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Study of genetic diversity in exotic germplasm of lentil

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Abstract

Genetic diversity was assessed using multivariate analysis among seventy one diverse genotypes of lentil. Mahalanobis D^2 analysis grouped genotypes into twenty clusters. Maximum genotypes were present in cluster I (43), followed by cluster II (6) and cluster XII (5). Remaining clusters had only one genotype in each. Genotypes belonging to cluster I, II and XII having high genetic diversity can be used as parents for hybridization programme for the development of high yielding lentil genotypes. The percentage contribution towards genetic divergence by 100 seed weight was maximum. Maximum inter cluster distance *i.e.*, 1509 was reported between cluster II (X2011S 189, X2011S 133, X2011S 87, X2011S 154, X2011S 111, X2011S 172) and XVIII (Flip 2010-96L). The hybridization between individuals belonging to these clusters may leads to the formation of superior segregants. On the basis of cluster mean values, cluster XIII had highest mean values for days to 50% flowering; cluster VII for days to maturity and seed yield per plant; cluster XVIII for plant height; cluster II for number of primary branches per plant and number of secondary branches per plant; cluster XV for number of pods per plant; cluster XVII for number of effective pods per plant; cluster IX for number of seeds per pod; cluster XII for 100 seed weight; cluster III for biological yield per plant and cluster XX for harvest index. Genotypes viz., Idleb 2, FLIP 2011-43L, FLIP 2010-91L, FLIP 2010-96L & JL 3 were identified as highly divergent and better performing on the basis of their high cluster mean values and can be given due importance for the development of high yielding genotypes of lentil.

Keywords: Genetic divergence, diversity, cluster analysis, intra-, inter-cluster distances

Introduction

Lentil is the third most important cool-season grain legume in the world after chickpea and pea. Global annual lentil production was around 5 million metric tons from nearly 4.3 million ha in 2013. Canada was the largest producer, contributing 38% of the world's production, followed by India, Turkey, and Australia (FAO, 2015) [6].

Assessments of genetic diversity and relationships among preserved germplasm have important implications both for facilitating reliable documentation of genetic resources and for identifying material with possible utility for specific breeding purposes, particularly in cultivated lentil and other species with a narrow genetic base. Considerable genetic diversity has been reported in *Lens* genetic resources for agro-morphological and phenological characteristics (Erskine and Choudhary, 1986 [5]; Erskine *et al.*, 1989 [4]; Lazaro *et al.*, 2001 [11]; Zaccardelli *et al.*, 2012 [18]; Cristóbal *et al.*, 2014 [3]; Gautam *et al.*, 2014 [7]; Katiyar and Kant, 2015) [9].

Cluster analysis helps to understand the genetic relation among the accessions and also to facilitate the selection of genetically diverse parents in hybridization programme resulting in considerable amount of heterosis and wide range of segregation. Hence, the study was taken to investigate the extent of genetic diversity of various traits on seed yield in lentil.

Materials and Methods

The materials for the present investigation comprised of 71 lentil genotypes of diverse origin which were procured from ICARDA, Syria in a Randomized Complete Block Design with three replications at the Seed Breeding Farm, JNKVV, Jabalpur during Rabi 2013-14. Each individual plot consisted of 2 rows of 4 mt length with 20 cm and 10 cm spacing between and within rows, respectively. Recommended doses of fertilizers were applied and all necessary precautions including irrigation, weed control and pest control management were followed.

The data were recorded from 10 randomly selected plants from each treatment/replication on thirteen distinct quantitative traits namely days to 50% flowering, days to pod initiation, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of effective pods per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). Days to 50% flowering, days to pod initiation and days to maturity were recorded on

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plot basis. The data were subjected to multivariate analysis as suggested by Mahalanobis, 1936 [12] and genotypes were grouped into different clusters based on Tocher's method (Rao, 1952) [13].

Results and Discussion

On the basis of D^2 statistics, all the 71 genotypes were grouped into 20 clusters (Table 1). The pattern of distribution of the genotypes into different clusters showed considerable genetic divergence. It can be depicted from the table that maximum number of genotypes (43) were included in cluster I, followed by 6 genotypes in cluster II and 5 genotypes in cluster XII. Remaining cluster has 1 genotype each. The pattern of group constellation shows that geographical diversity was not related to the genetic diversity, which may be attributed to the distribution of different gene constellation into a geographical region. Genetic diversity among genotypes belonging to the same geographical region might be due to different adaption selection criteria, selection pressure and environments (Hair *et al.*, 1998) [18].

The intra- and inter-cluster distance values are given in Table 2. Highest intra cluster distance was reported for cluster II (269.00), followed by cluster XII (261.34) and cluster I (173.55). Remaining clusters have only one genotype. This suggested that genotypes occupying the same cluster have low level of diversity and selection of parents within the cluster may not be considered promising for developing good segregants through hybridization programme. Generally, the genotypes within a group showed little divergence from each other than from the genotypes of different groups as has been observed by Kumar, *et al.*, 2004 [10], Sultana, *et al.*, 2005 [16], Sirohi, *et al.*, 2007 [14], Solanki, 2007 [15], Tyagi and Khan 2010 [17] and Asghar, *et al.*, 2010 [1]. Hybridization among the genotypes of same group may not be fruitful. Variation within the group may be due to different genetic makeup of the genotypes and different sources of collection as reported by Bharawadraj, *et al.*, 2001 [2].

The highest inter cluster divergence was observed between genotypes of cluster II and XVIII (1509.00), followed by cluster VII and cluster II (1303.46), cluster XII and cluster II (1284.96), cluster XIII and cluster XII (1178.99), cluster XI and cluster X (1150.10), cluster VIII and cluster II (1128.57), cluster XX and cluster XIII (1062.32), cluster XVIII and cluster XII (1047.62) and cluster XV and cluster VIII (1009.21). Most of the clusters showed high inter cluster distance. The lowest inter cluster distance (63.22) was found between cluster VIII and cluster V. Therefore, hybridization between lines selected from different clusters is likely to produce more heterotic hybrids. The relative divergence of each cluster from other cluster (i.e., inter-cluster distance) has been of high order and divergence particularly between the members of cluster IV with members of all other clusters. The large inter-cluster distance between members of any two clusters indicates that genotypes falling in such clusters would be more genetically divergent. Therefore, the crosses between genotypes selected from those clusters may give desirable transgressive segregants.

The cluster means for different characters are given in table 3. Cluster XX reported lowest mean value for days to 50% flowering (58.67 days) and days to pod initiation (68.33 days). Cluster II showed highest mean values for number of primary branches per plant (4.56); cluster XVI had highest number of secondary branches per plant (12.37); cluster XV reported highest number of pods per plant (96.17); cluster XVII had maximum number of effective pods per plant

(85.10); cluster IX showed maximum number of seeds/pod (3.10); cluster XII had more 100 seed weight (5.44); cluster III had more biological yield per plant (78.53); cluster XX had maximum harvest index (5.93%) and cluster VII had highest seed yield per plant (3.47g), indicating that genotypes of outstanding mean performance from these clusters may be identified as potential parents and could be utilized in hybridization programme for developing high yielding varieties.

The percent contribution of each character was ranked on the basis of percent contribution to that character (table 3). 100 seed weight (34.57%) contributed maximum variance (34.57%), followed by days to 50% flowering (14.57%), total number of pods per plant (13.32%), biological yield per plant (10.38%), days to maturity (8.81%), plant height (8.69%) and harvest index (4.39%). Therefore, these characters should be given more stress for the selection and choice of parents for hybridization.

Table 1: Average inter and intra-cluster (bold values) distances among different cluster in lentil

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI	Cluster XVII	Cluster XVIII	Cluster XIX	Cluster XX
Cluster I	173.55																			
Cluster II	796.11	269.00																		
Cluster III	262.27	907.85	0.00																	
Cluster IV	268.90	902.30	308.31	0.00																
Cluster V	353.42	898.25	482.41	76.98	0.00															
Cluster VI	323.30	498.94	245.56	480.90	562.21	0.00														
Cluster VII	288.32	1303.46	310.89	540.40	685.10	552.12	0.00													
Cluster VIII	511.27	1128.57	654.77	165.48	63.22	827.80	852.33	0.00												
Cluster IX	276.44	991.40	427.21	99.62	104.07	590.13	548.21	123.83	0.00											
Cluster X	301.64	708.74	90.35	325.88	459.94	135.62	479.53	622.53	450.89	0.00										
Cluster XI	262.19	594.66	188.89	127.10	144.60	269.74	521.88	242.29	191.97	1150.10	0.00									
Cluster XII	690.59	1284.96	512.43	378.79	352.29	835.70	917.87	300.80	385.60	501.12	264.35	261.34								
Cluster XIII	269.06	1096.15	395.75	559.21	735.62	511.16	244.44	950.35	582.56	509.01	629.43	1178.99	0.00							
Cluster XIV	296.12	912.00	174.48	539.63	652.42	207.50	274.15	867.47	624.84	214.46	385.46	847.73	220.53	0.00						
Cluster XV	458.93	550.18	302.90	700.17	765.56	117.88	503.59	1009.21	793.53	193.35	343.39	870.30	630.96	236.98	0.00					
Cluster XVI	345.68	520.04	425.42	414.37	445.02	146.74	681.18	674.84	581.37	321.78	339.39	934.61	530.62	349.63	392.24	0.00				
Cluster XVII	472.79	674.08	294.54	425.06	462.96	227.67	642.48	587.31	505.81	158.12	183.63	454.22	774.88	375.68	178.35	465.45	0.00			
Cluster XVIII	396.84	1509.00	435.35	551.93	461.25	725.88	362.24	961.26	460.78	639.92	677.24	1047.62	398.75	634.36	903.97	934.43	860.15	0.00		
Cluster XIX	409.08	871.10	596.40	630.16	593.66	667.43	455.07	630.94	520.86	643.57	441.11	839.31	686.69	646.71	662.10	605.84	823.68	924.31	0.00	
Cluster XX	577.03	822.53	536.41	486.48	487.19	799.45	732.36	461.86	433.63	580.71	261.33	411.03	1062.52	907.90	700.08	894.56	532.88	943.56	352.31	0.00

Table 2: Cluster means values for different traits of lentil

Traits	Days to 50% flowering	Days to pod initiation	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Number of pods/plant	Effective pods/plant	Number of seeds/pod	100-seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/plant (g)
I	76.4	84.7	118.0	40.4	2.9	6.8	39.9	24.2	1.8	3.1	54.4	2.7	1.4
II	60.8	69.8	100.6	29.2	4.6	12.4	51.9	44.2	1.3	2.9	34.8	3.9	1.4
III	73.3	80.7	111.3	46.4	2.2	5.7	79.7	43.2	1.8	3.3	78.5	2.8	2.2
IV	79.3	87.7	113.0	41.3	2.6	5.1	24.3	15.3	1.7	4.3	50.3	2.3	1.2
V	80.7	87.3	118.0	36.4	3.3	5.5	24.3	11.2	2.3	4.7	31.2	4.1	1.3
VI	73.3	81.7	110.7	36.4	2.7	5.0	84.4	62.4	1.3	2.7	45.9	3.3	1.5
VII	79.3	87.3	124.0	45.3	3.2	7.2	43.0	38.6	1.1	2.7	76.4	4.6	3.5
VIII	79.0	87.3	121.3	34.8	2.7	6.3	23.4	8.0	2.9	5.3	33.8	4.0	1.3
IX	79.0	87.0	121.0	43.8	2.5	6.7	26.0	8.4	3.1	4.4	38.5	1.3	0.5
X	72.3	81.3	110.7	42.3	2.6	5.5	86.2	67.1	1.3	3.4	76.6	1.7	1.3
XI	71.7	79.7	112.0	39.8	3.4	6.9	57.3	39.6	1.4	4.2	54.0	3.4	1.8
XII	73.0	81.5	117.1	44.2	2.9	6.9	67.9	44.4	1.6	5.4	57.2	4.1	2.1
XIII	83.0	90.7	120.0	40.8	2.8	10.3	42.4	19.7	2.2	2.2	73.8	1.6	1.2
XIV	80.0	87.3	118.0	36.7	3.0	7.7	90.9	52.2	1.7	2.7	74.7	3.0	2.2
XV	70.0	78.0	111.0	38.8	4.1	8.8	96.2	84.8	1.1	2.8	64.3	4.6	2.9
XVI	74.7	84.0	111.0	24.5	2.2	3.2	52.4	30.4	1.7	2.8	32.2	5.4	1.7
XVII	74.3	83.3	111.7	43.0	3.2	9.3	92.4	85.1	1.1	4.1	50.0	5.0	2.5
XVIII	80.3	83.3	121.0	61.7	2.5	6.4	39.5	13.2	3.0	2.7	47.1	2.1	1.0
XIX	63.0	72.0	123.0	29.8	2.6	7.0	25.0	16.7	1.5	3.2	59.3	4.8	2.8
XX	58.7	68.3	112.3	44.2	3.6	11.2	38.0	32.1	1.2	4.5	56.3	5.9	3.3
% contribution	14.57	0.04	8.81	8.69	0.20	2.74	13.32	1.17	0.12	34.57	10.38	4.39	1.10

Table 3: Distribution of 71 genotypes in different clusters

Cluster No.	No. of genotypes	Genotypes included
1	43	Flip 2011-26L, 93-034L, Flip 2011-33L, Flip 2011-18L, Flip 2010-95L, Flip 2011-20L, 97-067L, 97-039L*99R060, Flip 2011-14L, Flip 2011-44L, Flip 2010-97L, JL-1, Flip 2010-81L, Flip 95-30L, Flip 2011-25L, Flip 2011-12L, Flip 2011-42L, Flip 2010-23L, Flip 2011-61L, Flip 2011-49L, Flip 2011-57L, Flip 2011-36L, Flip 89-63L, Flip 2011-54L, Flip 2010-94L, 95-005L-98H027, Flip 2011-48L, Flip 2011-35L, Flip 86-35L, Flip 2011-37L, Local masoor, Flip 2011-41L, Flip 2010-26L, Flip 2011-56L, Flip 2011-64L, Flip 92-36L, Flip 2010-104L, Flip 2011-19L, Flip 84-51L, Flip 96-46L, Flip 2011-51L, Flip 2011-9L, Flip 2011-32L
2	6	X2011S 189, X2011S 133, X2011S 87, X2011S 154, X2011S 111, X2011S 172
3	1	Flip 2010-91L
4	1	Flip 96-15L
5	1	Flip 2011-13L
6	1	Flip 2010-101L
7	1	Idleb 2
8	1	Flip 86-51L
9	1	Flip 2011-7L
10	1	Flip 2010-105L
11	1	Flip 2011-40L
12	5	Flip 2011-17L, 98-0331*99HSO50, Flip 96-50L, Flip 89-71L, Flip 90-25L
13	1	Flip 2010-19L
14	1	Flip 87-22L
15	1	Flip 2010-106L
16	1	Flip 2011-11L
17	1	Flip 2011-43L
18	1	Flip 2010-96L
19	1	Flip 86-45L
20	1	JL-3

Conclusion

The findings of the present study suggested that the material involved in this investigation had sufficient amount of diversity for important agronomic traits and may be exploited with great extent by resorting to hybridization which subsequently would result into the development of superior lines.

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