Indian J. Genet., 49(3): 349–353 (1989)

GENETIC DIVERSITY AND STABILITY IN CHICKPEA

V. SINGH* AND F SINGH

Department of Agricultural Botany
Meerut University, Meerut 250005

(Received: August 30, 1988; accepted: December 17, 1988)

ABSTRACT

Sixty six genotypes of chickpea (*Cicer arietinum* L.) were grown over nine microenvironments created by different combinations of sowing dates, spacing and fertilizer doses over 3 years. Pooled data of nine characters over environments were analysed for D^2 statistic. Clusters of genotypes were formed on the basis of D^2 estimates. Joint regression analysis revealed highly significant differences due to genotypes, environments, and genotype × environment interaction for all characters. Stability of individual genotypes was worked out on the basis of two stability parameters—regression coefficient (bi) and deviation from regression (S^2di). Further, 14 genotypes were sorted out with high grain yield per plant (higher than grand mean over environments) and stable for grain yield and for other yield contributing characters. On the basis of intra- and intercluster distances, crossing among these selected genotypes was suggested to recombine the genes for stability and high yield.

Key words: Chickpea, genetic diversity, stability

A commercially desirable genotype should be stable for grain yield per plant with high mean value. In self-pollinated crops like chickpea, development of hybrid varieties is not successful due to crossing barrier and cost of seed production. However, it is important to select divergent parents with stable performance for yield as well as other morphological characters for hybridization and to obtain desirable segregants through selection in the advanced breeding generations. Keeping this in view, genetic divergence analysis was done to identify suitable parents on the basis of intra- and intercluster distances for realising heterosis and desired recombinants.

MATERIALS AND METHODS

Sixty six genotypes of chickpea were grown over nine microenvironments at Meerut University Research Farm, Meerut. Microenvironments were created through different combinations of sowing dates, spacings and fertilizer doses over three years. Nine microenvironments consisted of one environment in rabi 1982-83 with a spacing of 30 × 15 cm (row × plant) and fertilizer dose of N : P : K 20 : 50 : 40 kg/ha plus eight environments with different combinations of two sowing dates having differences of about a fortnight (spacing in first sowing 50 × 20 cm and in second

*Present address: National Research Centre for Groundnut, Junagadh 362015.

sowing 30 × 15 cm) and two levels of fertilizers (control and N : P : K 20 : 50 : 40 kg/ha) in two years, i.e., rabi seasons of 1983-84 and 1984-85, respectively. The material was planted in RBD of three replications in each environment. The plot size for each treatment was one row of 3 m length spaced as per combination in the environments.

Data were recorded on nine morphological characters, namely, plant height, days to flowering, days to maturity, primary branches per plant, secondary branches per plant, pods per plant, 100-grain weight, harvest index, and grain yield per plant. Generalised distance was estimated by D^2 statistic [1, 2] and clusters of genotypes were formed by Tocher's method given by Rao [1]. Estimates of divergence were calculated based on pooled data of nine characters over nine environments. Further, joint regression analysis was done using the method of Perkins and Jinks [3]. Stability parameters were computed using the method of Eberhart and Russell [4]. A genotype having unit regression coefficient (bi = 1) and nonsignificant deviation from regression (i.e., $S^2di = 0$) was considered stable.

RESULTS AND DISCUSSION

Genetic divergence. The clustering on the basis of D^2 values of pooled data formed only four clusters. Cluster I had the maximum, 61 genotypes. Cluster II had three genotypes, viz. F 370, P 992 and P 6308, while cluster III and IV included only one genotype each (Table 1). Clustering showed that genotypes P 9695, ICC 8149, F 370, P 992 and P 6308 were distinct from the other genotypes, as the first two were represented in single-genotype clusters and the other three formed different clusters. Maximum intercluster distance was observed between clusters I and IV followed by II and IV, I and III, II and III, and I and II (Table 2). Least intercluster distance was observed between clusters III and IV. Maximum intracluster distance was observed for cluster II, followed by cluster I. Cluster III and IV had 0 intracluster distance, since each of them was represented by a single genotype. On the basis of intra- and intercluster distances, it is suggested that for creating maximum genetic variability, crossing between the genotypes of clusters I and IV, II and IV and I and III would be useful.

Table 1. Distribution of 66 genotypes of chickpea among four clusters on the basis of D^2 analysis

Cluster	Genotypes
I	ICC 1097, P 678, WR 315, BG 212, HMS 17, P 289, HMS 25, HMS 5, HMS 19, Annigeri, P 179, P184–1, H77–111, H77–78, P345–1, ICC 1994, HMS 21, HMS 27, BG 209, JG 35, ICCC 3, ICCC 4, ICC 1134, NEC 2383, H 77–108, H 76–104, H 77–56, P 3765, P 1179, H 77–104, HMS 6, F 6 Wilt 1965, NEC 249, F 6 Wilt 315, H 76–105, H 77–19, P 1786, H 77–74, PG 72-84, E 100, ICC 7710, C 235, H 77–110, H 77–103, H 77–112, H 77–106, L 345, H 77-62, JG 221, P 4116–1, ICCC 2, H 76–101, F 6 Wilt 115, GC 665, 12–071–05093, PRR-1, NEC 2305, ICC 3651, NEC 1128, H 77-57, H 77–70
II	F 370, P 992, P 6308
III	ICC 8149
IV	P 9695

Table 2. Pooled average intra- and intercluster D^2 values

Clusters	I	II	III	IV
I	**6.26**	18.52	40.68	94.88
II		**9.29**	22.21	54.85
III			**0.00**	15.19
IV				**0.00**

Joint regression analysis. Highly significant differences were observed due to genotypes, environments and genotype × environment interaction for all the nine characters (Table 3). A highly significant variation due to environments indicated presence of significant variation due to different combinations of spacing, sowing time and fertilizer doses. Significant linear component of G × E for grain yield per plant, days to maturity, primary branches per plant, secondary branches per plant, pods per plant, and harvest index indicated predominance of predictable component for these characters. Linear mean squares as well as remainder mean squares were significant for plant height, days to flowering and 100-grain weight. Significant linear component against its remainder for days to flowering showed that the major component for differences in stability was due to linear regression. Plant height and 100-grain weight showed nonsignificant linear component against their remainder mean squares, indicating unpredictable nature of these characters. However, predictions of G × E interaction in individual lines for plant height and 100-grain weight were also made on the basis of their bi and S^2di values.

Table 3. Joint regression analysis for nine characters of 66 genotypes of chickpea grown over nine microenvironments

Source of variation	d.f.	Mean squares								
		plant height	days to flowering	days to maturity	primary branches per plant	secondary branches per plant	pods per plant	100-grain wt.	harvest index	grain yield per plant
Genotypes	65	130.0$^{\times\times}$**	64.7$^{\times\times}$**	9.7$^{\times\times}$**	0.56$^{\times\times}$**	6.25$^{\times\times}$**	853.0$^{\times\times}$**	88.4$^{\times\times}$**	144.6$^{\times\times}$**	18.9$^{\times\times}$**
Environments	8	3741.8$^{\times\times}$**	4108.3$^{\times\times}$**	9129.4$^{\times\times}$**	70.78$^{\times\times}$**	596.36$^{\times\times}$**	83586.3$^{\times\times}$**	75.8$^{\times\times}$**	8131.0$^{\times\times}$**	3011.2$^{\times\times}$**
Genotypes × environment	520	9.5**	4.7**	2.1**	0.23**	2.0**	197.4**	2.0**	36.9**	6.0**
Linear	65	10.3*	13.1^{++}**	6.0**	0.61**	3.72**	529.0**	2.1**	47.2*	16.1**
Remainder	455	9.4**	3.5**	1.7	0.18	1.85	150.1	2.0**	35.4	4.6
Error	1170	7.2	2.1	1.8	0.17	1.84	140	1.3	32.9	4.5

*, **Significant at 5% and 1% levels against error mean squares, respectively.
××Significant at 1% level against genotype × environment mean squares.
++Significant at 1% level against remainder mean squares.

Table 4. High yielding genotypes stable for various characters

Genotype	Stable characters									Total stable characters
	1	2	3	4	5	6	7	8	9	
P 4116–1	+	+	+	+	+	+	+	+	+	9
ICCC 4	+	+	+	+	+	+		+	+	8
H 77–70		+	+	+	+	+		+	+	7
H 77–103	+	+	+		+		+		+	6
H 77–56	+	+	+	+	+		+	+	+	8
NEC 2383			+	+	+	+		+	+	6
ICCC 2	+		+	+	+				+	5
PRR 1	+		+	+	+	+	+		+	7
H 77–110	+	+	+	+	+	+	+	+	+	9
H 77–62	+				+	+		+	+	5
F 370	+		+		+	+	+	+	+	7
P 992	+		+		+	+	+	+	+	7
ICC 8149	+		+	+		+			+	5
P 9695		+	+	+	+			+	+	6

Characters: 1) Plant height, 2) days to flowering, 3) days to maturity, 4) primary branches/plant, 5) secondary branches/plant, 6) pods/plant, 7) 100-grain weight, 8) harvest index, 9) grain yield/plant.

Table 5. High yielding genotypes stable for grain yield/plant forming different clusters on the basis of D^2 analysis

Cluster	Genotype	Xi	bi	S^2di	No. of other stable characters
I	P 4116–1	H (11.28)	1.1563**	−3.906	8
	ICCC 4	H (10.58)	0.9810**	−0.534	7
	H 77–70	H (10.23)	1.2093**	2.731	6
	H 77–103	H (9.89)	1.2136**	−1.662	5
	H 77–56	H (9.85)	1.2547**	0.230	7
	NEC 2383	H (9.69)	0.8366**	−2.351	5
	ICCC 2	H (9.67)	1.1679**	3.026	4
	PRR 1	H (9.65)	0.9464**	1.267	6
	H 77–110	H (9.58)	1.2022**	−0.289	8
	H 77–62	H (9.28)	1.0185**	2.542	4
II	F 370	M (6.91)	0.9886**	−2.796	6
	P 992	H (8.92)	1.1734**	−1.402	6
III	ICC 8149	H (8.33)	1.0147**	−2.357	4
IV	P 9695	M (7.71)	1.2138**	3.739	5

Note. 1. Grand mean of population 8.27 g/plant.

2. H—high yield (8.27) g and above/plant); M—medium yield (6.60–8.26 g/plant).

**Significant against error mean square at 1% level.

Stability parameters showed that out of 66 genotypes 26 were stable for grain yield with high mean performance (higher mean than grand mean over environment). These were P 4116–1, ICCC 4, H 77–70, H 77–103, H 77–56, NEC 2383, ICCC 2, PRR 1, H 77-110, H 77–62, H 77-112,H 77–111, P 179, P 992, P 1179, H 76–101, HMS 19, L 345, HMS 27, H 77–104, H 76–104, P 345–1, F_6 Wilt 1865, Annigeri, ICC 8149 and JG 221. Out of these 26 genotypes 14 were sorted out having higher yields and stable for most of the yield contributing characters (Table 4).

D^2 and stability. The 14 genotypes selected on the basis of stability and higher mean for grain yield belong to different clusters, e.g., 10 belong to cluster I, 2 to cluster II, and one each to clusters III and IV, respectively (Table 5). Therefore, considering the D^2 analysis and stability of yield and yield contributing characters, making crosses among the selected genotypes of cluster I (P 4116–1, ICCC 4, H 77–70, H 77–103, H 77–56, NEC 2383, ICCC 2, PRR 1, H 77–110 and H 77–62) with the genotypes of clusters IV (P 9695) and III (ICC 8149) is recommended. Similarly, crossing P 9695 with the genotypes of cluster II (F 370 and P 992) is also suggested. Crosses in the above combinations are expected to provide enough genetic variability to select for high yielding and stable segregants in the segregating generations.

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