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Generation mean analysis for seed yield and it's contributing quantitative traits in chickpea (*Cicer arietinum* L.)

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Abstract
The present investigation was conducted in *rabi* seasons during 2015-16, 2016-17 and 2017-18 at G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand with the objectives to study gene effects for ten yield and yield attributing traits. The experimental material consisted of three families (GL 10006 X DCP 92-3, DKG 876 X H 208 & GL 10006 X H 208) developed from four parents, each family comprised of six generations as P_1, P_2, F_1, F_2, BC_1 and BC_2. Scaling test, three parameter model, six parameter model and joint scaling test were used for gene action studies. Predominant and significant role of non-additive gene action i.e. dominance (h) and dominance × dominance (l) components which are non-fixable. Duplicate type of epistasis was prevalent than complementary epistasis in almost all the crosses in different traits.

Keywords: Chickpea, crosses, quantitative and generation mean analysis

Introduction
Chickpea is a self-pollinated diploid (2n = 2x = 16) crop species with a genome size of 740 Mb and presently grown on global area of 17.81 million ha with 17.19 million tons production (FAOSTAT 2019) [4]. In India it was grown in 9.44 million ha area with production of 10.13 million tons having productivity of 1073 kg/ha in the year 2018-2019 accounting for 55-60% of global chickpea production (Directorate of Economics and Statistics 2019) [3]. The genus Cicer consists of 43 species with 9 annuals, 33 perennials and one unclassified (Van der Maesen, 1987) [14]. Ladizinsky and Adler (1976) [9] considered *C. reticulatum*as the wild progenitor and south eastern Turkey as the centre of origin for the cultivated chickpea. It can be considered as a model legume crop having a smaller genome than other legume crops. Its substantial nutritive value makes it a valuable source for both food and feed (Gil *et al.*, 1996) [5].

An understanding of the mode of gene action, knowledge of genetic variances, levels of dominance, and the importance of genetic effects may help plant breeders to enhance yield potentials. In a polygenic system underlying a quantitative character, the allelic and non-allelic interactions play a greater role in the manifestation of gene effects and inheritance pattern. Although, diallel and line × tester analysis are useful in imparting the knowledge about additive variance, dominance variance, gca, sca variances and effects but they do not provide the estimates of nonallelic interactions. However, partitioning of total genetic variance in to all its components i.e., additive, dominance and all types of epistasis with regard to individual crosses will be of immense value in formulating an effective breeding programme. Generation mean analysis using first degree statistics is an accurate technique to partition total genetic variance in to different components in relation to individual crosses. Generation mean analysis (Mather and Jinks, 1971) [10], besides providing estimates of main gene effects (additive and non-additive) also provide estimates of non-allelic (digenic) interactions viz., additive × additive [i], additive × dominance [j] and dominance × dominance [l] cross-wise. This helps in the proper understanding and selection of potential parents or crosses for the pedigree selection or heterosis exploitation.

Experimental material

The experimental materials consisting of three crosses, namely GL10006 X DCP 92-3, DKG876 X H208 and GL10006 X H208. Experimental lines were sown in 4 m long rows. The row-to-row distance was maintained at 30 cm and plant to plant at 10-15 cm. The standard package of practices for chickpea cultivation was followed. Crosses were attempted using hand emasculation followed by immediate pollination between resistant and susceptible parents for botrytis grey mould disease during *rabi* season of 2015-16. The F_1 seeds of desired crosses obtained in previous season were planted in *rabi* 2016-2017 in between their parental lines to observe botrytis grey mould in comparison to their parents. The backcrosses were attempt with both the parents. When, the F_1's were backcrossed with female parent (P_1), it was designated as BC_1P_1. Similarly, when it was backcrossed to the male parent (P_2), it was designated as BC_1P_2. The F_1's, F_2's, BC_1P_1 and BC_1P_2 along with their parents were sown during *rabi* season of 2017-18.

Statistical analysis

The adequacy of three parameter model (additive-dominance model) was tested by using joint scaling test given by Cavalli (1952) [2]. In case of inadequacy of three parameter model (significant $\chi 2$ test) further analysis was done as per six parameter model suggested by Hayman (1958) [7].

Result and discussion

Results of scaling test revealed that simple additive-dominance model was inadequate for most of the crosses for almost all the characters studied except for number of primary branches per plant and number of seeds per pod in all the crosses, days to flowering in crosses DKG876 X H208 and GL10006 X H208, plant height in crosses DKG876 X H208, number of pods in crosses GL10006 X H208, seed yield in crosses DKG876 X H208 and biological yield in crosses GL10006 X H208. It indicated the importance of non-allelic interactions in most of the cases.

Additive (intra-locus) and additive x dominance (inter-locus) gene effects were significant and negative in cross GL 10006 X DCP 92-3 under study for number of days to 50 % flowering. Since, opposite sign of dominance [h] gene effects and dominance x dominance [l] gene interaction exhibited the presence of duplicate gene action. The dominance x dominance [l] is negative; hence it would tend to reduce the heterosis effect for number of days to 50 % flowering. Six parameter model for the crosses GL 10006 X DCP 92-3 and DKG 876 X H 208 revealed that additive x dominance [j] inter-locus gene interactions were found significant in both the crosses. Dominance gene effects, additive x dominance [j] and dominance x dominance [l] interaction in the cross GL 10006 X H 208 was significant for the number of days to maturity. The opposite direction of [h] and [l] exhibited the presence of duplicate gene action for all the three crosses.

Additive [d] & dominance [h] type intra locus gene interaction and additive x additive [i], additive x dominance [j] & dominance x dominance [l] type inter-locus gene effect were significant for cross GL 10006 X DCP 92-3 for plant height. None of the intra and inter locus effects were found significant for cross GL 10006 X H 208. The signs of dominance gene effect [h] and dominance x dominance gene interactions [l] suggested the presence of duplicate gene action for crosses GL 10006 X DCP 92-3 and GL 10006 X H 208. In cross GL 10006 X DCP 92-3, dominance gene effect [h], additive x additive gene interaction [i] and dominance x dominance [l] gene interactions were significant. Additive gene effect [d] and additive x dominance [j] gene interaction was significant in the cross DKG 876 X H 208. The sign of dominance gene effect [h] and dominance x dominance [l] gene interactions was in opposite directions for cross GL 10006 X DCP 92-3 revealing duplicate gene action for number of pods per plant. The sign of [h] and [l] were same in the cross DKG 876 X H 208 revealing the complementary gene action for number of pods per plant.

Results of six parameter model revealed that both type of intra- locus gene effects for DKG 876 X H 208 and only additive gene effects [d] for GL 10006 X H 208 were found significant for hundred seed weight. Whereas, additive x dominance [j] gene interaction in GL 10006 X DCP 92-3, additive x dominance [j] & dominance x dominance [l] gene interactions in DKG 876 X H 208 and additive x additive [i] & additive x dominance [j] gene interactions in GL 10006 X H 208 were found significant. Opposite direction of [h] & [l] indicates that there was presence of duplicate gene action in crosses GL 10006 X DCP 92-3 and DKG 876 X H 208. Whereas, sign of [h] and [l] in cross GL 10006 X H 208 was similar indicating the presence of complementary type of epistasis.

Dominance gene effect [h], additive x dominance [j] and dominance x dominance [l] gene interactions were significant in GL 10006 X H 208. In cross GL 10006 X DCP 92-3, dominance gene effect [h] and additive x dominance [j] were significant. Opposite direction of [h] & [l] indicates that there was presence of duplicate gene action in both the crosses for seed yield per plant. Six parameter model for the cross GL 10006 X DCP 92-3 revealed that dominance [h] type of intra-allelic, additive x additive [i], additive x dominance [j] and dominance x dominance [l] type of inter-allelic interactions were present. Cross GL 10006 X DCP 92-3 had opposite signs for [h] and [l] signifying duplicate gene action. Significant values of additive x dominance [j] type of gene interaction were found for cross DKG 876 X H 208. Opposite signs for [h] and [l] reveals presence of duplicate type of epistasis for both of the crosses for biological yield per plant. Six parameter model for all the crosses revealed that additive x additive [i] and additive x dominance [j] gene interactions were found to be significant for cross GL 10006 X DCP 92-3. Only additive x dominance [j] epistatic interaction had significant value for cross GL 10006 X H 208. Sign of [h] and [l] were found in opposite direction for all the crosses, thus, signifying duplicate gene action for harvest index.

Significane of scaling test and joint scaling test revealed the presence of epistasis for seed yield per plant, number of pods per plant, 100-seed weight, biological yield per plant, harvest index, number of days to 50 % flowering, days to maturity and plant height. Similar results for above traits except for harvest index were observed by Sundaram *et al*. (2018) [13]. The significance of [d], [h], [i] and [l] revealed the importance of both additive and non additive gene actions for the expression of different traits in three crosses. Earlier Patil *et al*. (2004) [12], Bhardwaj and Sandhu (2007) [1] and Gupta *et al*. (2007) [6] also reported that both additive and non-additive gene actions were important for yield and yield contributing characters in chickpea.

The presence of significant value of [h] for different traits indicated that selection should be delayed until heterozygosity was reduced in segregating generations. The non-significant value of [d] effect for most of the traits revealed that these traits were under the control of complex gene pathway in these crosses involving several minor genes of small effect

with different expression. These results are similar to the findings of Mathews *et al*. (2008) [11]. The gene action was considered to be duplicate type for maximum characters studied *viz*., seed yield per plant, number of pods per plant, 100 seed weight, biological yield per plant, harvest index, days to 50 % flowering, days to maturity and plant height, since the estimates of dominance and dominance x dominance effect had opposite signs. The findings of Kumhar *et al*. (2013) [8] were in similar direction to the present research findings.

Table 1: Components of generation means based on best fit model for different yield attributing traits in chickpea

Traits	Crosses	m	[d]	[h]	[i]	[j]	[l]	Chi-square	Epistasis
DF	C_1	78.633**	-1.533*	1.367	1.067	-5.433**	-3.933	67.309**	D
	C_2	82.20**	-0.40	-1.400	-	-	-	3.085^{NS}	-
	C_3	83.067**	0.067	-2.667	-	-	-	2.491^{NS}	-
DM	C_1	145.817**	0.333	2.900	0.333	8.633**	-6.933	87.560**	D
	C_2	146.967**	0.133	0.233	-0.933	8.700**	-11.267	85.440**	D
	C_3	146.367**	0.267	8.100	4.667	7.833**	-18.200**	62.061**	D
NPB/P	C_1	3.500**	0.167	-1.833	-	-	-	4.027^{NS}	-
	C_2	3.000**	-0.133	-0.333	-	-	-	3.002^{NS}	-
	C_3	3.233**	-0.033	-0.633	-	-	-	3.575^{NS}	-
PH	C_1	46.633**	-6.933**	-27.633**	-22.000**	-9.700**	55.667**	105.360**	D
	C_2	44.400**	3.000**	7.933	-	-	-	5.010^{NS}	-
	C_3	47.033**	3.133	-2.767	1.867	0.767	5.400	4.370^{NS}	D
NP/P	C_1	43.150**	0.000	31.033**	-24.333**	0.300	59.067**	25.855**	D
	C_2	37.150**	-5.933*	11.967	6.467	-6.567*	6.933	15.307**	C
	C_3	73.433**	-0.300	90.100**	-	-	-	2.205^{NS}	-
NS/P	C_1	1.633**	-0.033	-0.700	-	-	-	4.194	-
	C_2	1.600**	-0.067	-0.333	-	-	-	1.996	-
	C_3	1.033*	-0.033	1.033	-	-	-	1.086	-
100 SW	C_1	18.165**	0.061	-0.898	-0.542	-3.524**	0.824	191.525**	D
	C_2	17.181**	0.913**	-1.364**	-0.333	1.760**	4.569**	77.801**	D
	C_3	17.743**	0.813**	1.138	2.929**	-2.340**	1.175	150.058**	C
SY/P	C_1	10.859**	0.136	-1.732*	0.277	-2.364**	2.435	53.678**	D
	C_2	13.534**	0.661**	-6.942	-	-	--	3.900^{NS}	-
	C_3	11.294**	0.116	-2.623*	-0.673	-2.452**	4.960*	37.445**	D
BY/P	C_1	28.448**	-0.279	-7.881**	-5.079**	-3.013**	12.855**	36.764**	D
	C_2	29.401**	0.655	1.106	0.665	2.829**	-1.448	15.884**	D
	C_3	33.877**	1.091**	-2.889	-	-	-	2.703	-
HI	C_1	0.384**	0.010	0.052	0.079*	-0.036*	-0.107*	10.068**	D
	C_2	0.384**	-0.028	-0.093	-0.082	-0.036	0.173	6.557	D
	C_3	0.346**	-0.003	-0.067	-0.007	-0.068**	0.141	29.463**	D

*, ** significant at 5 % and 1% level, respectively

Here DF-Days to 50 % flowering, DM-Days to maturity, NPB/P-Number of primary branches/plant, PH-Plant height, NP/P-Number of pods/plant, NS/P- Number of seeds/pod, 100 SW-100 Seed weight, SY/P- Seed yield/plant, BY/P-Biological yield/plant, HI-Harvest index, D-Dominance epistasis, C- Complementary epistasis

Conclusion

The overall study revealed that there was predominant and significant role of non-additive gene action i.e. dominance (h) and dominance × dominance (l) components which are non-fixable coupled with duplicate type of epistatic interactions. The preponderance of non-additive gene action might have been exploited through heterosis breeding; however, the possibility of exploiting heterosis in chickpea is remote due to absence of male sterile lines, strict self pollination and high seed rate. However, it would be better to adopt biparental approach or intermate desired segregants in early generations followed by delayed selection for the improvement of traits studied.

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