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Genetic diversity analysis for quantitative traits in lentil germplasm

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Abstract
The present investigation was undertaken with the objectives, to estimate the genetic divergence between different genotypes and to group different genotypes into suitable cluster. Genetic divergence was assessed among 30 germplasm lines of lentil collected from Gadhinglaj, Ajara and Chandgad tahsils of Kolhapur district using Mahalonobis's D^2 analysis. Presence of diversity pave way for exploitation of genotypes in breeding programme intended to improve yield and yield attributing traits. Genotypes from different geographical locations have been observed in same cluster and vice versa indicating that clustering of populations does not follow their geographic or location distribution. The 30 genotypes of lentil were grouped into 7 clusters. Cluster II was found to be the largest comprising 14 genotypes, followed by cluster III having 5 genotypes. Clusters IV and VII had single genotypes each. The intra cluster distance was observed to be highest for cluster VI thereby indicating greater genetic divergence between genotypes belonging to this cluster. The maximum inter cluster distance was observed in cluster IV and VII followed by cluster IV and VI. Thus, hybridization among these cluster pairs is recommended for getting high transgressive segregants in F_2 population. The characters number of secondary branches per plant, seed yield per plant, 100 seed weight and number of pods per plant contributed more towards divergence.

Keywords: Genetic divergence, Intra and inter cluster distance, Lentil

Introduction
Lens culinaris L. is diploid (2n=2x=14). It belongs to family Fabaceae and tribe *Vicieae*. Lentil is self-pollinated crop and have less than 1.66 per cent cross pollination (Baum *et al*, 1997) [3]. The plant is annual, herbaceous, erect, semi erect or spreading and compact growth. Lentils are highly nutritious and easily digestible pulse crop. It contains protein, vitamin A, fiber, starch, potassium, B vitamins and iron. It is versatile source of nutrients for man, animals and soil, containing on an average 25.1 per cent protein, 59 per cent carbohydrate, 0.5 per cent fat, 2.1 per cent animal minerals and sufficient amount of vitamins *viz*., vitamin A 16U; thiamine 0.23 mg and vitamin C at the rate 2.5 mg per gram (Anonymous, 2003 and Fredrick *et al*, 2006) [1, 6]. History of lentil is as old that of agriculture, small seeded (2-3 mm) types of lentil was recovered 8000-7500 B.C. in the Marybeth, Northern Syria. Lentil is originated in Near East centre of origin (Zohary, 1996) [13] and subsequently spread to Central Asia and Mediterranean Basin (Cubero, 1981) [5] from where it spreads to Egypt, India, Southern and Central Europe, Pakistan, Afghanistan and Ethiopia (Bahl *et al.* 1993) [2]. As far as crop improvement programme is concerned, germplasm plays the vital role. Modern agriculture relies on selection of desirable parents. These desirable parents are used for hybridization programme. The selection of suitable divergent parents for hybridization is required because the cross involving diverse parents offer great possibility of obtaining desirable segregants in the segregating generations. D^2 analysis measures the degree of diversification and determines the relative proportion of each component character to the total divergence. Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes (Gaur *et al.* 2020) [7]. The D^2 technique is developed by Mahalonobis (1936) and is based on multivariate analysis. This analysis provides a measurement of relative contribution of different components on diversity both in inter cluster and intra cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combination and wide variability in segregating generation (Tocher method, Rao 1952) [11]. D^2 analysis also provides information to know about parallelism between genetic divergence and geographical distribution of the genotypes. D^2 analysis quantifies the degree of divergence in germplasm.

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Material and Methods

The experiment was conducted to evaluate 30 germplasm at PG farm, RCSM College of Agriculture, Kolhapur in randomized block design with three replications. The thirty germplasms were collected from Gadhinglaj, Ajara and Chandgad tahsils of Kolhapur district. Observations were recorded on randomly selected five plants from each entry in three replications for nine quantitative traits. The characters under study were days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant. Genetic diversity was estimated by calculating Mahalanobis (1936) [9] D^2 statistics. The genotypes were further grouped into different clusters as per Tocher's method (Rao, 1952) [11].

Results and Discussion

The distribution of 30 lentil genotypes in seven clusters is given in Table 1. The highest number of genotypes appeared in cluster II which contained 14 genotypes followed by cluster III having 5 genotypes. Cluster I, V and VI consist 3 genotypes each. Clusters IV and VII were solitary. Similar trends were also reported by Bayoumi (2008) [4] where he observed that cluster II was the largest cluster among all the clusters formed. The trends reported by Kumar *et al.* (2014) [8] were in proximity and showed that the cluster IV and VII was solitary. The estimates of intra and inter cluster distance for 7 clusters are presented in Table 2. The highest intra-cluster distance was observed for cluster VI (D^2=7.02) followed by cluster III (D^2=6.43), cluster II (D^2=5.09), cluster V (D^2=5.03) and cluster I (D^2=3.38). The clusters IV and VII showed no intra cluster distances being mono-genotypic. The maximum inter-cluster distance observed between cluster VII and IV (D^2=16.82) followed by clusters VI and IV (D^2=15.94), clusters VII and V (D^2=15.48), cluster VII and II (D^2=13.55) and cluster VI and II (D^2=13.04). The minimum inter-cluster distances between cluster IV and II (D^2=6.55), cluster VII and I (D^2=7.57) and cluster VI and I (D^2=7.92) and cluster V and II (D^2=8.12) indicating proximity with each other. The trends reported by Kumar *et al.* (2014) [8] were in proximity and showed that the cluster IV and VII was solitary. The minimum inter cluster distance was observed between cluster II and IV. The crosses involving parents from clusters having maximum inter cluster distance may exhibit high heterosis for desirable traits.

Table 1: Distribution of 30 genotypes of lentil into different clusters

Clusters	Number of genotypes included	Genotypes
I	3	Kudnur-3, Kudnur-8, Kudnur-6
II	14	Nesari Local-4, Sambra-2, Rajgoli-1-a, Belgavi masoor, Kalkundri-2-a, Itagi local, Kudnur-4, Kudnur, Nesari Local-3, Rajgoli-2, Kalkundri-3, Kudnur-1, Kalkundri, Bhakati
III	5	Kudnur-7, Kalkundri-2-b, Kudnur-2, Nashik Local, Nesari Local-1
IV	1	Nesari Local-5
V	3	Nesari Local -2-a, Local masoor-1, Local masoor-2
VI	3	Gandingan Local, Local masoor-3, Sambra-1
VII	1	Rajgoli-1-b

Table 2: Average intra and inter cluster D^2 and D values of seven clusters formed from genotypes under study

Clusters	I	II	III	IV	V	VI	VII
I	3.38	8.66	8.90	11.50	10.25	7.92	7.57
	(1.83)	(2.94)	(2.98)	(3.39)	(3.20)	(2.81)	(2.75)
II		5.09	9.07	6.55	8.12	13.04	13.55
		(2.26)	(3.01)	(2.56)	(2.85)	(3.61)	(3.68)
III			6.43	10.21	11.02	12.06	10.05
			(2.54)	(3.19)	(3.32)	(3.47)	(3.17)
IV				0.00	8.39	15.94	16.82
					(2.89)	(3.99)	(4.10)
V					5.03	11.64	15.48
					(2.24)	(3.41)	(3.93)
VI						7.02	9.17
						(2.65)	(3.03)
VII							0.00

Bold figures represents intra cluster distance

The cluster mean for 9 characters are presented in Table 3. The genotype included in solitary cluster IV (36 days) exhibited early flowering while, cluster IV (40.56 days) had late for days to 50 per cent flowering. The genotype included in solitary cluster IV (80.67 days) was earliest to mature while, cluster V (87.33 days) had late maturity. The highest cluster mean for plant height was observed in case of cluster VI (33.17 cm) followed by cluster I (32.02 cm) and cluster V (31.98 cm). The lowest cluster mean for plant height was found in cluster III (28.68 cm). Considering the variation in number of primary branches per plant cluster VII showed highest mean value (5.33) while, cluster IV (3.67) had lowest value for number of primary branches per plant. The highest cluster mean for number of secondary branches per plant was observed for cluster VII (19.07) while, genotypes with very low number of secondary branches were found to be grouped in cluster II. The genotypes included in solitary cluster VII (50.37) recorded maximum and solitary cluster IV (15.97) recorded minimum number of pods per plant, respectively. The highest cluster mean for number of seeds per pod was observed for cluster VI (1.63) and the lowest cluster mean for the number of seeds per pod was exhibited by the cluster III (1.42). Cluster mean for 100 seed weight was maximum for cluster VI (4.31 g) while, minimum for solitary cluster IV (2.58 g). The highest cluster mean for seed yield per plant was maximum for solitary cluster VII (3.21 g) while, minimum for

solitary cluster IV (1.09 g). The mean performance for character number of pods per plant was high for cluster VII. The results obtained were in accordance with results of Sharma *et al.* (2014) [12] where they reported that mean performance for character seed yield per plant was high for

cluster VII. Also, the results reported by Maurya *et al.* (2018) [10] were in conformity and they observed that mean performance for character days to 50 per cent flowering and days to maturity was high for cluster V.

Table 3: Mean performance of 7 clusters of 9 characters on 30 lentil genotypes

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
I	37.67	82.56	32.02	5.02	14.31	36.99	1.58	2.83	2.94
II	36.36	83.69	30.11	4.17	11.24	33.21	1.47	2.75	1.59
III	39.07	87.13	28.68	4.18	18.85	34.84	1.42	2.68	1.62
IV	36	80.67	29.56	3.67	12.8	15.97	1.43	2.58	1.09
V	40.56	87.33	31.98	4.4	11.76	25.56	1.38	4.27	1.39
VI	38.78	84.22	33.17	4.91	14.75	44.58	1.63	4.31	3.07
VII	35.67	84.33	28.85	5.33	19.07	50.37	1.61	2.61	3.21

The per cent contribution of the 9 characters studied towards the total divergent is presented in Table 4. The estimates of per cent contribution of different characters for divergence revealed that number of secondary branches per plant (28.05%), seed yield per plant (24.83%), 100 seed weight (20.69%) and number of pods per plant (18.85%) contributed

more towards divergence. Days to maturity (2.98%), days to 50 per cent flowering (1.84%), number of seeds per pod (1.15%) and plant height (0.92%) contributed less towards divergence. Number of primary branches per plant (0.69%) contributed the least towards divergence.

Table 4: Per cent contribution of characters under study for divergence in lentil

Sr. No.	Characters	No. of times appeared 1st in ranking	Percent contribution %
1.	Days to 50% flowering	8	1.84
2.	Days to maturity	13	2.98
3.	Plant height (cm)	4	0.92
4.	No. of primary branches per plant	3	0.69
5.	No. of secondary branches per plant	122	28.05
6.	No. of pods per plant	82	18.85
7.	No. of seeds per pod	5	1.15
8.	100 seed weight (g)	90	20.69
9.	Seed yield per plant (g)	108	24.83
	Total	435	100

Conclusion
The seven clusters in the aforesaid divergence analysis contained genotypes of heterogenous origin. The highest inter cluster distance was observed between cluster IV and VII, followed by cluster IV and VI. The lowest inter cluster distance was observed between cluster II and IV followed by cluster I and VII, which indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between the genotypes belonging to the clusters separated by low inter cluster distances are unlikely to generate promising recombinants in segregating generations. Also, proposed hybridization between lines belonging to clusters separated by large inter cluster distances in lentil. The cluster mean for 9 characters revealed considerable differences between clusters in respect of cluster means. The intra and inter cluster D^2 values revealed that the genotypes of same cluster had little divergence from each other. It is suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter cluster distance.

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