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Generation mean analysis for seed yield and its contributing traits in chickpea (*Cicer arietinum L.)*

R.A. Deshmukh[1] and V.L. Gawande[2]
Department of Agriculture Botany,
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444 104 (M.S.), India.
1 Post Graduate Scholar, 2 Associate Professor (Agri. Botany) & Corresponding Author
vlgawande@yahoo.co.in

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Abstract
Generation mean analysis study in chickpea was undertaken to estimate the gene action operating in the inheritance of yield and its components. Six basic generations *viz.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 of two crosses, namely ICCV 2 × PKV Harita and ICCV 2 × HC 5 were studied. Joint scaling test was applied to test the adequacy of additive-dominance model for the traits under investigation. Significant χ^2 values indicated the presence of higher order interactions except for days to maturity in ICCV 2 × PKV Harita cross and number of primary branches per plant and number of pods per plant in ICCV 2 × HC 5 cross. The dominance component was higher in magnitude than additive component for all the characters studied along with duplicate type of epistasis in most of the cases. Both, additive, and non-additive gene action contribute significantly in the inheritance of various quantitative characters in chickpea. Moderate to high broad sense heritability and low narrow sense heritability was noticed for most of the traits studied. Further low to moderate genetic advance coupled with low genetic advance as *per cent* of mean was detected for most of the characters studied indicating the great influence of environmental effects. Hence, the biparental approach or inter-mating of desired segregants in early generations followed by delayed selection would be ineffective.

Key words**:** Chickpea, gene action, generation mean analysis, seed yield, yield components,

Introduction

Chickpea is one of the most important pulse crops of India, playing a crucial role in agricultural production by enriching the soil through biological nitrogen fixation. Chickpea has special significance predominantly in the vegetarian diet as it plays an important role in human nutrition as a source of protein (12.4 to 31.5 %), carbohydrate (48.2 to 67.6 %), starch (41 to 50 %), fat (6 %) vitamins and minerals for large population sectors in the developing world and is considered a healthy food in many developed countries (Jodha and Subbarao, 1987).

Hybridization followed by selection to isolate desirable recombinant from the superior crosses is one of the important breeding methods for breaking yield barriers and combining different traits in one variety. The ability of parents to combine well depends upon complex interaction among genes, which cannot be predicted from yield performance and adaptability of the parents (Allard, 1960). The precise knowledge of the nature of gene action for yield and yield attributing traits helps to choose an effective breeding strategy to accelerate the pace of genetic improvement of seed yield and other important traits. Most of the reports for gene action in chickpea are based on the diallel mating which does not provide information regarding non-allelic gene actions. The non-allelic gene actions could inflate the measures of additive and dominance components. Estimation of gene effects based on generation mean analysis provides requisite information to formulate the breeding strategy. Thus, it is imperative to generate the information on gene action for chickpea improvement. Estimates of heritability and genetic advance also give some idea about the gene action involved in the expression of various polygenic traits. Keeping this aspect in view, the present investigation was undertaken to study the gene action, heritability and genetic advance for yield and its components in two chickpea crosses.

Materials and Methods

Plant Material

The six generations of two crosses were developed by using three genotypes namely ICCV 2, PKV Harita and HC 5. The F_1s were developed by effecting crosses between ICCV 2 × PKV Harita and ICCV 2 × HC 5 during *rabi* 2011-2012 and were selfed to get F_2 seeds as well as backcrossed with both parents to get BC_1 and BC_2 generations during *rabi* 2012-2013 at the research field of Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola.

Field Trial-

These six generations of above mentioned two crosses and a check *viz.*, JAKI 9218 were evaluated in Randomized Block Design with three replications at the research field of Pulses Research Unit, Dr. P.D.K.V., Akola, during *rabi* 2013-14. One row each of P_1, P_2 and F_1; two rows each of BC_1 and BC_2 generations and four rows of F_2 generation of both the crosses were grown in each replication with row to row 30 cm and plant to plant 15 cm spacing. The data were recorded on plant basis from each entry in each replication on randomly selected 5 plants in parents, check and F_1s; 10 plants in backcrosses and 20 plants in F_2s for all the traits studied.

Statistical Analysis

Data were subjected to analysis of variance as per procedure suggested by Panse and Sukhatme (1954). The adequacy of three parameter model (additive-dominance model) was tested by using joint scaling test given by Cavalli (1952). In case of inadequacy of three parameter model (significant χ^2 test) further analysis was done as per six parameter model suggested by Hayman (1958). The value of heritability was estimated as per Warner (1952). Further, genetic advance and genetic advance as per cent of mean were estimated as per Johnson *et al*. (1955).

Results And Discussion

Analysis of variance revealed that, mean squares due to treatments were highly significant for all the traits studied indicating the presence of sufficient amount of variation for all the characters studied (Table 1). Further, Joint Scaling Test (Cavalli, 1952) was applied to find out the presence or absence of epistatic gene interactions and to estimate the m, d and h parameters (in case of adequacy of additive-dominance model). Significant Chi square (χ^2) values of joint scaling test suggested the inadequacy of the additive-dominance model and it was considered appropriate to use six parameter model of Hayman (1958) for the estimation of genetic components. The χ^2 value was found significant for most of the characters in both the crosses except for days to maturity in ICCV 2 × PKV Harita cross and for number of primary branches per plant and number of pods per plant in ICCV 2 × HC 5 cross (Table 2). Hence, in case of inadequacy of the additive-dominance model, the further analysis was done as per six parameter model given by Hayman (1958) and in case of adequacy of additive-dominance model, estimated values of m, d and h (Cavalli, 1952) were used to draw further conclusions.

Among the major gene effects additive (d) and dominance (h) effects including additive × additive (i) and dominance × dominance (l) epistatic gene interactions were found significant in ICCV 2 × PKV Harita cross for days to 50 per cent flowering. Whereas, in ICCV 2 × HC 5, dominance (h) gene effect with additive × additive (i) and dominance × dominance (l) interaction were found significant for days to 50 *per cent* flowering. The magnitude of dominance (h) gene effect was relatively greater than additive gene effect in both the crosses with duplicate type of epistasis in ICCV 2 × PKV Harita cross and complimentary in ICCV 2 × HC 5 cross. The value of dominance × dominance (l) gene interaction was relatively greater than additive × additive (i) interaction indicated its predominant role in the inheritance of this trait in both the crosses. The presence of epistatic interaction suggests that this trait was governed by more than one gene. Here, it was concluded that both additive and non-additive type of gene action played a major role in the inheritance of this trait, which has also been reported earlier by Verma and Waldia (2010). In view of parallel role of both additive and non-additive gene effects determining the inheritance of the character, simultaneous exploitation through adoption of biparental approach or early generation mating was suggested, further the selection should be delayed in subsequent generations.

The additive-dominance model was found adequate in ICCV 2 × PKV Harita for the trait days to maturity. Main effects *viz.*, average effect (m), additive (d) and dominance (h) were found significant. In case of ICCV 2 × HC 5, dominance (h) gene effect and additive × additive (i) and dominance × dominance (l) epistatic interactions were deciphered significantly. The parameters m, d and j were non-significant. In respect of ICCV 2 × HC 5 cross, dominance (h) gene effect and additive × additive (i) and dominance × dominance (l) epistatic interactions were involved in the inheritance of this trait but the relative magnitude of dominance × dominance (l) gene interaction prevailed over additive × additive (i) gene interaction. The sign of dominance (h) and dominance × dominance (l) was observed opposite suggesting duplicate type of non-allelic interaction in the inheritance of this trait. The findings are in confirmation with Patil *et al.* (1987). The relative magnitude of dominance effect was higher than additive (d) effects in ICCV 2 × PKV Harita cross indicated that the character was predominantly under the control of dominance gene action although substantial additive effect was also present. Bicer and Sakar

(2008) also reported the same results. Hence, selection should be delayed to subsequent generations for this trait in both the crosses due to predominant effect of non-additive gene action.

The major gene effect i.e. dominance (h) with dominance × dominance (l) type of epistatic interaction were found to be significant for the trait number of primary branches per plant in ICCV 2 × PKV Harita cross. The parameters *viz.*, additive (d) and additive × additive (i) and additive × dominance (j) epistatic interactions were observed to be non-significant. The value of dominance (h) gene effect and dominance × dominance (l) digenic interaction were detected with opposite sign which showed that genes have duplicate epistatic interaction in ICCV 2 × PKV Harita cross. Non-additive gene effect indicated a poor gain under selection in early generations. Hence, selection should be delayed to later generations with some sort of intermating in early generations. In cross ICCV 2 × HC 5, three parameter model was found adequate with significant dominance (h) gene effect in the inheritance of this trait. The character showed the simple inheritance by dominance (h) gene action. Hence, the selection in early generation should be avoided.

As regards the number of pods per plant, the major gene effects, additive (d) and dominance (h) were found to be significant with all the three epistatic gene interactions in ICCV 2 × PKV Harita cross. Higher magnitude of dominance (h) gene effect revealed the preponderance of dominance (h) over additive effect indicating the importance of dominance (h) gene effect for inheritance of this trait. Among the interaction effects, all the three non-allelic interactions were significant in ICCV 2 × PKV Harita cross but the higher magnitude of epistatic interactions indicated its importance for controlling inheritance of this trait mostly with non-additive gene action. Further, presence of duplicate type of epistatic interaction was also detected. The similar findings were also reported by Verma and Waldia (2010). In view of parallel role of both additive and non-additive gene effects determining the inheritance of different characters, their simultaneous exploitation through adoption of biparental approach or early generation mating was suggested. In ICCV 2 × HC 5 cross, three parameter model was found adequate to explain the genetic variation with significant additive (d) and dominance (h) gene effect. The dominance (h) gene effect played a major role in the inheritance of this trait in ICCV 2 × HC 5 cross. Hence, delayed selection in subsequent segregating generations may help for isolating desirable segregants.

For 100 seed weight, dominance (h) component and dominance × dominance (l) interaction were found to be significant in both the crosses alongwith duplicate type of epistasis. These results are in accordance with the previous findings of Kumhar *et al*. (2012). The dominance (h) gene effect alongwith additive × additive (i) and dominance × dominance (l) interaction were found significant with duplicate type of epistasis for seed yield per plant in ICCV 2 × PKV Harita and ICCV 2 × HC 5 cross. The greater magnitude of dominance × dominance (l) interaction as compared to additive × additive (i) indicated the importance of dominance × dominance (l) interaction in the inheritance of this trait with dominance (h) gene effect as has been reported earlier by Patil *et al*. (1987). Intermating of early generation segregants followed by delayed selection in subsequent segregating generations for increasing 100 seed weight and seed yield per plant would be effective.

High estimates of broad sense heritability were recorded for days to maturity and seed yield per plant in both crosses (Table 3). Moderate level of broad sense heritability was detected for days to 50 per cent flowering, number of pods per plant and 100 seed weight in both the crosses. The findings were in line with Nimbalkar (2000) and Vekaria *et al.* (2008). Low level of broad sense heritability was recorded for number of primary branches per plant in both the crosses. Moderate level of narrow sense heritability was noticed for seed yield per plant in both crosses and also for number of pods per plant in ICCV 2 × HC 5 cross. However, low level of narrow sense heritability was recorded for days to 50 per cent flowering, days to maturity, number of primary branches per plant and 100 seed weight in both crosses and number of pods per plant in ICCV 2 × PKV Harita cross. Most of the character showed the moderate to low level of broad sense and narrow sense heritability which revealed that the characters were highly influenced by the environmental effects and genetic improvement through selection will be little bit difficult due to masking effect of the environment on the genotypic effects.

High genetic advance was recorded for the character days to maturity in ICCV 2 × PKV Harita cross. The results are in conformation with Nimbalkar (2000) for plant height. The character days to 50 per cent flowering and days to maturity in ICCV 2 × HC 5 cross recorded moderate genetic advance. Low genetic advance was noticed for number of primary branches per plant, number of pods per plant, 100 seed weight and seed yield per plant in both crosses and days to 50 per cent flowering in ICCV 2 × HC 5 cross. Data revealed that, low to moderate genetic advance was recorded for days to 50 per cent flowering, number of primary branches per plant, number of pods per plant, 100 seed weight and seed yield per plant in both the crosses indicating the major role of non-additive gene action in the inheritance of these traits. It was found that days to 50 per cent flowering and days to maturity in ICCV 2 × PKV Harita recorded high genetic advance as per cent of mean as reported earlier by Nimbalkar (2000). Moderate level of genetic advance as per cent of mean was recorded for 100 seed weight and seed yield per plant in both the crosses. Whereas, days to maturity, number of primary branches per plant and number of pods per plant in ICCV 2 × HC 5 cross showed moderate genetic advance as per cent of mean. It was revealed that low genetic advance as per cent of mean was recorded for days to 50 per cent flowering in ICCV 2× HC 5. Whereas, for plant height, number of primary branches per plant and number of pods per plant in ICCV 2 × PKV Harita cross exhibited low genetic advance as per cent of mean.

The result showed that there was no consistency in magnitude of genetic parameters observed in any cross population. However, the crosses ICCV 2 × PKV Harita and ICCV 2 × HC 5 exhibited high magnitude of heritability coupled with high genetic advance as per cent of mean for the traits days to maturity and plant height, respectively, which indicates that the heritability was due to additive gene effects and which could be helpful for improvement of these trait by simple selection. Low heritability percentage coupled with low genetic advance as per cent mean was recorded for number of primary branches per plant in both the crosses indicating the great influence of environmental effects and hence selection would be ineffective for these traits in respective cross, as has been reported earlier by Arshad *et al.* (2002). Non-additive gene action coupled with low heritability percentage and low genetic advance as per cent of mean was observed for number of primary branches per plant in cross ICCV 2 × PKV Harita indicating a poor gain under selection in early generations, hence, for improvement of the traits selection must be delayed to the later generations.

The overall study revealed that there was significant role of additive (d) and additive × additive (i) components which are fixable in both the crosses for most of the traits. However, predominant and significant role of non-additive gene action i.e. dominance (h) and additive × dominance (j) and dominance × dominance (l) components which are non-fixable coupled with duplicate type of epistatic interactions in most of the cases followed by low level of narrow sense heritability and genetic advance estimates were also noticed. 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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Table 1. Analysis of variance for seed yield and other characters in chickpea

Source	d.f.	Mean sum of squares					
		Days to 50 % flowering	Days to Maturity	No. of primary branches/ plant	No. of pods per plant	100 seed weight	Seed yield per plant
Replications	2	10.19	6.08	1.47	78.26	0.4	56.67
Treatments	11	58.14**	65.39**	2.93**	121.58**	8.92**	3.11**
Error	22	17.7	28.02	0.9	38.05	2.77	2.2

(** Significant at 1% level of significance)

Table 2. Estimates of joint scaling test and gene effects for different characters in chickpea

Character/ Parameter	Days to 50% flowering	Days to maturity	No. of primary branches per plant	No. of pods per plant	100 seed weight	Seed yield per plant
	Six parameter model (Hayman, 1958) or Three parameter model (Cavalli, 1952)					
Cross I	ICCV 2 X PKV *Harita*					
m	47.00	85.00**	13.53	49.13	18.48	10.30
d	-4.33**	-5.00*	-0.50	-4.00**	0.08	0.16
h	-8.66**	14.35**	-8.86**	-33.70**	6.08**	-5.40*
i	-10.00**	-	-3.80	-39.60**	0.33	-7.30*
j	2.33	-	0.86	-1.16**	-1.16	0.93
l	9.33**	-	4.53*	59.13**	-4.23**	8.76**
χ^2	18.91**	6.88(NS)	14.35*	18.01**	12.05*	13.67*
Interaction	Duplicate	-	Duplicate	Duplicate	Duplicate	Duplicate
Cross II	ICCV 2 × HC 5					
m	48.00	86.33	6.96	43.26**	26.65	10.80
d	0.33	-2.00	1.30	-6.13**	1.64	0.16
h	-4.16**	14.16*	2.03*	9.40**	-17.89**	-7.40*
i	-2.00**	16.00*	-	-	-9.40	-9.30**
j	8.83	4.16	-	-	-1.55	0.93
l	-10.33**	-35.00**	-	-	10.84**	10.76**
χ^2	88.60**	116.71**	8.88 (NS)	6.19 (NS)	47.97**	21.05**
Interaction	Complementary	Duplicate	-	-	Duplicate	Duplicate

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

Where : m-mean, d-additive gene effects, h-dominance gene effects, i-additive × additive gene interaction, j-additive × dominance gene interaction, l-dominance × dominance gene interaction.

Table 3. Estimates of heritability and genetic advance in two crosses of chickpea for seed yield and other traits.

Character	Days to 50 % flowering		Days to maturity		No. of branches per plant		No. of pods per plant		100 seed weight		Seed yield per plant	
Cross	**I**	**II**	**I**	**II**	**I**	**II**	**I**	**II**	**I**	**II**	**I**	**II**
Heritability in b. s. (%)	58.04	51.66	66.66	89.53	6.37	12.88	41.87	33.56	42.16	31.40	70.53	70.53
Heritability in n. s. (%)	17.27	29.50	1.57	5.20	2.10	9.95	3.61	32.55	8.71	8.60	41.20	41.20
Genetic advance	10.75	3.15	38.06	11.61	0.25	0.88	3.53	5.19	2.48	3.19	1.45	0.99
Genetic advance as % of mean	22.87	6.81	41.32	13.45	2.61	12.92	8.26	13.05	12.44	17.29	16.47	11.30

(b.s.- broad sense, n.s.- narrow sense)

Cross I - ICCV 2 × PKV *Harita*
Cross II- ICCV 2 × HC 5