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Ponnuru Akhil
Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

GM Lal
Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

Munagala Sai kiran
Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

Genetic diversity studies in chickpea (*Cicer arietinum* L.) germplasm

Ponnuru Akhil, GM Lal and Munagala Sai Kiran

Abstract
The present investigation consists of 51 genotypes of chickpea including one check, these genotypes were obtained from ICAR – Indian Institute of Pulses Research, Kanpur, U.P. The experiment was conducted during *Rabi*, 2018-19 at Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj in RBD having three replications. The data was recorded on 15 characters to study genetic divergence using Mahalanobis D2 Statistics. Based on D2 values, 51 genotypes were grouped into eight clusters. The cluster V consisted of maximum 18 genotypes, followed by Cluster VIII and cluster II, which had 11 and 9 genotypes, respectively. Intra cluster values varied from 9.93 to 44.84. The maximum intra cluster distance was found in cluster II (44.84) followed by cluster IV (42.49), V (42.44), cluster VIII (39.26) and cluster VII (37.15). Inter cluster values varied from 31.09 to 75.10. However, maximum inter cluster distance was noticed between cluster II and cluster VII (75.10), followed by cluster V and cluster VII (70.13), cluster VI and cluster VII (68.83), cluster III and cluster VII (63.11) and cluster II and cluster IV (62.35). whereas, seed yield of the plant (44.86%) followed by protein content (22.90%), 100 seed weight (7.60%), number of seeds per plant (7.13%) and number of secondary branches per plant (6.66%) contributed maximum towards diversity. Divergence analysis revealed that highest inter cluster distance (75.10) was found between clusters II and VII indicates that there is ample scope for selection of better parents. Based on inter cluster distances and Per se performance IPC 57-29, Phule G-5, GNG 1581 and IPC 05-66 were identified for inclusion in hybridization programme for realizing desirable transgressive segregates.

Keywords: Chickpea (*Cicer arietinum* L.), cluster analysis, D^2 statistics, inter cluster distance and intra cluster distance and genetic diversity

Introduction
Chickpea *(Cicer arietinum* L.) is a self - pollinated diploid with 2n= 2x=16. Chickpea is the third most important cool season food legume crop of the world. It is a vital source of protein and vitamins for millions of people. Being a leguminous crop it fixes nitrogen biologically into the soil and enriches soil fertility. It is mainly cultivated in *Rabi* in world. India is the largest chickpea producer accounting a share of about 67% in global chickpea production with about 10.57 million ha area, 11.15 million tonnes production and 1056 kg/ha productivity (DES, Ministry of Agril. & FW (DAC & FW), Govt. of India; 2017-18* - IIIrd Adv.Est.). The area occupied under chickpea cultivation in Uttar Pradesh is 6.11 million hectares which contributes 5.78% of total chickpea area of India with a Production of 6.84 lakh ha which contributes the 6.13% of total chickpea production of India and productivity of 1013 kg/ha (DES, Ministry of Agril. & FW (DAC & FW), Govt. of India; 2017-18* - IIIrd Adv. Est.). Genetic diversity is the base for survival of plants in nature and for crop improvement. Genetic divergence among the parents plays a vital role in cultivar improvement due to more variability in segregating generations, which can be exploited for improvement (Nimbalkar *et al*., 2017) [12]. Inclusion of diverse parents in hybridization helps in isolation of superior recombinants. Mahalanobis's D2 statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis has greatly been emphasized (Murty and Arunachalam, 1966) [11]. Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters towards divergence and effectiveness of selection (Venkateswarlu, 2001; Manivannan *et al*., 2002; Bisht *et al*., 2005) [18, 10, 2]. The present study aims to find out the genetic diversity among 100 promising chickpea genotypes.

Materials and Methods
The experimental material for the present investigation consisted of 51 genotypes obtained from the ICAR – Indian institute of pulses research, Kanpur, U.P. The present experiment was conducted in randomized block design at Field Experimentation Centre,

Correspondence
Ponnuru Akhil
Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

Department of Genetics and Plant Breeding, SHUATS, Prayagraj, U.P. during *Rabi* 2018-19. Each genotype was sown in a two rows of 1 m length with spacing of 30 cm between rows and 10 cm between plants. Recommended cultural practices were followed to raise healthy crop. Five competitive plants from each genotype were randomly selected for recording observations on fifteen characters, viz., Days to 50 per cent flowering, Days to 50 per cent pod setting, Plant height (cm), Chlorophyll content, Number of primary branches per plant, Number of secondary branches per plant, Number of days to maturity, Number of pods per plant, Number of seeds per pod, Number of seeds per plant, Biological yield per plant (g), Harvest index (%), 100 Seed weight (g), Protein content (%) and Seed yield per plant (g). Data were calculated by Mahalanobis D2 statistics (1936) [9] and the genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952) [16]. Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1979). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated.

Results and Discussion
Fiftyone genotypes in the present study could be grouped into eight clusters (Table 1) on the basis of Tocher's method of clustering utilizing D^2 values. Which revealed that the genotypes varied significantly for all the characters studied indicating considerable variable in the germplasm. Clustering pattern indicated that cluster V is the largest cluster comprising 18 out of 51 genotypes. indicating that the genotypes had narrow genetic divergent among them. The similarity in the base population, from which they had been evolved, might be the cause of genetic uniformity. However, the unidirectional selection potential for one particular trait or a group of linked traits in several places may produce similar phenotypes which can be aggregated into one cluster irrespective of their geographic origin (Joshi *et al*., 2006 and Parashi *et al*., 2013) [6, 13]. On the other hand, cluster VIII comprised 11 genotypes, cluster II comprised 9 genotypes, cluster I, cluster IV and VII comprised 3 genotypes each, cluster III and cluster VII comprised 2 genotypes each. The pattern of group constellation proved the existence of significant amount of variability. Highest intra cluster distance was observed for cluster II (44.84) which comprised nine genotypes differing mainly for days to 50% flowering and number of seeds per plant. The genotype IPC 57-29 belonging to this cluster on the basis of per se performance

was recorded as highest number of seeds per plant. In the present study the highest inter cluster distance (75.10) was found between clusters II and VII followed by clusters V and VII (70.13), cluster VI and cluster VII (68.83), cluster III and cluster VII (63.11), cluster II and cluster IV (62.35), cluster IV and cluster VI (58.16) indicating that these clusters are quite divergent from each other and the genotypes belonging to them can be used for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give high heterotic response resulting in better recombinants. Similar findings have been reported by Lal *et al*., (2001) [8] and Dwevedi and Lal (2001) [8]. The genotypes contained in cluster II, V, VI and cluster VII seem to be quite promising for many of the characters like day to 50% flowering, pods per plant, 100 Seed weight, number of seeds per plant, harvest index, biological yield per plant and seed yield per plant. Mean performance of a cluster is the mean of over all values of individual correlated variables of all genotypes included in that cluster. Cluster II recorded maximum valued for days to 50% flowering number of seeds per plant. Cluster III recorded maximum values for chlorophyll content, number of days to maturity and harvest index. Cluster IV recorded maximum values for number of primary branches per plant, number of secondary branches per plant, number of pods per plant and protein content. Cluster V recorded maximum values for days to 50% pod setting. Cluster VI recorded maximum values for plant height and number of seeds per pod. Similarly, the genotypes of cluster VII shown increased mean values for 100-seed weight. Cluster VIII recorded maximum values for biological yield and seed yield per plant. The present study revealed that seed yield per plant (44.86%), protein content (22.90%), 100 seed weight (7.60%), number of seed per plant (7.13%) and number of secondary branches per plant (6.66%) contributed to 89.15% of total divergence (Table 2) followed by number of pods per plant (4.15%) and number of primary branches per plant (3.45%). Parashi *et al*., (2013) [13] reported number of seeds per plant contributed maximum towards genetic diversity. Pahre *et al*., (2014) and Kuldeep *et al*., (2015) [7] reported that 100 seed weight and number of pods per plant contributed maximum towards genetic diversity. Based on inter cluster distances and Per se performance IPC 57-29, Phule G-5, GNG 1581 and IPC 05-66 were identified for inclusion in hybridization programme for realizing desirable transgressive segregates. This finding is in accordance with that of Dwevedi and Lal (2009) [3] and Gaikwad *et al*., (2014) [5].

Table 1: Composition of Fiftyone chickpea genotypes into different clusters

Clusters	Number of genotypes	Genotypes included
I	3	IPC 08-103(Green); JG.3.14.16; ILC 3279
II	9	JG-130; Phule G-5; HC-5; ICC 4958; JGM 7; IPC 57-29; IPC 05-66; L 550; IPC-71
III	2	CSJ 512; IPC 05-62
IV	3	Pusa 209; IPC 05-59; IPCK 06 -78
V	18	IPC 05-28; CSG 8962; IPC 10-134; EC 556270; BGD -72; PG 96006; BGD -9971; BG 212; IPC 04 -52; IPC 04–01; JG-37; ICC5439; RSG 931; GNG 2226; IPC 2K-2000-25; KPG-59; NBeG 47; ICCV 16303.
VI	2	IPC 06-11; IPC 11-85
VII	3	GNG1581; IPCK 09-165; Pusa 362
VIII	11	DEP 92-3; JG-14; JAKI-9218; IPC 06-77; JG-24; ICC-1205; IPC 10-72; BG 1053; IPCK 11-201; IPCK 02-29; IPCK 9767.

Table 2: Cluster means of different characters to genetic diversity in chickpea

Characters / Clusters	DF	DP	PH	CC	NPB	NSB	DM	NPP	NSP	TNSP	BY	HI	TW	PC	SYP
I	81.00	100.11	59.31	55.51	2.00	2.93	122.56	23.02	0.89	25.76	11.87	42.91	22.22	18.80	5.76
II	81.52	101.52	58.86	64.02	2.27	4.37	119.37	37.39	1.78	64.43	13.64	44.14	17.22	19.09	6.23
III	81.17	101.33	61.00	73.43	2.00	3.13	123.67	20.77	1.00	28.50	9.80	46.71	17.00	19.81	4.57
IV	80.89	100.78	65.02	58.87	2.93	7.40	120.11	69.62	1.00	35.96	15.11	45.41	28.00	22.57	6.87
V	81.28	101.54	60.26	53.93	2.36	4.08	120.44	36.96	1.50	63.56	15.44	46.19	17.67	18.76	7.20
VI	81.00	100.50	67.50	54.83	2.00	3.07	122.33	28.87	2.00	38.60	11.07	46.68	17.00	18.45	5.17
VII	81.00	101.00	66.07	66.29	2.27	3.93	121.44	35.09	1.33	29.84	11.16	43.01	34.67	22.09	4.80
VIII	81.03	101.36	66.54	58.38	2.44	4.39	121.64	32.73	1.36	48.73	15.51	45.85	22.27	20.53	7.32
Total	648.88	808.14	504.55	485.26	18.26	33.31	971.56	284.45	10.86	335.38	103.59	360.90	176.05	160.09	47.91

DF = Days to 50% flowering, DP = Days to 50% pod setting, PH = Plant height (cm), CC = Chlorophyll content, NPB = Number of primary branches, NSB = Number of secondary branches, DM = Days to maturity, NPP = Number of pods per plant, NSP = Number of seeds per pod, TNSP = Total number of seeds per plant, By = Biological yield, HI = Harvest index (%), TW = Test weight (gm), PC = Protein content, SYP = Seed yield per plant.

Table 3: Intra (diagonal) and inter cluster average distances (D^2) for different characters

Cluster	I	II	III	IV	V	VI	VII	VIII
I	14.89	50.41	31.09	42.64	45.34	37.60	40.05	34.29
II		44.84	37.31	62.35	42.75	33.93	75.10	46.17
III			9.93	55.13	36.42	18.94	63.11	35.24
IV				42.49	57.96	58.16	47.22	47.38
V					42.44	33.34	70.13	42.82
VI						11.67	68.83	36.89
VII							37.15	56.05
VIII								39.26

Table 4: Percentage contribution of individual characters towards total divergence

Characters	No. of First Rank	% Contribution
days to 50% flowering	2	0.1569
days to 50% pod setting	0	0.0000
plant height	0	0.0000
chlorophyll content	8	0.6275
primary branches	44	3.4510
secondary branches	85	6.6667
no of days to maturity	6	0.4706
no of pods per plant	53	4.1569
no of seeds per pod	1	0.0784
no of seeds per plant	91	7.1373
biological yield	13	1.0196
harvest index	11	0.8627
100 seed weight	97	7.6078
protein content	292	22.9020
seed yield per plot	572	44.8627
Total	1275	100

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