, (2007), Verma and Waldiya (2010), Bhatt *et al.*, (2013) and Monparaand Gaikwad (2014).

General combining ability

Seed yield plant^{-1}

For seed yield parents JG 14 and JG 16 inall the three environments. ICCV 96029 in E_1 and E_2 and ICCV 96030 in E_1 exhibited the desirable gca for the traits parents JG 14 in E_1 and E_2 and JG 16 in E_3 have been considered as the best general combiners

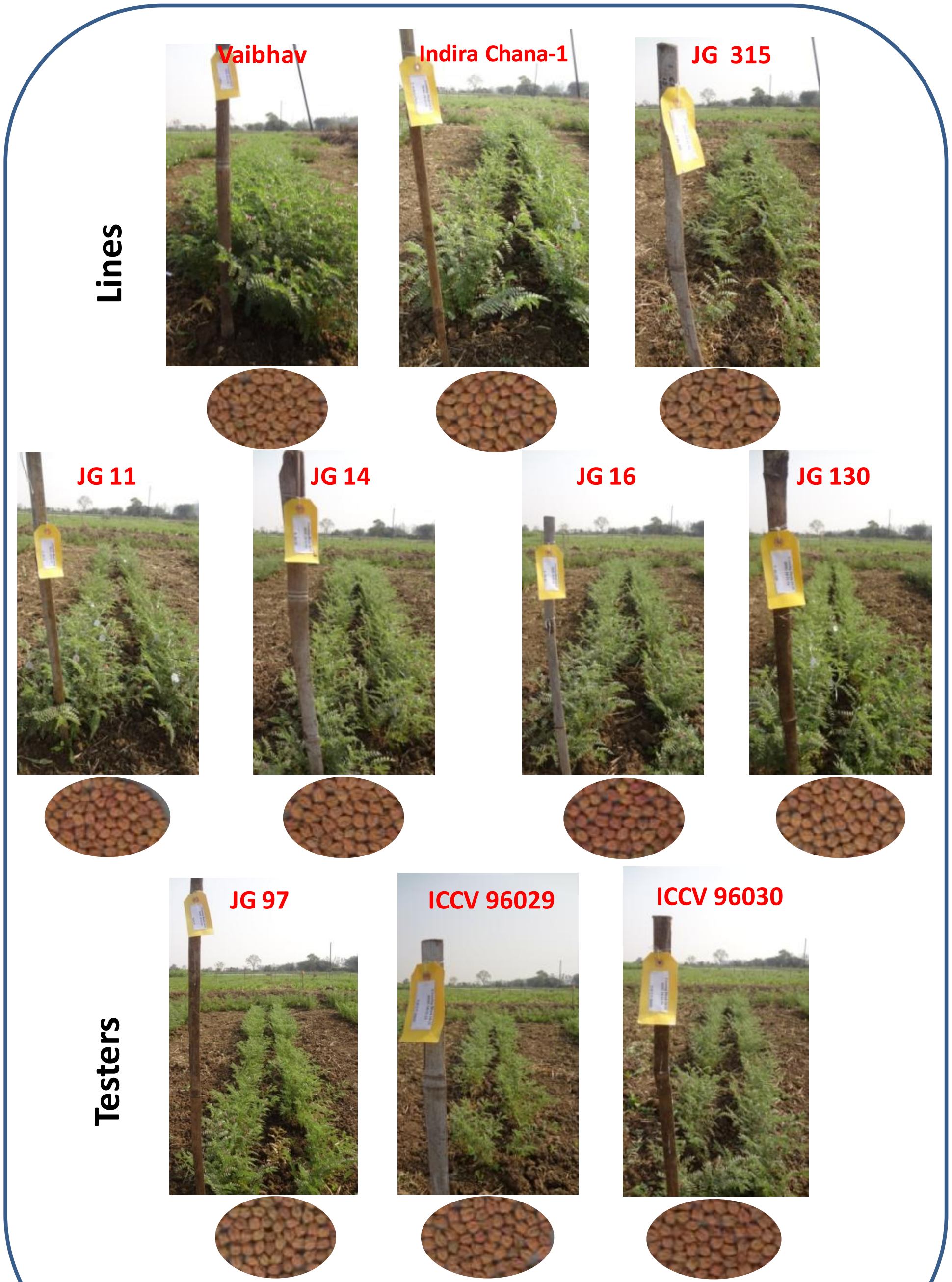

Fig: 1 Parents involved in hybridization programme

Sowing of field experimentation

Crop view

Laboratory experimentation

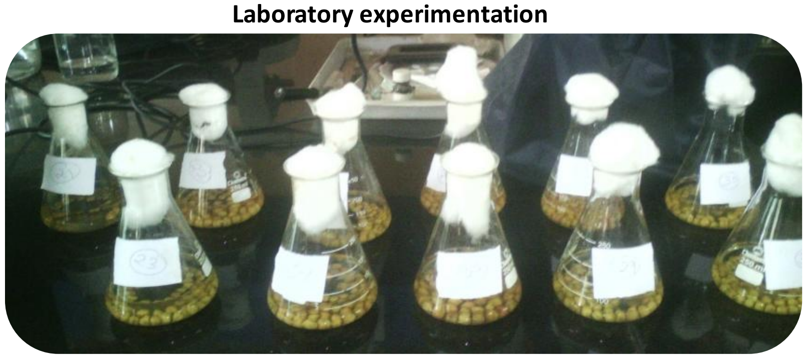

Fig: 2 General view of experimentation

Table.1 Analysis of variance for L x T for yield, its attributes and quality characters under E_1, E_2 and E_3 in chickpea

Source of variation	D.F.	Mean sum of squares														
		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	Secondary branches plant^{-1}	Pods plant^{-1}	Biological yield plant^{-1} (g)	Harvest index (%)	100-seed weight (g)	Seed yield plant^{-1}(g)	Seed volume (ml seed^{-1})	Hydration capacity seed^{-1} (g)	Hydration index	Swelling index	Protein content (%)
E_1: After harvest of early rice variety of 90-110 days																
Genotypes	30	26.55**	12.190**	40.370**	6.140**	376.02**	9197.4**	881.57**	341.26**	20.60**	301.12**	0.02**	0.0213**	0.0032**	3.920**	2.160**
Parents	9	58.56**	29.50**	24.97	0.254	5.17**	162.47	151.15**	342.80**	13.445**	26.87*	0.0018**	0.022342**	0.000198**	1.6848**	1.09499
hybrids	20	13.48**	2.25	46.68**	2.371**	172.56**	3560.1**	177.62**	231.13**	13.07**	269.77**	0.0019**	0.02035**	0.000391**	4.45436**	2.1739**
Par Vs Hyb	1	0.035	59.32**	52.81**	134.59**	7783.4**	20325.8**	21530.8**	2530.08**	235.67**	3398.34**	0.0091**	0.03172**	0.000009**	13.5610**	11.6757**
Line	6	30.43*	5.300**	46.31	1.431	342.98**	3832.58**	150.4*	367.58**	23.59**	355.410**	0.0032**	0.03488**	0.00065**	8.1970**	4.2395*
Tester	2	4.22	0.863	33.34	2.301	205.75**	4563.94**	127.22	93.15	2.984**	86.820**	0.0036**	0.000343*	0.000026**	2.3092	0.2188
Line x Tester	12	6.57**	0.960	49.10*	2.853	81.82**	3256.67**	199.63**	185.89**	9.5**	257.440**	0.0011**	0.0160**	0.000317**	2.9404**	1.467*
Error	30	1.00	1.35	16.33	0.510	0.1448	366.95	35.064	51.041	0.3535	9.55	0.00008	0.00006	0.000001	0.08136	0.77683
E_2: After harvest of medium rice variety of 111-135 days																
Genotypes	30	32.79**	27.66**	102.14**	4.037**	310.01**	6475.9**	731.99**	239.4**	22.18**	317.15**	0.023**	0.209**	0.0032**	3.45**	1.898**
Parents	9	78.2721**	73.755**	20.9032	0.11912	0.9205	65.1731	16.2659	54.7656	134.488**	4.076253	0.00186**	0.022556**	0.000198**	2.123	1.386*
hybrids	20	13.795**	2.2312*	51.1851**	2.83924**	176.833**	3915.12**	193.9875**	333.513**	13.0775**	254.3312	0.00168**	0.019547**	0.00039**	3.65876**	1.692**
Par Vs Hyb	1	3.4257	121.51**	1852.51**	63.26703**	5755.24**	115389.4**	17933.6**	21.6914	283.045**	4391.305	0.0174**	0.033053**	0.000003*	11.2353**	10.679**
Line	6	30.484**	4.493*	49.540	5.271*	495.255**	5097.094	223.300	367.1	23.595*	341.309	0.0024	0.03327	0.000659	7.3596**	1.386*
Tester	2	5.453	0.170	33.810	2.366	68.437	2439.246	46.908	45.441	2.983	56.443	0.0031	0.00054	0.000027	3.0566	1.691**
Line x Tester	12	6.8411**	1.443	54.900**	1.702*	35.688	3570.089**	203.84**	364.728**	9.500**	243.823**	0.00103	0.01558**	0.000317**	1.9086**	10.679**
Error	30	0.88064	0.96505	14.5232	0.43312	17.9776	526.3379	57.3844	56.8828	0.36509	12.31574	0.000078	0.000094	0.000001	0.16528	0.549
E_3: After harvest of late rice variety of above 135 days																
Genotypes	30	32.09**	26.587**	60.40**	1.993**	262.75**	684.75**	462.16**	255.53*	23.07**	163.47**	0.019**	0.206**	0.0031**	3.124**	2.385**
Parents	9	74.7999**	70.1163**	10.6922	0.254	2.8315432	310.1801**	26.998**	88.2691	13.45041**	5.358101	0.001545**	0.02236**	0.000199**	1.819**	1.365*
hybrids	20	15.0953**	2.49531**	64.3968	2.371	170.12143	479.5344**	198.412**	326.8023**	13.07754**	103.991**	0.0018431**	0.0193**	0.000387**	3.294**	2.175**
Par Vs Hyb	1	0.44140	91.7343**	428.097	134.59**	4454.602	8160.025**	9653.697**	335.781**	309.6514**	2776.236**	0.00773**	0.0333**	0.000012**	11.492**	15.754**
Line	6	31.151*	5.429**	154.37**	2.831**	475.26**	391.651	387.821**	335.262	23.595*	164.049	0.00291*	0.0331	0.000634	5.978*	4.241*
Tester	2	1.2388	0.667	24.300	1.340	8.588	47.012	170.346	647.832	2.984	14.553	0.00363**	0.00026	0.000027	2.435	0.222
Line x Tester	12	9.3768**	1.333	26.092*	0.651	44.469*	595.562**	108.385**	269.067**	9.500**	88.860**	0.0010**	0.0154**	0.000325**	2.0942**	1.466
Error	30	0.73334	0.72311	9.77124	0.458789	11.83804	83.76560	21.69353	120.4268	0.364980	9.886743	0.000074	0.000134	0.000001	0.367	0.588

*Significant at 5 % level; **Significant at 1 % level of probability

Table.2 Analysis of variance for combining ability and genetic components for seed yield, its attributes and quality characters under E_1, E_2 and E_3 in chickpea

Source of variation	D.F.	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	Secondary branches plant^{-1}	Pods plant^{-1}	Biological yield plant^{-1} (g)	Harvest index (%)	100-seed weight (g)	Seed yield plant^{-1}(g)	Seed volume (ml seed^{-1})	Hydration capacity seed^{-1} (g)	Hydration index	Swelling index	Protein content (%)
E_1: CSI																
GCA	9	58.56**	29.50**	24.97	0.254	5.17**	162.47	151.15**	342.80**	13.445**	26.87*	0.0018**	0.022342**	0.000198**	1.6848**	1.09499
SCA	20	13.48**	2.25	46.68**	2.371**	172.56**	3560.1**	177.62**	231.13**	13.07**	269.77**	0.0019**	0.02035**	0.000391**	4.45436**	2.1739**
Error	30	1.00	1.35	16.33	0.510	0.1448	366.95	35.064	51.041	0.3535	9.55	0.00008	0.00006	0.000001	0.08136	0.77683
Genetic components																
σ^2gca		1.065	0.211	-0.927	-0.099	19.254	94.158	-6.082	4.447	0.378	-3.632	0.0002	0.0001	0.0000025	0.2312	0.0762
σ^2sca		2.777	-0.256	15.274	1.0774	30.703	1395.5	75.11	77.453	4.554	124	0.0005	0.0082	0.000158	10874	0.3786
σ^2gca/ σ^2sca		0.384	-0.824	-0.061	-0.092	0.627	0.067	-0.081	0.057	0.083	-0.029	0.400	0.012	0.016	0.000	0.201
σ2A		4.260	0.844	-3.708	-0.396	77.016	376.632	-24.328	17.788	1.512	-14.528	0.001	0.000	0.000	0.925	0.305
σ2D		11.108	-1.024	61.096	4.310	122.812	5582.000	300.440	309.812	18.216	496.000	0.002	0.033	0.001	43496.000	1.514
h2(ns)		30.926	12.467	-13.079	-11.910	40.948	7.876	-5.308	9.069	14.432	-9.353	7.968	3.745	0.625	46.224	20.757
E_2: CS-II																
GCA	9	78.2721**	73.755**	20.9032	0.11912	0.9205	65.1731	16.2659	54.7656	134.488**	4.076253	0.00186**	0.022556**	0.000198**	2.123	1.386*
SCA	20	13.795**	2.2312*	51.1851**	2.83924**	176.833**	3915.12**	193.9875**	333.513**	13.0775**	254.3312	0.00168**	0.019547**	0.00039**	3.65876**	1.692**
Error	30	0.88064	0.96505	14.5232	0.43312	17.9776	526.3379	57.3844	56.8828	0.36509	12.31574	0.000078	0.000094	0.000001	0.16528	0.549
Genetic components																
σ^2gca		1.112	0.0887	-1.322	0.211	24.615	19.808	-6.874	15.845	0.3788	4.494	0.0002	0.0001	0.0000025	0.3299	0.1341
σ^2sca		2.888	0.2476	20.422	0.564	5.446	1457.8	75.26	95.77	4.5525	96.691	0.0005	0.0079	0.0001583	0.8313	0.125
σ^2gca/ σ^2sca		0.385	0.358	-0.065	0.374	4.520	0.014	-0.091	0.165	0.083	0.046	0.400	0.013	0.016	0.397	1.073
σ2A		4.448	0.355	-5.288	0.844	98.460	79.232	-27.496	63.380	1.515	17.976	0.001	0.000	0.000	1.320	0.536
σ2D		11.552	0.990	81.688	2.256	21.784	5831.20	301.04	383.080	18.210	386.764	0.002	0.032	0.001	3.325	0.500
h2(ns)		26.421	2.479	-9.065	37.762	60.039	2.263	-6.967	42.783	13.442	10.912	6.933	0.383	0.625	73.001	43.841
E_3; CS-III																
GCA	9	74.7999**	70.1163**	10.6922	0.254	2.8315432	310.1801**	26.998**	88.2691	13.45041**	5.358101	0.001545**	0.02236**	0.000199**	1.819**	1.365*
SCA	20	15.0953**	2.49531**	64.3968	2.371	170.12143	479.5344**	198.412**	326.8023**	13.07754**	103.991**	0.0018431**	0.0193**	0.000387**	3.294**	2.175**
Error	30	0.73334	0.72311	9.77124	0.458789	11.83804	83.76560	21.69353	120.4268	0.364980	9.886743	0.000074	0.000134	0.000001	0.367	0.588
Genetic components																
σ^2gca		0.681	0.171	6.324	0.1434	19.74	-37.62	17.069	22.248	0.3789	0.0435	0.0002	0.0001	0.0000005	0.2112	0.0763
σ^2sca		4.242	0.284	7.579	0.0422	14.91	268.65	51.521	110.23	4.5525	38.96	0.0005	0.0077	0.000161	0.8125	0.3792
σ^2gca/ σ^2sca		0.161	0.602	0.834	3.398	1.324	-0.140	0.331	0.202	0.083	0.001	0.400	0.013	0.003	0.260	0.201
σ2A		2.724	0.684	25.296	0.574	78.960	-150.480	68.276	88.992	1.516	0.174	0.001	0.000	0.000	0.845	0.305
σ2D		16.968	1.136	30.316	0.169	59.640	1074.600	206.084	440.920	18.210	155.840	0.002	0.031	0.001	3.250	1.517
h2(ns)		16.598	5.009	72.098	46.790	57.512	-39.161	28.222	47.342	12.935	0.201	8.388	0.388	0.129	48.399	20.531

*Significant at 5% level; **Significant at 1 % level of probability

Table.3 GCA effects of the parents of crosses showing SCA effects for seed yield plant^{-1} under E_1, E_2 and E_3 in chickpea

Environments	Cross combination	**SCA effects**	**GCA effect of females parent**	**GCA effect of male parent**
E_1(CS-I)	JG 130 x JG 97	25.430 **	1.370 (L)	**-2.870 (L)**
	JG 14 x JG 97	11.280**	10.400**(H)	**-2.870 (L)**
	JG 315 x JG 97	9.700**	-6.300**(H)	**-2.870 (L)**
	Indira Chana-1 x JG 97	5.200*	1.340 (L)	**-2.870 (L)**
	JG 11 x JG 97	4.800**	-8.430**(H)	**-2.870 (L)**
	JG 315 x ICCV 96029	3.300**	-6.300**(H)	**1.600* (H)**
	Vaibhav x ICCV 96029	2.970**	-7.300**(H)	**-2.870 (L)**
E_2(CS-II)	JG 130 x JG 97	23.650**	-0.250 (L)	**-2.230 (L)**
	JG 14 x JG 97	12.800**	10.620**(H)	**-2.230 (L)**
	JG 315 x JG 97	8.390**	-6.580**(H)	**-2.230 (L)**
	Indira chana-1 x JG 97	7.230*	1.550 (L)	**-2.230 (L)**
	JG 315 x ICCV 96029	3.560**	-6.580**(H)	**1.670* (H)**
E3(CS-III)	JG 130 x JG 97	11.200**	2.850 (L)	**0.420 (L)**
	JG 16 x JG 97	7.360**	7.560**(H)	**0.420 (L)**
	JG 14 x JG 97	7.140**	4.210**(H)	**0.420 (L)**
	JG 315 x JG 97	7.080**	-2.650*(H)	**0.420 (L)**
	JG 315 x ICCV 96029	**4.490****	**-2.650*(H)**	**0.750 (L)**

*and**Significant at P= 0.05 and 0.01 level of probability H: High combining ability L: Low combining ability

Table.4 Top ranking *per se* performance and sca effects and heterosis of F_1‘s and gca effects of the parents for seed yield plant^{-1} in chickpea

Environments	Hybrids	*Per se* performance seed yield per plant (g)	sca effects	gca effect of female	gca effect of male	Heterosis (%)	
						RH	HB
E_1 (CS-I)	JG 130 x JG 97	71.30	25.430 **	1.370	-2.870	113.154**	**100.450****
	JG 14 x JG 97	56.00	11.280**	10.400**	-2.870	47.504**	**25.561****
	JG 315 x JG 97	42.40	9.700**	-6.300**	-2.870	43.171**	**35.334****
	JG 11 x JG 97	34.30	4.800**	-8.430**	-2.870	20.140**	**9.480**
	JG 315 x ICCV 96029	29.10	3.300**	-6.300**	1.600*	-0.157	**-11.173**
	Indira Chana-1 x JG 97	28.10	5.200*	1.340	-2.870	-15.944	**-20.912**
E_2 (CS-II)	JG 130 x JG 97	66.55	23.650**	-0.250	-2.230	40.351**	**35.959****
	JG 14 x JG 97	55.25	12.800**	10.620**	-2.230	7.153	**-9.091**
	JG 315 x JG 97	37.65	8.390**	-6.580**	-2.230	37.761**	**27.584***
	Indira chana-1 x JG 97	29.85	7.230*	1.550	-2.230	-4.921	**-10.306**
	JG 315 x ICCV 96029	29.55	3.560**	-6.580**	1.670*	0.922	**-11.553**
E3(CS-III)	JG 130 x JG 97	40.55	11.200**	2.850	0.420	49.635*	**42.361**
	JG 14 x JG 97	41.75	7.140**	4.210**	0.420	94.915**	**76.923****
	JG 315 x JG 97	36.65	7.080**	-2.650*	0.420	77.255**	**73.846****
	JG 16 x JG 97	32.65	7.360**	7.560**	0.420	62.931*	**45.385**
	JG 315 x ICCV 96029	**26.05**	**4.490****	**-2.650***	**0.750**	**82.500****	**75.200****

*&**Significant at P= 0.05 & 0.01 level of probability; H = High combining ability and L=Low combining ability RH = Relative heterosis and HB =Heterobeltiosis.

Specific combing ability

Even though SCA effect does not contribute tangibly in the improvement of self-pollinated crops, except in situations where exploration of heterosis is feasible, best crosses are expected to generate transgrasive segregants which could be selected as potent homozygous lines.

Result of sca analysis revealed that some exhibited significant desirable sca estimates in all the environment for one or more characters whereas, for other trait they shared significant SCA in one or two environment. Hence, in order to draw some valid conclusions result of the crosses exhibited significant sca for the traits under all the environments have discussed. The hybrid Vaibhav x JG 97 exhibited desirable negative SCA for days to 50 % flowering in all the three environments. The hybrid Vaibhav x ICCV 96029 exhibited desirable positive SCA in all the environments for 100 seed weight and seed volume. The hybrid Indira chana-1 x ICCV 96029 exhibited desirable negative SCA for days to 50 % flowering and desirable positive SCA for swelling index and protein content in all the environments. The hybrid Indira Chana-1 x ICCV 96030 exhibited desirable positive SCA for pods plant^{-1}, 100 seed weight, seed volume and hydration capacity seed^{-1} in all the three environments. The hybrid JG 315 x JG 97 exhibited significant positive SCA for harvest index seed yield plant^{-1} and seed volume in all the three environments.

The hybrid JG 315 x ICCV 96029 showed positive desirable SCA for seed yield plant^{-1} in all the three environments.ie. E_1, E_2 and E_3.The hybrid JG 11 x ICCV 96029 exhibited desirable positive SCA for swelling index in all the three environments. The hybrid JG 11 x ICCV 96030 exhibited desirable positive SCA for 100 seed weight in all the three environments. The hybrid JG 14 x JG 97 exhibited positive significant desirable SCA for harvest index, 100 seed weight, seed yield plant^{-1} and hydration index in all the three environments. The hybrid JG 16 x ICCV 96029 exhibited desirable negative SCA for days to 50 % flowering whereas, it had desirable positive SCA for plant height, 100 seed weight and swelling index in all the environments. The hybrid JG 130 x JG 97 exhibited desirable positive SCA for pods plant^{-1}, biological, harvest index, 100 seed weight and seed yield plant^{-1}in all the three environments. The hybrid JG 130 x ICCV 96030 exhibited significant positive desirable SCA for hydration index in all the three environments. Similar finding were reported by Khan *et al.*, (2006), Gupta *et al.*, (2007) and Bhatt *et al.*, (2013) for days to maturity. Jayalakshmi *et al.*, (2009) and Naveed *et al.*, (2012) for plant height. Sewak *et al.*, (2012), Gadekar and Dodiya (2013) and Mishra *et al.*, (2013) for primary branches plant^{-1}and Secondary branches plant^{-1}. Bhardwaj *et al.*, (2010) for pods plant^{-1}, Biological yield, harvest index, 100 seed weight and seed yield plant^{-1}. Naveed *et al.*, (2012)for harvest index, Sidramappa *et al.*, (2008), Malik *et al.*, *(*2011) and Mishra *et al.*, (2013) for 100 seed weight and seed yield plant^{-1}.

Per se performance seed yield plant^{-1} is the ultimate and most important traits presented in table 3. In the present investigations, the degree of heterosis for seed yield varied considerably. Out of 21 crossed 2 crosses (JG 130 x JG 97 and JG 315 x JG 97) exhibited significant positive mid and better parents heterosis in all three environments. However, the highest mean value was sown JG 130 x JG 97(71.30 g plant^{-1}) in E_1, 66.55 g plant^{-1}in $E_2$and 40.55 g plant^{-1}in E_3. The crosses JG 14 x JG 97 performed MP and BP parents heterosis in E_1 and $E_3$and JG 315 x ICCV 96029 performed positive MP and BP parents heterosis in $E_3$for high seed yield should be utilized for future hybridization programme

Line x Tester analysis mean sum of square due to genotypes was highly significant for all the traits in E_1, E_2 and E_3. Analysis of variance for combining ability revealed that the variance due to gca were highly significant for all the characters in all the environments except for days to maturity in E_1, plant height and primary branches plant^{-1} in E_1, E_2 and E_3, secondary branches, seed yield and harvest index in E_2 and E_3, pods plant^{-1} in E_1 and E_2, biological yield plant^{-1} in E_2 and protein content in E_1.

Similarly variance due to sca were highly significant for all the characters in all the environments except days to maturity in E_1, plat height, primary branches plant^{-1} and secondary branches plant^{-1} in E_3, seed yield plant^{-1} in E_2 indicated the importance of both additive and non-additive gene effect in their expression.

Per se performance seed yield plant^{-1} is the ultimate and most important traits presented in table 4. In the present investigations, the degree of heterosis for seed yield varied considerably. Out of 21 crossed 2 crosses (JG 130 x JG 97 and JG 315 x JG 97) exhibited significant positive mid and better parents heterosis in all three environments. However, the highest mean value was sown JG 130 x JG 97(71.30 g plant^{-1}) in E_1, 66.55 g plant^{-1}in $E_2$and 40.55 g plant^{-1}in E_3 for high seed yield should be utilized for future hybridization programme

Acknowledgement

The Author are great full to All India Coordinated Research Project on chickpea, Research cum Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur for providing funding and field for the experiment and also thanks full to Major Advisor Dr. R.N. Sharma, Professor/ Principal Scientist, GPB at this university.

References

Anonymous, Descriptors for chickpea (*Cicer arietinum* L.). IBPGR/ ICRISAT/ ICARDA ROME. ICRISAT, Patancheru, India, 1993, pp.1-31.

Anonymous, Project Coordinator's Report, All India Coordinated Research Project on chickpea. Indian Institute Pulses Research, Kanpur, 2014, p.-29.

Bhardwaj, R., Sandhu, J.S. and Gupta, S.K., Gene action and combining ability estimates for yield and other quantitative traits in chickpea. (*Cicer arietinum* L.). Indian J. Agric. Sci., 2009, 79, 897-900.

Bhardwaj, R., Sandhu, J.S. and Singh, I., Heterosis in relation to combing ability in chickpea (*Cicer arietinum* L.). Crop Improvement, 2010, 37,126-132.

Bhatt, H., Anju, A. and Panwar, R.K., Genetic studies for yield contributing characters in chickpea (*Cicer arietinum* L.). Pantnagar J. Res., 2013, 11,214-218.

Gadekar, M.S. and Dodiya, N.S., Heterosis and combining ability analysis for yield and yield contributing traits in chickpea (*Cicer arietinum* L.*)*. Legume Research, 2013, 36, 373-379.

Gupta, S.K., Sandhu, J.S. and Kumar, A., Line x Tester analysis in chickpea (*Cicer arietinum* L.). Crop Improvement, 2007, 34,170-172.

Jayalakshmi, V., Reddy, C.K.K. and Reddy, M.S., Heterosis and combining ability in chickpea under moisture stress condition in chickpea (*Cicer arietinum* L.). J. Food Legumes, 2009, 22, 56-58.

Kempthorne, O., An introduction to genetic statistics, New York. John Wiley and Sons, 1957, 2nded; London: Chapam and Hall, Ltd.

Khan, H., Ahmad, F. and Iqbal, N., Genetic variability and correlations among quantitative traits in gram. Sarhad J. Agric., 2006, 22: 55–59.

Malik, S. R., Saleem, M., Iqubal, U., Zahid, M.A. Baksh, A and Iqubal, S.M., Genetic analysis of physiochemical traits in chickpea (*Cicer arietinum* L.) seeds. Int. J. Agric. Bio., 2011, 13, 1033-1036.

Mishra, N., Awasthi N.C. and Chaturvedi, S.K., Heterosis and inbreeding depression in wide crosses of chickpea (*Cicer arietinum* L.). Current Advances in Agric. Sci., 2013, 5, 23-26.

Monpara, B.A. and Gaikwad S.R., Combining high seed number and weight to improve seed yield potential of chickpea (*Cicer arietinum* L.) J. African Crop Sci., 2014, 22, 1-7.

Monpara, B.A., and Dhameliya, H.R., Genetic behaviour of earliness related traits and seed yield in chickpea (*Cicer arietinum* L.). Pakistan J. Biological Sci., 2013, 16, 955-959.

Naveed, M.T., Ali, Q., Saeed, U. and Babar. H., Combining ability analysis for various quantitative traits in chickpea (*Cicer arietinum* L.). IJBPAS, 2012, 1, 503-511.

Sewak, S., Iquebal, S.M., Singh, M.A., Solanki, N.P. and Sarika R.K., Genetic diversity studies in chickpea (*Cicer arietinum* L.) germplasm. J. Food Legumes, 2012, 25, 31-36.

Sidramappa, S., Patil, A. Salimath P.M. and Kajjidoni, S.T., Genetic variation for productivity and its related traits in recombinant inbred lines population of Chickpea. Karnataka J. Agric. Sci., 2008, 21, 488- 490.

Verma, P. and Waldiya, R.S., Diallel analysis for nodulation and yield contributing traits in chickpea (*Cicer arietinum* L.). J. Food Legumes, 2010, 23, 117-120.

How to cite this article:

Johnson, P.L., R.N. Sharma and Nanda, H.C. 2019. L X T Analysis of Yield Characters in Chickpea (*Cicer arietinum* L.) under Rice Based Cropping System. *Int.J.Curr.Microbiol.App.Sci.* 8(06): 1640-1651. doi: https://doi.org/10.20546/ijcmas.2019.806.196