Electronic Journal of Plant Breeding, 6(2): 493-499 (June 2015)
ISSN 0975-928X

Research Note

Adaptability of exotic genotypes of lentil (*Lens Culinaris* [medik]) for rainfed farming condition of Madhya Pradesh

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(Received: 13 Oct 2014; Accepted: 22 Dec 2014)

Abstract

One hundred accessions from different lentil growing countries namely Egypt (17), Ethiopia, Iran (16), Iraq (3), Jordan (19), Lebanon (9), Morocco (15), Syria (20) and Turkey (20) were evaluated in the year 2012-13 for assessment of yield and yield characters viz., plant height, 50% flowering, days to maturity, primary branches, secondary branches, total pods per plant, filled pods per plant, unfilled pods per plant, seeds per plant, 100 seed weight and yield per plant. The genotypes had wide range of yield per plant. The genetic variability was highest in the accessions of Morocco for seeds per plant and 100 seed weight. The Lebanon accessions have 56.2 percent variation for seed yield plant^{-1}. The exotic accessions have high variability for seed yield plant^{-1} (40.03%), number of filled pods (39.58%), total pods plant^{-1} (36.04%) and number of filled pods (39.58%). Germplasm has been grouped into 13 and 21 clusters as per group average and complete linkage basis. The clusters having single genotypes have higher inter cluster genetic distance than clusters having more than two genotypes. The genetic distance in the present germplasm is independent of geographical origin.

Keywords
Lens culinaris, Cluster analysis, Genetic diversity, Correlation

Lentil (*Lens culinaris* [Medik]) is the second most important food legume of winter season in Madhya Pradesh after chickpea. It is grown in about 5.0 lakh hectares with annual production of 3.84 lakh tons. The productivity of lentil in the state is only 584 kg/ha which is below national average of 678 kg/ha. Lentil is mainly grown in marginal land with least management practices with zero (or) least irrigation in the state. The major constrains of low productivity is unavailability of improved cultivars with wilt resistance and of quality seeds. Quantitative traits provide an estimate of genetic diversity and various numerical taxonomic techniques have been successfully used to classify and measure the pattern of phenotypic diversity in the relationship of germplasm collections in a variety of crops by many scientists as in lentil (Ahmed *et al.*, 1997, Fratini *et al*., 2007 and Tullu *et al.*, 2008). Presently available high yielding varieties have longer duration of 120-135 days which suffer during terminal drought as few of the farmers afford to supply irrigation for the lentil crop. To combat this problem Indian Council of Agriculture

Research with the cooperation of International Centre for Agricultural Research for Dry land Areas launched the program of Pre-breeding in lentil for identification and development of lentil genotypes suitable to dry land farming. The major objectives of the project in Madhya Pradesh are – identification and development early maturing, wilt resistant genotypes through evaluation and identification of exotic accessions and through introgressions from the crosses of wild relatives of lentil with cultivated ones. Many workers emphasized the importance of genetic divergence in selection of parents for hybridization. The more diverse the parents, within the reasonable range the more would be the chance of improving the characters of question. Barulina (1930) first recorded detailed morphological descriptions of lentil landraces and species from Asia. The main characters in her study to define subspecies were pods, seeds and distinct differences in the length of flowers and secondary characters included size of leaflets, length of vegetation and height of plants. Erskine and Witcombe (1984) classified the world collection of lentil germplasm on the basis of morphological variations as days to flowering, days to maturity, plant height, seed yield, biomass yield, straw yield and 100-seed weight. Tullu et al. (2001) suggested that there was considerable genetic variation for phenological and morphological traits in the core collection of lentil that can be used to breed higher biomass and seed yielding cultivars. Morphological characterization is the first step in the classification and description of any crop germplasm (Smith and Smith, 1989). With this background, the present investigation was carried out to assess the genetic diversity among lentils of diverse eco geographical origin.

The material for present investigation comprised of 100 lentil accessions of diverse ecogeographical origin. These were screened for 9 morphological yield characters. The experiment was conducted at the research field of RAK College of Agriculture, Sehore, during winter of 2012-13. Each genotype was sown in one row plot of 4 m length with inter and intra row spacing of 30 cm and 10 cm, respectively in randomized block design with three replications. In each entry, ten plants were randomly tagged and used to collect data on nine distinct traits, namely, plant height, days to 50% flowering, days to maturity, number of pods per plant, number of seeds per plant, biological yield, harvest index, 100 seed weight and yield per plant following internationally recognized descriptor (Erskine and Williams,1980). The data were subjected to statistical analysis using D^2 statistics (Mahalanobis, 1936) and Tocher Method as described by Singh and Choudhary (1977) was used for determining the group constellations.

*Genetic Variability:*The highest range of variability for days to 50% flowering was observed in the accessions of Lebanon (63-79 days), closely followed by Iran (68-83 days), while for days to maturity it was observed in the accessions of Morocco and Lebanon (103-115 days). Accessions from Iran exhibited highest coefficient of variation for primary branches plant^{-1}(19.3%) and secondary branches plant^{-1} (29.9%). However, the range of variation was higher for primary branches plant $^{-1}$ in the accessions from Jordan, ranging from 2.0-4.3.The magnitude of variation for total number of pods plant^{-1} was highest (39.89%), ranging from 38.0 to 138.7in the accessions from Jordan, closely followed in the accessions from Lebanon (38.86%)., Percent of variation although was found highest (48.22%) in the accessions of Lebanon for total number of filled pods plant $^{-1}$ (33-107), the range of variation was higher (31-127) in the accessions of Jordan (Table 1).

Number of un-filled pods is a trait of negative significance. The least the un-filled pods, less the seed loss per plant. On this negative ranking, accessions from Jordan exhibited low coefficient of variation (23.85%) for number of un-filled pods plant^{-1} (6.7-13.7). Maximum number of seeds/pod (163 seeds plant^{1}) were found in one of the accessions of Morocco (IG 112128) and one from Egypt (158 in IG 129317). Overall seed size ranged from 2.0-3.2 g 100 seeds^{-1} in whole accessions. Per cent of variability was highest in the accessions of Morocco (25.19%), followed in the accessions from Egypt (22.56%). The highest grain size (3.2 g 100 seeds^{-1}) was found in IG 129319 of Egypt. For seed yield plant^{-1}, Lebanon accessions exhibited highest coefficient of variation (56.22%). However, the accession of highest seed yield plant^{-1} was observed in the IG 112128 (4.8 g) of Morocco. This accessions had both highest number of seeds plant^{-1}as well as seed yield plant^{-1}(Table 1). The incidence of highly significant variation among the accessions for the majority of the studied morphological traits is a sign of the presence of high degree of genetic variation implying great potential of the accessions in future breeding programs through selection. Considerable variations among the characters for use in breeding and selection programs have also been reported for various morphological characters (Sindhu and Mishra, 1982; Ramgiry et al., 1989; Sarker and Erskine, 2001).

On the basis of frequency of ranking of yield and component characters, high frequency of 1st ranking traits was observed in the accessions of Morocco (3/8), followed by in the accessions of Lebanon, Jordan and Iraq (2/8). Highest frequency of 2nd ranking traits was observed in the accessions of Lebanon (3/8), followed by Jordan and Egypt (2/8). These exotic accessions are being used in hybridization with Indian high yielding cultivars-JL 3 and JL2 for introgression of favorable yield characters. Significant positive association was observed of total pods per plant, filled pods per plant and seeds per plant with seed yield (Table 2).

*Genetic Diversity and relatedness:*The genetic distance analysis using unweighted pair group method of arithmetic means (UPGMA) dendrogram was constructed for measuring genetic diversity and relatedness among the accessions (Fig. 2). Cluster analysis indicated the extent of genetic diversity that is of practical use in plant breeding (Sultana et al., 2006). As per Group Average Classification, the genotypes formed 13 major groups + 10 single genotypic groups.

One of the landrace from Morocco (IG 112137) was independent of all the clusters in group average diversity. It showed its wider distance, independent of all the clusters formed. It also had the highest seed yieldplant^{-1}. Therefore, this accession can be used for introgression of yield in Indian cultivars. The two landraces (IG 129185, IG 129317) from Egypt also showed a separate cluster group with high yielding ability, Accession IG 12937 had high yield of 4.29 g plant^{-1}. This accession may be used for yield enhancement in Indian genotypes. These independent clusters of single genotypes are very different and diverse. These diverse genotypes independently can be used for hybridization with Indian cultivars for better introgression of genes for yield. The maturity of these cultivars is only between 107-117 days. Therefore, early maturing cultures of Indian origin can be improved for yield enhancement along with early maturity.

The intra cluster distances presented in Table 3 showed a range of 0.148 in cluster I to 0.983 in cluster XIII (Table 4). Inter cluster distances ranged from 0.974 (cluster III & X) to the highest of 2.124 (Cluster VI & XI). Exceptionally, inter cluster distance expressed between the clusters having more than two genotypes is lower than the independent genotypic clusters. This range was from 1.25 to 2.75. The highest inter cluster distance exhibited in between the genotypes of cluster VI and IG 2385 (Table 4). Genotypes of cluster VI (Lebanon IG 129214 Morocco (IG 112128) showed maximum diversity with many independent genotypes- IG 149 (2.58), IG 71456 (2.29), IG 2159 (2.53) and IG 482 (2.29) Table 3. It showed its wide diversity in genetic constitution of these genotypes from other ones. The genotypes included in these clusters were independent of geographical origin. No definite correspondence between geographic origin and genetic diversity of lentil has been observed in other crops like field pea (Gemechu et al., 2005) and safflower (Khan et al., 2008) suggesting that parental selection should be made on the basis of systematic assessment of genetic distance in a specific population rather than on geographic difference. Crop improvement is made through generating variability in desired traits followed by selection. Continued success in crop improvement can only be realized when new substantial variability is found and used in a population. Divergence between any two parents expresses the allelic differences between them (Dias et al., 2003). Crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants. Consequently, a crossing program should be conducted with putative parents belonging to different characters. Therefore, crosses between the members of clusters separated by inter-cluster distances are likely seemed to be beneficial for further improvement (S.Roy, 2013). The most important traits in the first principle component could preferably and mainly be represented by seed yield and pods per plant. Seed yield is the most interrelated variable to the rest of the traits. The first principle component, therefore, could be identified as yield related variables. The most significant variables of the second, third and fourth principle components included days to flowering, secondary branches and seed number per pod whereas the rest of the traits did not contribute enough (Abdul Latief et al, 2011).

Acknowledgment

The authors are thankful to International Centre for Agricultural Research in Dry Areas and Indian Institute of Pulses Research, Kanpur for providing seed material.

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Table 1. Range and variation for yield characters in accessions of lentil from different geographical origin

Origin& No. of accessions	Statistics	Plant height (cm)	Days to 50 % flowering	Days to maturity	No. Of Primary Branches	No. Of secondary Branches	No. Of Total Pod	No. Of filled Pods	No. Of unfilled Pods	Seeds per Plant	100 Seed Weight	Yield per plant	Frequency of traits ranked first	Frequency of traits ranked second
Egypt	% variation	8.97	4.32	3.44	11.37	14.58	31.41	35.35	34.92	39.42	22.56	35.00		
(13)	Rank	6	7	5	7	7	6	6	5	2	2	5	000/8	002/8
	Max.	35.0	81.0	115.0	3.7	8.0	128.3	115.7	20.3	158.3	**2.9**	4.3		
	Min.	25.5	71.0	103.0	2.7	5.0	47.3	37.3	6.0	42.0	**1.1**	1.3		
Ethiopia	% variation	7.88	2.19	0.82	15.93	10.47	15.24	18.13	23.85	24.11	11.91	22.83		
(7)	Rank	7	8	8	8	8	8	8	2	8	8	8	000/8	001/8
	Max.	31.5	79.0	111.0	3.7	8.7	88.0	75.0	14.0	114.3	2.0	3.0		
	Min.	25.0	73.0	108.0	2.3	6.0	56.3	47.3	7.0	58.3	1.3	1.4		
Iran	% variation	6.50	7.31	3.64	19.30	29.91	33.43	33.03	70.43	46.60	21.47	44.11		
(11)	Rank	8	**2**	4	1	1	5	7	8	6	3	3	002/8	001/8
	Max.	27.5	**83.0**	115.0	**4.0**	**11.7**	108.3	88.3	**34.7**	120.7	2.4	3.6		
	Min.	23.0	**68.0**	104.0	**2.3**	**4.7**	45.3	38.0	**4.0**	10.0	1.1	1.0		
Jordan	% variation	16.23	6.29	3.95	18.98	25.95	39.89	43.82	23.85	36.85	19.52	28.11		
(11)	Rank	4	3	3	2	4	1	2	1	4	4	6	002/8	002/8
	Max.	35.0	85.0	117.0	**4.3**	10.0	**138.7**	**126.7**	13.7	127.0	2.9	2.7		
	Min.	19.5	68.0	104.0	**2.0**	3.7	**38.0**	**31.3**	6.7	39.3	1.5	1.1		
Lebnon	% variation	9.97	7.52	4.46	14.80	29.73	38.86	48.22	62.69	40.66	18.68	56.22		
(6)	Rank	5	1	2	5	2	2	1	7	3	5	1	002/8	003/8
	Max.	30.5	79.0	**115.0**	3.7	**9.0**	**122.7**	**106.0**	37.0	127.3	2.4	**4.3**		
	Min.	23.5	63.0	**103.0**	2.3	**3.7**	**41.0**	**32.7**	7.3	41.7	1.3	**1.0**		

Table 1 contd.

Origin	Statistics	Plant height (cm)	Days to 50 % flowering	Days to maturity	No. of Primary Branches	No. of secondary Branches	No. of Total Pod	No. of filled Pods	No. of unfilled Pods	Seeds per Plant	100 Seed Weight	Seed yield per plant	Frequency of traits ranked first	Frequency of traits ranked second
Morocco	% variation	17.29	4.72	4.77	13.86	27.77	36.01	**36.91**	52.82	28.32	25.19	46.05		
(9)	Rank	3	5	1	6	3	3	4	6	1	1	2	003/8	001/8
	Max.	41.5	82.0	**115.0**	3.7	9.7	152.0	126.7	27.3	163.0	**3.2**	**4.8**		
	Min.	22.5	69.0	**103.0**	2.3	4.7	52.0	44.0	4.7	61.3	**1.5**	**1.2**		
Syria	% variation	19.25	3.72	2.43	8.82	22.49	27.70	33.33	34.27	33.67	16.43	35.74		
(13)	Rank	2	6	6	8	6	7	3	3	5	7	4	000/8	001/8
	Max.	**37.0**	85.0	117.0	3.7	10.0	103.0	94.0	19.3	123.7	2.5	3.8		
	Min.	**16.5**	75.0	108.0	2.7	4.7	38.0	28.0	6.7	33.7	1.3	1.1		
Turkey	% variation	29.96	6.25	3.29	24.15	24.70	39.66	40.80	51.86	40.98	27.49	33.24		
(11)	Rank	1	4	7	3	5	4	5	5	7	6	7	001/8	000/8
	Max.	**32.0**	84.0	116.0	3.7	8.3	103.0	88.3	18.7	117.3	2.5	2.7		
	Min.	**13.0**	72.0	107.0	2.0	4.3	36.3	29.7	5.7	36.7	1.3	1.1		
	General Mean	27.08	76.89	110.78	3.01	6.90	74.47	62.83	11.65	80.22	1.91	2.12		
	CV %	15.32	6.05	3.88	16.48	24.37	36.047	39.58	50.40	38.95	22.17	40.03		

Table 2. Correlations of yield contributing traits in lentil germplasm and proportion of variance explained by the characters

Characters	Plant height	Days to 50 % flowering	Days to maturity	Primary Branches	secondary Branches	Total Pods/plant	Filled Pods/plant	Unfilled Pods/plant	Seeds / Plant	100 Seed Weight	Seed yield per plant
Plant height		-0.179	0.057	0.128	-0.012	0.243	0.266	-0.028	0.303	0.069	0.186
Days to 50 % flowering			0.526**	0.077	0.026	-0.152	-0.130	-0.146	-0.117	-0.144	-0.261
Days to maturity				0.109	0.249	-0.040	-0.015	-0.114	-0.003	-0.287	-0.237
Primary Branches					0.540**	0.197	0.204	0.015	0.215	-0.075	-0.026
Secondary Branches						0.190	0.241	-0.146	0.215	-0.226	-0.081
Total Pods/plant							0.887**	0.350*	0.827	0.034	0.600**
Filled Pods/plant								0.163	0.850**	0.029	0.601**
Unfilled Pods/plant									0.189	0.026	0.202
Seeds / Plant										-0.047	0.643**
100 Seed Weight											0.271
Eigen values	2.38	2.00	1.03	0.22	0.97	1.64	0.11	1.09	0.55	0.66	0.31
Proportion of % variance explained	21.64	18.24	9.42	1.99	8.84	14.97	0.98	9.92	5.01	6.06	2.87

Table 3. Genotypes included in cluster with their sources

Clusters	Genotypes & source	
	Group Average Classification	**Nos**
I	Jordan (IG 20), Morocco (IG 71432, IG 71433)	3
II	Egypt (IG 129313), Iran (IG 134327)	2
III	Jordan (IG 2148, IG 9)	2
IV	Iran (IG 2374), Egypt (IG 129287, IG 129304)	3
V	Syria (IG 73710), Jordan (IG 73798)	2
VI	Lebanon (IG 129214), Morocco (IG 112128)	2
VII	Turkey (IG 161), Ethiopia (IG 129560), Syria (IG 71646)	3
VIII	Syria (IG 26, IG 4448), Jordan (IG 2), Egypt (IG 129293)	4
IX	Egypt (IG 129185, IG 129317)	2
X	Lebanon (IG 842), Egypt (IG 70238, IG 129302), Turkey (IG 70203, IG 71498, IG 70208, IG 5431, IG 73945) , Jordan (IG 5069), Ethiopia (IG 69502, IG 69522, IG 69568), Morocco (IG 71434, IG 130219), Syria (IG 71531), Iraq (IG 54)	16
XI	Lebanon (IG 840), Jordon (IG 21, IG 5190), Syria (IG 73920, IG 71603, IG 4545), Iran (IG 136607, IG 223, IG 2334), Turkey (IG 70198)	10
XII	Turkey (IG 70191, IG 70233), Lebanon (IG 485, IG 2280), Ethiopia (IG 936, IG 69549, IG 70174), Morocco (IG 71451, IG 112131), Jordan (IG 5305), Iran (IG 71352, IG 2284, IG 2413), Egypt (IG 129315, IG 71487, IG 129291, IG 129319)	17
XIII	Syria (IG 71519, IG 71685, IG 73712, IG 73717, IG 71685), Jordan (IG 73816), Turkey (IG 563)	7
XIV		
XV		
XVI		
XVII		
XVIII		
XIX		
XX		
XXI		
	Individual genotypic clusters(Independents)	
	Iran (IG 2159, IG 2385, IG 134356), Morocco (IG 71456, IG 112137), Turkey (IG 149), Egypt (IG 129309), Lebanon (IG 482), India (JL 3), Jordan (IG 5320),	9

Table 4. Intra and inter cluster distances of genotypes (Based on Group average)

Cluster	C-I	C-II	C-III	C-IV	C-V	C-VI	C-VII	C-VIII	C-IX	C-X	C-XI	C-XII	C-XIII
C- I	**0.148**	1.328	1.715	1.460	1.758	0.875	1.246	1.774	0.780	1.347	1.792	1.764	1.609
C-II		**0.469**	1.450	1.068	1.156	1.539	1.470	1.895	1.539	1.338	1.943	1.480	1.937
C-III			**0.630**	1.548	1.205	**2.140**	1.377	1.458	1.843	0.974	0.894	1.013	1.002
C-IV				**0.740**	1.477	1.094	1.037	1.536	1.142	1.200	1.874	1.368	1.683
C-V					**0.778**	1.895	1.163	1.642	1.244	1.107	1.154	1.090	1.154
C-VI						**0.802**	1.548	**2.080**	1.220	1.883	**2.022**	**2.124**	2.145
C-VII							**0.860**	1.637	1.230	1.126	1.451	1.298	1.179
C-VIII								**0.874**	1.678	1.897	1.158	1.088	1.322
C-IX									**0.870**	1.397	**2.032**	1.836	1.733
C -X										**0.916**	1.077	1.999	1.706
C-XI											**0.926**	1.604	1.542
C-XII												**0.948**	1.529
C-XIII													**0.983**
Individuals													
IG 2159	1.84	1.83	1.08	1.85	1.55	**2.53**	1.49	1.47	2.1	1.25	1.15	1.08	1.39
IG 71456	1.58	1.72	1.77	1.91	1.37	**2.29**	1.68	1.68	1.62	1.27	1.59	1.56	1.61
IG 149	**2.43**	**2.36**	1.89	2.07	2.2	**2.58**	1.86	1.78	**2.5**	1.73	1.34	1.29	1.38
IG 2385	1.78	1.67	1.18	1.98	1.41	**2.75**	1.82	1.88	**2.26**	1.37	1.5	1.69	1.69
IG 129309	**2.16**	1.68	0.86	1.59	1.88	2.09	1.79	1.4	2.15	1.35	1.53	1.02	1.56
IG 134356	2.00	1.79	1.59	2	1.84	**2.17**	1.78	1.67	2.04	1.52	1.58	1.63	1.19
IG 482	**2.40**	1.82	1.89	1.68	**2.32**	**2.29**	**2.24**	2.10	**2.49**	1.9	**2.15**	1.76	1.98
JL 3	1.79	2.02	1.67	1.61	1.49	2.07	1.58	1.78	1.73	1.56	1.95	1.77	1.82
IG 5320	1.74	1.49	1.35	1.19	1.46	1.97	1.45	1.59	1.12	1.15	1.68	1.36	1.69
IG 112137	2.15	1.89	2.11	1.15	**2.20**	1.08	1.67	2.18	1.77	1.80	**2.43**	1.81	2.1