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GENETIC DIVERSITY ON THE BASIS OF PHOTOSYNTHETIC AND YIELD RELATED TRAITS IN CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

Genetic diversity was assessed in a collection of 52 true breeding advanced generation lines and two check varieties of chickpea on the basis of photosynthetic and yield related traits, including nodulation parameters to identify physiologically efficient types. The study revealed enormous diversity in the material as indicated by the wide range of D^2 values from 53.9 (between the genotypes ICCV 90125 and ICCV 90127) to 15054.0 (between the genotypes ICVV 90103 and ICCV 90113). The genotypes fell in nine clusters when grouped using the Tocher's method. Cluster V had the highest number of genotypes. The intercluster distances ranged from 339.4 between clusters I and V to 15054.0 between VIII and IX. The cluster means for different characters were worked out and the future strategies are discussed after identifying genotypes as potential sources of genes for photosynthetic and yield related traits.

Key words: Photosynthetic traits, yield related traits, diversity, chickpea.

Accumulation of different desirable traits spread over diverse genotypes is important to rapid advance in yield improvement of any crop. The morpho-physiological traits of the plant related to photosynthesis have a telling effect on dry matter accumulation and its partitioning which ultimately decides productivity. Very little information is available on genetic variability for photosynthetic traits in chickpea. The utility of techniques like Mahalanobis D^2 analysis to detect divergence in a group of genotypes and to identify genotypes which can effectively be used in crossing programmes has been stressed repeatedly. Potential sources of genes for different characters can be identified by taking into consideration the clusters of genotypes which excel in each trait and the diversity

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between the genotypes. The present study aims at the assessment of genetic diversity in a collection of 52 advanced generation true breeding lines of chickpea on the basis of 15 photosynthetic and yield related traits including nodulation parameters.

MATERIALS AND METHODS

The field experiment was conducted at the Agricultural Research Station, Dharwad during rabi 1990-91 using 52 true breeding advanced generation lines and two check varieties (Table 1) of chickpea (*Cicer arietinum* L.) to assess the genetic diversity in the material on the basis of photosynthetic and yield related traits. The trial was laid out in

Table 1. List of chickpea genotypes under study and their pedigree details

Entry No.	ICCV No.	Parentage
1	90101	(ICCX-750073-4-1P-1P-BP x JG 74) x ICCX-750073-4-1P-1P-BP
2	90102	ICCC 30 x Annigeri
3	90103	Phyle G-12 x JG 1265
4	90104	2375 x ICCC 30
5	90105	Phule G-12 x ICCC 22
6	90106	18-7-2-1 x JG 315
7	90107	(K 850 x ICCX-770535-6P-2P-BP) x (JG 62 x ICC 506-EB)
8	90108	" "
9	90109	ICCC 10 x H 75-35
10	90110	K 850 x Redhey
11	90111	[(K 850 x G 130) x K 850] x G 130
12	90112	BG 209 x H 75-35
13	90113	" "
14	90114	(HMS 4 x RPSP 322-1) x ICCL 80074
15	90115	ICCL 79080 x BG 203
16	90116	HMS 4 x H 75-35
17	90117	BG 209 x H 75-35
18	90118	ICCL 79048-3EB x H 208
19	90119	P 9847 x ICC 5264-EB-EB
20	90120	L 550 x Pant G-114
21	90121	P 9847 x Phule G-5
22	90122	K 850 x H 355

(Contd.)

Table 1 *(contd.)*

Entry No.	ICCV No.	Parentage
23-30	90123 to 90130	(WR 315 x BG 203) x BG 203
31	90131	(K 850 x ICCX 770535-6P-2P-BP) x (JG 62 x ICC 506-EB)
32	90132	(P 2426-1 x K 1170) x GL 769
33	90133	(WR 315 x BG 203) x BG 203
34	90134	P 324 x P 2161
35	90135	GL 769 x H 75-35
36	90136	ICCL 79048-3EB x ICCL 80101-2EB
37	90137	ICC 7770-EB-EB x ICC 2793-EB-EB
38	90138	(HMS 4 x RPSP 322-1) x ICCL 80074
39	Annigeri 1 (Local check)	—
40	K 850 (Check var.)	—
41	90152	ICCL 79048-3EB x H 208
42	90151	ICCL 79048-3EB x (G 130 x Chaffa)
43	90150	Pant G-114 x (JG 62 x F 496)
44	90149	ICCL 78043 x K 850
45	90148	ICCC 10 x H 75-35
46	90147	P 324 x ICCC 5
47	90146 to 90144	(WR 315 x BG 203) x BG 203
50	90143	Annigeri x Phule G-5
51	90142	Phule G-5 x JG 315
52	90141	(H 208 x F 61) x ICCC 4
53	90140	ICCL 13 x Annigeri
54	90139	ICCL 78043 x K 850

randomized block design with two replications. Three plants per replication in each genotype were sampled in both the replications 60 and 75 days after sowing (DAS) for recording observations on leaf area, total dry matter (TDM) and partitioning of dry matter into leaf, stem and reproductive parts. These plants were dried in hot air oven at 60°C to a constant weight and their dry weight determined. Leaf area per plant was calculated as described by Kvet et al. [1]. Different physiological traits like leaf area indices (LAI) at 60 and 75 DAS, leaf area duration (60-75 DAS), and specific leaf weight (SLW) etc. were determined. The total chlorophyll content of leaves at 60 and 75 DAS was estimated following the procedure of Arnon [2]. For recording the nodulation parameters, three plants in each replications were harvested at peak flowering stage and the number of nodules per plant were counted. These nodules were oven dried to determine their dry weight. The data on number of pods, seed yield per plant, and harvest index were recorded at harvest. Mahalanobis D^2 statistic was used to assess genetic divergence between genotypes. The grouping of genotypes was done using Tocher's method as described by Rao [3]. Canonical analysis was carried out by calculating the first two vectors or canonical roots. The first two vectors accounted for 94.1% of the total variability. The mean values for the first two canonical vectors for the 54 genotypes were plotted on a two dimensional graph and the D^2 clusters superimposed over it.

RESULTS AND DISCUSSION

The Mahalanobis D^2 analysis using 54 genotypes based on 15 characters produced 2916 D^2 values. They ranged from 53.9 (between genotypes ICCV 90125 and ICCV 90127) to 15054.0 (between genotypes ICCV 90103 and ICCV 90113). The wide range of D^2 values indicated enormous diversity present in the material studied. Similar results were also reported earlier [4]. Moreover, with the recent emphasis on the physiological mechanisms influencing seed yield, the presence of sizeable diversity for the photosynthetic and yield related traits in the present study can be considered as an encouraging situation.

The genotypes included in the study were the derivatives of single, three-way and four-way crosses involving best commercial varieties like Annigeri-1, 2375, Phule-G 12, K-850, Radhey, BG-209 and L-550, etc., crossed with important donor parents like WR-315, IG-315, H-7535, HMS-13 etc., confering resistance to biotic stresses and other yield related traits. The genotypes fell into nine clusters when grouped using the Tocher's method [3]. Cluster V was the largest, accommodating as many as 34 genotypes (Table 2, Fig. 1). Cluster

Table 2. Distribution of fifty four chickpea genotypes in different clusters

Cluster No.	No. of genotypes	Genotypes (ICCV Nos.)
I	2	90128, Annigeri 1
II	2	90144, 90140
III	2	90136, 90141
IV	3	90110, 90137, K-850
V	34	90101, 90102, 90104, 90106, 90107, 90108, 90109, 90111, 90112, 90114, 90115, 90118, 90119, 90122, 90123, 90124, 90125, 90126, 90127, 90129, 90130, 90131, 90132, 90133, 90135, 90152, 90149, 90148, 90147, 90146, 90145, 90143, 90142, 90139
VI	8	90105, 90116, 90117, 90120, 90121, 90134, 90151, 90150
VII	1	90138
VIII	1	90113
IX	1	90103

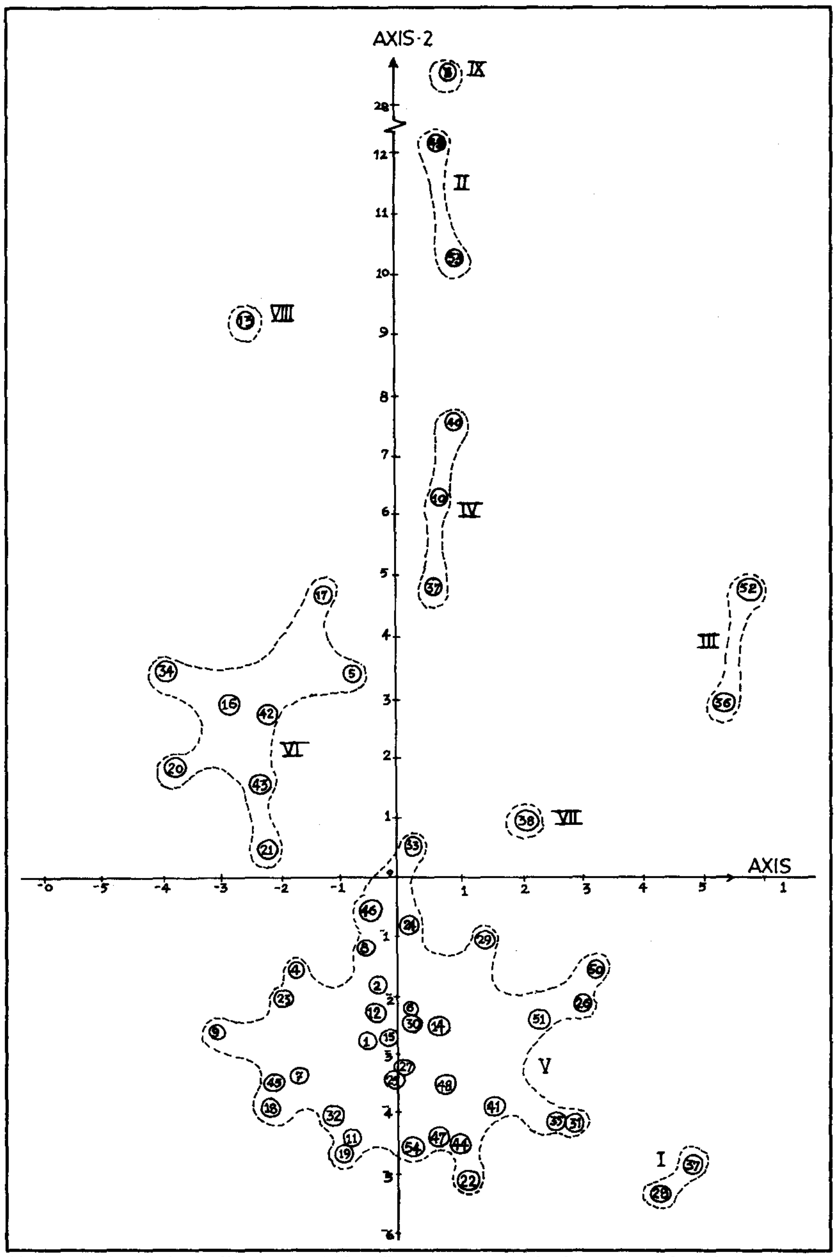

Fig. 1. **Canonical diagram of the first two canonical vectors showing relative positions of fifty four genotypes of chickpea.**

VI had eight genotypes. There were three solitary clusters; clusters VII, VIII and IX, with ICCV 90138, ICCV 90113 and ICCV 90103 genotypes, respectively.

Some of the genotypes used in the study were the descendants of the same cross. As expected, many such derivatives fell into the same cluster. For example, genotypes ICCV Nos. 90123, 90124, 90125, 90126, 90127, 90129, 90130, 90147 and 90148 originating from the cross (WR-315 x BG-203) x BG-203 were grouped together in cluster V. However, the grouping pattern also indicated that in spite of common ancestry, many derivatives of the same cross fell in different clusters. For instance, genotypes ICCV 90112 and ICCV 90113 had the common origin from the cross BG-209 x H-75-35, but fell in clusters V and VI, respectively. Similarly, genotype ICCV 90144 fell into cluster II although it was isolated from the same cross (WR-315 x BG-203) x BG-203 as the genotypes ICCV 90147 and ICCV 90145, which were placed in cluster V. It is generally expected that the different lines derived from the same cross reveal low diversity. However, when diverse parents are used in a cross, the lines selected may reveal greater diversity despite the common parentage. Similar observations were earlier reported by Katiyar [5]. He explained such situations by (i) some degree of heterogeniety either through balanced polymorphic system, (ii) directional selection for some agronomic characters under domestication, and (iii) genetically diverse nature of parents used in evolving the genotypes or genetic drift and selection forces under diverse environments. It may be wrong to generalise that all segregates sharing common parentage will always have low diversity among them.

The average intra- and intercluster D^2 and D values are given in Table 3. The intracluster distances ranged from 137.3 to 332.7 for clusters I and VI, respectively, and did not transgress

Table 3. Average intra- (in bold) and intercluster distances between different clusters of chickpea genotype

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**137.3**	404.9	583.2	365.9	333.5	339.4	440.6	517.3	3151.5
	(11.7)	(20.1)	(24.1)	(19.1)	(18.3)	(18.4)	(21.0)	(22.7)	(56.1)
II		**199.2**	652.9	458.7	379.9	390.5	456.2	529.7	2950.4
		(14.1)	(25.6)	(21.4)	(19.5)	(19.8)	(21.4)	(23.0)	(54.3)
III			**227.1**	602.4	603.6	611.1	745.8	773.3	5516.6
			(15.1)	(24.5)	(24.6)	(24.7)	(27.3)	(27.8)	(74.3)
IV				**271.8**	394.5	391.7	474.3	544.2	2962.5
				(16.5)	(19.9)	(19.8)	(21.8)	(23.3)	(54.4)
V					**297.1**	440.6	472.7	542.9	2961.5
					(17.2)	(21.0)	(21.7)	(23.3)	(54.4)
VI						**332.7**	499.8	580.9	3475.5
						(18.2)	(22.4)	(24.1)	(59.0)
VII							**0.0**	824.0	7397.0
							(0.0)	(28.7)	(86.0)
VIII								**0.0**	15054.0
								(0.0)	(122.7)
X									**0.0**
									(0.0)

Note. Values in parentheses are D values.

the limits of any of the intercluster distances. Clusters VIII and IX were the most diverse, the intercluster distance between them (15054.0) being maximum. The intercluster proximity was maximum between clusters I and V, hence they were closely related.

The mean values of each of the 15 characters for the nine clusters (Table 4) show that the different clusters were superior in respect of different characters. Cluster IX, which was most diverse, had very high nodule dry weight (250.0 mg) and nodule number (23.5). Clusters II and III also represented entries with high nodule number and nodule dry weight (25.2 and 121.7 mg for cluster II and 21.2 and 71.7 for cluster III, respectively). These clusters could be regarded as useful sources of genes for nodulation parameters. Cluster VII with

Table 4. Meann values of different characters in nine clusters of chickpea

Character	Character means in different clusters								
	I	II	III	IV	V	VI	VII	VIII	IX
Nodule number	6.2	25.2	21.2	21.5	12.7	19.7	17.5	18.0	23.5
Nodule dry weight (mg)	7.0	121.7	71.7	85.6	20.1	57.6	48.5	10.5	250.0
Days to 50% flowering	53.5	57.5	56.2	54.2	54.4	59.1	44.0	61.5	52.0
Pods/plant	85.6	55.6	84.0	57.8	56.3	36.7	64.0	34.6	48.6
Seed yield/plant (g)	9.7	6.6	9.0	8.8	7.5	6.0	8.7	5.6	7.7
Total dry matter 60 DAS (g/plant)	11.7	10.9	10.4	10.5	9.7	9.4	9.6	10.7	11.5
Total dry matter 75 DAS (g/plant)	19.7	18.8	21.0	18.0	17.0	16.4	17.6	18.3	15.2
Total dry matter 90 DAS (g/plant)	25.0	19.6	23.7	22.5	21.5	20.1	20.2	22.1	20.3
Harvest index (%)	0.4	0.3	0.4	0.4	0.4	0.3	0.4	0.2	0.4
Specific leaf weight (mg/cm^2)	48.5	42.5	48.5	48.3	45.7	48.2	46.5	50.5	47.0
Chlorophyll content 60 DAS (mg/g)	2.4	1.7	2.2	1.8	1.8	1.7	2.5	1.5	1.4
Chlorophyll content 75 DAS (mg/g)	1.4	1.3	1.5	1.1	1.3	1.2	1.6	1.2	1.2
Leaf area index 60 DAS	3.4	2.5	4.4	3.2	2.5	1.9	3.3	1.3	1.7
Leaf area index 75 DAS	4.4	3.0	4.8	3.4	3.3	2.9	3.8	2.7	2.7
Leaf area duration 60–75 DAS	56.4	41.8	68.4	49.3	42.8	36.3	53.7	30.1	33.0

the lowest number of days to 50% flowering (44 days) can be regarded as a good source for earliness. Cluster I and III are good sources for high pod number and seed yield (i.e. 85.6 and 9.7 g, respectively, for cluster I and 84.0 and 9.0 g for cluster III). Clusters III and I also represent types with good dry matter accumulation at different stages of crop growth. Cluster I also presented high mean performances with regard to leaf area indices at 60 and 75 DAS and leaf area duration (60–75 DAS). Cluster VII included genotypes with efficient partitioning of dry matter as revealed by the high harvest index. The genotypes of this cluster can also be considered as useful source of genes for total chlorophyll content at 60 and 75 DAS stages of crop growth. The genotypes from these clusters may therefore be selected as parents in crossing programmes to incorporate the characters for which they have shown superiority.

Crosses between the genotypes of clusters I and III, which exhibited excellence for agronomic and photosynthetic traits, with the genotype of cluster IX with excellent nodulation parameters and dry matter accumulation may yield promising derivatives. Similarly, genotypes of these clusters crossed with those from cluster VII with a very efficient dry matter partitioning, as shown by the highest harvest index, may also produce derivatives with better physiological efficiency in accumulating and partitioning of dry matter.

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