Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(2): 2705-2709
Received: 23-01-2018
Accepted: 25-02-2018

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Genetic diversity in elite lines of chickpea (*Cicer aritinum*) for phenological and quantitative traits

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Abstract
Assemblage and assessment of divergence among genotypes is essential to know the spectrum of diversity. Recently developed 70 elite lines of desi chickpea from diverse sources sown in RCBD in seed breeding farm, JNKVV, Jabalpur (2016-17). Maximum % contribution towards the divergence observed for total number of pods plant^{-1} followed by height of first fruiting node, harvest index and biological yield. These characters were responsible for expressing maximum diversity between the clusters should be considered prime during selection. On the basis of D^2 values 70 elite lines were grouped into 11 clusters, the maximum lines were grouped in cluster I (24 lines) followed by cluster II and VII (11 lines), IV (10 lines), III (8 lines) and cluster V, VI, VIII, IX, X and XI had only one line in each. Cluster VII was the most diversified, having highest Intra-cluster distance followed by cluster VI, III, II and I, whereas cluster V, VI, VIII, IX, X, XI were mono-genotypic. The inter cluster divergence was observed maximum between genotypes of cluster VII and VIII followed by cluster V and VIII, cluster VI and X, cluster VI and VIII, cluster V and X. Cluster VI showed maximum mean value for 100 seed weight, biological yield plant^{-1} had high mean value in cluster VIII, harvest index were recorded maximum in cluster V, seed yield plant^{-1} showed maximum value in cluster VI. Divergence elite lines *viz*., SAGL 152210, ICCX-090021-P19, IPC 2012-31, JG 14,JG 2016-141611, N BeG 873, Phule G 0805-17-5, JAKI 9218 grouped in different clusters, intercrossed for inducing variability in the respective characters and their rationale improvement for increasing seed yield in chickpea.

Keywords: genetic diversity, phenological traits, quantitative traits

1. Introduction
Knowledge of genetic divergence in the available genotypes has an immense importance and in tune with immediate need in the selection of parents to be used in hybridization program for obtaining desirable genetic recombination. It is difficult for the breeder to select most suitable genetically diverse parents for successful hybridization programme unless provides necessary information on genetic variation and genetic divergence present in the available genetic material. The more diverse the parents are more the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generations. Mahalanobis D^2 statistic is a powerful tool used to quantify the degree of genetic divergence between the genotypes and relate clustering pattern with the geographic origin. The genetic distance had a definite role to play for efficient choice of parents for hybridization programme. Hence, utilization of prominent genotypes falling in distant clusters into breeding programme may lead to development of potential genotypes having broadened genetic base.

2. Material and Methods
Seventy elite lines of desi chickpea from different sources viz., JNKVV(Jabalpur), ICRISAT(Patencheru), IIPR (Kanpur), MPKV(Rahuri), ZARS(Nandyal) and RVSKVV (Sehore) (Table 1) were grown in randomized completely block design with three replications during Rabi 2016-17 at Seed Breeding Farm, College of Agriculture, Jabalpur (M.P.). Observation were recorded on 15 quantitative and phenological traits viz., days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity, plant height, height of first fruiting nods, number of primary branches plant^{-1}, number of secondary branch plant^{-1}, total number of pods plant^{-1}, number of effective pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight, biological yield plant^{-1}, harvest index and seed yield plant^{-1}. The mean data were subjected to standard statistical techniques to estimate genetic divergence through Mahalanobis D^2 analysis (1928).

Table 1: Details of elite lines of desi chickpea

S.no.	Entry name	Source	S.no.	Entry name	Source
1	IPC 2013-25	IIPR,Kanpur	36	SAGL 152278	RVSKVV, Sehore
2	IPC 2014-48	IIPR, Kanpur	37	SAGL 152317	RVSKVV, Sehore
3	IPC 2014-120	IIPR, Kanpur	38	SAGL 152401	RVSKVV, Sehore
4	IPC 2015-105	IIPR,Kanpur	39	SAGL 152402	RVSKVV, Sehore
5	IPC 2015-120	IIPR,Kanpur	40	SAGL 152403	RVSKVV, Sehore
6	IPC 2015-85	IIPR,Kanpur	41	SAGL 152404	RVSKVV, Sehore
7	IPC 2014-112	IIPR,Kanpur	42	SAGL 152405	RVSKVV, Sehore
8	IPC 2013-83	IIPR,Kanpur	43	JG 2016-111	JNKVV,Jabalpur
9	IPC 2012-49	IIPR,Kanpur	44	JG 2016-1614	JNKVV,Jabalpur
10	IPC 2012-98	IIPR,Kanpur	45	JG 2016-141611	JNKVV,Jabalpur
11	IPC 2012-30	IIPR,Kanpur	46	JG 2016-634958	JNKVV,Jabalpur
12	IPC 2012-31	IIPR,Kanpur	47	JG 2016-638474	JNKVV,Jabalpur
13	IPC 2010-25	IIPR,Kanpur	48	JG 2016-921814	JNKVV,Jabalpur
14	IPC 2010-14	IIPR,Kanpur	49	JG 2016-1206301	JNKVV,Jabalpur
15	IPC 2007-13	IIPR,Kanpur	50	JG 2016-55224111	JNKVV,Jabalpur
16	IPC 2008-11	IIPR,Kanpur	51	JG 2016-96054958	JNKVV,Jabalpur
17	IPC 2008-83	IIPR,Kanpur	52	JG 2016-960506301	JNKVV,Jabalpur
18	IPC 2011-28	IIPR,Kanpur	53	ICCX-060029- P30	ICRISAT,Patencheru
19	IPC 2006-127	IIPR,Kanpur	54	ICCX-070127-P20	ICRISAT,Patencheru
20	IPC 2010-216	IIPR,Kanpur	55	ICCX-080026-P4	ICRISAT,Patencheru
21	Phule G 0805-17-5	MPKV,Rahuri	56	ICCX-080062-P1	ICRISAT,Patencheru
22	Phule G 0808-30-9	MPKV Rahuri	57	ICCX-080062 -P3	ICRISAT,Patencheru
23	Phule G 0913-2-11	MPKV Rahuri	58	ICCX-080065-P2	ICRISAT,Patencheru
24	Phule G 0914-6-6	MPKV Rahuri	59	ICCX-090020-P5	ICRISAT,Patencheru
25	Phule G 0914-6-17	MPKV Rahuri	60	ICCX-090021-P19	ICRISAT,Patencheru
26	Phule G 0914-7-13	MPKV Rahuri	61	ICCX-090026-P11	ICRISAT,Patencheru
27	Phule G 0914-8-14	MPKV Rahuri	62	ICCX-090033-P21	ICRISAT,Patencheru
28	Phule G 0914-8-20	MPKV Rahuri	63	ICCX-090034-P2	ICRISAT,Patencheru
29	Phule G 0919-4-8	MPKV Rahuri	64	ICCX-090036-P17	ICRISAT,Patencheru
30	Phule G 14101	MPKV,Rahuri	65	ICCX-090042-P5	ICRISAT,Patencheru
31	N BeG 776	ZARS, Nandyal	66	ICCX-090042-P12	ICRISAT,Patencheru
32	N BeG 873	ZARS, Nandyal	67	ICCX-090044-P14	ICRISAT,Patencheru
33	SAGL 152199	RVSKVV, Sehore	68	ICCX-090044-P18	ICRISAT,Patencheru
34	SAGL 152210	RVSKVV, Sehore	69	JAKI 9218	JNKVV,Jabalpur
35	SAGL 152216	RVSKVV, Sehore	70	JG14	JNKVV,Jabalpur

3. Result and Discussion

Genetic diversity helps in the selection of genetically divergent parents for their exploitation in hybridization programmes. It measures the degree of diversification and determines the relative proportion of each component character to the total divergence. The forces of differentiation are measured at two levels i.e. inter-cluster and intra cluster levels. This technique provides reliable estimates of divergence and a large number of germplasm lines can be evaluated at a time for genetic diversity by this technique.

The % contribution towards genetic divergence by 15 quantitative characters (Table 2) revealed that, total number of pods per plant contributed most towards genetic divergence followed by height of first fruiting node, harvest index and biological yield plant^{-1}, These characters were responsible for expressing of maximum diversity between the clusters should be considered prime during selection .Remaining characters exhibited very low or negligence contribution towards divergence.

Seventy elite lines of chickpea assessed for nature and magnitude of genetic divergence were grouped into 11 clusters (Table 3) out of which five were polygenotypic and six was monogenotypic indicated sufficient diversity in the material. Cluster I was the largest among all the clusters comprising 24, followed lines by cluster II and cluster VII consisted of 11 lines. Cluster IV consisted 10. Cluster III 8 lines, cluster V lines, VI, VIII, IX, X and XI comprising one line in each. The D^2 values of the genotypes and clustering pattern indicates that the material is highly diverse. Distributions of genotypes into different clusters were presented in Table 4. Intra cluster distance ranged from 0.00 to 111.7. Cluster VII was the most diversified, having highest Intra-cluster cluster followed by cluster VI, cluster III, cluster II and cluster I, whereas cluster V, VI, VIII, IX, X, XI were mono-genotypic. The highest inter cluster divergence was observed between genotypes of cluster VII and cluster VIII, followed by cluster V and cluster VIII, cluster VI and cluster X, cluster VI and cluster VIII, cluster V and cluster X, suggesting the presence of high variability in genetic make-up of genotypes included in these clusters. The highest inter cluster divergence was observed between the genotypes of cluster VII and cluster VIII. Crossing between the genotypes of these most divergent clusters may lead to maximum recombinant / sergeants in the material. High heterotic combinations will obtain when genotypes of these distinctly placed clusters were crossed would give high heterosis/heterotic sergeants. Inter cluster distance was lowest between cluster I and cluster II indicating existence of closer proximity between these clusters. These results are in conformity with the finding of Dwevedi and Gaibriyal, 2009 [3], Sial *et al*. 2003 and Parashi *et al*. 2013. Divergence elite lines viz., SAGL 152210, ICCX-090021-P19, IPC 2012-31, JG 14,JG 2016-141611, N BeG 873, Phule G 0805-17-5, JAKI 9218 grouped in different clusters, there is no correlation between geographical distribution and genetic divergence of genotypes. Genotypes from the same source distributed different clusters. Genotypes select from different

clusters intercrossed for inducing variability in the respective characters for exploitation in future breeding programmes.

The cluster mean for different characters are presented in Table 5. Wide range of variation was noted for all the characters under study. Cluster VI showed maximum mean value for 100 seed weight, biological yield plant^{-1} had high mean value in cluster VIII, harvest index were recorded maximum in cluster V, seed yield plant^{-1} showed maximum value in cluster VI. Cluster X had high mean value for days to maturity, total number of pods plant^{-1}, days to pod initiation. Cluster III and Cluster VII showed high mean value for phenological characters viz., days to maturity, days to pod initiation and total number of pods plant^{-1}. Cluster I had high mean value for harvest index. Cluster V and VI showed high mean value for days to maturity. Promising elite lines grouped in cluster III are Phule G 0805-17-5, JG 2016-96054958, IPC 2010-216, SAGL 152401, JG 2016-921814, Phule G 0914-6-17, JG 2016-634958, IPC 2015-120 and in cluster VII are ICCX-080026-P4, JAKI 9218 , SAGL 152404, ICCX-080062-P1, N BeG 873, SAGL 152402, IPC 2012-49, SAGL 152403, SAGL 152317, ICCX-090036-P17, ICCX-070127-P20. Early, high yielding JG 14 having high harvest index, grouped in cluster XI. Intercrossing of lines involved in these clusters could be practiced for inducing variability in the respective characters and their rationale improvement for increasing seed yield. Based on cluster means, Rao and Singh (1994) [18] also reported wide range of variation for days to maturity, total number pods plant^{-1} and harvest index, while Darshanlal *et al*. (2001) reported that grouping of genotypes in different clusters was due to the traits viz., plant height, yield plant^{-1}, seeds pod^{-1}, total number of pods plant^{-1}, followed by plant height and 100 grain weight were the main yield contributing character to genetic divergence in chickpea. The findings of present investigation are in accordance with the earlier findings of Parameshwarappa *et al*. 2012 [14], found highest mean value for days to maturity, plant height, number of seeds pods^{-1}, 100 seed weight and seed yield and Syed *et al*. 2012 found highest mean value for total number of pods plant^{-1}. On the basis of these characters superior genotypes are selected from the clusters having wide inter cluster distance to create maximum variability in segregating generation and selected genotypes used in hybridization programme as a donor parent. Heterosis is generally attributed to genetic divergence among the parental lines involved in the crosses. These findings confirm in earlier studies of Gupta and Krishna (1996) [5], Tripathi (1997) [22], Pooranchand (1999) [16], Harisatyanarayan and Reddy (2000) [7], Jeena *et al*.(2005) [9], Singh *et al*. (2006) [19] Dwevedi and Gaibriyal (2009) [3], Hahid *et al*.(2010) [6], Sreelakshmi *et al*. (2010) [20], Parameshwarappa *et al*. (2011) [14], Prakash and Shekhawat (2012), Babbar and Thakur (2012) [1], Pandey *et al*.(2013) [13], Gaikwad *et al*.(2014) [4], Verma and Waldia (2013) [23], Malik *et al*., (2014), Jayalakshmi *et al*.(2014) [8] and Naveed *et al*., (2015) [12], Dhuria and Babbar (2016) [2]. Considerable amount of genetic divergence was present among the elite lines. Intercrossing of genotypes for different clusters showing superior mean performance may help in obtaining higher yield.

Table 2: Contribution (%) of characters towards divergence

S. No.	Source	Times ranked 1st	Contribution %
1	TNPPP	517	21.41
2	HFFN	503	20.83
3	HI	310	12.84
4	BY	303	12.55
5	DFI	222	9.19
6	PH	196	8.12
7	100SW	196	8.12
8	SPP	70	2.9
9	SY	68	2.82
10	DPI	10	0.41
11	DFF	8	0.33
12	DM	6	0.25
13	SB	4	0.17
14	PB	2	0.08
15	EPPP	-	-

Table 3: Distribution of genotype in different clusters using Mahanlobis D^2

Cluster No.	No. of genotypes	Genotypes included in the cluster
1	24	ICCX-080062-P3, ICCX-080065-P2, Phule G 0914-7-13, Phule G 0914-8-20, ICCX-090020-P5, JG 2016-55224111, ICCX-090033-P21, SAGL 152199, ICCX-060029-P30, SAGL 152278, JG 2016-638474, IPC 2008-83, Phule G 0808-30-9, Phule G 0913-2-11, Phule G 0914-8-14, ICCX-090044-P18, IPC 2007-13, Phule G 0914-6-6, ICCX-090042-P5, ICCX-090026-P11, JG 2016-141611, JG 2016-111, Phule G 14101, SAGL 152216
2	11	Phule G 0919-4-8, SAGL 152405, JG 2016-960506301, JG 2016-1206301, IPC 2011-28, IPC 2006-127, N BeG 776, IPC 2008-11, JG 2016-1614, IPC 2015-85,ICCX-090042-P12
3	8	Phule G 0805-17-5, JG 2016-96054958, IPC 2010-216, SAGL 152401, JG 2016-921814, Phule G 0914-6-17, JG 2016-634958, IPC 2015-120
4	10	IPC 2014-120, IPC 2012-98, IPC 2010-25, IPC 2013-25, IPC 2015-105, IPC 2014-112, IPC 2012-30, IPC 2014-48, IPC 2013-83, IPC 2010-14
5	1	SAGL 152210
6	1	ICCX-090021-P19
7	11	ICCX-080026-P4, JAKI 9218 , SAGL 152404, ICCX-080062-P1, N BeG 873, SAGL 152402, IPC 2012-49, SAGL 152403, SAGL 152317, ICCX-090036-P17, ICCX-070127-P20
8	1	ICCX-090044-P14
9	1	ICCX-090034-P2,
10	1	IPC 2012-31
11	1	JG 14

Table 4: Inter and intra cluster D^2 values for different clusters

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	17.5	28.6	41.6	40.7	29.4	25.8	40.1	58.6	33.2	49.9	45.0
Cluster II		23.2	62.5	44.4	46.6	53.6	47.5	69.7	53.6	41.0	40.6
Cluster III			27.7	79.2	81.9	46.7	83.6	46.1	40.1	75.9	53.4
Cluster IV				28.3	56.2	74.8	63.9	82.5	56.8	56.9	64.6
Cluster V					0.0	22.7	39.6	105.1	61.6	86.6	87.9
Cluster VI						0.0	47.2	86.6	48.3	90.8	77.3
Cluster VII							42.6	111.7	68.7	82.1	74.3
Cluster VIII								0.0	54.3	46.0	64.4
Cluster IX									0.0	45.2	31.9
Cluster X										0.0	36.6
Cluster XI											0.0

Table 5: Cluster mean for yield and its component characters

S. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
1	DFI	51.9	55.06	50.6	61.7	48.0	43.0	51.2	56.0	54.3	49.3	55.6
2	DFF	58.3	61.09	57.6	68.3	54.6	50.6	57.4	61.0	60.3	57.3	63.3
3	DPI	66.9	68.4	66.4	73.2	65.3	68.6	66.5	66.6	67.3	64.6	68.0
4	DM	107.3	107.5	110.1	110.5	104.0	104.0	104.5	109.6	111.3	111.6	70.0
5	PH	52.1	51.1	52.2	61.9	50.6	48.0	42.02	54.5	49.3	55.8	49.2
6	HFFN	19.1	12.0	20.7	19.0	22.6	23.9	19.6	17.1	17.9	6.2	8.2
7	PB	3.2	3.2	3.07	3.5	3.1	3.3	2.9	3.6	3.6	3.6	2.8
8	SB	7.1	7.1	7.1	7.7	7.6	6.6	7.03	8.8	8.3	6.8	7.0
9	TNPPP	47.3	36.4	62.3	50.	34.3	45.3	38.4	69.3	86.2	66.9	67.6
10	EPPP	41.4	31.4	55.3	39.8	24.1	40.1	32.5	64.3	74.1	58.2	57.2
11	SPP	1.1	1.2	1.1	1.3	1.35	1.05	1.1	1.09	1.1	1.09	1.1
12	100SW	26.7	23.5	26.5	20.9	29.2	32.2	19.2	29.8	29.4	20.4	21.8
13	BY	25.6	24.9	37.8	23.0	12.9	23.9	18.9	50.7	24.3	33.8	26.9
14	HI	61.0	57.1	70.8	53.6	80.9	71.8	59.1	46.1	77.1	36.2	75.0
15	SY	15.4	13.9	26.1	11.9	10.4	17.1	10.7	23.1	18.5	12.3	20.1

Where,
FI = Flower initiation, 50% F = Days to 50% flowering, DPI = Days to pod initiation, DM = Days to maturity, PH = Plant height (cm), HFFN = Height of first fruiting node (cm), PB = Number of primary branches per plant, SB = Number of secondary branches per plant, TNPPP = Total number of pods per plant, EPPP = Number of effective pods per plant, SPP = Number of seeds per pod, 100 SW = 100 Seed weight (g), BY = Biological yield per plant per plant (g), HI = Harvest index (%), SY = Seed yield per plant/ plant (g).

4. Conclusion

The percentage contribution towards genetic divergence observed high for total number of pods per plant followed by height of first fruiting node, harvest index biological yield, thus selection for characters would be effective. On the basis of D^2 values, the 70elite lines of chickpea were grouped into 11 clusters out of which five were polygenotypic and six was monogenotypic indicated sufficient diversity in the material. The highest inter cluster divergence was observed between the lines of cluster VII and cluster VIII. Crossing between the genotypes of these most divergent clusters may lead to maximum recombinant / sergeants in the material. Divergence elite lines viz., SAGL 152210, ICCX-090021-P19, IPC 2012-31, JG 14,JG 2016-141611, N BeG 873, Phule G 0805-17-5, JAKI 9218 grouped in different clusters,there is no correlation between geographical distribution and genetic divergence of genotypes.

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