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Genetic diversity analysis in genotypes of chickpea (*Cicer arietinum* L.) suitable for mechanical harvesting

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Abstract
This experiment was conducted during *rabi* 2017-18 using randomized complete block design with three replications. Forty one chickpea (*Cicer arietinum* L.) genotypes including three check was used in the experiment for genetic diversity analysis and data were recorded on eleven quantitative traits and one morphological trait. Inter and intra cluster distances, cluster mean and contribution of each characters towards divergence was analysed. This analysis indicated presence of adequate genetic diversity among investigated genotypes and found H 14-01, NBeG 865 and RVSSG 66 as highly diverse genotypes. Hence, these genotypes can be utilized as parents in future hybridization programmes in chickpea genotypes.

Keywords: Chickpea, divergence, genetic diversity, genotypes

Introduction
Chickpea [(*Cicer arietinum* L.) 2n=2x=16] belongs to genus *Cicer*, family fabaceae, subfamily papilionaceae. It is an annual, self-pollinating, diploid pulse crop with a genome size of ~738 Mbp. On the basis of cultivated area, chickpea ranks 19th among the crops, and is grown in 34 countries of the world. It is an important pulse crop of India, grown in an area of 10.76 million ha with the annual production of 11.16 million tonnes and an average productivity of 1037 kg ha^{-1}. In Chhattisgarh, it is cultivated in around 0.307 million ha with an average productivity of 1171 kg ha^{-1} (Anonymous, 2018). In general chickpea is harvested manually in India because of lack of varieties suited to mechanical harvesting. Availability of chickpea varieties suited to mechanical harvesting will reduce production cost and attract farmers to chickpea cultivation. In chickpea first pod height at ≥30cm from surface has been considered as desirable trait for mechanical harvesting in accordance with erect to semi erect plant type growth habit. Such plant types can accommodate more number of plants per unit area and may also give higher seed yield. Diversity analysis helps in understanding about the nature and magnitude of diversity present between various genotypes. The current study will be conducted to obtain total genetic divergence which might be helpful in selecting genotypes for better yield and also suitable for mechanical harvesting.

Materials and Methods
The experiment was conducted in randomized block design. In the experiment 41 genotypes including three check namely BGM-2, NBeG-47 and Indira Chana-1 were taken for study which were replicated into 3 blocks. Each block was divided into various plots of size 4.8 m^2 each. These plots were divided into 4 rows of length 4 m. A spacing of 30 cm was maintained between two rows and 10 cm space was given between two plants. Fertilizer was applied in the ratio of 20 N: 40 P_2O_5: 20 K_2O kg/ha. Genetic diversity analysis was done by using formula proposed by Mahalanobis (1936) [7]. Mahalanobis D^2 and clustering was done according to Tocher's method as described by Rao (1952) [10].

Results and Discussion
ANOVA indicated significant MSS for several traits due to genotypes barred no. of primary branches plant^{-1} and no. of secondary branches plant^{-1}. As per the result obtained on ANOVA presence of abundant variability was noticed which will be helpful in further analysis on the material under investigation.

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All the 41 genotypes were grouped into 8 clusters exhibiting significant variability for selecting genotypes for further breeding programmes. Cluster I and II were noticed as biggest cluster with 19 and 10 genotypes respectively. While, cluster III, IV and V comprised of 4, 3 and 2 genotypes respectively. On the other hand cluster VI, VII and VIII comprising 1 genotype in each.

The cluster mean for different characters are presented in Table 2. The observations obtained from overall cluster means indicated that, cluster VI have high cluster mean for no. of primary branches plant[-1] (3.2), no. of secondary branches plant[-1] (5.4), pods plant[-1] (52.0), biological yield plant[-1] (27.2), harvest index (66.0), 100-seed weight (34.2) and seed yield plant[-1] (17.8). Cluster V had shown high value of cluster mean for days to 50% flowering (65.5), days to maturity (103.5) and height of first pod from ground level (37.2). Cluster VIII had shown high cluster mean for plant height (64.7).

Regarding the contribution of different characters towards diversity, the unity of D^2 analysis is enhanced by its estimate the relative contribution of different traits towards genetic divergence (Table 3). The present study revealed that days to 50% flowering (29.15%) had highest contribution towards genetic divergence followed by biological yield plant[-1] (15.21%), pods plant[-1] (12.69%) and days to maturity (12.19%). Other characters *viz.,* height of 1st pod (8.16%), 100-seed weight (6.33%), no. of primary branches plant[-1] (5.03%), seed yield plant[-1] (4.00%), no. of secondary branches plant[-1] (3.76%) and plant height (3.43%) showed low percentage of contribution, whereas harvest index exhibited no contribution towards divergence.

The experimental result showed that cluster V exhibited highest intra cluster distance (50.7), followed by cluster I (37.8), III (34.5), II (34.2) and IV (33.4). The highest inter cluster distance was observed between genotypes of cluster V and VIII (288.0), followed by III and VIII (267.2), VI and VIII (231.9), V and VII (211.5), VII and VIII (196.0), I and VIII (181.9), IV and V (173.2), VI and VII (163.4). The low inter cluster distance was found between cluster II and IV (72.0), cluster I and VI (71.2), cluster I and V (66.6), cluster I and III (60.7), cluster III and V (58.1) and cluster V and VII (54.0) in descending order of magnitude. The value of inter cluster and intra cluster distances are presented in table 4.

These findings are in accordance with that of Dwevedi *et al.,* 2011, Wadikar *et al.,* 2010 [12], Akhtar *et al.,* 2011 [1], Jayalakshmi *et al.,* 2012 [6], Jain *et al.,* 2013, Pandey *et al.,* 2013 [8], Puri *et al.,* 2013 [9] and Gaikwad *et al.,* 2014 [4].

Conclusion
On the basis of result obtained we found that cluster V and VIII showed maximum genetic diversity and hence genotypes belonging to these clusters *viz.,* H 14-04, NBeG 865 and VIII RVSSG 66 can be utilized as parents for future hybridization programme.

Table 1: List of genotypes used in the experiment

Entry No.	Entries	Pedigree
1	BGM-2 (ch)	Mutant of Annageri 1
2	NBeG-47 (ch)	ICCV 2 X PDG 84-16
3	Indira Chana-1 (ch)	JG 74 X ICCL 83105
4	RG 2010-10-03	RG 06-04 X RG 06-03
5	RG 2016-01	PG-92-97 X *C. reticulata*
6	RG 2016-14	ICCV 93001 X JAKI 9218
7	RG 2016-19	(ICCC 37 X JG 130) X ICC 4958
8	RG 2016-20	(ICCC 37 X JG 130) X ICC 4958
9	RG 2016-22	(ICCV 93001 X JAKI 9218) X BG 256
10	RG 2016-75	Selection from ICC 269703
11	RG 2016-84	Selection from RG 2015-05
12	RG 2016-114	Selection from ICCV 11501
13	RG 2016-115	Selection from ICCV 11501
14	RVSSG 65	JAKI 9218 X ICCV 00108
15	DVGB 212	ICCV 03112 X ICCV 93954
16	GL 15039	GL 22044 X GL 24021
17	RG 2011-02	Selection from IPG-2008-24
18	H 14-21	HC 5 X ICC 4958
19	JG 2017-48	(JG 315 X ICCV 96029) 48
20	BG-3094	BG 362 X (BGD 9812 X HC 5)
21	CSJ 944	RSG 974 X RSG 907
22	Phule G 1005-5-4	Phule G 00108 X Phule G 96006
23	CG-Chana-2	PG-92-97 X *C. reticulata*
24	CSJ 1044	RSG 888 X HC 5
25	RG-2015-04	GJG 107 X Vaibhav
26	PG 144	PG 037 X JSC 47
27	GNG 2300	HC 5 X GNG 663
28	NBeG 868	ICCV 03112 X JAKI 9218
29	JG 16	ICCC 42 X ICCV-10
30	H 14-04	H 03-56 X H 04-31
31	RVSSG -64	BGD 112 X JG 16
32	DBGV 216	ICCV 9107 X ICCV 10
33	NBeG 865	ICCV 10 X ICC 10369
34	BG 3093	BGD 9812 X HC 5
35	Phule G 1012-15	Selection from ICCV 09112
36	RG-2010-10-5	RG 2006-04 X RG 2006-03
37	PG 209	ICCV 2 X PBG 5
38	RVSSG 66	Sonali X ICCV 00108
39	IPC 2014-28	HC 5 X WR 315
40	GL 15003	PBG 1 X ICC 424318
41	RG 2015-08	PDE-90-2E X JG 97

Table 2: Analysis of variance for different characters in chickpea genotypes

MEAN SUM OF SQUARES											
Source of variation	Degree of freedom	DF	DM	PH	PB	SB	HFP	PP	BY	HI	SW	SY
Replications	2	8.593	4.545	6.292	0.205	0.024	2.570	10.252	5.322	68.349	4.541	0.690
Treatments	40	90.684**	45.007**	76.834**	0.435**	1.235**	31.899**	154.417**	29.138**	111.322**	45.574**	15.706**
Error	80	3.243	4.853	18.819	0.093	0.240	3.957	13.894	4.101	49.841	6.716	1.602

Table 3: Grouping of chickpea genotypes into different clusters

Cluster	No. of genotypes	Name of genotypes
I	19	CSJ 944, RG-2010-10-5, GL 15039, BG-3094, PG 144, RG-2016-75, BGM-2, RG-2011-02, PG 209, RVSSG 65, RG-2016-22, DVGB 212, RG-2015-04, H 14-21, RG-2015-08, CSJ 1044, RG-2016-84, CG-Chana-2
II	10	Indira Chana-1, RG-2016-114, JG 16, RG-2016-19, RG-2016-115, RG-2016-01, NBeG-47, RG-2016-20, RG-2010-10-03, RG-2016-14
III	4	RVSSG-64, GL 15003, IPC 2014-28, GNG 2300
IV	3	Phule G 1005-5-4, Phule G 1012-15, JG 2017-48
V	2	H 14-04, NBeG 865
VI	1	DBGV 216
VII	1	BG 3093
VIII	1	RVSSG 66

Table 4: Cluster mean for yield and its component traits of chickpea genotypes

Cluster	DF	DM	PH	PB	SB	HFP	PP	BY	HI	SW	SY
I	61.0	98.2	58.0	2.7	4.2	34.0	36.2	22.7	53.1	25.7	12.0
II	54.6	92.7	58.1	3.0	4.8	32.9	35.0	24.7	59.1	28.1	14.6
III	63.3	101.0	57.6	2.9	4.8	32.4	31.3	17.0	52.8	20.9	8.9
IV	50.3	97.1	50.8	2.6	4.0	28.3	46.1	20.8	64.3	24.2	13.2
V	65.5	103.5	60.4	3.1	4.3	37.2	27.9	18.0	59.3	28.3	10.6
VI	60.3	99.6	52.9	3.2	5.4	30.2	52.0	27.2	66.0	34.2	17.8
VII	50.0	94.6	64.7	2.4	3.6	29.6	48.6	16.0	61.4	23.9	9.0
VIII	44.0	95.0	54.9	3.1	3.6	30.6	24.3	24.6	50.1	25.8	12.4

Table 5: Contribution of different characters towards divergence in chickpea genotypes

S. No.	Character	Contribution towards divergence (%)
1.	Days to 50% flowering	29.15
2.	Days to maturity	12.19
3.	Plant height	3.43
4.	Primary branches plant[-1]	5.03
5.	Secondary branches plant[-1]	3.76
6.	Height of 1st pod	8.16
7.	Pods plant[-1]	12.69
8.	Biological yield	15.21
9.	Harvest index	0
10.	100-seed weight	6.33
11.	Seed yield	4.00

Table 6: Average inter and intra cluster distance in chickpea genotypes

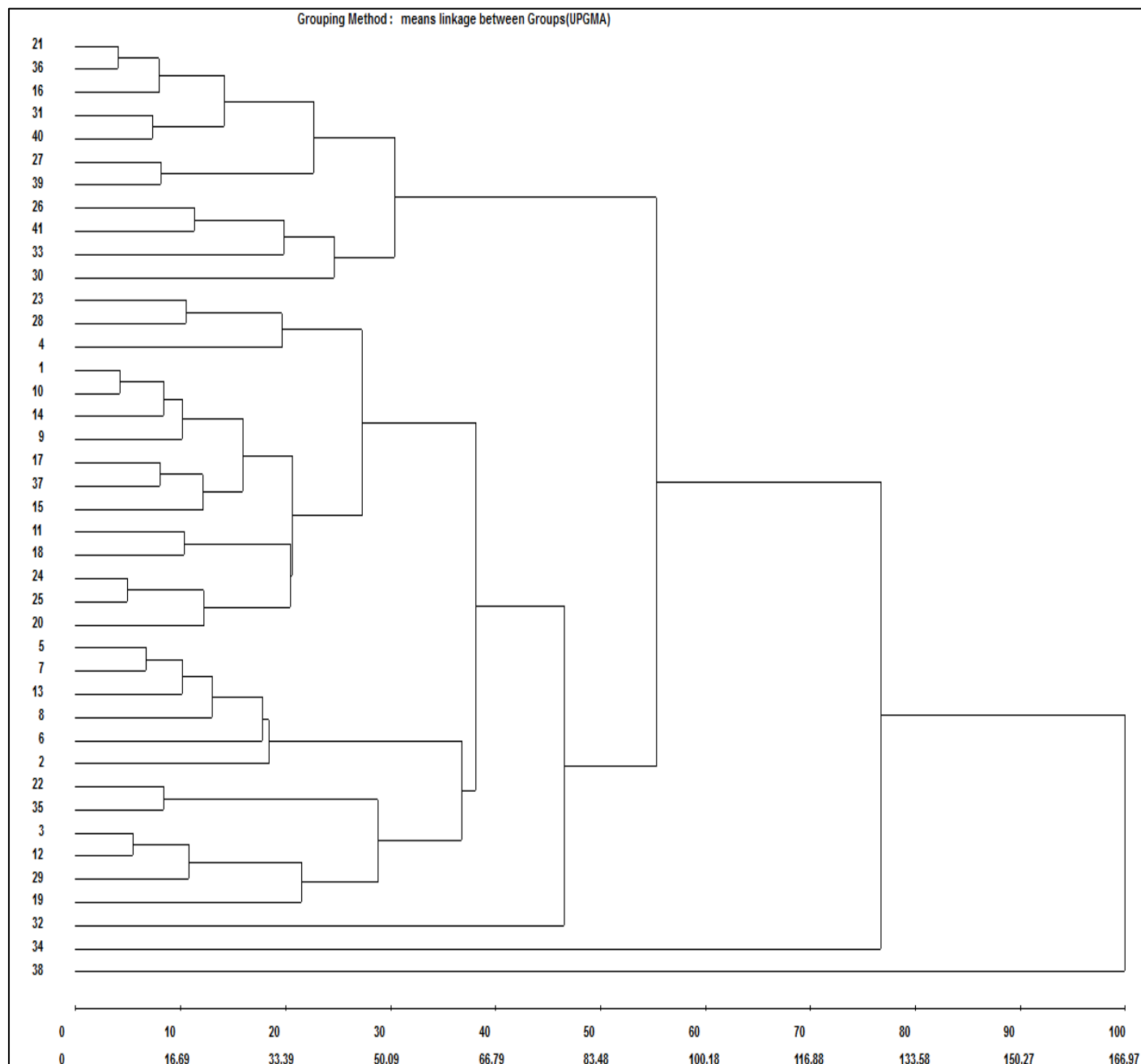| Cluster	I	II	III	IV	V	VI	VII	VIII
I	37.8	73.9	60.7	84.7	66.6	71.2	120.2	181.9
II		34.2	136.5	72.0	144.1	84.7	142.5	82.1
III			34.5	119.5	58.1	117.3	133.3	267.2
IV				33.4	173.2	94.0	54.0	109.2
V					50.7	109.3	211.5	288.0
VI						0.0	163.4	231.9
VII							0.0	196.0
VIII								0.0

Fig 1: Grouping of genotypes into different clusters

References

1. Akhtar LH, Pervez MA, Nasim M. Genetic divergence and inter-relationship studies in chickpea (*Cicer arietinum* L.). Pak. J Agri. Sci. 2011; 48(1):35-39.
2. Anonymous. Project Coordinator's Report, All India Coordinated Research Project on chickpea. Indian Institute of Pulses Research Kanpur, 2018, 29.
3. Dwevedi KK, Gaibriyal ML. Assessment of genetic diversity of cultivated chickpea (*Cicer arietinum* L.). Asian J Agric. Sci. 2009; 1(1):7-8.
4. Gaikwad AR, Desai NC, Pawar GH, Langhi AM. Genetic divergence in chickpea. Int. J Agric. Sci. 2014; 10(2):812-815.
5. Jain S, Indapurkar YM, Singh AK. Genetic architecture, interrelationship and path coefficient analysis in chickpea cultivars (*Cicer arietinum* L.). Trends in Biosciences. 2014; 7(2):133-135.
6. Jayalakshmi V, Reddy CKK, Jyothirmayi G. Genetic study on drought tolerance attributes in chickpea (*Cicer arietinum* L.). J Food Legumes. 2012; 25:94-96.
7. Mahalanobis PC. On generalized distance in statistics. Proc. Nat. Ins. Sci. India 1936; 2:49-55.
8. Pandey A, Gupta S, Kumar A, Thongbam PD, Pattanayak A. Genetic divergence, path coefficient and cluster analysis of chickpea (*Cicer arietinum* L.) cultivars, in the mid-altitudes of Meghalaya. Indian J Agric. Sci. 2013; 83(12):1300-1304.
9. Puri MK, Johnson PL, Sharma RN. Study of variability, diversity and association analysis of chickpea (*Cicer arietinum* L.) germplasm under normal and late sown condition of Chhattisgarh state. Trends Biosci. 2013; 6(6):723-731.
10. Rao CR. Advance statistical methods in biometrical research. Wiley and Sons, New York, 1952, 390.
11. Varshney RK. The chickpea genome: an introduction. Retrieved from Springer, 2017. Link: link.springer.com
12. Wadikar PB, Ghodke MK, Pole SP. Genetic divergence for productivity traits in chickpea (*Cicer arietinum* L.). J Food Legumes. 2010; 23:245-246.