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Genetic diversity analysis in chickpea (*Cicer arietinum* L.) grown under rainfed and irrigated conditions for quality and yield attributing traits

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ABSTRACT

Genetic diversity among 30 chickpea genotypes was assessed for quality and yield attributing and traits at Regional Agricultural Research Station, Nandyal during *rabi* 2016-17 under both rainfed and irrigated conditions individually. The genotypes were grown in randomized block design (RBD) with three replications each. Genetic diversity study grouped 30 chickpea genotypes into five different clusters under both the tested environments. 100 seed weight followed by cooking time for soaked seeds contributed maximum towards diversity under rainfed as well as irrigated conditions. Inter cluster average D² values stretched between 9.32 and 21.96 under rain fed condition, while it was comparatively lower and varied from 3.77 to 15.76 under irrigated condition. Cluster II under rainfed and cluster V under irrigated were identified to be the most divergent clusters. Under irrigated, genotype RVSSG- 37 from cluster II, NBeG-840, CSJK- 25, CSJK- 24, MNK- 1, NBeG-459 from cluster III, genotype NBeG-833 from cluster IV, KAK- 2, Vihar, ICCV- 15308 from cluster V and under irrigated condition, the genotype NBeG 831 of cluster II, RVSSG- 37, NBeG-459, CSJK- 25, NBeG-840, PKV-4 from cluster III, KAK- 2 from cluster IV and Vihar from cluster V were identified to be superior and were from genetically divergent clusters so could be used in hybridization programme to produce transgressive segregants.

Key words: Cleistogamous, Clusters, Supplemental irrigation, Phyto chemicals, Subsistence, Transgressive segregants.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is currently the second most important food legume in the world after common bean Gowda *et al.* (2015). It is a cleistogamous, self-pollinated crop with chromosomal complement 2n=2x=16 and known to be originated in south-eastern Turkey from where, it spread to other parts of the world. *Cicer reticulatum* is the progenitor of existing cultivated chickpea. It is a highly nutritious grain legume and an important source of energy, protein (20-22%), minerals (Zn, K, Fe and P), vitamins (Thiamine and Niacin), fibre and other potentially health beneficial phyto chemicals Geervani (1991).

Globally, chickpea is grown in an area of 14.80 million ha. with a production of 14.23 million tons and a productivity of 962 kg per ha. India is the largest producer of chickpea with a production of 9.98 million tons from an area of 10.74 million ha. with a productivity of 920 kg per ha FAOSTAT (2016). Madhya Pradesh is the single largest producer in India, accounting for over 40 percent of total production. In Andhra Pradesh, the area under chickpea cultivation has increased dramatically from 71 thousand ha (1992-93) to 4.71 lakh ha (2015-16) with the production of 5.00 lakh tones touching the highest productivity of 1061 kg per ha (Project Coordinator's Report, AICRP on Chickpea, 2015-16).

In India demand for extra-large seeded types met through import mainly from Mexico and Turkey as the introduced extra-large seeded varieties are poorly adapted Yadav et al. (2004). Farmers also showing interest in largeseeded kabuli chickpea growing as the market prices of these kabuli types are higher by 150 to 200% compared to desi varieties. Breeding and selection for new large-seeded kabuli chickpea varieties, therefore, is an urgent requirement to meet the growing farmer's interest. Also, this situation offers to raise the status of chickpea from a poor farmer's subsistence crop to a cash crop Kashiwagi et al. (2007). Hence, there is a need to develop large-seeded kabuli types which are adaptable for wide range of environmental conditions. The international trade recognizes three groups based on seed diameter in Europe and Australia viz., large seeded (>9 mm), medium seeded (8-9 mm) and small seeded (7-8 mm).

Early maturity is important in chickpea for its adaptation to short-season environments and for escaping terminal drought, which is the main constraint to chickpea productivity in Andhra Pradesh. So, there is a need to develop varieties for extra-large seeded and high yielding cultivars which are suitable for rainfed condition and also varieties which respond to one or two supplemental irrigations to meet the demand and to make chickpea cultivation more profitable.

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MATERIALS AND METHODS

The experiment was conducted at Regional Agricultural Research Station, Nandyal with 30 chickpea genotypes during rabi 2016-17 in randomized block design (RBD) with three replications each under rainfed and irrigated conditions (two supplemental irrigations were given at 35 and 55 days after sowing). Each genotype was sown in a single row in a plot of 4m row length at a spacing of 30 cm between rows and 10 cm between plants within the row. Observations were recorded on 19 traits viz., plant height (cm), days to 50 per cent flowering, days to physiological maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed diameter (mm), SCMR, number of seeds per plant, harvest index (%), seed yield (g), 100 seed weight (g), shoot biomass (g), protein content (%), 100 grain volume (ml), water absorption after soaking (g/seed), volume expansion after soaking (ml/seed), cooking time for soaked seeds and cooking time for raw seeds. Data were subjected to divergence analysis using Mahalanobis D² statistic (1936) and the genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

Selection of most desirable and genetically diverse parents for running a successful hybridization programme requires the information of divergence existing in the available material. These genetically diverse genotypes are likely to produce heterotic effect and superior segregants when involved in hybridization for the crop improvement programs. Therefore, an attempt was made to identify the most divergent lines among 30 genotypes of *kabuli* chickpeas through multivariate analysis (Mahalanobis D²). The results were discussed here under.

The average inter-cluster distance values ranged from 9.32 to 21.96 and 3.77 to 15.76 under rainfed and irrigated conditions respectively (Table 1). Under rainfed condition, the maximum inter-cluster distance was observed between cluster III and V (21.96) followed by cluster III and IV (19.12). While under irrigated condition, maximum inter-cluster distance was observed between cluster III and V (15.76) followed by cluster II and V (15.64) indicating that the genotypes included in these clusters had wide genetic divergence. So, genotypes of clusters III and V under both conditions could be used as parents for crossing programme to obtain high heterotic effect and transgressive segregants with high variability. Inter cluster distance values were comparatively high under rainfed situation indicating the differential expressivity of genotypes under stress conditions. Maximum intra-cluster distance was noticed in cluster II (7.88) followed by cluster III (7.73) and cluster I (6.59) under rainfed condition while in cluster V (8.01) followed by cluster I (6.35) and cluster III (4.43) under irrigated condition. Maximum intra cluster distance indicated the presence of greater diversity among the genotypes allocated in those respective clusters.

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Cluster	Ι		П		Ι	II	IV		V	
	rainfed	irrigated	r	i	r	i	r	i	r	i
I	6.59	6.35	10.57	7.85	9.32	8.25	15.67	7.57	17.67	11.96
II			7.88	0	15.03	3.77	11.53	10.86	11.47	15.64
III					7.73	4.43	19.12	10.62	21.96	15.76
IV							0	0	10.56	12.01
V									0	8.01

Table 1: Average inter and intra cluster distances in 30 chickpea genotypes under rainfed and irrigated conditions during rabi 2016-17.

Table 2: Distribution of 30 genotypes of chickpea into different clusters under rainfed, irrigated conditions during rabi 2016-17.

Number	of genotypes	Genotype(s)						
rainfed	irrigated	rainfed	irrigated					
17	20	NBeG-839, NBeG-843, NBeG-845,	PG- 12407, ICCV- 14507, NBeG-805,					
		NBeG-832, NBeG-830, NBeG-841,	NBeG-119, NBeG-460, NBeG-846,					
		NBeG-834, NBeG-838, NBeG-842,	NBeG-831, NBeG-834, NBeG-830,					
		MNK- 1, PG- 12407, NBeG-460, NBeG-	NBeG-836, NBeG-839, NBeG-832,					
		805, NBeG-731, NBeG-846, PG- 05107,	NBeG-843, NBeG-838, NBeG-842, PG-					
		CSJK- 24	05107, NBeG-731, PKV- 4, NBeG-841,					
			NBeG-845					
6	1	NBeG-119, ICCV- 15308, ICCV- 14507,	RVSSG- 37					
		NBeG-831, NBeG-836, NBeG-833						
5	5	RVSSG- 37, PKV- 4, NBeG-459, CSJK-	NBeG-840, CSJK- 25, CSJK- 24, MNK-					
		25, NBeG-840	1, NBeG-459					
1	1	KAK- 2	NBeG-833					
1	3	Vihar	KAK- 2, Vihar, ICCV- 15308					
	Number rainfed 17 6 5 1 1	Number of genotypes rainfed irrigated 17 20 6 1 5 5 1 1 1 3	Number of genotypes Genoty rainfed irrigated rainfed 17 20 NBeG-839, NBeG-843, NBeG-845, NBeG-832, NBeG-830, NBeG-841, NBeG-834, NBeG-834, NBeG-838, NBeG-842, MNK- 1, PG- 12407, NBeG-460, NBeG-805, NBeG-731, NBeG-846, PG- 05107, CSJK- 24 6 1 NBeG-119, ICCV- 15308, ICCV- 14507, NBeG-831, NBeG-831, NBeG-833, S5 5 5 RVSSG- 37, PKV- 4, NBeG-459, CSJK-25, NBeG-840 1 1 KAK- 2 1 3 Vihar					

The distribution of the 30 genotypes into different clusters using Toucher's method was presented in Table 2 under rainfed and irrigated conditions. Cluster I had maximum of 17 genotypes followed by cluster II with six and cluster III with five genotypes. The clusters IV and V had single genotype of each under rainfed situation. Cluster I comprised of maximum of 20 genotypes followed by cluster III with five and cluster V with three genotypes, whereas clusters II and IV had single genotype each under irrigated condition. This indicated that there was no association among geographical distribution of genotypes and their divergence. It might be attributed to the free exchange of genetic material among the breeders from different places or unidirectional selection adopted by breeders while exercising selection process. The highest number of genotypes were placed in cluster I under rainfed (17) and irrigated (20) conditions and showed less divergence, this might be due to some similar characteristics or common parentage among the genotypes which led to their grouping in the same cluster. These results are similar to the earlier findings of Jeena and Arora (2002); Jeena et al. (2005) and Parameshwarappa et al. (2012).

The number of times each character appeared first and their relative contribution towards genetic divergence in percentage was presented in Table 3 under rainfed and irrigated situations. 100 seed weight among the studied traits contributed maximum of 42.30 per cent under rainfed and 30.57 per cent under irrigated by ranking first for 184 and 133 times under rainfed and irrigated conditions respectively followed by cooking time for soaked seeds (rainfed : 17.7 per cent by ranking first for 77 times and irrigated : 27.13 per cent by ranking first for 118 times). Greater contribution of 100 seed weight towards genetic divergence of the existing study is in accordance to the earlier findings of Jeethava *et al.* (2000); Dwivedi and Gaibriyal (2009); Hahid *et al.* (2010); Jivani *et al.* (2013) and Jayalakshmi *et al.* (2014). The character 100 seed weight could be considered as prime trait during selection.

Under rainfed condition (Table 4), cluster V recorded higher means for seven traits *viz.*, number of primary branches (4.13), number of secondary branches (14), number of pods per plant (23), number of seeds per plant (25.67), shoot biomass (14.47), protein content (22.47) and seed yield (7.5). Whereas genotypes of cluster III recorded high means for six traits *viz.*, plant height (51.09), 100 seed weight (62.57), seed diameter (8.81), 100 grain volume (60.15), water absorption after soaking (0.68) and volume expansion after soaking (0.63). Harvest index (53.13) was higher in genotypes of cluster IV and SCMR was highest (52.68) in cluster II.

Under irrigated condition (Table 4), higher means were recorded by the genotypes of cluster III for five traits *viz.*, 100 seed weight (65.56), seed diameter (8.75), 100 grain volume (64.39), water absorption after soaking (0.67) and volume expansion after soaking (0.66). Number of primary branches (3.91), number of secondary branches (13.22), number of pods per plant (21.78) and number of seeds per plant (21.44) were high in genotypes of cluster V. High SCMR (58.73), shoot biomass (18.80) and seed yield (9) values were noted in genotypes of cluster IV. Plant height (60), harvest index (53.1) and protein content (19.83) were higher in cluster II.

 Table 3: Relative contribution of 18 characters for genetic diversity in 30 chickpea genotypes under rainfed, irrigated conditions during rabi 2016-17.

Character	Times ra	nked First	Contribution (%)			
	rainfed	irrigated	rainfed	irrigated		
Days to 50% flowering	0	3	0.0%	0.69%		
Days to maturity	2	6	0.5%	1.38%		
Plant height (cm)	4	2	0.9%	0.46%		
No. of primary branches	1	0	0.2%	0.00%		
No. of secondary branches	0	0	0.0%	0.00%		
SCMR	0	0	0.0%	0.00%		
No. of pods per plant	0	0	0.0%	0.00%		
No. of seeds per plant	0	0	0.0%	0.00%		
Shoot biomass (g/plant)	21	7	4.8%	1.61%		
Harvest index (%)	60	8	13.8%	1.84%		
100 seed weight (g)	184	133	42.3%	30.57%		
Seed diameter (mm)	5	2	1.2%	0.46%		
100 grain volume (ml)	0	9	0.0%	2.07%		
Protein content (%)	12	90	2.8%	20.69%		
Water absorption after soaking (g/seed)	48	24	11.0%	5.52%		
Volume expansion after soaking (ml/seed)	11	31	2.5%	7.13%		
Cooking time for soaked seeds (min)	77	118	17.7%	27.13%		
Seed yield(g/plant)	10	2	2.3%	0.46%		

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Table 4	: Cluster means	for 18	characters in	30 cl	hickpea	genotypes	under rai	infed,	irrigated	conditions	during	rabi	2016-17.
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Character	Cluster Number										
-	Ι			Ш		III		IV		V	
	rainfed	irrigated	rainfed	irrigated	rainfed	irrigated	rainfed	irrigated	rainfed	irrigated	
Days to 50% flowering	36.51	37.12	36.06	34.00	34.2	37.33	46.67	37.67	48.33	46.89	
Days to maturity	77.92	80.93	77.06	85.00	81.00	83.73	83.33	76.67	84.00	87.22	
Plant height (cm)	48.89	52.74	47.64	60.10	51.09	51.69	34.2	45.37	41.17	42.53	
No. of primary branches	3.15	3.50	3.18	3.60	3.15	3.12	3.33	3.40	4.13	3.91	
No. of secondary branches	10.14	11.05	9.22	10.67	11.13	10.73	9.33	10.00	14.00	13.22	
SCMR	51.74	56.16	52.68	55.70	51.03	54.79	48.27	58.73	47.73	55.71	
No. of pods per plant	11.04	13.97	15.94	12.33	10.33	13.53	14.67	18.67	23.00	21.78	
No. of seeds per plant	13.57	15.63	18.89	12.33	12.4	16.00	17.33	20.33	25.67	21.44	
Shoot biomass (g/plant)	10.52	13.97	11.73	12.13	10.48	14.89	7.63	18.80	14.47	13.67	
Harvest index (%)	40.29	45.18	49.57	53.10	38.17	45.37	53.13	48.37	52.00	49.41	
100 seed weight (g)	56.28	57.38	47.72	64.17	62.57	65.56	35.87	57.50	37.23	37.77	
Seed diameter (mm)	8.59	8.50	8.04	8.70	8.81	8.75	7.27	8.67	7.23	7.90	
100 grain volume (ml)	54.15	56.16	44.66	63.23	60.15	64.39	33.63	55.57	35.57	36.29	
Protein content (%)	21.32	18.63	19.12	19.83	20.87	19.20	15.4	14.73	22.47	19.47	
Water absorption after soaking	0.58	0.57	0.47	0.66	0.68	0.67	0.34	0.50	0.39	0.38	
(g/seed)											
Volume expansion after soaking	0.56	0.56	0.45	0.62	0.63	0.66	0.30	0.50	0.31	0.33	
(ml/seed)											
Cooking time for soaked seeds	50.43	53.73	45.22	72.67	66.6	73.00	40.00	54.33	41.67	41.89	
(min)											
Seed yield(g/plant)	4.19	6.27	5.76	6.30	4.01	6.65	4.07	9.00	7.50	6.86	

CONCLUSION

The genotype NBeG 831 from cluster II, RVSSG-37, NBeG-459, CSJK- 25, NBeG-840, PKV-4 from cluster III, KAK- 2 from cluster IV and Vihar from cluster V under rainfed condition were found to be promising. However, under irrigated, genotype RVSSG- 37 from cluster II, NBeG-840, CSJK- 25, CSJK- 24, MNK- 1, NBeG-459 from cluster III, genotype NBeG-833 from cluster IV, KAK- 2, Vihar, ICCV- 15308 from cluster V identified to be superior. These genotypes were found from genetically divergent clusters characterized by cluster means for their respective characters and these could be used in hybridization programme to produce transgressive segregants. Under both the conditions, genotypes NBeG-459, CSJK- 25, NBeG-840 from cluster III and Vihar from cluster V found to be promising to utilize for genetic improvement of seed size besides yield.

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