Genetic Diversity of Yield Attributing Components and Seed Yield in Lentil (*Lens culinaris* Medik.)

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Author's contribution

The sole author designed, analysed, interpreted and prepared the manuscript.

Original Research Article

ABSTRACT

The experiment was conducted using 140 lentil genotypes at (farm name?) Bihar Agricultural University, Sabour, Bhagalpur in 2017-18. The genetic divergences were estimated using D^2 analysis where a number of clusters were formed considering all genotypes of indigenous and exogenous types. Genetic variation of genotypes in considerable traits was significant for selection of desired type that can be utilised in future breeding programme. The study on correlation, genotypic variability, and path analysis of seed yield and yield components were essential for determining the relevance of considerable traits in enhancement of seed yield. The total genotypes were grouped into 5 clusters viz. Cluster I was found to be the largest comprising 121 genotypes, followed by cluster III of 12 genotypes. Cluster II, IV had three genotypes each and V was monogenic. Seeds per plant, days to maturity and pods per plant contributed extreme divergence among the genotypes which can be integrated in enhancement of productivity of lentil. On the basis of cluster mean, intra and inter cluster distance and per se cluster III, IV and V may be used for their desired characters in breeding strategy. The genotypes BRL-1, BRL-2, BRL-3 LKH-1, LKH-2, LKH-3, FLIP 2010-73L-2, FLIP 2010-86L and X2011S-111-2 may be considered in breeding to gain high heterotic effect and also to improve the desirable transgressive segregants.

1. INTRODUCTION

Lentil (*Lens culinaris* Medik.) is herbaceous annual self pollinated diploid (2x=2n=14) pulse crop with erect or sub erect growth habit belonging to *Leguminosae* family. It is grown for its excellent nutrient status particularly protein and is an important part of the vegetarian diet in India. It is one of the principal crops cultivated in semi arid regions.

Globally, lentil shares only 5.38 percent of the total pulse production with annual production of 49.52 lakh tonnes and productivity 1140 kg/ha in the year 2013, compared to the productivity (786 kg/ha) of India during the year 2014-15. To mitigate the gap in Indian scenario, adaptation of suitable cultivation techniques with selection of appropriate genotypes is needed.

The major constraints of low productivity of lentil are reluctant nature of farmer particularly in use of seed and soil. Non availability of quality seeds, late sowing in rice fallow area, lack of suitable varieties, poor management in diseases, weed menace in addition to terminal drought are the cause of declining yield. In genetic improvement of a crop the type and extent of variability is desired in considerable characters. Information on the nature and magnitude of genetic divergence in population helps for choosing of diverse parents in meaningful hybridization [1]. The study of genetic diversity among genotypes is helpful in designing effective crop breeding strategy in lentil [2,1,3,4,5,6].

For determination of the extent of variability, the cluster analysis has importance [7]. D^2 statistical analysis is a quantitative measure of genetic divergence, though the clustering pattern of genotypes is arbitrary. The classification using generalized distance is functional, where the number of entries is not very large. Vairavan et al. [8] showed canonical analysis for initial grouping of large number of rice germplasm collections. But simple two-dimensional representation of multidimensional disposition of genotypes cannot be as precise as the Tocher's method of grouping takes into account the full multidimensional space, even when the two canonical vectors justify high proportion of variation [9]. In the present study, 140 indigenous and exotic germplasm were collected from different places with the objective of conservation of variability for their further used in varietal development/ improvement.

2. MATERIALS AND METHODS

The present experiment was conducted in Rabi 2017-18 at Bihar Agricultural University, Sabour, Bhagalpur. A number of 140 germplasm were collected from different regions of Bihar, IIPR(Kanpur), G.B.P.U.A.&T (Pantnagar), ICARDA (Lebanon) and NBPGR (New Delhi). The observations were recorded from five randomly selected plants of each entry considering ten plant traits *i.e.* days to maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, effective pods per plant, seeds per plant, seeds per pod, 100-seed weight and seed yield per plant. Genetic diversity was estimated by calculating [7] D^2 analysis. The genotypes were further grouped into different clusters considering Tocher's method [10].

3. RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating adequate genetic variability in the experimental material (Table 1). Genetic divergence among lentil germplasm lines was determined for seed yield and its components. The significant estimates of 'V' statistics during the analysis revealed significant differences among mean values of different correlated variables, thus analysis of genetic divergence among the tested lentil germplasm was considered to be relevant. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relations. The composition of clusters and values of inter and intra clusters distances are given in Tables 2 and 3, respectively. The results revealed that the inter cluster distance in most cases was larger than intra cluster distance suggesting wider diversity among the germplasm of different groups. These genotypes were grouped into 5 clusters. Cluster I was found to be the largest comprising 121 genotypes followed by cluster III having 12 genotypes in such a way that germplasm lines having minimum genetic distance were grouped in same cluster and *vice versa*. Cluster II, IV had three genotypes each and V was monogenic.

Table 1. Mean, S.E, critical difference and coefficient of variation of quantitative traits of lentil germplasm lines

Sl. No.	Traits	Mean ±SEM	CD Value		CV %
			5%	1%	
1.	Days to maturity	110.1 ± 0.51	1.51	2.02	0.87
2.	Plant height	34.3 ± 0.52	1.66	2.22	3.14
3.	Number of primary branches per plant	2.5 ± 0.17	0.37	0.40	7.38
4.	Number of secondary branches per plant	5.2 ± 0.29	0.53	0.71	6.61
5.	Total number of pods per plant	51.2 ±1.31	3.49	4.63	5.55
6.	Number of Effective pods per plant	36.8 ± 1.15	3.21	4.22	5.59
7.	Number of seeds per plant	58.9 ±1.33	3.38	4.41	3.58
8.	Number of seeds per pod	1.7 ±0.002	0.11	0.15	5.68
9.	100-seed weight (g)	2.2 ±0.09	0.13	0.20	4.98
10.	Seed yield per plant (g)	1.4 ±0.01	0.27	0.41	14.35

The distribution of genotypes from different eco-geographical regions into these clusters was apparently random [11] Genotypes of similar origin were grouped into different clusters and *vice versa*, thereby indicating non-relationship between geographical and genetic diversity. This tendency of genotypes to occur in clusters cutting across geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity [12]. This also suggests that the genotypes within cluster may have some degree of ancestral relationship. Similar findings were also reported by Sirohi et al. [13]. The genetic divergence is an outcome of several factors such as genetic drift, changing of breeding material, natural variation and artificial selection other than geographical and ecological diversification [14]. Therefore, genetic diversity should be given priority rather than geographic diversity to get more heterotic recombinants and desired transgressive segregants. However, such crosses may not yield proportionate heterotic response [15], and hence, recklessness should be taken in selecting divergent genotypes. Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high means for almost all component traits. Moreover, these divergent parents should have better combining ability to give results proportionate to heterotic response.

The intra cluster average D^2 values ranged from 443.39 to 719.46 (Table 3). The highest intra cluster distance (719.46) was observed in the cluster I, indicating wide genetic variation among the genotypes included in the cluster. It is reported that genotypes would produce more desirable breeding materials for achieving maximum genetic distance with regard to yield *per se*, provided that there is adequate complementation of gene effects of parental lines [16]. Therefore, genotypes from cluster I should be given emphasis, while selection of parents for hybridization programme since most of the elite breeding cultivars were included in this cluster.

The inter cluster D^2 value ranged from 365.41 to 9338.50. Minimum inter cluster D^2 value was obtained between clusters III and II (D^2=365.41) indicate that the genotypes of these clusters were genetically least diverse and almost of the same genetic architecture. Such genotypes can also be used in breeding programmes for developing biparental crosses between the most diverse and closest groups to break the undesirable linkages between yield and its associated traits (Haddad *et al.*, 2004) cluster V and I (D^2=9338.50), followed by cluster IV and I (D^2=8411.30), cluster V and II (D^2=4219.15) and cluster V and III (3295.54), revealing that genotypes included in these clusters are genetically diverse and may give rise to high heterotic response [17]. Similar results were also found by Qian and He [18].

Cluster means of germplasm for ten characters in lentil (Table 4) revealed that cluster V had maximum number of primary branches per plant (3.37), number of secondary branches per plant (7.21), total number of pods per plant (171.0), number of effective pods per plant (132.0), number of seeds per plant (233.10) and seed yield per plant (4.29 g). Cluster IV reported to be highest number of seeds per pod (2.41), whereas cluster I early maturing average plant type with highest 100- seed weight (2.25g). These clusters can be preferred in selecting germplasm lines for respective traits as they recorded good means.

Table 2. Distribution of genotypes in different clusters

Cluster	No. of genotypes	Percentage of total
I	121	89.09
II	3	0.73
III	12	8.47
IV	3	0.82
V	1	0.89
Total	140	100

Table 3. Average inter and intra cluster D^2 values for different clusters

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**719.46**				
Cluster II	1534.38	**0.00**			
Cluster III	2347.86	365.41	**443.39**		
Cluster IV	8411.30	3123.31	2642.63	**0.00**	
Cluster V	9338.50	4219.15	3295.54	1445.10	**0.00**

Table 4. Cluster mean for yield and yield contributing traits of 140entil genotypes

SI. No.	Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1.	Days to maturity	107.98	113.97	114.09	116.77	110.11
2.	Plant height	34.28	33.10	39.09	30.93	35.77
3.	Number of primary branches per plant	2.96	2.74	2.92	2.78	3.37
4.	Number of secondary branches per plant	5.19	6.75	5.83	6.71	7.21
5.	Total number of pods per plant	45.11	64.87	81.98	96.35	171.00
6.	Number of Effective pods per plant	31.60	58.07	65.39	81.56	132.00
7.	Number of seeds per plant	47.96	104.95	127.09	201.12	233.10
8.	Number of seeds per pod	1.41	1.67	1.74	2.41	1.61
9.	100-seed weight (g)	2.25	2.09	2.11	1.83	1.70
10.	Seed yield per plant (g)	1.08	1.49	2.09	3.87	4.29

Table 5. Contribution (%) of different characters towards clustering

SI. No.	Source	Times ranked 1st	Contribution %
1.	Days to maturity	2483	26.66
2.	Plant height	383	3.89
3.	Number of primary branches per plant	17	0.19
4.	Number of secondary branches per plant	147	1.48
5.	Total number of pods per plant	1309	12.94
6.	Number of effective pods per plant	119	1.29
7.	Number of seeds per plant	4497	46.12
8.	Number of Seeds per pod	38	0.39
9.	100-seed weight	561	5.63
10.	Seed yield per plant	139	1.41

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times, each of the yield component character appeared first in rank and its respective per cent of contribution towards genetic divergence was presented in Table 5. The results showed that number of seeds per plant (46.12%) contributed highest towards genetic divergence by taking 4497 times first rank, followed by days to maturity (26.66%) by 2483 times, total number of pods per plant (12.94%) by 1309 times, 100-seed weight (5.63%) by 561 times and plant height (3.89%) by 383 times.

4. CONCLUSION

The results indicated that the indigenous and exotic germplasm lines studied had a considerable level of variability that could be exploited in future breeding programs. On the basis of cluster mean, intra and inter cluster distance and per se cluster III, IV and V may be used for their desirable characters in breeding programme of lentil. Germplasm lines like, BRL-1, BRL-2, BRL-3 LKH-1, LKH-2, LKH-3, FLIP 2010-73L-2, FLIP 2010-86L and X2011S-111-2 were selected which could be intercrossed to obtain high heterotic effect and also to recover desirable transgressive segregants.

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COMPETING INTERESTS

Author has declared that no competing interests exist.

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