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IDENTIFICATION OF SUITABLE QUANTITATIVE TRAITS IN CHICKPEA THROUGH BIPARENTAL PROGENY ANALYSIS

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Abstract

Information regarding additive and dominance properties of gene of the quantitative traits is very important to improve any crops. Five chickpea genotypes were taken as a base material for this study and five different crosses were made between the genotypes to raised F_1, F_2 and biparental (BIP's) family. Analysis of variance showed significant differences among the families in almost all the cases. Higher magnitude of additive component than that of dominance component along with high narrow sense heritability and high genetic advance recorded for pod weight plant^{-1} in cross-4 and cross-5; number of seeds plant^{-1} in cross-3, cross-4 and cross-5; while seed weight plant^{-1} in cross-3 and cross-5. This is signifying that the selection of these traits for the respective crosses will be very effective for the improvement of chickpea yield. Regression item in some cases was significant which revealed good relationship between biparental families and their parents and vice-versa. Significant linkage in both coupling and repulsion phases were detected.

Introduction

Pulses are the second most important crop in Bangladesh in terms of cultivation, which highlights its importance in the country's diet. Among pulses, chickpea (*Cicer arietinum* L.) as dry seeds are important sources of healthy human's food all over the world. Bangladesh is a low chickpea producing country and imports chickpea from other countries to meet up the demand (Rezia *et al.* 2021). Hence, pulse breeders of Bangladesh are continuously paying their attention to improve an average chickpea yield. Thus, estimates of additive and non-additive components of genetic variance are required first to improve any high yielding crop, which makes available information about of how a particular trait could be selected for a population improvement program. Among the existing mating design, Mather (1949a) suggested biparental mating (BIP's) design is very simple random mating designs. BIP's also exhibited improved estimates of heritability and genetic advance (Koli *et al*. 2018). Therefore, the present investigation was aimed to know the gene action as well as to identify the suitable traits of chickpea through the biparental progeny analysis.

Materials and Methods

Five chickpea genotypes namely BARI chola-1, BARI chola-3, BARI chola-4, BARI chola-7 and BARI chola-8 were collected from Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh and used as a base material. Five different crosses such as Cross-1(8 × 3); Cross-2 (8 × 1); Cross-3 (8 × 4); Cross-4 (4 × 8) and Cross-5 (8 × 7) were made between the genotypes to raise F_1, F_2 and BIP's family population.

The experiment was set in the botanical research field of the University of Rajshahi, in four consecutive *rabi* crop seasons from 2009-2010 to 2012-2013. In the first year, seeds were sown and hybridization was done to raise F_1 seeds. In the following year F_1 seeds were sown to get F_2

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seeds. At the same time fresh F_{1s} were also maintained. In the third year, F_2 and fresh F_1 generations were grown in the field. From the F_2 generations, 20 plants were selected randomly in pairs and marked as male and female parents and crosses were made between the mates of a pair. At the same time for linkage test, selected F_2 considered as male was crossed with the selected F_1 plants. Thus, seeds of 10 F_1 families and 10 ($F_1 \times F_2$) families were obtained for each cross from that year. Seeds from each mate of a pair (10 pairs) treated as P_1 and P_2 of the F_2 population were also collected and marked as 10 P_1 and P_2 families. Finally, in the fourth year, seeds of 10 F_1, 10 P_1, 10 P_2 and 10 ($F_1 \times F_2$) families along with their F_2 generations were sown and plants were raised.

Thirteen yield and yield components namely, date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at harvest (PWH), number of pods plant^{-1}(NPd/P), pod weight plant^{-1}(PdW/P), number of seeds plant^{-1}(NS/P) and seed weight plant^{-1}(SW/P) were considered for this experiment. Data were collected and recorded on individual plant basis.

The collected data were analyzed according to the biometrical technique of analysis of Kearsey and Jinks (1968) which an extension of North Carolina Design III of Comstock and Robinson (1952). The test of linkage has been done by comparing total variance (σ^2) of any pair of three generations such as F_2, F_2 (BIP's) and $F_1 \times F_2$ (L_{3i}) for all the thirteen characters following Jinks and Perkins (1970). In calculating F value for significance test, the lower variance was considered as denominator.

Results and Discussion

The result of analysis of variance (ANOVA) of biparental progeny (BIP's) is presented in Table1. All the items of the ANOVA of BIP's were tested by within family. Except DMF in cross-1; NSBFF and NPd/P in cross-4 and DMF, NPBMF, NSBMF, NPd/P, PdW/P and SW/P in cross-5 all the characters and crosses were significant regarding between families items. Significance of family variance suggests the suitability of the present materials for further breeding research. Kearsey (1965) and Sharma *et al.* (1979) also obtained a greater extent of genetic varition in the population of BIP's in their materials. Similar results were reported by Ojha and Roy (2001) in sunflower and Husain *et al.* (2009) in chili. Interaction item (F×R) was noted to be non-significant in maximum cases.

Table 2 revealed regression item was significant only NPBMF in cross-4 and PHFF, NPBMF and PdW/P in cross-5 which indicated a good relationship between biparental progenies and their parents. Due to non-significant regression values in maximum cases, parent-offspring relationship bear the complex situations and there were involved non-linear components and vice versa. De Toledo *et al.* (2000) also marked the same situation in soybean. Regression item was non-significant due to high standard error values in this material. Regression coefficients (bi) when tested with their standard error, in most of the cases standard errors were greater than the regression coefficient indicating the complex nature of parent-offspring relationship. Therefore, it is suggested that biparental progenies and their mid-parents were related regarding the inheritance of these characters in the crosses.

Table 3 showed that the extent of additive component (D_R) was higher than that of the respective dominance component for NPBMF, NSBMF and PdW/P in cross-1; for DFF, NSBFF, DMF, PHMF, NPBMF and NSBMF in cross-2; for NPBFF, NPBMF, PdW/P, NS/P and SW/P in

Table 1. MS values of BIP's ANOVA of thirteen characters of five crosses in chickpea.

Source	df	Cross	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
Replication (R)	2	1	6.3880	12.4763	0.1613	0.0333	10.5880	15.7953	0.1373	1.1773	32.2314	717.7080	90.9228	1258.2613	66.9989
		2	3.1080	6.2074	0.1373	0.7453	12.9333	25.6991	0.2973	1.3173	387.4043	1481.6693*	130.1306*	1879.8893*	71.1304
		3	0.5880	1.1597	0.0213	0.6173	2.8373	2.3448	0.1773	0.1240	21.0661	3.5453	2.4177	1.3440	0.0914
		4	1.9373	0.1956	0.0173	0.4813	2.8853	26.3176	0.0120	2.6413	1233.2317	390.5453	47.2080	527.7640	30.9990
		5	3.0653	5.8693	0.1213	0.5173	7.3453	0.0232	0.0173	1.3240	351.4537	19.6653	68.7216	11.9080	50.0205
Between families (F)	9	1	14.1630*	14.9530**	0.4570**	1.5022**	7.1895	26.5616**	0.9732**	2.3764**	973.3864**	1410.0356**	102.5731**	1722.2858**	66.9115**
		2	27.6681**	25.2556**	0.3717**	0.8037*	26.2844**	49.3670**	0.2579*	4.6436**	2171.3816**	1045.1372**	112.6306**	1191.9639*	74.5934*
		3	10.4861**	10.6631**	1.3169**	0.7705**	16.9535**	13.8948**	0.4007**	2.6139**	561.0883**	706.6615**	53.5069*	742.6461**	35.7772*
		4	21.6446**	54.7443**	0.1695*	0.2799	4.7924**	50.6797**	0.2828**	2.6319*	3123.3111**	463.5231	90.5841*	1165.1053**	76.7342**
		5	17.1076**	23.7255**	0.3283**	0.6443*	2.6999	27.8222**	0.2163	5.3090	2110.3918**	652.2621	74.6730	972.8201*	54.2952
F × R	18	1	6.4443	7.0437	0.1006	0.1444	6.2250	19.5181**	0.1403	0.4307	328.2723	532.2458	71.0099*	748.8658*	41.3258*
		2	9.6873	12.0649	0.0810	0.2890	4.5156	27.5523*	0.1388	0.9707	523.4904	748.8012**	86.5235**	1008.5456**	60.6802*
		3	8.0621*	9.9668*	0.0613	0.1892	8.7099*	6.9818*	0.1625	0.6944	446.6114*	428.3690*	51.3864**	455.8581*	32.2731**
		4	8.6810	6.6444	0.0321	0.1865	1.7920	7.1944	0.1068	1.6487	411.4906	202.1987	27.8147	454.5818	13.1676
		5	4.2787	2.2432	0.0176	0.3159	3.6905	8.0025	0.1359	0.9877	263.3328	400.4550	53.8308	610.6784	39.8537
Within families	120	1	7.0129	4.3840	0.1310	0.2952	3.8835	8.9715	0.1864	0.5180	373.8332	345.7631	36.5899	443.3172	23.8842
		2	7.9140	7.7654	0.1065	0.3648	5.0927	14.5389	0.1288	0.9927	383.3814	354.3013	37.9430	466.2098	29.8318
		3	3.9505	4.9364	0.1607	0.2105	4.9876	3.6130	0.1332	0.7511	218.2650	220.7052	23.2756	247.4757	14.3333
		4	6.4882	8.1360	0.0823	0.2409	1.6711	10.8226	0.1053	1.1803	574.7309	241.5492	36.0139	414.4563	21.3708
		5	5.4454	4.7936	0.0794	0.2601	3.2708	6.2927	0.1248	1.1394	429.6626	334.9499	42.1503	466.7521	32.7241

* and ** indicate $P<0.05$ and $P<0.01$, respectively.

Table 2. MS values of regression analysis of ten BIP's families against their mid-parent of thirteen characters of five crosses in chickpea.

Source	df	Cross	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
Between families	9	1	29.4837**	17.2481**	0.7617**	2.5037**	11.9825**	36.8731**	1.6220**	3.9607**	1622.3106**	2018.2459**	143.4226**	2870.4763**	111.5192**
		2	46.1136**	42.0926**	1.4689**	1.3956**	43.8074**	81.3118**	0.4299**	7.7393**	3618.9693**	1741.8953**	187.7177**	1986.6064**	124.3224**
		3	18.8830**	26.2078**	2.1948**	1.2842**	28.2558**	18.5667**	1.0277**	3.3136**	935.1472**	1177.7691**	92.0542**	1167.0235**	52.8071**
		4	36.0743**	94.6878**	0.8953**	0.4664	7.9874**	54.2824**	1.6507**	4.3864**	5205.5184**	817.8311**	150.9736**	1941.8422**	127.8904**
		5	50.4978**	34.9069**	1.0154**	1.0738**	4.4998	46.3703**	1.7892**	8.8484**	3517.3197**	1087.1035**	347.4922**	1621.3669**	90.4921**
Regression	1	1	2.6377	2.1759	0.0782	0.1085	0.4455	2.9376	0.0515	0.0512	820.5829	279.4496	2.5337	169.2921	16.6276
		2	8.3066	5.6283	0.4153	0.0718	15.9217	1.8865	0.0229	1.0827	1105.9468	66.4779	45.3762	283.0368	12.3326
		3	9.3128	5.0023	0.4467	0.5847	1.4281	9.2191	0.1105	1.8691	130.6375	55.5744	24.2872	46.9920	2.9456
		4	1.0464	25.7573	0.2535	0.3912	0.2820	32.0194	0.8112**	2.7380	68.7056	3.5822	7.1134	27.8989	5.0284
		5	21.2170	36.2900**	0.0928	0.0303	0.0232	2.6659	0.7247*	1.2164	108.2844	12.5719	256.0582*	461.3387	10.8485
Remainder	8	1	6.3041	3.6088	0.1616	0.5498	2.6404	7.9292	0.3585	0.8848	262.4470	419.1741	31.9534	624.6957	23.0134
		2	9.3372	8.7673	0.2786*	0.3050	7.8665	18.0594	0.0939	1.6060	676.0247	383.6167	36.5645	411.6068	26.4310
		3	3.0846	5.2715	0.4380**	0.2159	6.1790	3.0251	0.2174	0.5119	194.0784	258.0513	17.6763	256.7063	11.5134
		4	7.9859	18.0851	0.1698*	0.0560	1.7619	8.2111	0.2700*	0.6447	1162.6534*	183.5642	33.0799	433.4271	28.1468
		5	8.7099	3.3178	0.2169**	0.2378	1.0095	10.1001	0.3120*	1.8388	777.8614	243.0268	46.1785	307.1402	19.0047
Within families	120	1	7.0129	4.3840	0.1310	0.2952	3.8835	8.9715	0.1864	0.5180	373.8332	345.7631	36.5899	443.3172	23.8842
		2	7.9140	7.7654	0.1065	0.3648	5.0927	14.5389	0.1288	0.9927	383.3814	354.3013	37.9430	466.2098	29.8318
		3	3.9505	4.9364	0.1607	0.2105	4.9876	3.6130	0.1332	0.7511	218.2650	220.7052	23.2756	247.4757	14.3333
		4	6.4882	8.1360	0.0823	0.2409	1.6711	10.8226	0.1053	1.1803	574.7309	241.5492	36.0139	414.4563	21.3708
		5	5.4454	4.7936	0.0794	0.2601	3.2708	6.2927	0.1248	1.1394	429.6626	334.9499	42.1503	466.7521	32.7241

* and ** indicate $P<0.05$ and $P<0.01$, respectively.

Table 3. Estimated values of D_R, H_R and E_W along with degree of dominance ($\sqrt{H_R/D_R}$) of BIP's of thirteen characters of five crosses.

Item	Cross	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
D_R	1	1.2593	1.2978	0.1926	0.2815	1.2311	1.2891	0.2163	0.4222	1247.2814	98.8889	6.8448	537.4430	26.3195
	2	4.5333	7.1250	0.0341	0.1111	5.1704	5.7821	0.0281	0.8000	1564.7142	251.3659	40.0662	538.5452	18.2145
	3	0.4652	2.3977	0.3007	0.7289	1.6563	1.3028	0.0519	0.3348	431.9965	45.1556	0.4567	62.6444	0.8362
	4	1.4178	8.7471	0.0148	0.3956	0.6474	8.9702	0.0400	1.6444	249.0062	78.1215	20.1232	189.2133	13.6508
	5	4.4652	4.1453	0.0652	0.1230	0.3822	4.2449	0.0296	1.5674	393.3046	135.1348	5.1192	92.7407	3.3686
H_R	1	3.1962	3.2454	-0.3902	0.3224	-3.8957	2.3566	0.0232	0.3866	-4301.0038	540.7535	6.2883	-1111.4572	-77.9864
	2	1.0463	-14.4301	0.1737	0.1045	2.5387	0.1406	0.0145	0.7177	-4501.1063	-689.3720	-132.4172	-1958.5346	-58.0170
	3	0.7249	-8.8480	0.1363	-2.2955	2.1679	2.1626	0.0467	0.7083	-1605.8773	116.2231	0.4352	55.3294	0.3931
	4	8.1567	16.3181	0.0872	-1.4827	0.6108	10.5037	0.0277	-5.5291	1896.5837	-33.7399	-13.5389	1.0385	13.2012
	5	-4.1766	6.3335	0.0706	-0.1415	-2.5856	4.1616	-0.0327	-1.6602	396.9777	-271.9450	1.7549	15.3216	1.9301
E_W	1	34.1506	20.9872	0.6799	1.3454	19.8404	44.0932	0.8735	2.4118	2363.7840	1602.7018	180.0595	2290.6234	127.4637
	2	38.2405	39.7515	0.4915	1.7768	23.6950	71.2225	0.6341	4.6287	2369.6860	1837.9223	204.5267	2563.6381	155.4835
	3	19.5001	25.7415	0.7025	1.3007	24.1173	17.3338	0.6445	3.5392	1284.4278	1070.4455	116.1824	1211.3429	71.3838
	4	30.5573	35.4336	0.3912	1.3837	8.0789	49.9011	0.5112	6.5272	2455.7936	1194.5417	177.5771	2024.7836	100.9659
	5	26.8940	21.7441	0.3676	1.2964	16.7432	29.6218	0.6229	5.6164	1975.5538	1691.9553	209.1427	2307.7023	162.4164
$\sqrt{H_R/D_R}$	1	1.5932	1.5814	-1.4233	1.0702	1.7789	1.3521	0.3277	0.9569	-1.8570	2.3384	0.9585	-1.4381	-1.7214
	2	0.4804	-1.4231	2.2581	0.9699	0.7007	0.1559	0.7167	0.9472	-1.6961	-1.6561	-1.8180	-1.9070	-1.7847
	3	1.2483	-1.9210	0.6732	-1.7746	1.1441	1.2884	0.9490	1.4544	-1.9280	1.6043	0.9762	0.9398	0.6856
	4	2.3986	1.3658	2.4265	-1.9361	0.9714	1.0821	0.8327	-1.8337	2.7598	-0.6572	-0.8202	0.0741	0.9834
	5	-0.9671	1.2361	1.0410	-1.0728	-2.6009	0.9901	-1.0507	-1.0292	1.0047	1.4186	0.5855	0.4065	0.7569

Table 4. Estimates of heritability (h^2_b, h^2_n) and genetic advance (GA_b, GA_n) of biparental progeny for thirteen characters of five crosses in chickpea.

Item	Cross	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
h^2_n	1	0.0177	0.0289	0.1419	0.0898	0.0316	0.0142	0.1095	0.0776	0.3261	0.0277	0.0185	0.1178	0.1086
	2	0.0556	0.0897	0.0309	0.0299	0.0961	0.0390	0.0216	0.0768	0.3860	0.0702	0.1046	0.1149	0.0607
	3	0.0208	0.0485	0.1695	0.3340	0.0325	0.0352	0.0380	0.0431	0.1965	0.0201	0.0020	0.0249	0.0058
	4	0.0213	0.0997	0.0176	0.1633	0.0378	0.0787	0.0372	0.1378	0.0408	0.0319	0.0546	0.0446	0.0614
	5	0.0795	0.0816	0.0780	0.0465	0.0117	0.0647	0.0235	0.1309	0.0866	0.0399	0.0121	0.0197	0.0102
h^2_b	1	0.0402	0.0651	-0.0018	0.1413	-0.0184	0.0272	0.1154	0.1132	-0.2362	0.1033	0.0270	-0.0040	-0.0523
	2	0.0620	-0.0011	0.1096	0.0440	0.1196	0.0395	0.0271	0.1113	-0.1692	-0.0260	-0.0683	-0.0940	-0.0360
	3	0.0117	-0.0410	0.2079	-0.1919	0.0538	0.0643	0.0551	0.0887	-0.1688	0.0460	0.0029	0.0359	0.0072
	4	0.0825	0.1926	0.0695	-0.1428	0.0557	0.1247	0.0500	-0.0939	0.1960	0.0250	0.0362	0.0448	0.0911
	5	0.0423	0.1439	0.1203	0.0197	-0.0280	0.0965	0.0105	0.0616	0.1303	-0.0002	0.0141	0.0213	0.0132
GA_n	1	0.2174	0.2821	0.2408	0.2316	0.2873	0.1972	0.2242	0.2637	29.3791	2.4092	0.5183	11.5894	2.4632
	2	0.7313	1.1646	0.0472	0.0839	1.0265	0.6916	0.0359	0.3611	35.7990	6.1174	2.9825	11.4590	1.5314
	3	0.1074	0.4966	0.3289	0.7187	0.3379	0.3118	0.0647	0.1750	13.4223	1.3885	0.0436	1.8203	0.1016
	4	0.2530	1.3600	0.0235	0.3703	0.2280	1.2236	0.0562	0.6934	4.6407	2.2988	1.5270	4.2331	1.3340
	5	0.8679	0.8472	0.1039	0.1101	0.0975	0.7636	0.0385	0.6599	8.4999	3.3843	0.3620	1.9672	0.2705
GA_b	1	0.4934	0.6349	-0.0031	0.3643	-0.1673	0.3775	0.2362	0.3844	-21.2749	8.9965	0.7563	-0.3943	-1.1861
	2	0.8157	-0.0147	0.1677	0.1234	1.2785	0.7000	0.0451	0.5230	-15.6912	-2.2711	-1.9460	-9.3776	-0.9075
	3	0.1910	-0.4197	0.4034	-0.4130	0.5591	0.5705	0.0938	0.3601	-11.5253	3.1753	0.0643	2.6241	0.1254
	4	0.9809	2.6285	0.0928	-0.3237	0.3355	1.9401	0.0756	-0.4723	22.3138	1.8024	1.0133	4.2447	1.9790
	5	0.4620	1.4944	0.1601	0.0468	-0.2324	1.1379	0.0172	0.3104	12.7896	-0.0210	0.4241	2.1297	0.3479

Table 5. Specific test of linkage based on comparisons of the total variance between the generations of thirteen characters of four crosses in chickpea.

Source	df	Cross	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
F_2(BIPs)	149	1	---	---	---	---	---	---	---	---	---	---	---	---	---
		2	34.7517**	34.3365**	0.4630	1.5626**	22.8143**	65.2011**	0.5549**	4.4127*	1743.4156	1600.1931	171.7930**	2096.4240*	132.9189**
		3	17.5231**	21.7417**	0.7342**	0.9253	22.1985**	16.2632	0.5828	3.2682	967.0464	983.2271	103.1995	1096.4922	63.7794
		4	28.5092**	36.8745**	0.3456	1.0161	7.2738*	47.8646**	0.4541	5.1465	2569.2728*	1030.3481*	154.4877**	1801.3271**	92.6986**
		5	23.5193	21.0859*	0.3434	1.1315	13.8785	27.9872**	0.5324	5.0459**	1894.1880**	1436.8308	181.6688**	2012.2325	140.5404**
F_2	29	1	---	---	---	---	---	---	---	---	---	---	---	---	---
		2	3.1828	14.6483	0.5471	1.3609	1.7575	14.6483	0.8517*	4.4931	1909.6612	1021.5276	37.9142	1125.5816	29.7698
		3	5.2057	24.2632**	0.3402	0.8092	3.1954	10.5039	0.7138	2.9989	1814.2755**	3191.0486**	203.9413**	8021.1954**	224.5893**
		4	4.4379	7.3575	0.6023**	1.2195	3.7483	7.3575	0.8609**	5.3851	1354.6437	2760.6023**	181.5006**	3894.2299**	104.4388**
		5	28.0517	10.5039	0.4368	0.7000	13.0402	10.5039	0.7138	2.9989	1814.2755	3191.6655**	203.9413*	8021.1954**	224.5893**
$F_1 \times F_2$	149	1	---	---	---	---	---	---	---	---	---	---	---	---	---
		2	30.7606**	21.4537	0.3562	0.9485	31.2573**	45.7651**	0.8723	3.3604	1527.3209	1618.3291	207.0988**	2179.4016*	126.2954**
		3	19.4284**	12.4617	0.4922	0.7517	17.9597**	33.8901**	0.5865	4.4201	1409.2199*	1315.0486*	123.7511	1577.3479*	60.0923
		4	16.7315**	14.8233**	0.2875	0.8528	17.2440**	33.9210**	0.5235	4.0367	1508.6107	748.5324	84.9751	1190.2640	51.2393
		5	22.9024	14.9990	0.6361**	1.5257**	32.3132**	56.8368**	0.7161*	3.9374	1277.1343	2018.6264*	120.4420	4748.1845**	77.2059

* and ** indicate $P<0.05$ and $P<0.01$, respectively.

Cross-3; for DMF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHMF, PdW/P, NS/P and SW/P in cross-5. A higher value of D_R indicates the relative importance of the additive gene action in the inheritance of these characters, which are related with homozygosity and also fixable. So, selection for these traits will be very effective. Mahalingam *et al*. (2011) stated that additive component of variation is the only component of variation which respond to selection so the presence of additive components in breeding materials is the precondition for the improvement through selection program. Therefore, these traits can improve by pure line selection, mass selection and or progeny selection. Manickavelue *et al*. (2006) and Thirugnana *et al*. (2007) also reported the same findings. On the other hand, dominance component (H_R) is linked with heterozygosity and unfixable, so it is ineffective to select these traits. Hence, to take advantage of dominance gene action, it is suggested that better traits should be selected from the later generations. The magnitude of H_R in some cases was negative. Science H_R is a variance component, it should not be negative. The probable cause of the negative value of H_R may be first due to lack of random mating amounting to assertive mating, secondly due to sampling error (Mather1949b) and lastly due to high genotype × environment interaction (Hill 1966). In case of degree of dominance ($\sqrt{H_R/D_R}$), over dominance was observed for the majority of the characters and crosses signifying the high influence of dominance components. The presence of over dominance was reported by Kanwar and Karla (2004) and Jayaprada *et al*. (2005) in their studied materials.

Table 4 showed that in the majority cases both narrow (h^2_n) and broad (h^2_b) sense heritability values were low. It seems that high estimates of environmental variation (E_w) and their prevalence of H_R components in this material deflated both narrow and broad sense heritability. Husain *et al*. (2009) and Alam (2012) reported low narrow and broad sense heritability for the majority of the traits in their study. Regarding genetic advance, both broad and narrow sense genetic advance was calculated as low.

Comparison between total variance (σ^2_s) of different generations such as F_2, F_2 (BIP's) and $F_1 \times F_2$ (L_{3i}) was made and the results are presented in Table 5. Linkage test was not possible for cross-1 due to unavailable material of L_{3i} families. In the presence of linkage, greater variance between the total variances as shown in F_2 (BIP's) and $F_1 \times F_2$ (L_{3i}) families in this investigation. Further in many cases F_2 and $F_1 \times F_2$ were intermediate. Hence in most of the comparison, total variances (σ^2_s) of the F_2 (BIP's) and $F_1 \times F_2$ families provided a sensitive test of the presence of linkage in these materials. Test of significance shows that linkage in both coupling and repulsion phases were present in most of the cases. Significant linkage was also reported by De Toledo *et al*. (2000) in soybean and Husain *et al*. (2009) in chilli.

From the above, it is concluded that additive gene action for the traits pod weight plant^{-1} in cross-4 and cross-5; number of seeds plant^{-1} in cross-3, cross-4 and cross-5; seed weight plant^{-1} in cross-3 and cross-5 is important due to its fixable heritable nature. Therefore, selection of these traits will be very effective for the improvement of chickpea yield.

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