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Non-allelic interaction of some quantitative traits in chickpea

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Abstract

In the present study five generations viz. P_1, P_2, F_1, F_2 and F_3 of chickpea were taken for the analysis of non-allelic interaction considering five yield and yield contributing characters like as date of first flower (DFF), number of primary branches at first flower (NPBFF), plant height at first flower (PHFF), number of pods per plant (NPd/P) and number of seeds per plant (NS/P). At first Mather's scaling test was done where scales C and D found to be significant and non-significant for all the traits, respectively. Potence was non-significant for all the characters, which revealed that there was no dominance. In the Cavalli's joint scaling test, the χ^2 values were found to be significant for all the characters, which confirm that additive-dominance model was inadequate and except additive and dominance effects there are other effects like non-allelic interaction, linkage, genotype × environment (G×E) interaction etc. are involved either individually or in combination in the inheritance of the studied traits.

Keywords: Scaling test; Potence; Non-allelic interaction; Chickpea

1. Introduction

Legumes are an excellent source of good quality protein in the diets of people and they are also valuable as animal feed. Legumes also increase and sustain the productivity of soil and when grown in rotation with cereals, and reduce chances of build 'up of diseases, insect-pests and weeds for the following cereal crops [1]. Pulse crops (food legumes) are the second most planted crops in Bangladesh after rice, reflecting the importance of pulses as a source of protein in Bangladeshi diets. The dominant pulse crops are lathyrus, lentil, chickpea, black gram and mungbean, and chickpea (*Cicer arietinum* L.) is the third most important food legume grown in 11m ha with 9 million ton production (https://www.fao.org). It is grown in over 45 countries in all continents of the world. It provides a high quality protein to the people in developing countries. People in the developed countries consider it as a healthy food. Green leaves/twigs of chickpea are used in preparing a nutritious vegetable in countries of South Asia. These are also used as high protein fodder mixed with cereal leaves. Chickpea stover is fed to the cattle/goats as a nutrient-rich supplement to their major cereal fodder in the lean season. Chickpea in particular is important, providing a high-level source of protein (21.7%) along with complex carbohydrates, dietary fibre, unsaturated fats and essential vitamins and minerals. Chickpea is a cool-season grain legume that may withstand hot temperatures during fruiting and ripening [2]. It was introduced to the Mediterranean Basin, to Africa and to the Indian subcontinent before 2000 BC [3]. *Cicer arietinum* L. grows from sea level to up to 2500 m in areas where temperatures ranges from 15°C to 29°C [3]. The plant is well adapted to tropical climates with moderate temperatures and is successfully cultivated under irrigation in the cool season of many tropical countries. Well-aerated sandy to sandy loam soils and black cotton soils with pH ranging from 5-7 or even higher are suitable but salinity and solidity should be avoided [2, 3]. In 2020, world production of chickpeas was 15 million tones, led by India with 73% of the global total, and Turkey, Myanmar, and Pakistan as secondary

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producers [4]. Most of the economic traits of the crop are quantitative in nature. Several statistical methods have been developed for the study of the inheritance of quantitative characters. To make Bangladesh self-sufficient with respect to protein sources, plants breeders are trying to improve the crops through breeding efforts and modern cultural technology. For successful breeding programmers breeders must have knowledge about the nature and extent of gene actions governing the various quantitative traits and should be able to determine and predict the magnitudes of these genes. Keeping this view in mind the present study was undertaken to see the adequacy of additive-dominance model and determine the simple relationship among the traits through the study of component of non-allelic interaction

2. Material and methods

2.1. Planting Material

The materials for this investigation consisted of three different varieties such as BARI chola_3, BARI chola_8, BARIchola_1collected from Regional Agricultural Research Station (RARS), Ishurdi, Pabna, Bangladesh. Five generations viz. P_1, P_2, F_1, F_2 and F_3 were raised from the two crosses as cross-1: (BARI chola_8 × BARI chola_3) and cross-2: (BARI chola_8 × BARI chola_1).

2.2. Field Experiment

The experiment was conducted during the Rabi crop season of 2013-2014 at botanical research field nearby the third science building of University of Rajshahi, Bangladesh. The surface layer of soil of the field was well pulverized by plugging before sowing of seeds. As the experimental field was sufficiently moist, no irrigation was given before or after the sowing of seeds. The experiment was conducted in a Randomized Complete Block Design (RCBD) with three replications. Five generation (P_1, P_2, F_1, F_2 and F_3) for each of the two crosses were evaluated in this study. The experimental field was comprised area of 1400×380cm^2. Each replication contained 50 rows where each row having 5 hills. Spaces between replications were 100 cm, gaps between rows and hills were 40 cm and 30 cm, respectively. In each hill, one plant was maintained. The seeds of different crosses were sown randomly following individual plant randomization in different replicated plots. The excess seedlings were removed from the experimental field and regular weeding was done. The insecticides were sprayed at two or three times of the total life cycle of this plant whenever it was necessary.

2.3. Data Collection and Analysis

Data were collected on individual plant basis. Data date of first flower (DFF) was recorded form the germination and on the opening of first flower in each of the plants. Plant height at first flower (PHFF) was measured in cm from the base of the stem to the tip of the plant at first flowering stage. The number of primary branches per plant (NPBFF) was counted and recorded at the time of first flowering. In case of number of pods per plant (NPd/P) all the pods of an individual plant (NPd/P) were collected, and then the total number of pods was counted and recorded. For number of seeds per plant (NS/P) all the seeds of an individual plant were collected, counted and dried up properly. The collected data were analyzed following the biometrical techniques as developed by Mather [5] based on the mathematical model of Fisher [6] and those of Allard [7], Hayman and Mather [8]. The analysis of variance of RCBD for each character under study was performed to test the differences among the five studied generations. Scaling tests was outlined as per Mather [5] and Hayman and Mather [8] model was performed to detect the presence of non-allelic interaction. The significance of scaling test implies the inadequacy of the simple additive-dominance model. The test of adequacy of scale is important because in most of the cases the estimation of additive and dominance components of variance is made assuming the gene interaction. Mather [5] and Hayman and Mather [8] gave four tests for scale effects. The significance of scaling tests and gene effects was performed using t-test as outlined dividing the effects of A, B, C and D by their respective standard error [9]. Due to absence of back cross generations, only C and D sales are used in this investigation and the computations are as follows:

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

$$D = 4\overline{F_3} - 2\overline{F_2} - \overline{P_1} - \overline{P_2}$$

When the scale is adequate, the values of the scales C and D should be zero within the limit of their respective standard errors (SE).Variances of above scales are as follows:

$$V_C = 16\overline{V}(\overline{F_2}) + 4\overline{V}(\overline{F_1}) + \overline{V}(\overline{P1}) + \overline{V}(\overline{P_2})$$

$$V_D = 16\overline{V(F_3)} + 4\overline{V(F_2)} + \overline{V(P_1)} + \overline{V(P_2)}$$

Where;

VP_1, VP_2, VF_1, VF_2, and VF_3 are the variance of P_1, P_2, F_1, F_2, and F_3 populations, respectively.

Standard errors (SE) of the above scales are:

$$S.E\ (C) = \sqrt{V_C}$$

$$S.E\ (D) = \sqrt{V_D}$$

Now, the 't' values are calculated as follows:

$$t_C = {}^{C}/_{S.E(C)} \text{ and } t_D = {}^{D}/_{S.E(D)}$$

The calculated value of 't' are to be compared with tabulated value of 't' at 5% level of significance. In each test, the degree of freedom is sum of the degrees of freedom of various generations (total number of observations - total number of replications) involved. Hayman [10] and Jinks and Jones [11] devised the five parameter model for the estimation of various genetic components which were estimated according to Hayman [10] as follows:

Mean,

$$m = \overline{F_2}$$

Additive effect,

$$d = {}^{1}/_{2}\overline{P_1} - {}^{1}/_{2}\overline{P_2}$$

Dominance effect, $h = {}^{1}/_{6}(4\overline{F_1} + 12\overline{F_2} - 16\overline{F_3})$

Dominance ×Dominance effect, $l = {}^{1}/_{3}(16\overline{F_3} - 24\overline{F_2} + 8\overline{F_1})$

Additive ×Additive effect, $i = \overline{P_1} - \overline{F_1} + ({}^{1}/_{2})(\overline{P_1} - \overline{P_2} + \overline{h}) - {}^{1}/_{41}$

Variances of above parameters are as follows:

$$Vm = V\overline{F_2}$$
$$Vd = {}^{1}/_{4}(V\overline{P_1} + V\overline{P_2})$$
$$Vh = {}^{1}/_{36}(16V\overline{F_1} + 144V\overline{F_2} + 256V\overline{F_3})$$
$$Vl = {}^{1}/_{9}(256V\overline{F_3} + 576V\overline{F_2} + 64V\overline{F_1})$$
$$Vi = V\overline{P_1} + V\overline{F_2} + {}^{1}/_{4}(V\overline{P_1} + V\overline{P_2} + h) + {}^{1}/_{16}V_1$$

Now, standard errors (SE) of the parameters are as follows:

$$S.E.m = \sqrt{Vm} \qquad S.E.d = \sqrt{Vd}$$

$$S.E.h = \sqrt{Vh} \qquad S.E\,I = \sqrt{V_I} \qquad S.E.i = \sqrt{Vi}$$

Now, the values of 't' are calculated as follows:

$$t_m = {}^{m}/_{S.E.\,m}$$

$$t_d = {}^{d}/_{S.E.\,d}$$

$$t_h = {}^{h}/_{S.E.h,}$$

$$t_l = {}^{l}/_{S.E.\,l}$$

$$t_i = {}^{i}/_{S.E.\,i}$$

The calculated value of 't' are to be compared with tabulated value of 't' at 5% level of significance. To see the adequacy of additive-dominance model, Cavalli's [12]joint scaling test was done based on 4-parameter model as m, [d], [i] and [l] and hence parameter [h] was excluded from this model due to non-significance of potence.

3. Results and discussion

Mean and variance of five generations viz. P_1, P_2, F_1, F_2 and F_3 were calculated separately for five quantitative characters viz. DFF, PHFF, NPBFF, NPd/P and, NS/P in each of the two crosses. Mather [5] scaling test was done for all the characters and the results are presented in Table 1.For the five characters scale C was significant and D found to be non-significant. Significant C scale indicated that the studied traits are largely influenced by 'l' type i.e. dominance × dominance non-allelic gene interaction which would confirm by the model fitting of Cavalli's [12] joint scaling test. The result of Mather's [5] scaling test noticed that the scales are inadequate to explain the relationship among the traits of different generations. The same results were reported by several research workers such as Samad et al. [13] in chickpea, Deb and Khaleque [15] in chickpea, Shahid [16] in wheat, Samad [17] in chickpea. Sarker et al. [14] in chickpea also made a result from Mather's [5] scaling test and observed that scales are inadequate for most of the cases. The test of potence was done in two crosses for the five characters and the results were given in Table 1 where it was showed that the potence was non-significant for all the characters. These results reflected to some extent the values as obtained in case of degree of dominance.

Table1 Mather's scaling test and test of potence of five characters in chickpea

Characters	C	D	Potence
DFF	6.2477**	-3.3653^{NS}	-1.1238^{NS}
NPd/P	93.219**	-138.1748^{NS}	1.6286^{NS}
NS/P	108.4477**	-146.3651^{NS}	-16.0572^{NS}
PHFF	7.7419**	-4.0309^{NS}	1.5428^{NS}
NPBFF	2.3522**	-3.47^{NS}	0.1334^{NS}

Estimated values of 5-parameters and their test of significance are given in Table 2. For the five characters values of m and [h] were significant and the values of [d] and [l] were non-significant. Another parameter [i] found to be non-significant in this study except the traits NPd/P and NS/P. Significant [h] and [i] items indicated the dominace gene action and additive × additive non-allelic interaction in the respective traits. Samad et al. [13] observed and revealed the significance [d], [h], [i] and [l] of both additive and non-additive gene actions for the expression of different traits in six crosses in chickpea. Moreover, the results of Saxena[18] in pigeonpea found the same in different traits and crosses, whereas Hooda et al. [19]and Sameer et al. [20] got significant [h] for plant height, branches per plant, pods per plant, 100-seed weight and seed yield in pigeonpea. In Shoba et al. [21] observation of [i] interactions in groundnut, most of the yield contributing traits was significant.

Table 2 Estimated values of 5-parameters and their test of significant of five characters in chickpea

Characters	m	[d]	[h]	[i]	[l]
DFF	82.4667**	-4.1904^{NS}	5.2848**	-5.09615^{NS}	-12.8173^{NS}
NPd/P	129.9000**	-24.8095^{NS}	155.8911**	58.034**	-308.525^{NS}
NS/P	140.6000**	-29.7857^{NS}	153.818**	56.0797**	-339.75^{NS}
PHFF	37.8000**	-o.3647^{NS}	9.3913**	3.24805^{NS}	-15.6970^{NS}
NPBFF	2.9333**	-0.0238^{NS}	4.0148**	2.5910^{NS}	-7.7629^{NS}

Cavalli's [12] joint scaling test ($\chi 2$) was done through the weighted least square techniques to test the goodness of fit of the observed generation means with that of the expected means based on 4-parameters viz. m [d], [i] and [l]. Other parameter [h] is not included in the model due to non-significant of potence value. The obtained $\chi 2$ values for each of the charactersare shown in Table 3. The $\chi 2$ values found to be significant for all the characters and indicated the inadequacy of the additive-dominance model.

Table 3 Joint scaling test of five characters in chickpea

Characters	DFF	NPd/P	NS/P	PHFF	NPBFF
$\chi 2$ Values	8.5424**	27.0861**	4678.3671**	87.7971**	2727.4743**

Joint sealing test of Cavalli [12] is more effective than any other test in detecting the adequacy of model, since it uses information from all of the generations available from each cross at a time. Inadequacy of the model showed that in the inheritance of these characters with the additive-dominance gene effects, non-allelic interaction and linkage may be a part.Significantχ^2values were noted by Deb[22] in lentil, Uddin [23] in wheat Rahman [24] in *Philosamia ricini*, Islam in brinjal [25] and Deb and Khaleque [15] in chickpea for different characters and crosses.

4. Conclusion

The significant result of scale C for all the traits indicated the simple additive-dominance modelis not adequate to getting the relationship and the studied traits are largely influenced by dominance × dominance [l] non-allelic interaction component. The χ^2 values were found to be significant for all the characters which noticed that additive-dominance model is quite unsatisfied to explain the nature of relationship among the traits and hence except additive, dominance and non-allelic gene effects, the studied traits bears the effects of genotype × environment (G×E) interaction or linkage. So in this case need to focus the parameters of G×E interaction and linkage to precisely measure the relationship of the studied traits.

Compliance with ethical standards

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Disclosure of conflict of interest

The authors declare that they have no conflict of interest.

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