

Study of Genetic Variability and Interaction of Some Quantitative Traits in Chickpea (*Cicer arietinum* L)

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Abstract

A study was conducted during 2007-08 and 2008-09 to identify the stable genotypes of chickpea (*Cicer arietinum* L.) for grain yield under diverse agronomic conditions. Twenty nine genotypes were evaluated in 4 environments under irrigated and un-irrigated conditions for their yield performance. Data on 10 yield component (days to flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod, 100- seed weight, biological yield, seed yield per plant and harvest index) were used to investigate the effects of genotype, environment and G x E. On partitioning these components into linear and non-linear components, both were responsible for expression of the traits. However, the linear component was found larger in magnitude than the non-linear component suggesting that variation in the performance of different cultivars could be predicted. The genotypes Pusa 1105, BG 2050, DG 5003 DG 5008 and DG 5009 were found suitable for irrigated environments for grain yield. For moisture stress environment four genotypes Pusa 1003, Pusa 1053, DG 5005 and DG 5055 were found stable for grain yield. For the days to maturity only two genotypes Pusa 1105 and Pusa 1105 were found stable across environments. Thus these genotypes could be used for commercial cultivation. The stability measures are useful in characterizing cultivars by showing their relative performance in various environments. High phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as percent of mean were reported for seed yield per plant, number seeds per pod and number of pods per plant indicating predominance of additive gene effects in controlling these characters

Key words: Chickpea, GXE interaction, moisture stress, yield components

Introduction

Chickpea (*Cicer arietinum*) is one of the most important pulse crop in country and is grown on 8.25 million ha area with 7.06 million tons of production with an average productivity of 856 kg/ha¹ during 2009-10. India is the largest producer of chickpea where the crop has great significance, particularly for meeting the protein demand of vegetarian population and restoring the soil fertility. In Jammu & Kashmir chickpea is grown about 4300 ha with a production of 2550 tons at an average yield of 593 kg/ha¹.

Besides management practices, poor soil fertility has been reported to be one of the major causes of low productivity of chickpea which is generally grown as a rain-fed crop in relatively poor soils^[10]. A considerable area of about 43,435 ha remains unutilized during *rabi* season in most parts of the hills and foothills of the Shivalik and Pirpanjal mountain ranges in subtropical rain-fed area of Jammu region especially after the harvest of long duration rice and maize crops. Chickpea can be good alternate crop under these conditions to encourage double cropping

in otherwise mono-cropped area. Though the chickpea is a rabi crop but its timely sowing greatly effects the productivity of the crop .As the temperature during sowing time varies in different growing areas of Jammu province due to different mini agro-climatic zones. It is necessary to develop widely adapted elite varieties with stability in yield and having good response to high levels of management under diverse agro-ecological conditions. Lack of stability in production is perhaps the major factor responsible for low material productivity rather than low potential of crops. In Chickpea also, lack of stable varieties for diverse agro-ecological conditions has been the main battle neck. There, fore the objective of the present study was to supplement the earlier efforts on this aspect by was of identifying stable genotypes with higher seed yields.

Materials and Methods

The experimental materials consisted of 29 genotypes of chickpea. All genotypes were evaluated during *rabi* season 2007-08 and 2008-09 under diverse environments at RARS, SKUAST-J, Rajouri (Irrigated and Rainfed) and IARI, Delhi (Irrigated and Rainfed). In each trail, genotypes were grown in a six rows of 4 m length in randomized block design with three replication .Under irrigated crop normal irrigations were applied, whereas under rainfed condition only pre-sowing irrigation was given to ensure good germination thereafter crop was left to utilize natural precipitation. Recommended package of practices was followed for raising the crop. The row-to-row and plant-to-plant distance was kept 40cm x 20cm, respectively. All the agronomic and plant protection practices applicable for commercial chickpea were adopted .Observations were recorded on

five randomly taken plants in each plot on ten characters, i.e. Days to 50 % flowering, Days to 50 % maturity, plant height (cm), branches/plant, pods/ plants, seeds/ pod, 100-seed weight (g), biological yield (kg), seed yield / plant (g) and harvest index (%).Standard statistical procedures were followed for estimating genetic constants i.e. Phenotypic and genotypic coefficients of variation^[2]. heritability in broad sense^[5] and expected genetic advance^[6]. Genotypic and phenotypic correlation coefficients were calculated following the formula suggested by Searle^[9] and path analysis following Dewey and Lu^[3] and stability analysis was done following Eberhart and Russell^[4].

Results and Discussion

The estimates of both phenotypic (PCV) and genotypic coefficients of variation (GCV) for the ten characters were studied and presented in Table-1. The variability estimates, in general, revealed that the estimates of PCV were greater than the estimates of GCV for all the traits; this suggested the role of environment in the expression of the characters. Highest GCV was obtained for seed yield per plant (23.63per cent) followed by harvest index(21.04 percent), number of seeds per pod (18.37 per cent) and number of pods per plant (17.75 percent).For all other characters GCV was low. The seed yield showed the estimate of PCV (26.63percent) in comparison to GCV of (23.63 percent) suggesting environmental influence on this character, which was confirmed by its heritability. The least difference between PCV and GCV for plant height suggested that this character is least affected by environment. In such a situation, selection can be effective on the basis of phenotype alone with equal probability of success.

On the basis of GCV, it is possible to determine the amount of heritable variation. It can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied [6]. Hence both heritability and genetic advance were determined to study the scope of improvement in various characters through selection. The heritability estimates ranged from 67.6 per cent for harvest index 96.70 per cent for number of seeds per pod. High estimates of heritability were also observed for number of seeds per pod, biological yield, plant height and 100- seed weight. Moderate estimates of heritability for these characters indicated that environmental effects constitute a sufficient portion of the total phenotypic variation and hence, selection for these characters will be less effective. Expected genetic advance and its estimated percent mean for various characters (Table 1) revealed that number of pods plant and biological yield exhibited the high genetic advance. These characters exhibited high GCV heritability together with high genetic advance indicated the predominance of additive gene effects in controlling these characters. This confirms the findings of earlier [1] that GCV together with heritability estimate would give a better picture of genetic advance to be expected from selection.

The analysis of variance for all the characters indicating significant differences among the genotypes over four environments. Pooled analysis of variance for stability is revealed the presence of significant differences among genotypes and environments for all the traits (table 2). Mean square due to genotypes x environment interaction was highly significant for all the characters except

100-seed weight against pooled error. It indicated the variable responses of genotypes to the environments^[11]. For the estimating the genotype x environment interaction, multiplication testing of genotype is essential. Further environment + (genotype x environment) interaction component were also significantly different in pooled analysis of variance for stability of all the characters except branches/plant and 100-seed weight^[12]. Genotype x environment (linear) was not significant for days to flowering. Pooled deviation suggested that the genotype differed considerably with respect to stability of all the traits except branches/ plant over the four environments. The environment (linear) component for all the traits was significant, indicating that variation among the environment is linear. The genotype x environment interaction was further partitioned into linear and non-linear components. Since G x E (linear) component was significant for all the traits except days to flowering, this indicates that practical utility of prediction would depend on relative magnitude of the two variances. For days to flowering it indicates unpredictable performance of genotypes over the environments.

Primary requisite for sustainable crop production is the requirement of a genotype with high yield and stable performance over different environments. The stability parameters are presented in Table 3. The best variety was categorized by regression coefficient (b_i) equal or close to one and mean square deviation (S^2d_i) equal or

close to zero and having high mean performance. For days to flowering only four genotypes Pusa 1108, Pusa 2024, Pusa 1105 and Pusa 1003 revealed regression co-efficient close to unity and non significant S^2_{di} value. For days to maturity three genotypes Pusa 1105, Pusa 1108 and Pusa 1003 revealed regression co-efficient close to unity and non significant S^2_{di} value. Further this genotypes also early maturity on the basis of pooled mean. For plant height one genotypes Pusa 2024 revealed high mean, regression co-efficient near to unity and significant deviation S^2_{di} . Seeds per pod high mean genotypes DG 5009 but not stable to over environments and significant to mean square deviation (S^2_d). Three genotypes namely Pusa 1053 DG 5000 and DG 5002 high mean performance, regression co-efficient close to unity and non-significant mean square deviation respectively. These genotypes were considered relatively stable for respective traits. For seed yield per plant five genotypes showed $b_i=1$ Pusa 1105, BG 2050, DG 5003, DG 5008 and DG 5009 revealed regression coefficient around 1 and non-significant S^2_{di} value except DG 5003 these genotypes considered stable for this trait^[7,8,11]. The significance of $G \times E$ interaction for various characters indicates that the performance of chickpea genotype

is very much influenced by environmental variations indicating scope of agronomical manipulations. The regression analysis was very useful in assessing the adaption of various genotypes in terms of predictability of variations in performance over environment. Joint consideration of pooled analysis of variance and response of individual genotypes suggests that one should directly attempt to see the response of a genotype in respect of the information obtained from analysis. Since the latter provides a clear picture of material individually, this may be more useful. These genotypes Pusa 1105, BG 2050, DG 5003 DG 5008 and DG 5009 were suitable for across environment and highly promising and stable for yield and other important yield components, thus besides acting as an important donor, can also be considered as future cultivar after further evaluation, while the genotypes Pusa 1003, Pusa 1053, DG 5005 and DG 5055 were suitable for rainfed environmental conditions.

Acknowledgements

The authors express grateful thanks to Dr. S.S. Yadav Former Principal Scientist (Chickpea Breeding) Division of Genetics, IARI, Delhi for supplying the seed materials.

Table 1 Estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and correlation coefficients of ten characters in chickpea.

Characters	Mean	Range		PCV (%)	GCV (%)	h ² (broad sense)	Genetic Advance	rg with harvest index
		Min	Max					
Days to 50 % flowering	123.8	117.0	139.0	3.77	3.55	88.4	8.50	0.160
Days to 50 % maturity	153.82	147.0	169.0	3.04	2.85	88.4	8.50	0.160
Plant height	90.18	78.30	103.55	8.93	8.65	93.8	15.56	0.456*
Number of branches/ plant	29.73	20.95	39.20	16.16	13.83	73.3	7.25	0.556**
Number of pods/ plant	87.88	62.45	130.95	18.24	17.75	94.7	31.28	0.446*
Number of seeds / pod	1.29	0.85	1.75	18.68	18.37	96.7	0.48	0.131
100-seed weight(g)	33.62	24.90	39.50	13.78	13.30	93.2	8.95	-0.440*
Biological yield	111.88	82.60	139.95	13.74	13.48	96.2	30.47	-0.149
Seed yield/plant	25.78	13.45	39.45	26.63	23.63	71.8	9.01	0.793**
Harvest index	23.13	15.54	34.57	21.04	21.04	67.6	6.78	1.00**

Table 2 Pooled analysis (mean squares) for different characters over environments

Source	df	Days to 50 % flowering	Days to 50 % maturity	Plant height	Branches/ plant	pods/ plant	seed s / pod	100-seed weight (g)	Biological yield	Seed yield/plant	Harvest index
Genotypes	28	16.54*	18.12**	1585.71**	91.03**	593.23**	0.11**	72.19*	593.13*	89.91**	193.26**
Environments	3	2826.24**	4725.44**	6805.11**	2407.56**	37944.05**	4.23**	35.51*	27642.41**	571.09*	8023.21**
Genotype x Env.	84	9.96**	9.37**	30.73**	24.17**	235.38**	3.71**	8.71	75.86**	16.86**	88.81*
Env.+ (Gen. x Env.)	87	107.08**	171.99*	264.33*	106.36	1535.87*	3.73**	9.64	1026.43**	35.97**	362.42**
Environments (Lin.)	1	8479.26**	14176.37**	20415.46**	7222.70**	113832.65**	4.71**	104.43**	82927.89**	23.34**	88.81
Gen.* Env.(Lin.)	28	9.97	4.95**	30.73**	24.17**	177.52**	2.95**	1.19**	27.97**	1713.26**	24069.98
Pooled Deviation	58	557.78**	11.18**	24.61**	26.69	255.48**	3.95**	12.04*	98.76**	13.15**	40.23
Pooled Error	112	2.71	2.74	5.51	5.76	24.24	47.10	1.4	13.91	7.40	26.72

Table 3 Mean and stability parameters of different genotypes in 4 four environments

Genotypes S. No	Days to 50% flowering			Days to 50 % maturity			Pods per plant		
	Mean	Regression coefficient (bi)	Mean square Deviation(S ² di)	Mean	Regression coefficient (bi)	Mean square Deviation(S ² di)	Mean	Regression coefficient (bi)	Mean square Deviation(S ² di)
Pusa1003	127.25	1.10	-0.42	160.50	1.05	-0.65	81.54	0.81	63.35
Pusa1053	126.00	1.21	3.51	159.75	1.06	2.15	94.66	0.82	65.20
Pusa1105	126.62	1.03	-1.24	159.25	1.04	-1.04	84.08	0.99	23.01
Pusa1108	126.75	1.06	-0.15	159.88	1.03	-0.01	89.03	0.87	-6.04
Pusa1088	127.25	1.12	3.77	160.38	1.06	4.57	93.24	0.67	885.48**
Pusa2024	126.75	1.06	-0.15	159.62	1.06	0.41	91.00	1.06	107.38*
Pusa2046	132.75	1.59	107.30**	165.88	1.28	121.03**	74.55	0.75	132.17
BG2050	127.25	1.25	19.76**	160.25	1.16	24.30**	69.21	0.97	30.80
BG2051	127.25	1.22	14.74*	160.75	1.14	18.24**	52.84	1.28	201.93*
BG2052	128.75	1.15	6.75	161.75	1.10	8.57	76.26	1.39	185.62*
BG2053	129.00	1.14	5.17	162.00	1.09	6.66	77.21	1.16	553.94**
BG2054	126.25	1.12	3.77	159.25	1.08	4.95	84.31	1.11	714.57**
DG5000	124.75	0.92	0.16	175.75	0.96	0.36	74.26	1.32	228.71*
DG5001	127.75	0.79	11.35	160.25	0.88	13.57*	58.09	1.02	13.45
DG5002	127.75	0.96	-0.93	160.25	0.98	-0.91	76.18	1.22	534.04**
DG5003	124.50	0.91	0.97	157.50	0.95	1.30	71.60	1.01	38.87
DG5004	124.50	0.91	0.97	157.50	0.95	1.30	77.30	1.17	346.64**
DG5005	125.00	0.77	0.97	158.00	0.95	1.30	69.75	0.80	69.27
DG5006	122.50	0.82	13.51*	155.50	0.87	16.14**	94.99	0.83	1.50
DG5007	123.75	0.80	7.53	156.75	0.90	9.05*	69.11	1.14	197.69*
DG5008	125.75	0.85	6.52	158.75	0.88	8.20*	82.36	0.96	176.56*
DG5009	125.00	0.81	2.42	157.62	0.87	4.27	67.74	0.78	94.64
DG5010	124.25	0.88	12.93*	157.25	0.90	14.91*	90.32	1.17	345.53**
DG5011	123.75	1.11	5.50	156.62	0.93	6.91	84.84	0.70	334.63**
DG5012	126.75	0.80	0.99	159.75	1.08	1.72	66.97	0.75	153.71*
DG5050	126.75	0.80	6.52	157.25	0.88	8.20	102.94	1.38	1265.87**
DG5055	124.25	0.82	7.53	158.25	0.90	9.05	78.57	1.15	193.92*
DG5056	125.25	0.97	-1.23	156.00	0.99	-1.24	85.38	0.97	13.65
DG5050	125.00	0.91	0.97	158.00	0.95	1.30	54.99	0.75	91.27
Pop (mean) 126.01						159.04			78.39
S.E. of mean 0.18						1.9			9.22
S.E. of b 1.00						0.15			0.25

Table 4. Mean and stability parameters of different genotypes in 4 four environments

Genotypes S. No	Seeds per pod			100-Seed weight			Seed yield per plant		
	Mean	Regression coefficient (bi)	Mean square Deviation(S ² di)	Mean	Regression coefficient (bi)	Mean square Deviation(S ² di)	Mean	Regression coefficient (bi)	Mean square Deviation(S ² di)
Pusa1003	1.14	3.30	0.00	26.61	1.59	0.93	19.27	0.69	-2.17
Pusa1053	1.49	5.72	0.15**	25.70	0.95	-0.73	26.71	0.96	-3.70
Pusa1105	1.23	1.31	0.01	35.49	2.51	42.72**	24.22	1.17	-1.09
Pusa1108	1.14	-0.96	0.08**	29.80	1.82	1.76	24.51	0.30	7.37
Pusa1088	1.49	3.26	0.00	30.07	0.96	-0.33	32.74	0.70	59.73**
Pusa2024	1.26	1.19	0.05	34.31	0.74	1.72	26.80	0.49	9.99*

Pusa2046	1.09	2.50	0.05	32.86	0.34	0.63	20.70	0.85	-3.54
BG2050	1.38	-3.00	0.00	36.60	1.35	4.05	27.28	1.05	-2.97
BG2051	1.22	-2.11	0.02	37.40	1.28	9.16	25.38	0.37	5.26*
BG2052	1.44	1.50	0.01	36.16	1.22	2.14	30.25	1.34	-1.84
BG2053	1.50	-0.85	0.00	34.49	1.46	10.97*	33.04	0.33	18.85**
BG2054	1.15	-1.69	0.01	30.42	0.34	4.73	31.35	0.32	5.36
DG5000	1.48	0.58	0.04	39.43	1.00	9.13	28.25	2.25	20.35**
DG5001	1.45	1.69	0.01	41.30	1.08	5.49	29.16	2.17	46.75**
DG5002	1.33	1.38	0.03	39.80	1.01	0.10	27.03	1.77	12.74*
DG5003	1.12	2.11	0.02	40.56	1.05	-0.19	29.61	1.03	11.32*
DG5004	1.42	2.99	0.04*	39.19	1.05	1.53	28.61	1.43	5.76
DG5005	1.05	0.00	0.0	38.20	0.67	0.51	24.90	1.20	-2.32
DG5006	1.25	-1.69	0.01	37.64	0.47	0.64	31.48	0.65	-1.65
DG5007	1.10	0.84	0.00	36.05	0.45	12.46*	25.25	1.86	17.35**
DG5008	1.00	-2.53	0.03	34.42	1.43	0.58	30.12	1.11	-2.18
DG5009	1.53	6.21	0.22**	36.95	0.44	24.93**	22.68	1.06	-2.88
DG5010	1.25	1.69	0.01	38.25	1.09	7.78	31.34	1.27	-3.00
DG5011	1.25	-3.38	0.05	37.39	0.91	-0.72	24.47	2.23	37.52**
DG5012	1.41	-3.19	0.03	32.91	-0.42	87.66**	24.59	0.95	-3.54
DG5050	1.15	5.07	0.12**	30.94	1.19	9.64	19.30	0.40	22.58**
DG5055	1.28	2.07	0.02	33.49	0.13	42.18**	13.26	0.89	-3.68
DG5056	0.90	2.53	0.03	28.71	1.42	16.52**	19.59	0.00	25.47**
DG5050	1.49	2.42	0.04	29.98	1.45	32.20**	20.60	0.90	1.99
Pop (mean)			1.25						25.94
S.E. of mean			0.11	34.65					2.09
S.E. of b			0.30	2.00					0.47
				0.18					

*,** Significant at P=0.05 and 0.01, respectively

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