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RESEARCH PAPER

Genetic diversity for seed and productivity traits in chickpea (*Cicer arietinum* L.)

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Abstract: The present investigation was conducted for assessing genetic divergence among eighty nine chickpea genotypes at College of Agriculture, Vijayapur campus during *Rabi* 2019.Based on D^2 values, the genotypes were grouped into seven clusters with highest inter cluster distance of 59.20 between Cluster I and VII. Cluster ranking, based on means showed Cluster IV at the top followed by Cluster II. With 72 genotypes, Cluster II was found to be largest, followed by Cluster III (6 lines), Cluster I (5 lines), while Cluster IV and VII had only 2 genotypes each. Intra cluster distance was highest in Cluster II (14.43) followed by Cluster III (6.22) whereas, inter cluster distance, varied between 12.89 (Cluster II and Cluster III) and 59.20 (Cluster I and Cluster VII).

Key words: Chickpea, D^2 statistics, Genetic diversity, Productivity

Introduction

Pulses are the prime group of crops and a wonderful boon of nature to the mankind, as they have deep root system, mobilize insoluble soil nutrients, restore soil fertility and bring qualitative changes in soil physical properties. Pulse crops are grain legumes, whose dry seeds are harvested and marketed distinguishing them from vegetable legumes. The term 'Pulse' was acquired from the Latin word "puls" or "putis" meaning "thick soup" or "potage". Globally among the major pulse crops, chickpea (*Cicer arietinum* L.) accounts for 40 per cent of the production and it remains the largest produced pulse crop. Chickpea is the only cultivated species under the genus '*Cicer*' with 2n=2x=16 chromosomes and relatively small genome size of 738.09Mbp (Varshney *et al.,* 2013). Chickpea belongs to the family Fabaceae, included in its subfamily Papilionaceae. The genus includes 43 species, among them, nine are annual and 33 are perennial while one is unclassified. It is an important cool season grain legume with indeterminate growth habit and largely cultivated throughout tropical and sub-tropical regions of the world (Gaur *et al*., 2012) across 33 countries and regions including Central-West Asia, Southern Europe, Ethiopia, North Africa and Australia. Van der Maesen (1972) believed that the species originates in the southern Caucasus and northern Persia.

The diversity present in crop genetic resources provide an assurance for future genetics progress and insurance against unforeseen threat to agricultural production. Assessment of genetic diversity in a set of genotypes or population is required for choosing divergent genotypes as parents in various crossing programs for breeding applications. Thus, genetic diversity analysis is of utmost importance in breeding not only for yield improvement but also for enhanced resistance to pest and disease and improved grain quality.

The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generation as already reported by earlier workers (Kumar *et al.,* 1994). D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop developed by Mahalanobis (1936). In the present study, an attempt has been made to identify genetic divergent lines, so as to select the potential parents for breeding programme to attain the anticipated improvement in grain yield.

Material and methods

A field experiment was conducted using eighty nine genotypes including checks during *Rabi* 2019-20 at I block, Regional Agricultural Research Station (RARS) Vijayapur, which is situated in Northern dry zone of Karnataka between 16°46' N latitude and 75°45' E longitude with an altitude of 595 meters above mean sea level (MSL). The experiment was laid out in augmented block complete design having four blocks with five checks repeated in each block. Observations on various seed and productivity traits along with phenological traits were recorded on five randomly selected plants from each genotype*viz.,* Initiation of first flower, Days to 50 per cent flowering, Initiation of first pod, Days to 50 per cent poding, Days to maturity, Number of primary branches per plant, Number of secondary branches, Plant height (cm), Number of pods per plant, Number of seeds per pod, Hundred seed weight (g), Seed yield per plant (g), Seed protein (%) using Bradford assay, Seed vigour (%) as per Ellis and Roberts (1980) and Seed moisture (%) using automatic moisture meter. Along with analysis of variance, genetic divergence was estimated using Mahalanobis (1936) D^2statistics and clustering was done according to Tocher's method as described by Rao (1952).

Results and discussion

The analysis of variance showed significant difference for genotypes for seven traits number of pods per plant, hundred seed weight and seed yield per plant, in addition to days to first flowering, days to 50 per cent flowering, days to first poding

Table 1. Analysis of variance for yield and yield related traits in chickpea

Source of variations	df	DFF	DFPF	DFP	DM	PH	NPB	NSB	NPP	NSP	SYPP	HSW	SM	SV	SP
Block (eliminating Check+Var.)	3	6.53	3.25	3.46	9.37	6.73	0.33*	0.37	30.26	0.003	2.12	0.62	1.08	0.60	0.53
Entries (ignoring Blocks)	88	62.17**	57.42**	53.50**	22.91	68.81 **	0.14	3.14**	697.54**	0.003	31.71**	77.73**	1.22*	0.51	0.41*
Checks	4	107.55**	66.67**	26.30*	60.17*	13.34 *	0.33*	11.80**	3783.14**	0.003	126.80**	32.50**	1.47*	0.60	0.54*
Varieties	83	57.93**	4.27**	54.39**	20.39	72.04 **	0.13	1.25**	399.29**	0.003	20.88**	80.45**	1.22*	0.51	0.41 *
Checks vs. Varieties	1	232.67**	281.73**	89.02**	82.82*	22.53 *	0.00	124.88**	13109.78 **	0.001	550.44**	33.55**	0.18	0.89	0.25
Error	12	3.61	11.87	5.80	16.17	3.22	0.06	0.21	14.78	0.004	2.82	0.97	0.43	0.57	0.16
C.D. (95%)		5.07	9.19	6.42	10.73	4.79	0.68	1.24	10.25	0.17	4.48	2.63	1.75	2.02	1.07

NOTE: * and ** indicates significance at 5%and 1% respectively

DFF: Days to first flowering
DFPF: Days to 50% flowering
DFP: Days to first podding
DM: Days to maturity
PH: Plant Height per Plant
NPB: Number of primary branches
NSB: Number of Secondary branches
SYPP: Seed Yield Per Plant
HSW: Hundred seed weight
SM: Seed moisture
SV: Seed vigour
SP: Seed protein
NPPP: Number of pods/plant
NSPP: Number of seeds/pod

and number of secondary branches per plant (Table 1) indicating presence genetic diversity.

Based on D^2 values, the test genotypes were grouped into 7 clusters and among them, Cluster II was the largest with 72 genotypes, followed by Cluster III (6 lines), Cluster I (5 lines), while Cluster IV and VII had 2 genotypes. The genotypes contrasting for seed traits falling in different clusters, give scope for choosing appropriate parents to create new variability through hybridization/ recombination. Intra and inter cluster distances are represented in Table 3 and Fig 1. Intra cluster distance was highest in Cluster II (14.43) followed by Cluster III (6.22) whereas, inter cluster distance, varying between 12.89 (Cluster I) and 59.20 (Cluster VII), was highest between Clusters I and VII and lowest between Clusters II and III. The highest contribution for the genetic divergence was found to by number of pods per plant seed yield per plant. Among phonological traits days to first flowering contributed highest followed by days to 50 per cent flowering.

Based on cluster means, individual clusters receive the score value based on which the ranking was given to clusters to identify the superior clusters consisting of desired genotypes. It is very useful to give rankings as the rank indicates the cluster superiority based on the trait mean values of genotypes. Here, the top rank among seven clusters was recorded by Cluster IV followed by Cluster II whereas Cluster VI ranked last. Similar studies on genetic diversity wherein clustering of the genotypes was done and useful information on genotypes and superior clusters was reported Pawar *et al.* (2002), Yadav *et al.* (2003) . It is also important to decipher the information on the trait contributing maximum for the diversity. The material used in the present study was carefully chosen to give sufficient opportunity to identify the genotypes differing in seed size, which was evident in diversity analysis with 100 seed weight contributing highest (20.32%) for the genetic divergence followed by number of pods per plant (18.36%).

The cluster means of 12 characters and overall score across all the clusters are presented in the Table 4. Based on the scores of individual trait means across

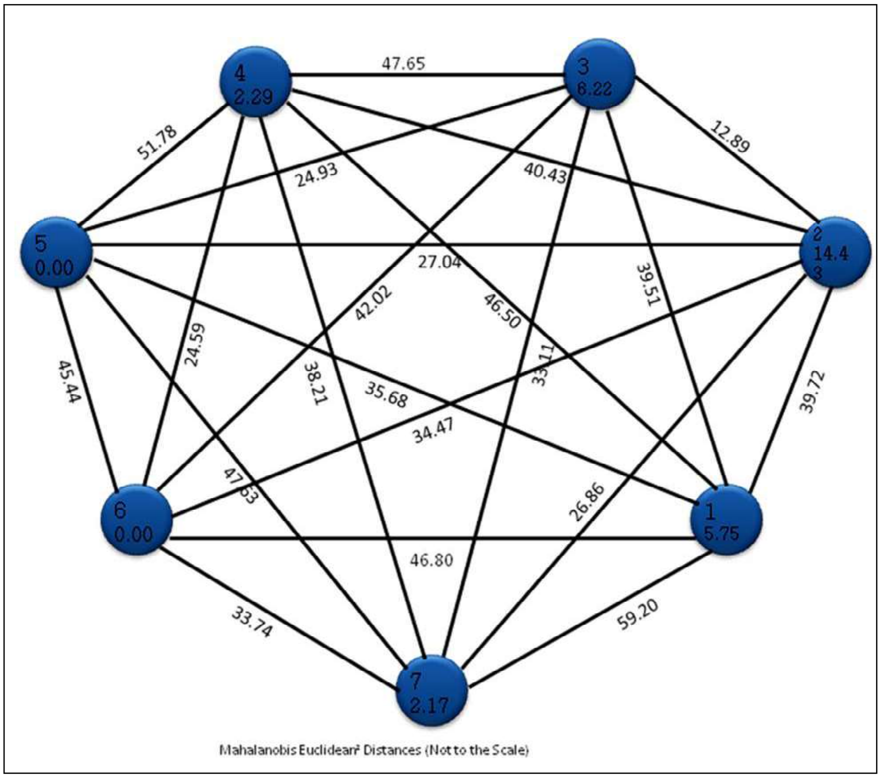

Fig. 1: Inter and intra cluster distances for 7 groups of 89 chickpea genotypes

Table 2. Grouping of chickpea genotypes based on D^2 analysis

Cluster number	Number of genotypes	Name of genotypes
I	5	JG 11, JG 16, JAKI 9218, BGD 103, A 1
II	72	ICC 637, ICC 11535, ICC 2263, ICC 1194, ICC 97114, ICC 456, ICC 10130, ICC 791, ICCV 92809, ICCV 92944, ICC 8277, ICC 16340, ICCL 86111, ICCV 05107, ICC 11551, ICC 1397, ICC 5402, ICC 5383, ICC 1205, ICC 6874, ICC 1398, ICC 1083, ICC 7305, ICC 16351, ICC 12346, ICC 9862, ICC 4954, ICC 4994, ICC 16487, ICC 12299, ICC 11449, ICC 9023, ICC 10301, ICC 5988, PUSA 261, PhG 5, ICC 12288, FLIP 97-437, S3-3, PUSA 244, ICC 14672, DG 5033, GL 22038, RSG 888, ICRISAT 3155, IPC 71, ICC 14240, ICC 10910, BGD 205, ICC 16129, KWR 108, ICC 14350, S8-17, BG 203, Local collection 1, BGD 121, NBeG 47, Dhanush, BGD 212, ICC 11617, Co 3, PhG00108, ICC 96029, BDNG 2001-21, AKG 58, ICCV 181667, BGD 223-1, ICCV 18608, ICCV 181112, ICCV 181117, Super Annigeri 1
III	6	ICC 11121, ICC 7184, P-18, Chaffa, ICC 515, ICC 11680
IV	2	ICCV 03112, ICCV 04502
V	1	ICCV 96030
VI	1	ICCV 93954
VII	2	ICC 5003, GL 12003

Table 3. Intra and inter cluster distances of seven clusters of chickpea genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	5.75	39.72	39.51	46.50	35.68	46.80	59.20
Cluster II		14.43	12.89	40.43	27.04	34.47	26.86
Cluster III			6.22	47.65	24.93	42.02	33.11
Cluster IV				2.29	51.78	24.59	38.21
Cluster V					0.00	45.44	47.63
Cluster VI						0.00	33.74
Cluster VII							2.17

Bold values indicate intra cluster D^2 values

Table 4. Cluster means for different traits in chickpea

Clusters	Characters														Productivity traits	
	DFF	DFPF	DFP	DM	PH	NPB	NSB	NPP	NSP	SYPP	HSW	SM	SV	SP	Score	Rank
1	46.06	53.86	57.91	94.54	33.90	2.29	5.01	54.25	1.02	13.26	21.70	8.86	46.23	20.51	53	3
	(4)	(3)	(4)	(4)	(5)	(3)	(4)	(4)	(2)	(6)	(6)	(2)	(4)	(2)		
2	40.00	47.50	54.25	98.25	34.05	2.64	7.25	83.35	1.00	18.05	22.60	8.69	46.20	19.89	52	2
	(6)	(6)	(6)	(2)	(4)	(1)	(1)	(1)	(4)	(2)	(5)	(3)	(5)	(6)		
3	46.50	51.50	55.75	92.75	32.65	2.08	2.80	46.40	1.05	15.07	34.70	9.24	46.62	20.48	55	4
	(3)	(5)	(5)	(6)	(6)	(5)	(7)	(6)	(1)	(5)	(1)	(1)	(1)	(3)		
4	49.75	59.25	63.25	96.25	42.60	2.64	3.78	57.65	1.05	16.57	25.60	8.48	46.56	20.94	34	1
	(2)	(2)	(2)	(3)	(2)	(1)	(5)	(3)	(1)	(3)	(2)	(5)	(2)	(1)		
5	38.75	46.50	47.75	91.50	43.75	2.64	5.60	52.00	1.00	15.73	24.20	8.85	46.11	20.26	65	6
	(7)	(7)	(7)	(7)	(1)	(1)	(3)	(5)	(5)	(4)	(4)	(4)	(6)	(4)		
6	42.00	53.50	58.25	93.00	39.45	2.18	6.55	74.60	1.00	21.40	24.85	7.76	46.23	19.97	55	4
	(5)	(4)	(3)	(5)	(3)	(4)	(2)	(2)	(5)	(1)	(3)	(7)	(4)	(7)		
7	54.25	66.50	73.00	100.2	25.25	2.33	3.70	27.95	1.00	9.81	13.30	7.81	46.44	20.20	59	5
	(1)	(1)	(1)	(1)	(7)	(2)	(6)	(7)	(5)	(7)	(7)	(6)	(3)	(5)		

Values in bracket indicates scores, Bold values indicate Rank

DFF: Days to first flowering
DM: Days to maturity
NSB: Number of Secondary branches
SM: Seed moisture
NPPP: Number of pods/plant
DFPF: Days to 50% flowering
PH: Plant Height per Plant
SYPP: Seed Yield Per Plant
SV: Seed vigour
NSPP: Number of seeds/pod
DFP: Days to first podding
NPB: Number of primary branches
HSW: Hundred seed weight
SP: Seed protein

clusters, Cluster III found to be top ranked and was followed by Cluster II, while III rank was shared by Cluster IV and Cluster V with same score values. Similarly, rank IV, V, VI and VII were designated to Clusters I, VI, VII and VIII, respectively.

In the present study, 18 genotypes were found to be bold seeded (100 SW >30g) while 10 genotypes with very small seeds (100SW <10g). Among the 18 bold seeded genotypes, ICCV 05107 and BGD 223-1 recorded more than 40g for 100SW.Considering the productivity, seed size and seed protein content, four genotypes *viz.,* NBeG 47, ICC 14672, BGD 103 and ICCV 04502were found to be promising.

Conclusion

Presence of significant difference for seed and maturity traits among the genotypes provides an opportunity to identify market suitable genotype through targeted breeding programmes. Based on cluster means, individual clusters receive the score value based on which the ranking is given to clusters to identify the superior clusters consisting of desired genotypes. The clusters can be preferred for the respective traits for which higher means are recorded. This cluster ranking can be utilized in decision making while selecting parents for hybridization programme to generate promising breeding material. In the present study genetically diverse chickpea lines were identified and promising genotypes will be exploited upon multi location evaluation. The genotypes promising for specific traits like seed size will be utilised in further breeding programme.

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