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ORIGINAL ARTICLE

Genetic Divergence and Character Association of Seed Yield and Component Traits of Lentil (*Lens culinaris* M.)

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ABSTRACT
Lentil germplasm comprising 100 genotypes were evaluated during rabi of 2012-13 to identify traits related to seed yield under rain-fed condition. All the characters showed significant differences and wide variation among the genotypes. Seed yield/plant (73.75), biological yield (87.38) and number of pods/plant (78.86) showed high heritability coupled with high genetic advance as percentage of mean of 37.9 and 25.9 respectively. The correlations revealed that pods/plant, seeds/plant, biological yield, harvest index and hundred seed weight had positive and highly significant correlation with seed yield. The genotypes were grouped into 8 clusters and 10 individual clusters as per group average basis. The cluster III with cluster V showed maximum inter-cluster distance, revealing wide genetic divergence between clusters. The individual clusters have higher inter- cluster distance with cluster V. Hence, the genotypes from these clusters may be useful in hybridization programmes.
Keywords: *Lentil, Genetic diversity, Cluster, Heritability, Dendogram.*

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INTRODUCTION

Pulses are the second source of human food crops after cereals that are used to feed the world population especially in developing countries. High yield is the major purpose of lentil breeding especially under stress conditions [11].Lentil (*Lens culinaris* ssp. *Culinaris)* is a diploid (2n=2x=14), autogamous species and is one of the oldest crops in the world, which originated in the near East [21]. Lentil was one of the first domesticated plant species and its remains are as old as those einkorn, emmer, barley and pea [7]. It is predominantly grown in Asia which accounts for 80-95% global area and production, respectively. Lentil seeds are relatively higher in protein content (25 percent), carbohydrates and calories than other legumes [13]. Lentil as legume has a positive impact on soil fertility (N_2 fixation) [2].

The correlation coefficient gives a measure of the relationship between traits and provides the degree to which various characters of a crop are associated with productivity. Selection based on yield components is advantageous, if different yield related traits have been well documented [16].

The coefficient of variation, heritability and repeatability of traits are important guides to selecting polygenic yield determining traits [14]. Grain yield improvement through breeding for yield components would be most effective, if their variability, heritability and genetic advances are understood [1].

Biological yield, harvest index, number of seeds/plant, number of the pods/plant, number of main and lateral branches and the number of seeds/pod are the yield components determining the amount of seed yield [5], [9].

Determination of genetic diversity in plants is the first step when developing breeding programmes. Success of crop improvement programme in lentil depends upon genetic diversity and the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. Many workers

emphasized the importance of genetic divergence in selection of parents for hybridization. D^2 statistic developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among the genotypes.

MATERIAL AND METHODS

The present study was carried out at the experimental farm of All India Coordinated Research Project on MULLaRP, Rafi Ahmad Kidvai College of Agriculture Sehore Madhya Pradesh during rabi season of 2012-13. 100 indigenous Lentil Germplasm were used as material. All genotypes were planted in RCBD in a single row of 3m. Length and spaced 30x10 cm. Uniform agronomy practices were followed for the maintenance of the crop. Ten random plants of each genotype were taken from each replication at maturity and data recorded on nine agronomic characters, namely, plant height, days to 50 percent flowering, days to maturity, pods per plant, seeds per plant, biological yield, harvest index, 100 seed weight and yield per plant. The analysis of variance for RBD was carried out following Panse and Sukhatme [15]. The phenotypic and genotypic coefficients of variance were computed using the formula suggested by Burton and Devane [3]. Heritability in broad sense and expected genetic advance as percent of means were calculated according to the methods suggested by Johnson *et al.* [8]. The genetic correlation was worked out by using the formula as suggested by Johnson *et al.* [12]. The data were subjected to statistical analysis using D^2 statistics [14] and Tocher Method as described by Singh and Chudhary (1985) was used for determining the group constellations [18].

RESULTS AND DISCUSSION

Analysis of variance and coefficient of variability

The performance of different lentil genotypes for seed yield and yield attributing characters exhibited significant variability among the genotypes for all the characters.

Information on genetic variability and heritability is useful to formulate selection criteria for improvement of seed yield. The phenotypic coefficient of variation was also higher as compared to their respective genotypic coefficient of variation (Table1).

Table 1: Estimates of variability, heritability and genetic advance in lentil.

character	Range	PCV	GCV	Heritability (broad sense)%	GA as percent mean
Plant Height	25.93-35.70	7.636	4.764	38.91	6.11
Day of 50% flowering	58.33-84.33	6.297	6.062	92.68	12.02
Day of maturity	102-137	6.554	6.285	91.95	12.4
Number of pods/plant	84.33-172	16.006	14.214	78.86	25.9
Number of seeds/plant	39.40-159.33	23.2440	18.7129	64.81	31.0
Biological yield	8.33-24.2	21.0857	19.7107	87.38	37.9
Harvest index	14.88-34.92	15.4888	9.1879	35.18	0.111
100 seed weight	2.16-4.27	16.5012	7.4022	20.12	0.068
Yield/plant	2.25-6.20	25.5663	21.9567	73.75	0.387

It was observed that the genotypic coefficient of variation was maximum for seed yield (21.95) followed by biological yield (19.71) and seeds/plant (18.71) (Table1). However, moderate genotypic coefficient of variation was observed for pods/plant (14.21) followed by harvest index (9.18) and 100 seed weight (7.40). The rest of the traits showed the low values of genotypic coefficient of variation. This shows the genetic variability between these characters. Phenotypic coefficient of variation was maximum for seed yield (25.56) followed by number of seeds/plant (23.24) and biological yield (21.08). Whereas 100 seed weight (16.50), pods/plant (16.00) and harvest index (15.48) showed moderate phenotypic coefficient of variation however rest of the traits showed low values of phenotypic coefficient of variation. Maximum variation (phenotypic and genotypic) was exhibited by yield/plant, biological yield, seeds/plant and 100 seed weight. Similar results on variability for different traits have also been reported by Tyagi and Khan, Singh et al. and Haddad et al.[19], [17] and [6].

Heritability and genetic advance

Values of heritability in broad sense were highest for days of 50% flowering (92.68%) followed by days of maturity (91.95%) and biological yield (87.38%). Moderate values were obtained from pods/plant (78.86%) followed by yield/plant (73.75%) and seeds/plant (64.81%) (Table1). Low heritability was

observed for plant height (38.91%), harvest index (35.18%) and 100 seed weight (20.12%). low heritability estimate for plant height and high heritability estimate for days to maturity and biological yield are also reported by Chouhan et al. [4]. Also they indicated that identification of important yield contributing characteristics is also helpful to establish a successful breeding programme.

Values of genetic advance as percent mean were higher for yield/plant (79.76%), 100 seed weight (40.48%) and biological yield (37.9%). Whereas seed/plant (31.0%), pods/plant (25.9%) and days of maturity (12.02%) showed moderate values. Lowest values were exhibited by day of 50% flowering (12.02%), plant height (6.11%) and harvest index (0.92%).

Table 2: Genotypic (Above diagonal) and phenotypic (below diagonal) correlation coefficient among various quantitative characters in lentil.

S.No.	Characters	Plant Height	Day of 50% flowering	Day of maturity	Number of pods/plant	Number of seeds/plant	Biological yield	Harvest index	100 seed weight	Yield/plant
1	Plant Height		-0.125	-0.146	-0.091	-0.073	0.005	-0.091	0.155	-0.043
2	Day of 50% flowering	-0.170924		0.720**	0.054	0.025	-0.000	0.093	0.016	0.048
3	Day of maturity	-0.197310	0.753314		0.119	0.111	0.111	0.031	-0.023	0.101*
4	Number of pods/plant	-0.190878	0.050099	0.140375		0.8049**	0.821**	0.403**	0.237*	0.933**
5	Number of seeds/plant	-0.229226	0.029561	0.137029	0.932288		0.663**	0.317**	-0.150	0.750**
6	Biological yield	0.053150	-0.014754	0.109168	0.911134	0.837553		-0.053	0.212*	0.801**
7	Harvest index	-0.447133	0.188589	0.125606	0.300741	0.337906	-0.051343		0.320**	0.540**
8	100 seed weight	0.412657	0.018338	-0.003864	0.254180	0.170257	0.344302	0.163797		0.367**
9	Yield/plant	-0.138510	0.053525	0.134531	0.967920	0.913648	0.889500	0.401741	0.413584	

Correlation analysis

Seed yield was positively correlated with all other traits except plant height at both genotypic and phenotypic levels and the magnitude of correlation was mostly higher. Traits like pods per plant, seeds per plant, biological yield and 100 seed weight and harvest index were strongly related with seed yield as compared to other traits. Positive and significant correlation of seed yield with above characters have also been reported in lentil by Vir et al. and Kumar et al. [20], [10] and according to Ciftic et al. and Karavadut et al. [5], [9] biological yield, harvest index, the number of seeds/plant, the number of pods/plant and hundred seed weight are the yield components determining the amount of seed yield. Positive phenotypic and genotypic correlation of pods per plant with seed per plant, biological yield, harvest index, 100 seed weight and yield was observed. It depicts that plants with more pods will produce more seeds ultimately increase seed yield. Likewise seeds per plant had positive association with biological yield, harvest index and yield. Similarly biological yield showed positive correlation with 100 seed weight and yield. A positive and significant relationship among the number of pod, biological yield and the number of seed/plant was also reported by Luthra and Sharma [11]. Thus above all the characters may be considered as important for improvement of seed yield. Positive and significant phenotypic correlation were observed for days to maturity with days to flowering (0.720); pods per plant with seed per plant (0.804), biological yield (0.821), harvest index (0.403), 100 seed weight (0.237) and seed yield (0.933); seeds per plant with biological yield (0.663), harvest index (0.3170) and yield (0.750); biological yield with 100 seed weight (0.212) and yield (0.801); harvest index with 100 seed weight (0.320) and yield (0.540); 100 seed weight with yield (0.367). Seed yield exhibited significant phenotypic correlation with pods per plant, seeds per plant, biological yield, harvest index and 100 seed weight, such relationships are useful in breeding and may improve seed yield.

Genetic divergence analysis

On the basis of group average the genotypes were grouped into 8 clusters (Fig.1) and 10 individual cluster genotypes. Cluster VIII was the biggest cluster comprising 49 genotypes. Cluster VII comprised of 17 genotypes, cluster VI had 11 genotypes, while cluster II, III and IV comprised of 3 genotypes each and cluster I and V of 2 genotypes each.

The intra cluster distance ranged from 0.60 to 0.86 with highest intra cluster distance for cluster VIII (0.86) followed by cluster V (0.76) and cluster IV (0.74) (Table 3). The cluster I showed minimum intra cluster values of (0.60) indicating more closeness between genotypes of cluster.

Table 3: 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- I	**0.601**	1.706	1.871	1.140	1.304	1.660	1.339	**2.057**
C-II		**0.681**	1.613	1.662	1.913	1.596	1.040	1.310
C-III			**0.689**	1.290	**2.484**	1.838	1.374	1.876
C-IV				**0.701**	1.642	1.791	1.193	1.979
C-V					**0.765**	1.791	1.710	**2.208**
C-VI						**0.657**	1.136	1.172
C-VII							**0.749**	1.143
C-VIII								**0.868**
Individuals								
IC 201680	1.145	1.547	1.174	**2.173**	**2.000**	1.296	1.034	1.590
IC201688	1.115	**2.457**	**2.502**	1.868	**2.153**	**2.538**	**2.188**	**2.869**
IC 267655	**2.275**	1.888	**2.103**	**2.111**	**2.081**	1.002	1.478	1.174
IC 267657	1.865	**2.016**	**2.191**	**2.250**	**2.555**	1.395	1.601	1.531
IC267662	**2.323**	**2.263**	**3.319**	**2.963**	**2.399**	1.747	**2.240**	**2.030**
IC 268236	1.911	1.694	**2.199**	**2.049**	**2.169**	1.374	1.425	1.266
IC 296887	**2.645**	**1.797**	**2.283**	**2.428**	**2.690**	1.613	1.633	1.005
IC 310826	**2.623**	1.726	**2.550**	**2.334**	**2.213**	1.787	1.756	1.415
IC 396796	1.932	1.469	1.395	1.654	**2.002**	1.118	1.113	1.355
JL 3	1.733	**2.264**	1.245	1.053	**2.355**	**2.496**	1.884	2.661

Table 4: cluster means of yield and yield traits in lentil germplasm.

Clusters	Characters								
	Height	50% Flow.	Maturity	Pods/Plant	No. of seeds/Plant	Bio. Yield	Yield/Plant (g)	HI %	100Seed Wt (g)
C- I	29.20	78.00	126.83	149.33	134.67	17.67	5.10	28.88	3.62
C-II	35.43	71.44	120.69	122.56	112.47	15.24	3.77	24.83	3.38
C-III	30.67	59.11	105.82	148.78	136.58	18.34	4.80	26.22	3.51
C-IV	29.63	69.78	119.33	150.17	135.80	21.33	5.06	23.80	3.75
C-V	29.37	83.17	134.67	152.92	135.17	18.55	4.02	21.72	2.97
C-VI	28.14	70.03	120.61	117.63	111.94	12.90	3.34	25.91	2.81
C-VII	31.18	70.20	116.61	126.90	116.74	15.85	3.97	25.13	3.42
C-VIII	31.18	68.80	113.32	105.85	90.15	12.45	2.96	23.85	3.33
G Mean	30.6	71.31625	119.735	134.2675	121.69	16.54125	4.1275	25.0425	3.34875
SED	2.2	7.0	8.6	18.2	16.8	3.0	0.8	2.1	0.3

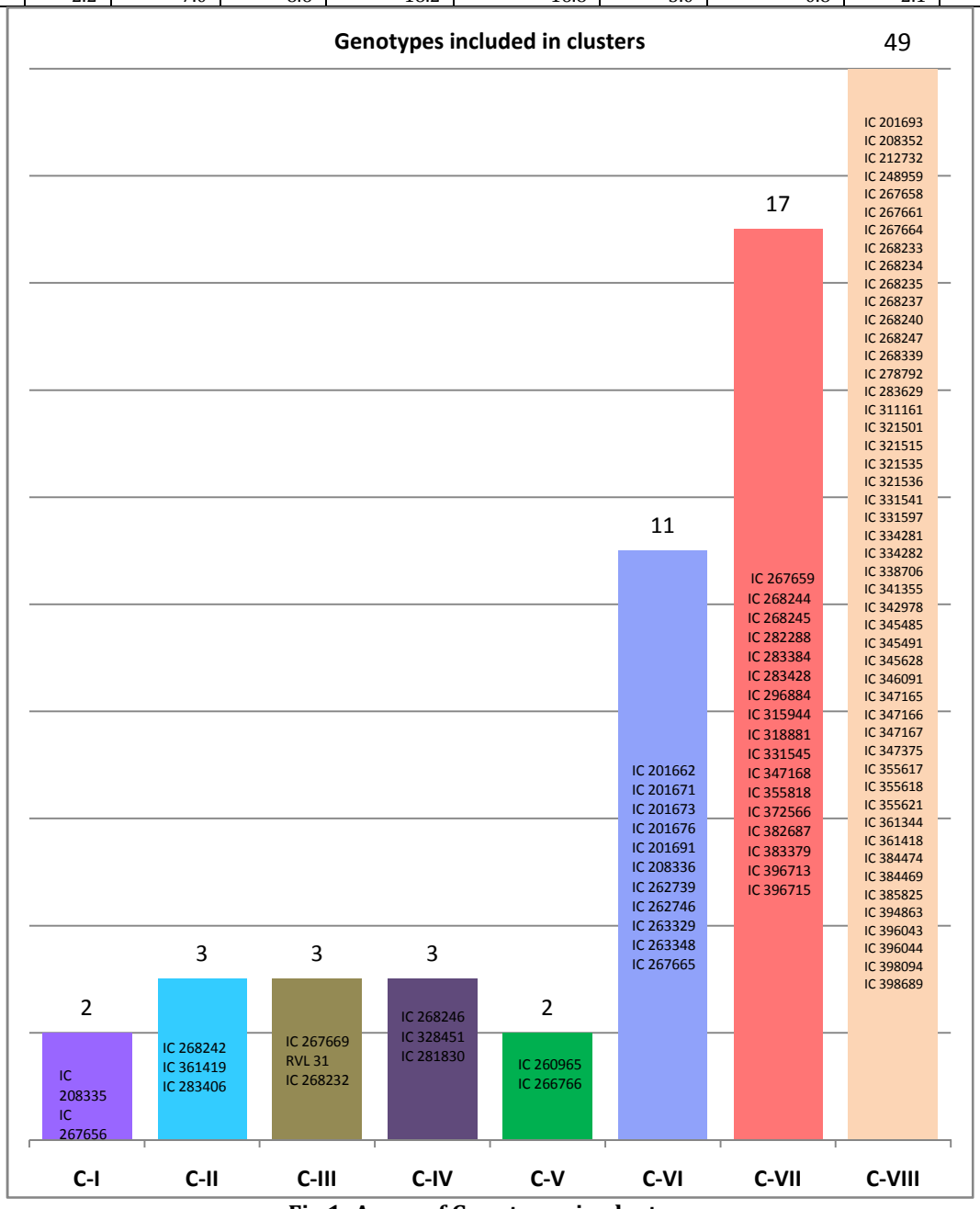

Fig 1: Array of Genotypes in clusters

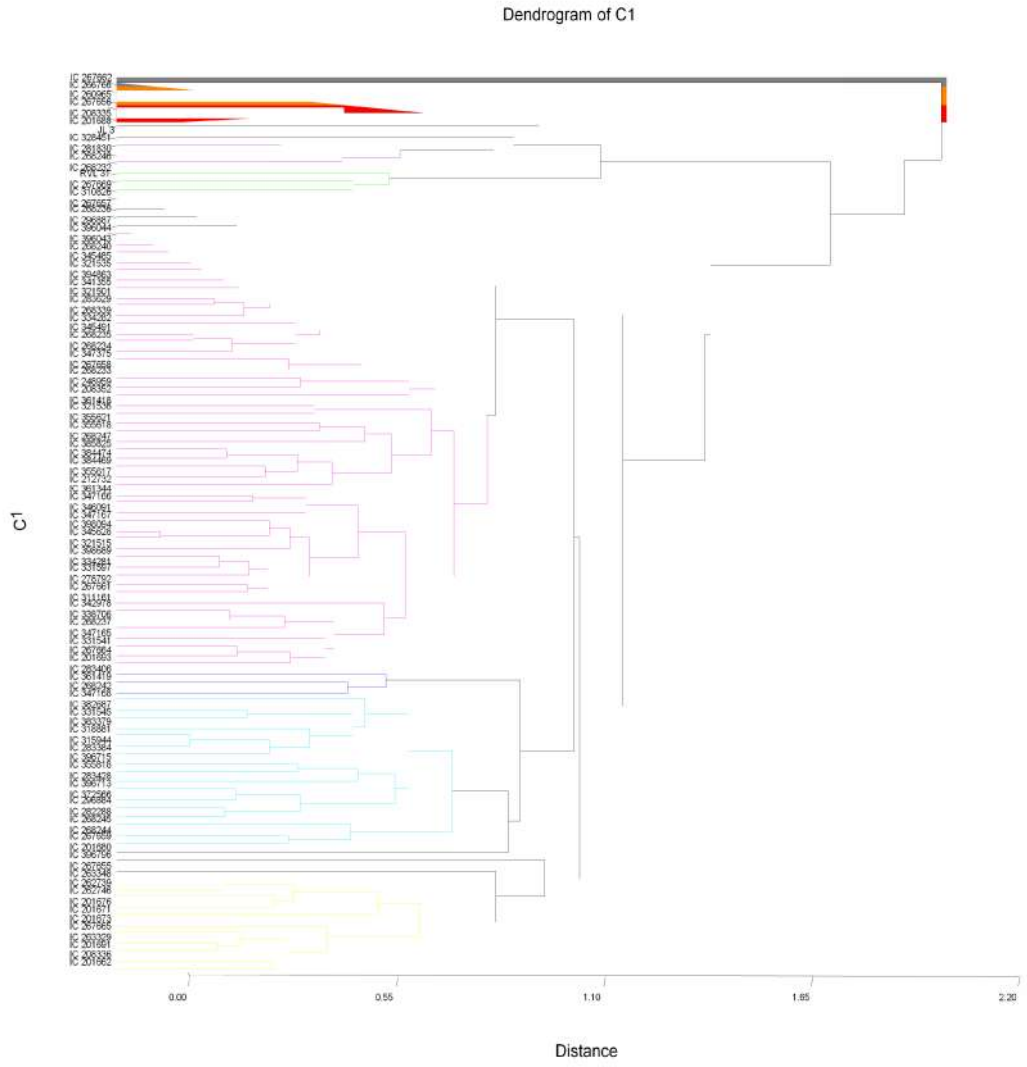

Fig 2: Dendogram of eight clusters based on group average linkage base in lentil Germplasm.

The inter cluster values on the basis of group average ranged from 1.04 to 2.48. The maximum inter cluster distance was observed between the clusters III and V (2.48) followed by cluster V and VIII (2.20) and cluster I and VIII (2.05). The minimum inter cluster distance was observed between cluster II and VII (1.04) indicating close relationship among the genotypes.

The cluster means for variable characters are presented in Table 4. The cluster number I and IV have significantly higher grain yield per plant along with more number of seeds per plant. However, there intercluster distance is very narrow indicating their closeness. The highest inter cluster distance between cluster III and V (2.484) along with above average yield per plant (4.80) and seeds per plant (136.58) would be of prime importance for making crosses to exploit maximum heterosis. Results showed that the crosses among the genotypes included in these clusters may give high heterotic response and thus better segregates.

All the single genotypes making individual cluster also exhibited higher intercluster distance with the genotypes of cluster V (Table 3) while 7 out of 10 genotypes exhibited significant inter cluster distance from cluster III and IV. The genotype IC 201688 had highest seed yield per plant (6.20g) and seeds per plant (145.4). It also had more divergence (2.153) with the genotypes of cluster V, III and II. The high yielding variety RVL 31 included in cluster III have more chance of elevation for seed yield per plant through present seed size of 3.66g/100 seeds to above 4g/100 seed weight.

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