Original Research Article

Assessment of Genetic Diversity in Extra Large and Large Seeded Kabuli Chickpea

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A B S T R A C T

To address the feasibility of developing demand for high yield, large seeded, protein rich and cooking quality of kabuli chickpea. Assessing for the diversity among kabuli chickpea was done which suggested for the crosses between the genotypes *viz.,* ICCV 171314, Vihar, NBeG 1010, ICCV 171313, Phule G 0517 from cluster IV with high cluster means for number of pods per plant, number of seeds per plant and seed yield per plant and NBeG 805 genotype from cluster VI with superior cluster means for SCMR, number of primary per plant, 100 grain volume and cooking time for soaked seeds can be used.

Introduction

Chickpea is one of the earliest food legumes cultivated. During the last five decades, its production has increased significantly which is primarily due to introduction of high yielding and disease resistant varieties and adoption of improved production technologies. India is the largest chickpea producer and consumer in the world. Among *desi* and *kabuli*, large seeded *kabuli* types have more consumer preference and hence fetch premium price to the farmers. Fortunately, the trading of extra-large seeded *kabuli* types is dominating the international market. Approximately one million tons of

chickpea were imported by Government, private organizations and other agencies. But the large seeded kabuli chickpea with high yields is a rare combination so far.

For this, genetic divergence among the parents can play a vital role in cultivar improvement because crosses involving genetically diverse parents are likely to produce high heterotic effects and also more variability in segregating generations when involved in hybridization programmes. Thus, the present investigation was a step to find the possible crosses by estimating the genetic divergence among 30 genotypes using Mahalanobis D^2 statistic for 19 traits.

Results and Discussion

Clustering of genotypes by tocher method

Based on the cluster analysis, 30 genotypes were grouped into six clusters under rainfed condition as presented in the Table 1 and Fig. 1. The highest number of genotypes *i.e* nine was found in cluster I and II. The other clusters *viz.,* cluster III and IV were with five genotypes and cluster V and VI were monogenotypic.

Inter and intra cluster distances

The average inter and intra cluster distances were presented in the Table 1 and Fig. 2. The range of inter cluster distance varied from 182.68 to 1696.22 which is higher than the range of Intra cluster distance varied from 0.00 to 162.98. Similar results were also reported by Syed *et al.,* (2012), Jain and Indapurkar (2013), Puri *et al.,* (2013), Jayalakshmi *et al.,* (2014), Singh *et al.,* (2016), Vijayakumar *et al.,* (2017), Gediya *et al.,* (2018). The highest inter cluster distance was observed between clusters IV and VI (1696.22), followed by II and VI (959.81), V and VI (950.94), I and IV (742.12) which indicated that the genotypes grouped in these clusters were highly divergent from each other.

While, the lowest inter cluster distance was found between cluster II and V (182.68), followed by cluster II and IV (241.68), cluster IV and V (266.54), cluster I and III (276.12) which indicated that the genotypes grouped in these clusters were less divergent from each other.

The maximum intra cluster distance was shown by cluster IV (162.98), followed by cluster III (130.18), cluster II (107.57) and cluster I (103.34). The clusters V and VI were monogenotypic and hence recorded zero intra cluster distance.

Cluster means for various characters

The cluster means obtained for 19 traits were presented in Table 2. Cluster means for days to 50% flowering ranged from 41.89 days to 57.13. The early flowering of 41.89 days was observed in the genotypes of cluster I and the delayed flowering of 57.13 days was recorded in the genotypes of cluster III.

Cluster means for days to physiological maturity ranged from early maturity of 76.78 days to late maturity of 89.93 days in the genotypes belonging to cluster I and cluster III, respectively.

SCMR cluster means ranged from maximum of 58.60 to minimum of 47.08 in the genotypes of cluster VI and cluster III, respectively.

The maximum value of cluster means of plant height observed in the genotypes of cluster V was 48.53 cm and the minimum value of cluster means of plant height observed in the genotypes of cluster I was 37.30 cm.

Cluster means for number of primary branches per plant ranged from maximum of 3.1 to minimum of 2.67 in the genotypes belonging to cluster VI and cluster V, respectively.

Number of secondary branches per plant cluster means ranged from maximum of 10.53 to minimum of 8.43 in the genotypes of cluster II and cluster III, respectively.

The genotypes in the cluster IV and cluster VI showed maximum value of 18.61 and minimum value of 11.01 for number of pods per plant, respectively. Cluster means for number of seeds per plant ranged from 24.55 to 15.33. The maximum value of 24.55 was recorded in the genotypes of cluster IV and the minimum value of 15.33 was observed in the genotypes of cluster VI.

Cluster means for seed diameter ranged from maximum of 8.47 mm to minimum of 7.53 mm in the genotypes belonging to cluster V and cluster IV, respectively.

The maximum value of cluster means for protein content observed in the genotypes of cluster III was 20.5% and the minimum value of cluster means of protein content observed in the genotypes of cluster VI was 15.2%.

The genotypes in the cluster VI showed maximum value of 39.33 ml and the genotypes in the cluster III and IV showed minimum value of 29.33 ml for 100 grain volume.

Cluster means for water absorption after soaking ranged from maximum of 60.81% to minimum of 51.98% in the genotypes of cluster V and cluster IV, respectively.

The maximum value of cluster means for volume expansion after soaking observed in the genotypes of cluster V was 67.56% and the minimum value observed in the genotypes of cluster VI was 54.15%.

Cluster means for cooking time for raw seeds ranged from a less time of 94.7 min to more time of 121.33 min in the genotypes belonging to cluster II and cluster V, respectively.

Cluster means for cooking time for soaked seeds ranged from 58.33 to 36.33 min. The less time of 36.33 min was observed in the genotypes of cluster V and the more time of 58.33 min was recorded in the genotypes of cluster VI.

The genotypes in the cluster V and cluster III showed maximum value of 47.33g and minimum value of 37.43g for 100 seed weight, respectively.

The maximum value of cluster means for shoot biomass per plant observed in the genotypes of cluster III was 18.47g and the minimum value observed in the genotypes of cluster VI was 15.76g.

Cluster means for harvest index ranged from 45.29% to 28.35%. The maximum of 45.29% was observed in the genotypes of cluster I and minimum of 28.35% was observed in the genotypes of cluster III.

Cluster means for seed yield per plant ranged from a maximum of 7.59g to minimum of 5.22g in the genotypes belonging to cluster IV and cluster III, respectively.

In a nut shell, genotypes of cluster V exhibited high cluster means for traits like plant height, seed diameter, water absorption after soaking, volume expansion after soaking, cooking time for soaked seeds and 100 seed weight, followed by cluster VI with superior cluster means for SCMR, number of primary branches per plant, 100 grain volume and cluster IV with excelled cluster means for number of pods per plant, number of seeds per plant, seed yield per plant and cluster I with superior cluster means for days to 50% flowering, days to physiological maturity, harvest index, followed by cluster III with higher cluster means for protein content, shoot biomass per plant and cluster II with superior cluster means for number of secondary branches per plant and cooking time for raw seeds.

Relative contribution of each character towards genetic divergence

The number of times each of the 19 characters appeared first and their respective percentage of relative contribution towards genetic divergence were presented in Table 3.

Table.1 Distribution of 30 genotypes of chickpea into different clusters under rainfed condition

Cluster No.	No. of genotypes	Name of the genotypes
I	9	NBeG 835, ICCV 171301, NBeG 837, NBeG 810, NBeG 723, ICCV 171305, NBeG 719, NBeG 119, Phule G 15307
II	9	NBeG 399, NBeG 724, NBeG 458, NBeG 789, KAK 2, NBeG 829, NBeG 833, NBeG 440, NBeG 844
III	5	ICCV 171302, ICCV 171306, JGK 5, RKGK 499, ICCV 171303
IV	5	ICCV 177314, Vihar, NBeG 1010, ICCV 171313, Phule G 0517
V	1	MNK 1
VI	1	NBeG 805

Table.2 Average inter and intra cluster distances in 30 chickpea genotypes under rainfed condition

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	103.34	298.97	276.12	742.12	390.23	340.76
Cluster 2		107.57	345.04	241.68	182.68	959.81
Cluster 3			130.18	626.88	294.33	537.37
Cluster 4				162.98	266.54	1696.22
Cluster 5					0	950.94
Cluster 6						0

Table.3 Cluster means for 19 characters in 30 chickpea genotypes under rainfed condition

| S.No.	Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
1	Days to 50% flowering	41.89	43.59	57.13	47.80	52.00	46.00
2	Days to physiological maturity	76.78	78.48	89.93	81.20	87.67	79.67
3	SCMR	50.05	51.26	47.08	48.37	48.10	58.60
4	Plant height (cm)	37.30	38.44	40.27	38.29	48.53	37.87
5	No. of primary branches per plant	3.00	3.09	2.98	2.89	2.67	3.10
6	No. of secondary branches per plant	10.09	10.53	8.43	9.74	8.52	9.59
7	No. of pods per plant	15.99	17.70	12.58	18.61	14.32	11.01
8	No. of seeds per plant	20.09	20.54	15.97	24.55	18.33	15.33
9	Seed diameter (mm)	8.05	7.67	7.81	7.53	8.47	8.00
10	Protein content (%)	18.80	16.98	20.50	18.30	16.63	15.20
11	100 grain volume (ml)	35.04	32.56	29.93	29.93	34.67	39.33
12	Water absorption after soaking (%)	54.33	55.10	57.10	51.98	60.81	56.13
13	Volume expansion after soaking (%)	58.15	57.23	62.56	58.76	67.56	54.15
14	Cooking time for raw seeds (min)	98.74	94.70	105.20	100.73	121.33	118.00
15	Cooking time for soaked seeds (min)	50.41	41.44	45.93	38.07	36.33	58.33
16	100 seed weight (g)	43.30	39.96	37.43	39.33	47.33	42.33
17	Shoot biomass per plant (g)	16.33	16.46	18.47	18.24	17.52	15.76
18	Harvest index (%)	45.29	44.37	28.35	41.56	42.60	33.28
19	Seed yield per plant (g)	7.39	7.31	5.22	7.59	7.50	5.62
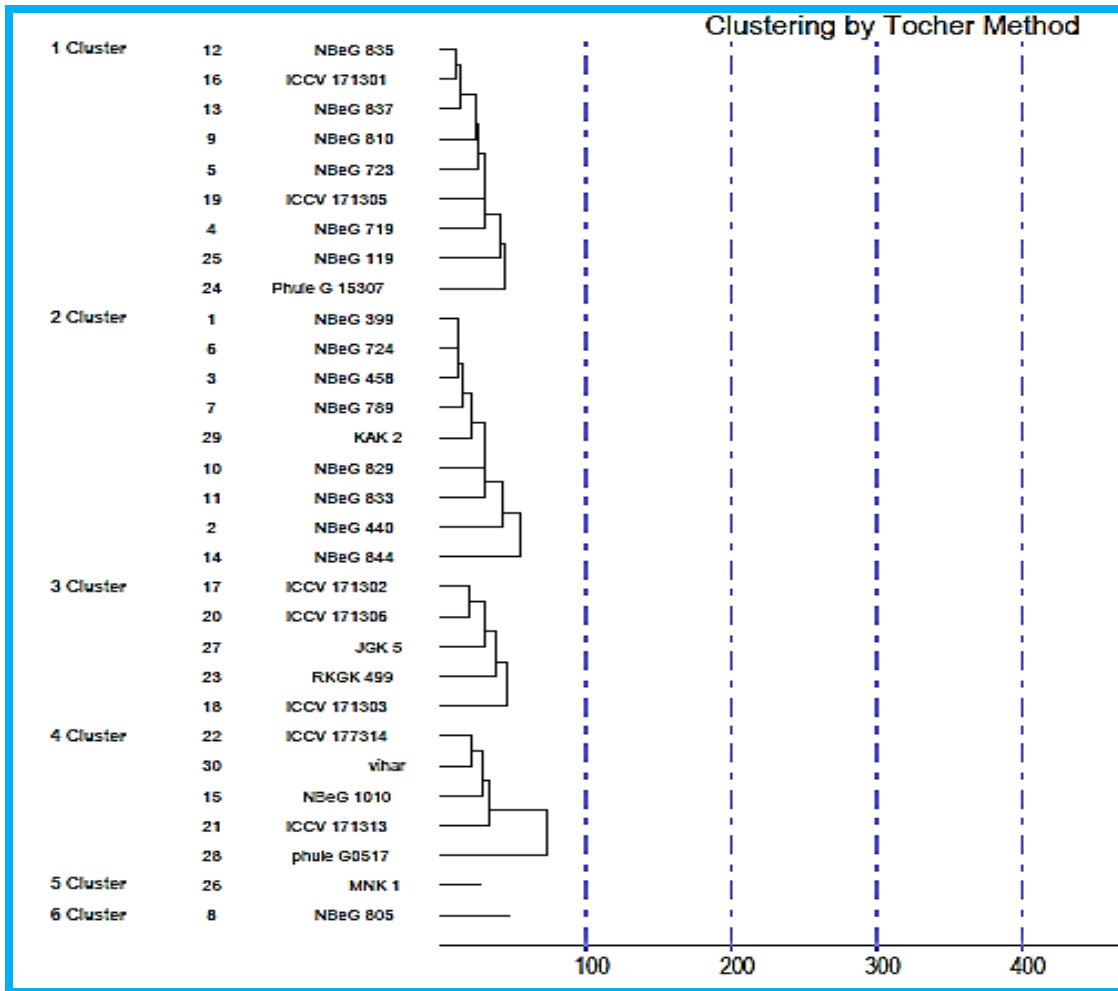
Fig.1 Grouping of genotypes into clusters using Tocher's method under rainfed condition
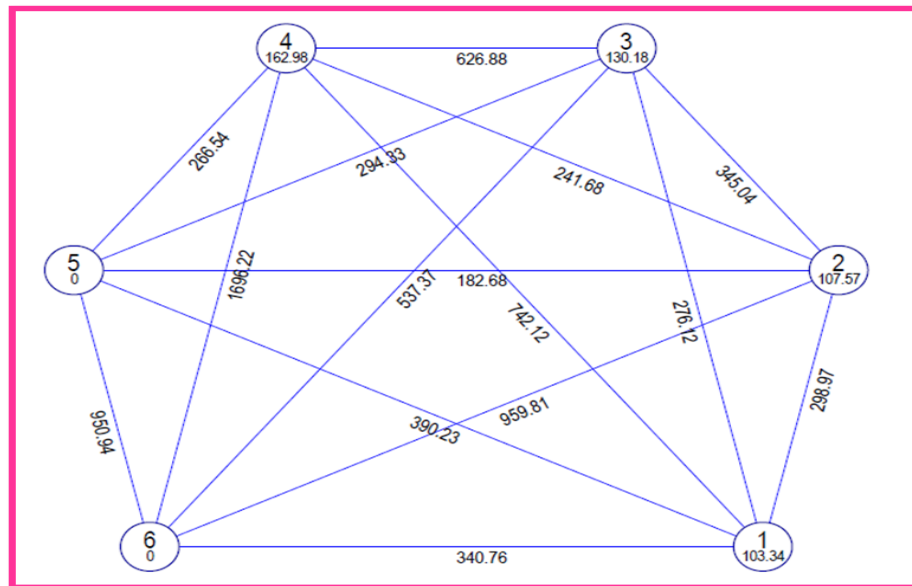

Fig.2 Average inter and intra cluster distances under rainfed condition

Cooking time for soaked seeds (69.66%) has the highest contribution for genetic divergence, followed by cooking time for raw seeds (8.51%), shoot biomass per plant (6.90%), days to physiological maturity (5.96%), 100 grain volume (2.76%) and 100 seed weight (2.53%).

The traits like days to 50% flowering (0.23%), number of primary branches per plant (0.23%) and number of pods per plant (0.23%), followed by protein content (0.46%) and seed yield per plant (0.46%), followed by SCMR (0.69%), seed diameter (0.69%) and water absorption after soaking (0.69%) contributed the least for genetic divergence. Plant height, number of secondary branches per plant, number of seeds per plant, volume expansion after soaking and harvest index showed zero contribution towards the genetic divergence.

Genotypes identified as parents for further breeding programme

The choice of parents belonging to the maximum divergent clusters is expected to manifest maximum heterosis in crossing and wide variability in genetic architecture (Chaudhry *et al*., 2002).

Hence, from the above findings, the genotypes *viz.,* ICCV 171314, Vihar, NBeG 1010, ICCV 171313, Phule G 0517 from cluster IV were with high cluster means for number of pods per plant, number of seeds per plant and seed yield per plant and NBeG 805 genotype from cluster VI were with superior cluster means for SCMR, number of primary per plant, 100 grain volume and cooking time for soaked seeds.

Both these clusters were with maximum divergence for inter cluster distance and cluster IV has maximum intra cluster distance also. Whereas, MNK 1 genotype included in

cluster V was with highest cluster mean for 100 seed weight (important trait to be selected for large seeded *kabuli*) and hence any of these promising genotypes belonging to these clusters can be utilized as parents for hybridization programme.

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