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Genetic diversity in lentil (*Lens culinaris*)

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Abstract

The investigation was carried out in a complete randomized block design with three replications with thirty lentil genotypes. The main objective of present research work was to assess the genetic divergence for yield and yield contributing character. The cluster II showed maximum number of genotypes. Generally, the genotypes within a group showed little divergence from each other than from the genotypes of different groups. The relative divergence of each cluster from other cluster 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. Cluster I reported lowest mean value for days to flowering (61.93 days) and days to maturity (123.75 days). Number of fruiting branches contributed maximum variance (29.66%) followed by 100 grain weight (22.42%), number of seeds per pod (11.26) etc. Therefore, these characters should be given more stress for the selection and choice of parents for hybridization. In view of considerable genetic diversity in lentil found in the present study, their appearance had sufficient scope for genotypic improvement through hybridization between the genotypes from divergent clusters.

Keywords: Genetic diversity, lentil.

Introduction

Lentil or Masur is one of the old Pulse crops, which provides a valuable and easily digestible protein (20.08-22.80). Lentil seeds are consumed as whole grains and as dehulled dhal. There are two types of lentil: the large seeded (macrosperma) and the small to medium sized seeded (microsperma) lentil. The color of seeds also varies with lines being brown, red, green or white. Lentil seeds are relatively higher in protein content (25 percentage), carbohydrates and calories than other legumes (Muehlbauer *et al.* 1981) ^[10]. Lentil is known by different names in various countries such as Lentil (French), Lenteja (Spanish), ados (Arabic), mereimek (Turkish), hiramame (japanese), and Masur (Hindi). It belongs to the family Leguminosae. Globally Lentil share only 5% of the total area under pulses where it occupies 3.765 million ha area and produces 3.165 million tons annually with productivity of 852 kg/ha (2002-03). It is predominantly grown in Asia which accounts for 80% of the global area and 75% of the world production. Highest productivity (2111kg/ha) has been reported from Australia followed by Canada (1265kg/ha), China, Syria, Turkey, Spain and Bangladesh (825kg/ha). In India Lentil is the second most winter pulse crop under which area, production and productivity is 1.32 million ha, 0.88million tonnes and 663kg/ha (2002-2003) respectively. The total production could be enhanced either by making horizontal expansion in area, which is not possible owing to high population growth, so none of the option left other than vertical expansion, which could be done opting a suitable breeding method. 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 (Zaccardelli *et al.*, 2012, Cristóbal *et al.*, 2014, Gautam *et al.*, 2014 and Katiyar and Kant, 2015) ^[17, 2, 3, 6]. 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. Recognizing the importance of genetic divergence in plant breeding experiments, the main objective of present research work was to assess the genetic divergence for yield and yield contributing character.

Materials and methods

The study was carried out in a complete randomized block design with three replications at the experimental farm of C.S.A.U.A. & T, Kanpur during Rabi 2003-04.

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with 30 lentil genotypes (K75, L4076, DPL 62, HUL 63, VL 508, PL 014, L4621, IPL 307, LL 933, LL 864, IPL 308, VL 509, PL 02, L4620, L 4652, IPL 408, L 4651, IPL 407, KLB 144, KLB 151, KLB 131, KLB 106, KLB 86-1, KLB 141, KLB 97-3, KLB 97-5, KLB 97-6, KLB-148, KLB 221-1). Each plot consisted six rows of 3 meter length. The distance between and within row was kept 30 cm and 10 cm respectively, standard agronomic package and practices were adopted to rise the good crop. The data were recorded on five randomly selected plants for eight quantitative characters viz., number of fruiting branches, 100 grain weight, plant height, grain yield per plant, number of pods per plant, number of seeds per pod, days to flowering and days to maturity. Genotypes were grouped into different clusters based on Tocher's method (Rao, 1952) ^[10]. The patterns of distribution of morphological variation were analyzed using Mahalanobis' generalized distances (D^2) (Mahalanobis, 1936) ^[36]. The D^2 is applied to estimate the distances within and between clusters.

Results and discussion

The D^2 value corresponding to all possible combination taking two varieties at a time were computed. The 30 diverse genotypes were grouped into 5 cluster with consideration that the genotypes within cluster had similar D^2 values among themselves than those from the inter cluster. Different clusters were formed according to closeness of the genotypes in respect of their D^2 values; intra cluster distances showed divergence among the genotypes within the cluster and inter cluster distance expressed relative divergence between the clusters. The intra and inter cluster distances have been presented in table 1. Grouping of genotypes into five clusters is in table 2. The Cluster 1 contains 8 genotypes viz., VL 508, PL 014, IPL 307, IPL 308, VL 509, KLB 97-5, and KLB 221-1. These genotypes took less time for days to flowering, days to maturity, medium number of pods per plant, medium 100 grains weight and grain yield per plant and maximum (1.80) number of seeds per pod among all the cluster and had medium bold seed. This cluster had the maximum distance from cluster III and minimum distance from cluster II. Intra cluster distance was (76.71). The cluster two consisted 10 genotypic viz. DPL 62, PL02, L4620, L4652, L4651, IPL407, KLB 144, KLB 131, KLB 106, KLB 97-6. This cluster showed maximum distance from cluster III and minimum from cluster IV and genotype included in this cluster are medium in plant height, days to flowering, days to maturity and had maximum in number of fruiting branches, number of pods per plant among the cluster and minimum in number of seeds per pod, 100 grain weight and average grain yield per plant. Intra cluster distance was (17.08). The cluster third consisted only three strain viz. IPL 408, KLB 141, KLB 97-3. This cluster had the maximum distance from cluster V and minimum from IV cluster. This cluster showed maximum in plant height, 100 grain weight and grain yield per plant and average in days to flowering, days to maturity, number of fruiting branches, number of pods per plant and number of seeds per pods. Intra cluster distance was (24.96). The cluster four included four genotypes namely HUL63, L4621, KLB 97-3 and LL864. The genotype in this cluster has maximum in days to maturity and minimum in plant height, number of fruiting branches among the cluster and average in days to flowering, number of pods per plant, number of seeds per

pod, 100 grain weight and grain yield per plant. The maximum distance of this cluster from cluster I and minimum distance from cluster III. Intra cluster distance was 21.10. K 75, L4076, KLB 86-6, KLB 86-1, KLB 148 genotypes were placed in cluster five. The genotypes includes in this cluster had maximum in number of days to flowering and minimum number of pods per plant and grain yield per plant and average in plant height, days to maturity, number of fruiting branches, number of seeds per pod and 100 grain weight among the cluster. The maximum distance from cluster II and the minimum distance from cluster I. 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 ^[8], Sultana, *et al.*, 2005 ^[15], Sirohi, *et al.*, 2007 ^[13], Solanki, 2007 ^[14], Tyagi and Khan 2010 ^[16] 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). 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 I reported lowest mean value for days to flowering (61.93 days) and days to maturity (123.75 days). Cluster II showed highest mean values for number of fruiting branches per plant (14.59) and number of pods per plant (104.41); cluster III had highest 100 grain weight (3.77 g) and grain yield per plant (5.26 g); cluster IV reported highest days to maturity (133.36 days); cluster V had maximum number of days to flowering (73.70 days), 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 4). No. of fruiting branches contributed maximum variance (29.66%) followed by 100 grain weight (22.42%), number of seeds per pod (11.26), plant height (10.34), grain yield per plant (9.88), Days to flowering (8.27), Number of pods per plant (7.29) and Days to maturity (0.82). Therefore, these characters should be given more stress for the selection and choice of parents for hybridization. Jeena and Singh (2002) ^[5], Kumar *et al.* (2002) ^[7], Haddad (2004) ^[4], Sarker *et al.* (2005) ^[16], Sirohi (2007) ^[13], Solanki (2007) ^[14] and Tyagi and Khan (2011) ^[17] also studied the genetic divergence in lentil. 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.

Table 1: Intra (diagonal) and inter cluster average distance (D²) in lentil genotypes.

	ClusterI	ClusterII	ClusterIII	ClusterIV	ClusterV
ClusterI	76.71	71.56	93.58	55.51	61.28
ClusterII		17.08	122.65	83.34	83.48
ClusterIII			24.96	97.62	112.14
ClusterIV				21.10	62.65
ClusterV					54.97

Table 2: Distribution of 30 lentil genotypes in different clusters.

Cluster No.	Number of genotypes	Name of genotypes included
I	8	VL 508, PL014, IPL 307, IPL 308, VL 509, KLB 151, KLB97-5, KLB 221-1,
II	10	DPL 62, PL 02, L4652, L4620, L4651, IPL407, KLB 144, KLB 131, KLB 106, KLB97-4,
III	3	IPL 408, KLB141, KLB 97-3
IV	4	HUL63, L 4621, LL 933, LL 864,
V	5	K 75, L-4076, KLB 86-6, KLB 86-1, KLB 148

Table 3: Mean values of five clusters for eight morphological characters in 30 lentil genotypes.

Cluster No.	Plant Height (cm)	Days to Flowering	Days to Maturity	No. of fruiting branches	No of pods/plant	No. of seeds/pod	100 grain weight (g)	Grain Yield/Plant (g)
I	40.08	61.93	123.75	11.07	88.86	1.80	2.78	4.30
II	41.12	64.97	130.15	14.59	104.41	1.58	2.69	4.50
III	42.98	63.73	129.45	13.42	87.17	1.62	3.77	5.26
IV	36.03	65.40	133.36	9.71	99.33	1.68	3.02	5.01
V	41.50	73.70	132.65	10.32	83.83	1.70	2.89	4.09
Max.	42.98	73.70	133.36	14.59	104.41	1.80	3.77	5.26
Min.	36.03	61.93	123.75	9.71	83.83	1.58	2.69	4.05

Table 4: Percent contribution of individual characters towards total divergence.

Characters	Times Ranked First	Contribution %
Plant Height (cm)	45	10.34
Days to Flowering	36	8.27
Days to Maturity	4	0.82
No. of fruiting branches	129	29.66
No of pods/plant	31	7.29
No. of seeds/pod	49	11.26
100 grain weight (g)	98	22.42
Grain yield per plant (g)	43	9.88
Total	435	99.86

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