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GENERATION MEAN ANALYSIS OF QUANTITATIVE TRAITS IN CHICKPEA

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Abstract

Nature of gene effects for 11 quantitative traits was analyzed in six crosses involving eight genotypes of chickpea through means analysis of basic five generations *viz.*, P_1, P_2, F_1, F_2 and F_3. The additive, dominance and epistatic gene effects were observed, indicating importance of both additive and non-additive gene actions for the expression of quantitative traits. Duplicate type of epistasis was prevalent than complementary epistasis in almost all the crosses in different traits. So, recurrent selection for these traits is suggested.

Introduction

As a biometrical technique in crop improvement, generation mean analysis reveals the estimates of main gene effects (additive [d] and dominance [h]) along with their digenic interactions (additive × additive [i], additive × dominance [j] and dominance × dominance [l]) and finally, helps which traits can be used for pure line or heterosis in further breeding program. Thus, the present investigation was undertaken to study the gene effects and epistasis for 11 quantitative traits in chickpea.

Materials and Methods

BARI-Chola (*Cicer arietinum* L.) 1, 2, 3, 4, 5, 6, 7 and 8 were procured from Regional Agriculture Research Station, Ishourdi, Pabna, Bangladesh. These varieties originated from ICRISAT line except BARI-Chola 5 which is collected from local cultivar of Pabna, Bangladesh. Selected varieties of chickpea were irradiated with irradiation source of Co^{60} at the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, Bangladesh. The radiation doses including control were 20 Kr = A, 30 Kr = B, 40 Kr = C and 0 Kr = D (control). After irradiation the varieties were regarded as lines. Trial of P_1, P_2, F_1, F_2, and F_3 generations was conducted in the Botanical research field, University of Rajshahi in 2010-2011. The data of 11 quantitative traits *viz.*, days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD, number of pods per plant (NPd/P), pod weight per plant (PdW/P), number of seeds per plant (NS/P), seed weight per plant (SW/P) and 1000-seed weight (1000-SW) were collected on individual plant basis following C.G.S system.

The presence or absence of epistasis in traits studied was detected by using C and D scaling test as suggested by Mather (1949) and Hayman and Mather (1955). Potence was done by comparing F_1 and F_2 means and joint scaling test by Cavalli (1952) was followed to see the adequacy of additive-dominance model. Here, two-parameter model (m and d) is done with five generations when potence is non-significant whereas, three-parameter (m, d and h) model is appropriate with significant potence values. Non-significant χ^2 value revealed that traits governed

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by only additive and dominance gene effects whereas, significant χ^2 value expressed the presence of non-allelic interaction in the concern traits. In this case, Hayman (1958) suggested five-parameter model. When dominance [h] and dominance × dominance [l] effect had the same sign the effects were complementary while different signs indicated duplicated epistasis by Kearsey and Poony (1996).

Results and Discussion

NPBMF, PWFD, RWD, PdW/P and NS/P were non-significant for either or both scaling test among all the crosses (Table 1). Besides, SW/P and 1000-SW expressed non-significant C and/or D values for all the crosses except $C_{5.}$ DMF for C_6, NPBMF for C_2, NPd/P for C_4 and PHMF for C_3, C_4 and C_6 exhibited significant C and D values while, the rest of the crosses for those traits had non-significant C and/or D values. Potence was only significant for RWFD, PdW/P and SW/P in C_5 and C_6; DMF, PWFD and NS/P in C_5; NPBMF and PHMF in C_2; NSBMF in C_3 and C_4 and 1000-SW in C_6. Scaling and joint scaling test was significant for most of the traits in all the six crosses. This observation was in accordance with the findings of Rahman and Saad (2000) in *Vigna sesquipedalis*. According to Ajay *et al.* (2012), the value interactions (inter-allelic interactions) play a key role in the expression of a character and additive-dominance alone is not sufficient. In such cases, populations have to be forwarded to next generations in order to arrive at the best fit model suggested by Mather and Jinks (1982).

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 six crosses (Table 1). Saxena (2008) in pigeonpea observed the same results for different traits and crosses. Among the gene effects, [d] was pronounced for DMF, whereas [h] was more prominent among PHMF, PWFD, RWFD, SW/P and 1000-SW. Hooda *et al.* (2003) and Sameer *et al.* (2009) in pigeonpea got significant [h] for plant height, branches per plant, pods per plant, 100-seed weight and seed yield. The presence of [h] for different traits indicated that selection should be delayed until heterozygosity was reduced in population. The non-significant [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 with finding of Mathews *et al.* (2008).

Among non-allelic interactions (epistasis): [i] was more prominent than [l] type for most of the traits among six crosses. Shoba *et al.* (2010) observed significant [i] interactions for most of the yield contributing traits. Though χ^2 test was significant for DMF in $C_1$and C_2, NPBMF in C_3; NSBMF in C_1 and C_6; PHMF in C_1; RWFD in C_3, C_5 and C_6; NPd/P in C_3; PdW/P in C_3 and C_6; NS/P in C_2 and C_3; SW/P in C_3 and C_6 but non-allelic interactions were not significant. This reveals that those traits are governed by higher order interactions or under complex genetic effects or they influence by large environmental variance which is suggested by Milus and Line (1986). Duplicate type of epistasis was in almost all the crosses in different traits. In this case, Kumar and Patra (2010) found that variability in segregating generation may be reduced which hinders the selection process. Presence of complementary gene action for NSBMF in C_1 and C_3; RWFD in C_5 and C_6 and PdW/P in C_4 indicates that parents selected for crossing are diverse. This is revealed by Reynolds *et al.* (2009).

Both additive and non-additive gene actions play a key role for the expression of the quantitative traits. Due to having duplicate and significant type of epistasis for PWFD and RWFD in C_2; PHMF and 1000-SW in C_3; NPBMF, PHMF and SW/P in C_4; PHMF in C_5 and PHMF, NPd/P and 1000-SW in C_6, selection should be done to later generations. Traits like NS/P and 1000-SW in C_1, NS/P in C_4, NSBMF in C_5 and NS/P in C_6 might be used for the development of pure line in further breeding research because of their adequacy of the additive-dominance model.

Table 1. Scaling tests, potence, gene action and epistasis for 11 quantitative traits in six crosses of chickpea.

Traits	Crosses	Scales		Potence	2 and 3-parameter				5-parameter					Epistasis
		C	D		m	[d]	[h]	χ^2	m	[d]	[h]	[i]	[l]	
DMF	C_1	−0.133^{NS}	−7.167^{NS}	2.183^{NS}	65.87**	−1.18	-	15.021**	67.07**	−1.2*	9.06*	2.36	−9.34	D
	C_2	15.217*	9.183^{NS}	−0.017^{NS}	87.86**	0.61	-	46.09**	92.37*	−1.48*	3.99	−6.54	−8.04	D
	C_3	19.567*	22.333*	0.683^{NS}	82.84**	−0.10	-	123.85**	90.52**	−1.25*	−0.48	−14.13**	3.69	D
	C_4	2.117^{NS}	22.783*	3.633^{NS}	86.38**	−2.63**	-	34.545**	87.52**	−2.98**	−6.51	−20.79**	27.56*	D
	C_5	3.367^{NS}	8.733^{NS}	3.883*	86.18**	0.66	9.92**	3.74^{NS}	-	-	-	-	-	-
	C_6	14.733*	12.4*	1.467^{NS}	85.54**	−3.12**	-	82.567**	92.18**	−1.75**	4.49	−9.31*	−3.11	D
NPBMF	C_1	−0.083^{NS}	−0.25^{NS}	0.183^{NS}	2.71**	0.14	-	2.162^{NS}	-	-	-	-	-	-
	C_2	−1.55*	−2.683*	0.5*	2.98**	−0.05	0.83**	22.43**	3.4**	0.03	1.76**	1.58**	−1.51	D
	C_3	−0.767^{NS}	−2*	−0.083^{NS}	2.87**	−0.32*	-	13.83**	2.88**	−0.35*	0.66	0.51	−1.64	D
	C_4	0.55^{NS}	−1.983*	−0.1^{NS}	3.12**	−0.02	-	13.36**	3.4**	−0.03	1.49**	1.36**	−3.38*	D
	C_5	0.05^{NS}	−1.55*	−0.3^{NS}	2.94**	0.03	-	10.53*	3**	0.13	0.47	1.29**	−2.13	D
	C_6	0.233^{NS}	−0.733^{NS}	0.117^{NS}	2.83**	−0.4**	-	4.972^{NS}	-	-	-	-	-	-
NSBMF	C_1	3.733^{NS}	4.067^{NS}	0.567^{NS}	12.29**	1.01	-	12.164**	13.38**	0.95	0.91	−0.19	0.44	C
	C_2	3.983^{NS}	−0.783^{NS}	−0.583^{NS}	11.50**	0.10	-	2.6977^{NS}	-	-	-	-	-	-
	C_3	18.217*	4.817^{NS}	−5.067*	15.11**	-1.39*	-2.23**	36.09**	16.82**	−0.43	-1.2	−1.03	−17.87*	C
	C_4	20.317*	2.517^{NS}	−5.067*	14.84**	2.51**	1.40	46.2**	18.02**	1.23*	1.73	4.16	−23.7**	D
	C_5	2.983^{NS}	2.783^{NS}	−0.133^{NS}	14.78**	2.24**	-	3.2183^{NS}	-	-	-	-	-	-
	C_6	4.433^{NS}	8.1*	−0.233^{NS}	14.43**	1.52**	-	14.065**	14.93**	0.7	−2.91	−3.26	4.89	D
PHMF	C_1	1.815^{NS}	0.778^{NS}	1.805^{NS}	49.60**	−0.81	-	37.882**	50.86**	−0.72	4.30	−1.66	−1.38	D
	C_2	−6.688^{NS}	−16.815*	4.443*	50.20**	1.16	7.67**	11.78**	54.45**	1.36	15.64**	12.8**	−13.50	D
	C_3	15.083*	−15.193*	1.592^{NS}	53.65**	0.62	-	160.11**	58.06**	−0.28	23.37**	12.09**	−40.4**	D
	C_4	22.648*	−15.403*	−2.186^{NS}	52.24**	3.70**	-	65.375**	58.11**	4.13**	20.99**	22.29**	−50.77**	D
	C_5	6.292^{NS}	−16.785*	−1.742^{NS}	52.96**	−1.59*	-	15.319**	54.59**	−1.64*	11.90**	8.96*	−30.77**	D
	C_6	14.658*	−15.718*	−2.758^{NS}	52.50**	−3.92**	-	31.004**	55.91**	−3.49**	14.73**	5.95	−40.50**	D
PWFD	C_1	−6.515^{NS}	−43.641*	2.75^{NS}	52.35**	0.44	-	30.989**	60.35**	0.28	30.25**	28.56**	−49.50	D
	C_2	28.198^{NS}	−22.08^{NS}	−3.822^{NS}	51.75**	1.63	-	10.563*	59.33**	1.45	25.87**	22.32*	−67.04*	D
	C_3	8.225^{NS}	−45.902*	10.94^{NS}	54.43**	−2.9	-	58.652**	66.72**	−1.56	57.96**	28.85*	−72.17	D
	C_4	9.967^{NS}	−11.42^{NS}	−1.0967^{NS}	51.59**	−13.98**	-	1.588^{NS}	-	-	-	-	-	-
	C_5	−15.83^{NS}	23.38*	17.315*	51.99**	−2.57	22.4**	4.73^{NS}	-	-	-	-	-	-
	C_6	−9.483^{NS}	3.483^{NS}	9.353^{NS}	51.85**	−11.19**	-	6.6047^{NS}	-	-	-	-	-	-
RWFD	C_1	1.232^{NS}	0.411^{NS}	−0.088^{NS}	2.40**	−0.23	-	6.023^{NS}	-	-	-	-	-	-
	C_2	1.858^{NS}	−1.485^{NS}	0.117^{NS}	2.88**	−0.25	-	19.62**	3.47**	−0.18	2.46**	0.93	−4.46*	D
	C_3	0.651^{NS}	2.085*	0.424^{NS}	2.38**	0.18	-	28.51**	2.62**	0.002	-0.11	−1.28	1.91	D
	C_4	0.183^{NS}	0.277^{NS}	0.136^{NS}	2.16**	−0.34**	-	2.038^{NS}	-	-	-	-	-	-
	C_5	−1.52^{NS}	−1.233*	0.820*	1.43**	0.08	1.01**	10.09**	1.87**	0.09	1.45**	0.75	0.38	C
	C_6	−1.749*	−0.836^{NS}	0.812*	1.62**	−0.27	0.69**	9.15*	1.84**	−0.37**	1.02*	−0.47	1.22	C

(Contd.)

(Contd.)

Traits	Crosses	Scales		Potence	2 and 3-parameter			5-parameter						Epistasis
		C	D		m	[d]	[h]	χ^2	m	[d]	[h]	[i]	[l]	
NPd/P	C_1	–1.233 ^{NS}	–41.1 ^{NS}	14.933 ^{NS}	93.83**	5.63	-	29.412**	101.52**	5.25	56.44**	37.69*	–53.16	D
	C_2	34.283 ^{NS}	–21.35 ^{NS}	0.217 ^{NS}	125.38**	6.65	-	6.2251 ^{NS}	-	-	-	-	-	-
	C_3	100.8*	32.167 ^{NS}	–11.65 ^{NS}	71.29**	–1.89	-	47.038**	93.45**	–0.75	22.46	–6.14	–91.51	D
	C_4	60.083*	77.317*	–9.983 ^{NS}	68.90**	–5.43	-	34.185**	78.13**	–2.38	–31.45	–46.3**	22.98	D
	C_5	11.617 ^{NS}	22.05 ^{NS}	0.583 ^{NS}	48.17**	–7.89**	-	5.1413 ^{NS}	-	-	-	-	-	-
	C_6	–0.296 ^{NS}	–52.32*	1.674 ^{NS}	46.89**	–2.51	-	24.855**	54.93**	–1.2	38.03**	32.43**	–69.36*	D
PdW/P	C_1	–4.572 ^{NS}	–1.745 ^{NS}	1.824 ^{NS}	17.52**	3.48**	-	3.0518 ^{NS}	-	-	-	-	-	-
	C_2	11.332 ^{NS}	–2.984 ^{NS}	–2.447 ^{NS}	24.68**	1.92	-	2.7753 ^{NS}	-	-	-	-	-	-
	C_3	18.536*	–1.892 ^{NS}	–1.632 ^{NS}	10.18**	1.07	-	20.057**	14.83**	0.09	10.36*	4.55	–27.24	D
	C_4	4.731 ^{NS}	7.796 ^{NS}	1.531 ^{NS}	9.98**	–4.97**	-	11.497**	11.23**	–3.0**	1.02	–10.42*	4.09	C
	C_5	–5.3 ^{NS}	–0.326 ^{NS}	4.301*	9.48**	–2.71*	5.82**	0.73 ^{NS}	-	-	-	-	-	-
	C_6	–5.676 ^{NS}	–11.18*	5.517*	6.48**	–1.20	9.71**	12.71**	11.56**	–1.35	14.70**	3.80	–7.34	D
NS/P	C_1	–4.683 ^{NS}	–35.75 ^{NS}	5.133 ^{NS}	77.47**	0.57	-	5.4102 ^{NS}	-	-	-	-	-	-
	C_2	61.733 ^{NS}	0.6 ^{NS}	–4.333 ^{NS}	110.54**	6.36	-	10.714*	123.83**	6.25	32.0	22.39	–81.51	D
	C_3	32.917 ^{NS}	31.617 ^{NS}	0.283 ^{NS}	57.87**	–5.38	-	8.5323*	64.52**	–7.68	1.43	–30.94	–1.73	D
	C_4	–2.833 ^{NS}	7.667 ^{NS}	0.683 ^{NS}	44.50**	–1.79	-	0.3042 ^{NS}	-	-	-	-	-	-
	C_5	–27.37 ^{NS}	–2.467 ^{NS}	18.717*	44.85**	2.89	22.85**	1.59 ^{NS}	-	-	-	-	-	-
	C_6	–7.8 ^{NS}	5.933 ^{NS}	0.4 ^{NS}	51.85**	3.05	-	0.6401 ^{NS}	-	-	-	-	-	-
SW/P	C_1	0.449 ^{NS}	1.681 ^{NS}	0.748 ^{NS}	13.42**	0.81	-	1.96 ^{NS}	-	-	-	-	-	-
	C_2	3.645 ^{NS}	–8.866 ^{NS}	1.445 ^{NS}	21.07**	1.97	-	10.026*	23.63**	1.78	11.23**	10.08*	–16.68	D
	C_3	11.454 ^{NS}	0.290 ^{NS}	0.294 ^{NS}	8.21**	0.95	-	24.379**	11.41**	0.04	8.03*	1.79	–14.89	D
	C_4	–8.216 ^{NS}	11.607*	2.906 ^{NS}	10.18**	–2.81**	-	8.51575*	7.78**	–2.17	–7.40*	–13.44**	26.43*	D
	C_5	–11.328*	7.968*	4.391*	8.99**	0.17	1.55	8.68*	7.53**	0.13	–4.08	–6.95*	25.73**	D
	C_6	–6.545 ^{NS}	-8.037 ^{NS}	4.986*	182.65**	40.08**	–42.54**	86.99**	8.44**	–0.94	10.97**	2.38	–1.99	D
1000-SW	C_1	51.696 ^{NS}	91.801 ^{NS}	–11.922 ^{NS}	176.09**	0.43	-	4.372 ^{NS}	-	-	-	-	-	-
	C_2	1.025 ^{NS}	–45.84*	5.833 ^{NS}	193.28**	1.06	-	16.876**	200.96**	0.97	42.91**	32.7*	–62.49	D
	C_3	1.303 ^{NS}	86.707*	3.227 ^{NS}	152.06**	4.38	-	21.1**	145.58**	2.35	–50.5**	–52.9**	113.87**	D
	C_4	35.031 ^{NS}	75.402*	–8.379 ^{NS}	147.69**	–0.37	-	25.42**	143.52**	0.70	–43.7**	–43.03**	53.83	D
	C_5	78.954*	151.22*	–16.289 ^{NS}	171.62**	27.88**	-	93.046**	160.12**	10.46**	–80.74**	–66.7**	96.35	D
	C_6	50.349*	155.163 ^{NS}	–17.654*	4.42**	–0.54	7.75**	11.19**	151.3**	17.30**	–105.2**	–60.44**	139.75**	D

C_1 = 1A × 3A, C_2 = 2A × 4D, C_3 = 4A × 7B, C_4 = 4C × 3C, C_5 = 6A × 5A and C_6 = 7A × 5A. C and D Mather's scaling test and χ^2 joint scaling test. m = mean of the base population, d = additive gene effect, h = dominance gene effect, i=additive × additive gene effect and l = dominance × dominance gene effect. C = complementary gene action and D = duplicate gene action. * and **significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

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