Study of Genetic Diversity on Yield and Yield Attributing Components in Lentil (*Lens culinaris* Medik.) Under Normal and Late Sown Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

The present investigation was carried out on thirty-six lentil genotypes at the farm of Bihar Agricultural University, Sabour, Bhagalpur in 2018-19. The genetic divergences were examined using Mahalanobis D2 statistics for two dates of sowing i.e normal sown and late sown condition. The presence of variation among genotypes was revealed by ANOVA for considerable traits which come out as significant for all traits under study except several primary branches per plant, the number of pods per cluster under both normal and late sown condition and the number of seeds per pod in late sown condition. The study on genotypic variability, correlation and path analysis was done to know the direct and indirect relationship on seed yield and yield components for enhancement of economic yield. The total genotypes were grouped into 7 clusters under a timely sown condition such as. Cluster I being the largest comprising 10 genotypes, followed by cluster II with 8 genotypes, cluster III with 7 genotypes, cluster IV had 6 genotypes. Cluster V with 3 genotypes and cluster VI and cluster VII was monogenic. Coming to late sown condition, five clusters were formed displaying cluster II with a maximum number of genotypes (18 genotypes) followed by cluster I (11genotypes), cluster III (5 genotypes) and lastly, cluster IV and V were

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monogenic. 100 seed weight contributed maximum towards genetic divergence followed by grain yield per plant and number of pods per plant in timely sown and 100 seed weight chased by the number of pods per plant and number of secondary branches per plant under a late sown environment which can be integrated into the enhancement of productivity of lentil. Owing to the results of inter-cluster distance and mean performance of clusters for different traits, the genotypes such as FLIP 2010-86L and X2011S-172-1 under normal sown and likewise, Pusa Vaibhav and IPL-406 under late sown environment are expected to trigger the heterotic combination and obtain the desirable segregants for yield and its determinants.

1. INTRODUCTION

Lentil (*Lens culinaris* Medik.) is herbaceous annual self-pollinated diploid (2x=2n=14) pulse crop with erect or suberect growth habit belonging to *Leguminosae* family. It is one of the nutritious food legumes with various uses as food and fodder. It is one of the principal crops cultivated in semi-arid regions. Globally, lentil shares only 5.38 per cent of the total pulse area with an annual production of 49.52 metric tonnes and with the productivity of 1140 kg/ha in the year 2013, compared to the productivity (786 kg/ha) in India during the year 2014-15. To lessen this gap in Indian scenario, we need appropriate genotypes for genetic improvement of a crop for which nature and magnitude of genetic divergence in the population should be known to identify genotypes in choosing of diverse parents in meaningful hybridization.

In the context to quantify the degree of divergence, D^2 statistics is the most potent biometrical tool used in various crops [1]. D^2 statistics employs multivariate distribution of natural variation to design the dispersion matrix. It tells about the genotypic and environmental variation. In D^2 analysis relative contribution of a character or traits is determined by the percentage of variation present in genotypes, that avoiding bias in choice [2]. Based on the D^2 value a bunch of different genotypes are classified into different clusters based on D2 statistical value of Tocher's method. In the present study, 36 indigenous and exotic germplasm were analysed from different places with the aim to known its variability for their further used in varietal development/ improvement.

2. MATERIALS AND METHODS

The present research was conducted in Rabi 2018-19 at Bihar Agricultural University, Sabour, Bhagalpur. Lentil lines were collected from different regions of Bihar, IIPR (Kanpur), G.B.P.U.A.&T (Pantnagar), ICARDA (Lebanon) and NBPGR (New Delhi). The data were noted from five randomly selected plants of each lines considering thirteen plant traits *i.e.* days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per cluster, number of pods per plant, filled pods per plant, seeds per pod, 100-seed weight and grain yield per plant, biological yield per plant and harvest index. Genetic diversity was estimated by calculating D^2 analysis. The genotypes were further organised into different clusters based on Tocher's method.

3. RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters except several primary branches per plant, the number of pods per cluster under both normal and late sown condition and number of seeds per pod in the late sown condition which indicated adequate genetic variability in the experimental material. A 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 3-6, respectively. The results revealed that the inter-cluster distance in most cases was larger than intracluster distance suggesting wider diversity among the germplasm of different groups. These genotypes were grouped into 7 clusters under timely sown condition. Cluster I being the largest comprising 10 genotypes, followed by cluster II with 8 genotypes, cluster III with 7 genotypes, cluster IV had 6 genotypes. Cluster V with 3 genotypes and cluster VI and cluster VII was monogenic. Coming to late sown condition, five clusters were formed displaying cluster II with a maximum number of genotypes (18 genotypes) followed by cluster I (11

genotypes), cluster III (5 genotypes) and lastly, cluster IV and V were monogenic as given in Tables 1 and 2 under normal and late sown condition respectively.

The distribution of genotypes from different eco-geographical regions into these clusters was random. 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 but also show some degree of ancestral relationship. Similar findings were also reported by Sharma et al. [3], Koul et al. [4]. 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. Therefore, genetic diversity should be given priority rather than geographic diversity to get more heterotic recombinants and desired transgressive segregants.

The inter-cluster distances were more than intracluster distance stating wide genetic diversity among lentil genotypes. Similar results were stated by Sharma et al. [3]. The intracluster average D^2 values ranged from 0 (VI and VII) to 32.52 (III) in normal condition (Table 3) while it ranged from 0 (IV and V) to 94.81 (II) in late sown condition (Table 4). Utmost intracluster distance was observed in cluster IV (116.83) showing wide diverse nature of genotypes in this cluster followed by cluster II (65.30) and cluster I (42.61) in normal sown condition whereas, within-cluster II (94.81) followed by cluster I (25.05) and cluster III (13.98) in late sown condition. The highest intra-cluster distance among genotypes from these clusters could be exploited as parental lines in lentil hybridization programmes owing to their mean performance within their group.

The inter-cluster D^2 value ranged from 167.94 to 10327.31 in normal sown and ranged from 147.84 to 9500.60 in late sown condition. The apex inter-cluster distance was observed between cluster VI and VII (10327.31), followed by cluster II and VII, cluster IV and VI and cluster III and VII in normal sown condition while in late sown condition the peak inter-cluster distance was noted between cluster IV and V (9500.62), followed by cluster II and V, cluster I and V and

cluster III and IV indicating enough genetic diversity among the genotypes between these aforesaid groups. Minimum inter-cluster D^2 value was obtained between clusters I and V (D^2=167.94) in a normal while between cluster I and III (D^2=147.84) in late sown condition indicate that the genotypes of these clusters were genetically least diverse and most 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. Earlier scientists have reported the same, hybridization between genetically distant genotypes to generate promising breeding material. The report is in congruity with reports of Gupta et al. [5], Singh and Gupta [6], Tyagi and Khan [7], Jewel et al. [8], Singh et al. [9].

Table 1. Distribution of genotypes in different clusters (Normal sown)

Cluster	No. of genotypes
I	10
II	8
III	7
IV	6
V	3
VI	1
VII	1

Table 2. Distribution of genotypes in different clusters (Late sown)

Cluster	No. of genotypes
I	11
II	18
III	5
IV	1
V	1

Cluster means of germplasm for different characters in lentil is presented in Tables 5 and 6 for normal and late sown condition respectively. The experiment revealed that cluster VII had the highest mean value for the number of pods per plant, the number of filled pods per plant, 100 seed weight, grain yield per plant, and biological yield per plant in normal sown condition advocating directly towards an increase in yield potential with the lowest mean value for plant height. But under late sown condition, cluster V had highest mean value for several secondary branches per plant, 100 seed weight, grain yield per plant, biological yield per plant and harvest index which influences better yield under heat

stress condition. Cluster VI showed the lowest mean value for days to 50% flowering and days to maturity in normal sown condition likewise, under late sown condition, cluster I showed lowest mean value for days to 50% flowering and days to maturity suggesting better yield potential. Cluster V had the highest mean value for the number of secondary branches per plant and cluster IV showed highest mean value for harvest index in normal condition indicating better yield potential and lastly, under late sown, Cluster IV had the highest mean value for number of pods per plant, number of seeds per pod, number of filled pods per plant with lowest mean value of plant height indicating direct increase in yield

potential of lentil. The statements are in agreement with Yadav et al. [10], Gupta et al. [5], Kumari [11], Sirohi et al. [12], Solanki et al. [13], Jewel et al. [8], Tyagi and Khan [7] and Singh et al. [14].

The characters contributing maximum divergence needs greater emphasis to identify the clusters for selection of parents in the respective cluster for hybridization for their respective environment. The results showed that the highest contribution in reference to genetic divergence was exhibited by 100-seed weight (92.86%) followed by grain yield per plant (2.54%), number of pods

Table 3. Average inter and intra cluster D^2 values for different clusters (Normal sowed)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	42.61	849.29	259.96	904.78	167.94	2191.67	3068.52
Cluster II		65.3	218.92	3340.17	1603.12	366.59	6976.6
Cluster III			32.52	1988.33	719.06	1013.91	4937.05
Cluster IV				116.83	375.58	5737.67	749.7
Cluster V					37.83	3357.32	1945.12
Cluster VI						0	10327.31
Cluster VII							0

Table 4. Average inter and intra cluster D^2 values for different clusters (Late sown)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	25.05	363.14	147.84	1854.39	3013.96
Cluster II		94.81	884.82	692.68	5253.4
Cluster III			13.98	2948.18	1907.59
Cluster IV				0	9500.62
Cluster V					0

Table 5. Cluster mean for yield and yield contributing traits of 36 lentil genotypes (Normal sowed)

Sr. no	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1	Days to 50% flowering	82.37	83.17	82.38	81.33	83.11	81.33	82.67
2	Days to maturity	123.73	124.92	124.67	125.44	126.56	122.33	122.33
3	Plant height	37.17	39.03	39.13	39.97	42.5	39.69	33.57
4	No. of secondary branches per plant	7.66	8.42	8.78	7.82	10.22	7.56	7.56
5	No. of pods per plant	99.18	119.38	110.5	139.7	136.73	125.93	151.13
6	No. of filled pods per plant	90.44	107.49	99.22	126.5	124.24	115.33	143.93
7	100 Seed weight	2.69	2.01	2.33	3.38	2.95	1.58	4.01
8	Grain yield per plant	4.63	4.15	4.36	8.33	7.7	3.25	12.09
9	Biological yield per plant	9.63	8.24	8.85	15.69	14.45	8.82	22.7
10	Harvest index	48.28	50.27	50.41	53.86	53.74	37.27	53.62

**Table 6. Cluster means for yield and yields contributing traits of 36 lentil genotypes
(Late sown)**

Sr. no	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1	Days to 50% flowering	61.24	61.65	62.87	64.67	63.33
2	Days to maturity	99.15	99.26	99.47	99.67	106
3	Plant height	40.58	39.93	39.68	39.01	42.88
4	No. of secondary branches per plant	7.07	7.14	7.47	5	8.44
5	No. of pods per plant	88.63	104.63	76.36	128.73	112.59
6	No. of seeds per pod	1.76	1.7	1.68	1.8	1.2
7	No. of filled pods per plant	77.02	90.21	65.49	104.8	103.24
8	100 Seed weight	2.53	2.12	2.79	1.52	3.82
9	Biological yield per plant	3.47	3.42	3.16	2.84	6.48
10	Harvest index	7.32	6.94	5.85	5.22	11.68
11	Grain yield per plant	47.62	49.14	55.58	54.92	55.97

per plant (1.59%), number of secondary branches per plant (1.43%), plant height (0.64%) and harvest index (0.48%) in normal sown condition while in late sown condition, 100-seed weight offered maximum towards genetic divergence (86.67%) followed by the total number of pods per plant (7.62%), number of secondary branches per plant (2.22%), grain yield per plant (1.11%), number of filled pods per plant (0.79%), plant height (0.64%) and biological yield per plant (0.48%).

4. CONCLUSION

The results indicated that the indigenous and exotic germplasm lines studied had a considerable level of divergence that could be exploited in future breeding programs. Based on cluster mean, intra and inter-cluster distance and per se cluster, VII and VI (for normal sown condition) and cluster IV and V (for late sown condition) may be used for their desirable characters in a breeding programme of lentil. Genotypes like X2011S-172-1, FLIP 2010-86L (normal sown condition) and IPL-406 and Pusa Vaibhav (for late sown condition) were selected which could be intercrossed to obtain the high heterotic effect and also to recover desirable transgressive segregants.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Haydar FMA, Paul NK, Khaleque MA. D^2 statistical analysis of yield contributing traits in maize (Zea *mays* L.) inbreds. Bangladesh Journal of Botany. 2015;44(4): 629-634.

2. Bersimis S, Psarakis S, Panaretos J. Multivariate statistical process control charts: An overview. Quality and Reliability Engineering International. 2007;23(5):517-543.

3. Sharma SR, Singh S, Gill RK, Kumar R, Parihar AK. Selection of promising genotypes of lentil (*Lens culinaris* Medik.) by deciphering genetic diversity and trait association. Agricultural Research Communication Centre LR-4056. 2018; 1-6.

4. Koul PM, Sharma V, Rana M, Chahota RK, Kumar S, Sharma TR. Analysis of genetic structure and interrelationships in lentil species using morphological and SSR markers. Springer 3 Biotech. 2017;7(83):1-11.

5. Gupta R, Begum SN, Islam MM, Alam MS. Characterization of lentil (*Lens culinaris* M.) germplasm through phenotypic marker. J. Bangladesh Agril. Univ. 2012;10(2):197–204.

6. Singh T, Gupta KK. Genetic diversity for yield and related traits in Lentil. (*Lens culinaris* Medik) Plant Archives. 2004;4(1): 39-43.

7. Tyagi SD, Khan MH. Genetic divergence in lentil. African Crop Science Journal. 2010; 18(2):69-74.

8. Jewel AA, Chowdhury AK, Alam AKMM, Latif MA, Hassan MM. Multivariate analysis in Lentil (*Lens culinaries* 1). Bangladesh Journal of plus Breeding and Genetics. 2010;23(1):9-12.

9. Singh P, Singh R, Kumar K, Singh DK. Estimates of genetic parametersin diverse genotypes of lentil. Journal of Food Legumers. 2011;25:66-69.

10. Yadav NK, Ghimire SK, Sah BP, Sarker A, Shrestha SM, Sah SK. Analysis of genetic variability and divergence for quantitative traits in lentil (*Lens culinaris* Medik.).

International Journal of Current Research. 2016;8(9):38422-38428.

11. Kumari A. Genetic divergence study in lentil (*Lens culinaris* medik.) genotypes (M.Sc). Bihar Agricultural University, Sabour, Bihar; 2016.

12. Sirohi SPS, Ramashray Yadav, Ranbir S. Genetic variability, correlatio-ns and path analysis of yield and its component characters in lentil (*Lens culinaris* L. Medik.). Plant-Archives. 2007;7(1): 295-299.

13. Solanki IS. Divergence analysis in lentil (*Le ns culinaris Medik.*). Natnl. J. Pl. Improv. 2007;9(2):123-125.

14. Singh RS, Sood BC, Naresh K. The nature and magnitude of variability and disease reaction of lentil (*Lens culinaris* Medik) genotypes across cropping systems. Agricultural Science Digest. 2012;32(1):66-70.

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