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The Pharma Innovation



ISSN (E): 2277-7695 ISSN (P): 2349-8242 NAAS Rating: 5.23 TPI 2023; 12(3): 3098-3101 © 2023 TPI www.thepharmajournal.com Received: 12-12-2022 Accepted: 15-01-2023

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Gene effects in desi x desi crosses of chickpea (*Cicer arietinum* L.) under timely and late sown condition

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Abstract

An experiment was conducted in chickpea to study of gene effects (through generation mean analysis), involving six generations (P₁, P₂, F₁, F₂, B₁ and B₂) of each of the three crosses namely RSG-807 × RSG-895, RSG-895 × HC-5 and RSG-974 × Avrodhi. This experiment was grown in compact family block design with three replications under two different environments *viz.*, timely (1st November) and late (1st December) sown conditions during *rabi* 2021-22 at Rajasthan Agricultural Research Institute, Durgapura, Jaipur (SKNAU, Jobner). The generation × environment interaction was found significant in all the crosses. Significant differences were also observed among the generations within cross in all the crosses under both the conditions. Out of four individual scaling tests, at least one scale was found significant in all three crosses under both the conditions. The significant value of 'm' component of gene effect was observed under studied in all the crosses. The magnitude of non-fixable gene effects (additive and additive x additive) for plant height in all three crosses under both the conditions. Therefore, selection in early segregating generation will be not effective.

Keywords: Gene effects, model and scaling test

Introduction

The chickpea (Cicer arietinum L.), which is currently cultivated on 15.01 mha worldwide with 95% of its production taking place in developing nations, is the second most significant pulse crop (after dry bean). India accounts for 65.62 percent of the world's acreage and 75.50 percent of its production (Anonymous, 2021 and FAOSTAT, 2021). The chickpea plays a distinctive role in the diet of India's largely vegetarian population since it has higher protein content and a different amino acid profile from cereals. Yet, during the past 30 years, chickpea production and productivity have remained constant. One of the main reasons is its sensitive to high temperature at critical stages. The precise knowledge of the nature of gene action for yield attributing traits helps in the choice of an effective breeding strategy to accelerate the pace of genetic improvement of seed yield. Most of the reports for gene action in chickpea are based on the diallel mating (Katiyar and Singh, 1980, Deshmukh and Bhapkar, 1982, Saxena et al., 2016 and Halladakeri et al., 2021)^[9, 4, 14, 7] which does not provide information regarding nonallelic gene actions. The non-allelic gene actions could inflate the measures of additive and dominance components. Further, Hayman (1958)^[8] suggested that the six-parameter model was good as the back cross studies for estimation of gene effects and gives satisfactory results. Keeping this in mind, the present investigation was carried out to determine the gene effects for plant height in three crosses of chickpea under timely and late sown conditions through generation mean analysis.

Material and Methods

Plant Material: Five desi chickpea cultivars *viz.*, HC-5, Avrodhi, RSG-974, RSG-807 and RSG-895 of diverse pedigree, seed size, origin and agro-climatic adaptation were crossed in three combinations viz., RSG-807 × RSG-895, RSG-895 × HC-5 and RSG-974 × Avrodhi. Six generations *viz.*, P₁, P₂, F₁, F₂ and B₁ and B₂ of these three crosses grown in a compact family block design with three replications during *rabi* 2021-22 at research farm of Rajasthan Agricultural Research Institute, Durgapur with two environments viz., timely sown (E1) condition and late sown (E2) conditions which were created by different date of sowing, first-November and first-December 2021, respectively. Seeds were sown in 3-meter-long rows. Keeping spacing between and within rows at 0.30 m x 0.15 m.

Parents and F_1 each were represented by two rows, F_{28} by 6 rows and B_1 and B_2 each by 4 rows.

Statistical Analysis: Pooled analysis of variance was done over two environments (timely and late sown conditions) according to Panse and Sukhatme (1985) ^[12]. The individual scaling test tests 'A', 'B', 'C' and 'D' (Mather, 1949) were applied to test the presence or absence of non-allelic interaction. Joint Scaling (Cavalli, 1952) ^[2] was applied to find out the presence of interaction. Significant χ^2 - values of joint scaling test suggested the inadequacy of additive-dominance model and it was considered appropriate to use six-parameter model of Hayman (1958) ^[8] for the estimation of gene effects under both the conditions.

Results and Discussion

The pooled analysis of variance over environments (timely and late sown conditions) was revealed significant differences between environments in all crosses for plant height (Table 1). Significant differences between the environments were indicating the effect of environment on expression of the character. Generation \times environment interaction was also significant for plant height in all the crosses. The mean sum of squares due to differences among generations within each cross was significant (Table 2). Kumhar *et al.* 2013 ^[10] also fund similar results for plant height in chickpea.

Gene effects

RSG-807 × **RSG-895** (C1)

In cross RSG-807 × RSG-895, individual scaling tests 'A' and 'C' were found significant under timely sown (E1) condition, while all individual scaling tests ('A', 'B', 'C' and 'D') were significant under late sown (E2) condition which suggested the inadequacy of additive-dominance model under both the conditions (E1 and E2). It was further supported by significant chi-square value of joint scaling test, which indicated the possibility of presence of diegetic interaction and/or linkage and/or higher order interactions under both the conditions (E1 and E2) (Table 3).

In six parameter model, significant estimates of dominance (h) followed by additive \times additive (i) gene effect had maximum role for inheritance of this character under E2 condition, while none of the component was found significant under E1 condition. No comment could be drawn about type of epistasis under both the conditions (E1 and E2).

RSG-895 × HC-5 (C2)

The additive-dominance model was failed to estimate the different components of genetic variance in the this cross RSG-895 \times HC-5 under both timely (E1) and late sown (E2) conditions due to significant values of individual scaling tests 'C' and 'D' under E1 condition, while scale 'B' under E2

condition were observed. It was further supported by significant chi-square value of joint scaling test, which indicating presence of diegetic interaction and/or linkage and/or higher order interactions (Table 3).

In six parameters model, all the components were found significant under E1 condition, except dominance \times dominance (l) component, while additive \times dominance (j) component was found significant under E2 condition. Among the significant components, dominance (h) followed by additive \times additive (i) and additive \times dominance (j) components contributed major role for genetic variation for plant height. No conclusion could be drawn about type of epistasis under both the conditions (E1 and E2).

RSG-974 × Avrodhi (C3)

The significant estimates of individual scaling tests 'B' and 'C' under timely sown (E1) and scales 'C' and 'D' under late sown (E2) conditions suggested the inadequacy of additive-dominance model in cross RSG-974 \times Avrodhi. Further, it was supported by significant chi-square value of joint scaling test, which indicated the presence of digenic interactions and/or linkage and/or higher order interactions under both the conditions (E1 and E2). Therefore, six parameter model was followed in this cross (Table 3).

Under E1 condition, additive \times dominance (j) component was observed significant, while under E2 condition, dominance (h) and additive \times additive (i) components were significant in this cross. Among the significant components, additive \times dominance (j) component under E1 condition and dominance (h) followed by additive \times additive (i) component under E2 condition contributed maximum for inheritance for this character. No conclusion could be drawn about type of epistasis under both the conditions (E1 and E2).

The results confirmed to the reports of Kumhar et al. (2013) ^[10], Deshmukh and Gawande (2016) ^[5] and Samad et al. (2016) ^[13] in different crosses of chickpea. Samad et al. (2016) ^[13] and Sundaram et al. (2018) ^[15] also observed significant values of individual scaling tests in different crosses of chickpea. Under the present research most of the crosses including were found to be controlled by both additive as well as non-additive gene effects with predominance of non-additive gene effects under both the conditions. Thus, exploitation of both types of gene effects will lead to the improvement of such characters. The selection programmed aiming to improve such characters in a population should accumulate favorable additive genes and simultaneously maintain heterozygosity in the population for manifestation of the dominance and epistasis gene effects. Use of reciprocal recurrent selection proposed by Comstock et al. (1949)^[3] has been suggested to improve the characters when both additive and non-additive gene effects are involved in the expression of characters.

 Table 1: Pooled analysis of variance (mean squares) for plant height in three crosses of chickpea

Crosses	Source of variations/d.f.						
C105865	Env. (1)	Rep. × Env. (2)	Gen. (5)	Gen. × Env. (5)	Error (20)		
Plant height (cm)							
RSG-807 × RSG-895 (C1)	153.778**	1.173	15.249*	1.466*	0.506		
RSG-895 × HC-5 (C2)	181.563**	1.833	58.667**	2.872*	0.915		
RSG-974 × Avrodhi (C3)	72.121**	0.696	8.033	4.212**	0.653		

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Crosses	Source of variations	d.f.	Plant height (cm)	
Crosses	Source of variations	a.i.	E1	E2
	Replications	2	0.064	2.281
RSG-807 × RSG-895 (C1)	Generations	5	5.322**	11.391**
	Error	10	0.285	0.725
	Replications	2	2.176	1.485
RSG-895 × HC-5 (C2)	Generations	5	30.810**	30.726**
	Error	10	0.947	0.883
	Replications	2	0.381	1.011
RSG-974 × Avrodhi (C3)	Generations	5	5.212**	7.031**
	Error	10	0.586	0.720

 Table 2: Analysis of variance (mean squares) among generations within cross for plant height in three crosses of chickpea under timely (E1) and late sown (E2) conditions

Table 3: Estimates of individual scaling tests, chi- square value (joint scaling test) and gene effects using six generations of three crosses for					
plant height (cm) under timely (E1) and late sown (E2) conditions					

	RSG-807 × RSG-895 (C1)		RSG-895 × HC-5 (C2)		RSG-974 × Avrodhi (C3)				
	E1	E2	E 1	E2	E1	E2			
	Individual scaling tests and chi-square (χ^2) value								
Α	-3.79*±1.65	-3.93*±1.77	2.19±1.79	1.99 ± 2.30	-2.00 ± 1.55	-1.59±2.43			
В	-1.26 ± 1.88	-4.33*±1.97	-2.66±1.71	-9.20**±1.84	-6.66**±1.77	-0.06±2.39			
С	-7.99*±3.72	-16.00**±3.14	-6.19*±2.72	-3.86±2.94	-8.26*±3.21	-14.40**±4.07			
D	-1.46 ± 1.74	-3.86*±1.7	-2.86*±1.37	1.66±1.69	0.20±1.67	-6.36**±2.24			
χ2	7.90*	28.21**	9.83*	27.57**	8.66*	14.21**			
	Gene effects (six parameter model) and type of epistasis								
m	50.80**±0.73	45.40**±0.64	55.71**±0.49	52.26**±0.58	49.80**±0.69	45.21**±0.87			
d	0.33 ± 0.92	1.66 ± 1.12	$-2.03*\pm0.95$	1.06 ± 1.23	1.73 ± 0.93	-0.19±1.39			
h	3.06±3.66	9.46**±3.53	9.19**±2.89	0.06 ± 3.51	0.13±3.45	14.56**±4.59			
i	2.93 ± 3.48	7.73*±3.41	5.73*±2.74	-3.33±3.39	-0.40±3.35	12.73**±4.48			
j	-1.26 ± 1.00	0.19±1.19	2.43*±1.14	5.59**±1.42	2.33*±1.11	-0.76±1.67			
1	2.13±5.25	0.53 ± 5.5	-5.26±4.67	10.53±5.75	9.06±4.94	-11.06±6.91			

Conclusion

The generation \times environment interaction was found significant in all the crosses. Significant differences were also observed among the generations within cross in all the crosses under both the conditions. Out of four individual scaling tests, at least one scale was found significant in all three crosses under both the conditions. The significant value of 'm' component of gene effect was observed under studied in all the crosses. The magnitude of non-fixable gene effects (dominance, additive x dominance and dominance x dominance) was found higher than fixable gene effects (additive and additive x additive) for plant height in all three crosses under both the conditions. Therefore, selection in early segregating generation will be not effective.

Acknowledgment

The authors are greatly thankful to the department of Plant Breeding and Genetics, Sri Karan Narendra Agriculture University, Jobner, Jaipur, Rajasthan for providing all necessary resources for the present study.

References

- Anonymous. Agricultural Statistics at a Glance, GOI, Ministry of A & FW, Department of A & FW, Directorate of E & S. (4th Advance Estimates); c2021. p. 67-70.
- 2. Cavalli LL. An analysis of linkage in quantitative inheritance. In: Quantitative Inheritance (ed E.C.R. Reeve and C.H. Waddington) HMSC, London; c1952. p. 135-144.

- 3. Comstock RE, Robinson HF, Harvey PH. A breeding procedure designed to make maximum use of both general and specific combining ability. Agronomy Journal. 1949;4:360-367.
- 4. Deshmukh RB, Bhapkar DG. Heterosis and combining ability for yield and its components in chickpea. Indian Journal of Agricultural Sciences. 1982;52(11):728-731.
- Deshmukh RA, Gawande VL. Generation mean analysis for seed yield and its contributing traits in chickpea (*Cicer arietinum* L.). Electronic Journal of Plant Breeding. 2016;7(1):86-93.
- FAOSTAT. Global area, production and productivity of chickpea. [Online] Available: http://faostat.fao.org; c2021.
- Halladakeri P, Arora A, Panwar RK, Verma SK. Genetic Architecture through Diallel Analysis in Chickpea for Yield and Related Traits. International Journal of Current Microbiology and Applied Sciences. 2021;10(3):2135-2145.
- 8. Hayman BI. The separation of epistasis from additive and dominance variation in generation means. Heredity. 1958;12:371-390.
- 9. Katiyar RP, Singh D, Verma VS. Heterosis response and inbreeding depression in chickpea. Tropical Grain Legumes Bulletin. 1980;19:41-43.
- Kumhar BL, Singh D, Bhanushally TB, Koli NR. Gene effects for yield and yield components in chickpea (*Cicer arietinum* L.) under irrigated and rainfed conditions. Journal of Agricultural Science. 2013;5(3):1-13.
- 11. Mather K. Biometrical Genetics: The Study of

Continuous Variation. Methen and Co. Ltd., London; c1949. p. 86-87.

- 12. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers, ICAR, New Delhi; c1985. p. 381.
- 13. Samad MA, Sarker N, Deb AC. Generation mean analysis of quantitative traits in chickpea. Bangladesh Journal of Botany. 2016;45(2):277-281.
- 14. Saxena K, Ravindrababu Y, Ram K. Study of heterosis using diallel analysis for yield and its component traits in chickpea. *The Bioscan.* 2016;11(2):943-947.
- Sundaram P, Samineni S, Sajja SB, Singh SP, Sharma RN, Gaur PM. Genetic studies for seed size and grain yield traits in kabuli chickpea. Euphytica. 2018;214(4):63.