

## Genetic variation in Lentil (*Lens culinaris* Medikus) genotypes

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### Abstract

Understanding the existence of genetic variability in crops is of utmost importance to plant breeders in yield improvement programs. A varietal trail was conducted with nineteen lentil germplasm accessions obtained from the All India Coordinated Research Project on MULLaRP in *Rabi-2021*. The genotypes were planted in RCBD and the data were collected for 8 morphological traits. Based on the trail, presence of genetic variability among the genotypes, association among yield and yield contributing factors with respect to environmental condition of Nagaland as well as the genetic diversity in the population has been explained. These genotypes exhibited significant variability in respect of days to fifty percent flowering, days to maturity, plant height, plant stand percentage, number of pods per plant, number of branches per plant, seed index and seed yield per plant. Genetic variability studies showed presence of good amount of variation among the twenty genotypes. The highest GCV and PCV were recorded for seed yield per plot followed by number of pods per plant. Medium estimates were obtained for plant stand percentage, plant height, Seed index and number of branches per plant. High heritability coupled with high genetic advance as percent of mean was observed for all the traits in study except for days to 50% flowering and days to maturity. Seed yield per plot was positively and significantly correlated with plant height, Plants stand percentage, number of branches per plant and number of pods per plant. However, path analysis revealed only plant stand percentage, number of branches per plant and number of pods per plant to be the most important traits for yield improvement. Simultaneously, the K-mean clustering and principal coordinate analysis disclosed the existence of moderate to high genetic diversity among the tested genotypes classifying them in four distinct clusters useful for crossing programs.

**Key words :** Genetic variation, Heritability, Correlation, Path analysis, Genetic diversity, K-means Clustering, Principle component analysis.

Since ancient times, the Mediterranean region has grown lentils (*Lens culinaris* Medik.), a type of legume. Its domestication and diversity are credited to the Fertile Crescent or west Asia, where it is still a significant crop grown in the winter. In the world, after chickpea and pea, lentil occupies third position in cool-season grain legumes. Cultivated lentil is self-pollinating annual diploids ( $2n=14$ ) and family is *Fabaceae*. Lentil is rich source of protein, fiber content and B-complex vitamins for balance human nutrient consumption. Its calorific value is equal to that of rice. It is a versatile source of nutrition for men and animals possessing about 25.1% protein, 59% carbohydrate, 0.5% fat, 2.1% minerals and sufficient amount of vitamins (Gowda and Kaul<sup>9</sup>). Lentil increases the soil nutrition level because it can fix the atmospheric nitrogen in soil through a symbiosis connection with *Rhizobium leguminosarum*. In India, lentil grows in 1.30 million hectares with production 1.10 million tons and average productivity 1195 kg ha<sup>-1</sup>. Yet the most significant determinants for lentil production are their cultivation on marginal terrain, inadequate management practices, use of local varieties and farmers' lack of awareness (Noor *et al.*<sup>17</sup>). Additionally, analysis of morphological features revealed that this crop's functioning gene pool has a limited level of diversity, which limits the germplasm<sup>19</sup>.

To save plant genetic resources, preserve the genotype-environment interaction, and increase output stability, agricultural diversity must be maintained. Understanding the available genetic variability and its possible application in breeding programmes for lentil crops requires understanding of genetic

variation and interactions between populations. Plant breeders and geneticists are particularly interested in understanding genetic variation between and within populations of crop species and its possible application in breeding programmes for lentil crops<sup>10</sup>. The availability of genetic variation for these variables appears to be necessary for the simultaneous increase of seed production and other agronomic traits.

The degree of variability present in the germplasm can be determined using genetic factors like genotypic coefficient of variation and phenotypic coefficient of variation<sup>11</sup>. For every crop development effort, the genotype with the best heritability and genetic advancement for a variety of traits may be the ideal parent. Another crucial task is to look at the relationships between the various yield-components in lentil harvests. Nevertheless, if the contribution of various characters to yield is measured using path coefficient analysis, selection for yield via strongly correlated characters becomes simple<sup>6</sup>. The stability of yield is a key goal of breeding programmes and this might be accomplished by having a better understanding of the factors influencing final yield. However, even for the same lentil genotype, these factors differ from year to year and from location to location<sup>16</sup>. Therefore, the secret to successful agricultural yield enhancement is continuous review of factors that contribute to yield including the impact of the environment on their expression. The current study is a varietal trail of lentil genotypes. The study intends to offer information regarding genetic variation, genetic diversity, relatedness, and association among the various morphological features with regards to the soil and climatic conditions of Nagaland. This knowledge

appears to be of extreme value, particularly in selection and hybridization.

Nineteen lentil germplasm accessions obtained from the All India Coordinated Research Project on MULLaRP were evaluated in the present study (Table-1). The trial was conducted during *Rabi-2021* at Department of Genetics and Plant Breeding farm of SASRD NU, Medziphema, India. Randomized complete block design (RCBD) was used to set up the trial. Over the course of the experiment, the suggested agronomic packages of practices were used. Eight quantitative characters were recorded of five randomly sampled plants of each genotype as per the standard protocol of AICRP on MULLaRP. Data were recorded on such morphological traits as days to 50% flowering (DF), days to maturity (DM), plant height (PH), plant stand percentage (PS%), number of branches per plant (NBPP), number of pods per plant (NPPP), Seed index (SI) and Seed yield per plot (SYPP). The data were subjected to statistical analysis. Analysis for variance, coefficient of variance, correlation, path

analysis k-mean clustering, Hierarchical cluster analysis, principal components, Eigen values and biplot between PC1 & PC2 were done by using R software, INDOSTAST and STAR.

In this investigation, a single trail data analysis in lentil crop has been carried out for eight agronomic traits. Nineteen genotypes were used in this trail to estimate their performance as studied under climatic condition of Nagaland. The experiment data quality was measured by following parameters *viz* *F*-value for the genotypic effect and the likelihood associated with it, coefficient of variance (CV) and heritability ( $h^2$ ). These parameters were linked to error variance. Coefficient of variation (CV) and standard error (SE) both are commonly used measures of trail precision. In this study, low standard error values were observed for days to 50% flowering, plant height, no. of branches per plant, no. of pods per plant and seed index that revealed a high trail precision. On the other hand, days to maturity, plant stand percentage and seed yield per plant showed high standard error values that signifies low trail precision either due to spatial

Table-1. List of Genotypes

S.No	Genotype	Trail	Seed type	S.No	Genotype	Trail	Seed type
1	LSS21-111	AVT1	Large seed	11	LSS21-121	AVT1	Large seed
2	LSS21-112	AVT1	Large seed	12	LSS21-122	AVT1	Large seed
3	LSS21-113	AVT1	Large seed	13	LSS21-123	AVT1	Large seed
4	LSS21-114	AVT1	Large seed	14	LSS21-11	AVT1	Small seed
5	LSS21-115	AVT1	Large seed	15	LSS21-12	AVT1	Small seed
6	LSS21-116	AVT1	Large seed	16	LSS21-13	AVT1	Small seed
7	LSS21-117	AVT1	Large seed	17	LSS21-14	AVT1	Small seed
8	LSS21-118	AVT1	Large seed	18	LSS21-15	AVT1	Small seed
9	LSS21-119	AVT1	Large seed	19	LSS21-16	AVT1	Small seed
10	LSS21-120	AVT1	Large seed				

variation present in the field or human error.

The Analysis of Variance (ANOVA) was carried out for all the traits under study. Analysis of variance revealed all traits getting a score of more than one about  $F$ -value, which indicated that the traits showed high and significant variance. All traits appeared to be highly heritable with high  $F$ -values which revealed that all the traits under study possessed valuable information about genetic variation among the tested genotypes. The quality of the present crop varietal trail can be considered as good since the  $F$ -values of genotypic effect were highly significant, heritability were relatively high and CV were relatively low for all the traits in study (Table-2).

The amount of genotypic and phenotypic variability that exists in a species is essential in developing better varieties and in initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population. All the traits under study, except for days to maturity, had PCV values only slightly higher than their corresponding GCV values showing

that their expressions were less influenced by environment. Whereas, the phenotypic expression for days to maturity, with low GCV and PCV was seen to be impacted by environment to a greater extent, thus building a hindrance to direct selection of such trait in lentil. High estimates of PCV and GCV observed for seed yield per plot and no of pods per plant showed the presence of high variability in these traits and indicated the potential for increasing yield by selection for these traits. Sakthivel *et al.*<sup>22</sup>, and Dugassa *et al.*<sup>7</sup>, noticed similar effect in number of pods per plant. Malik *et al.*<sup>15</sup>, observed high GCV and PCV for seed yield per plot. Medium estimates were obtained for plant stand percentage, plant height, seed index and no of branches per plant. Low estimate of PCV and GCV were found in case of days to 50% flowering and days to maturity indicating the presence of less variability in such traits with days to maturity being highly influenced by environmental factors. Chowdhury *et al.*<sup>5</sup>, noted low estimates of GCV and PCV for days to maturity and days to 50% flowering which is in line of with this study.

Table-2. ANOVA results for 19 lentil genotypes

Variable	Min	Max	Mean	Std Dev	S.E.	$h^2$	C.V.	F-value	F Prob.
DF50%	76.53	87.36	81.90	3.32	0.18	99.70	0.37	353.14	0.00
DM	77.34	114.73	109.27	8.07	7.71	8.80	12.22	1.10	0.39
PH	21.88	46.30	34.78	5.61	0.35	99.60	1.74	257.50	0.00
PS%	46.26	90.55	65.73	13.71	5.66	82.90	14.92	5.86	0.00
NBPP	3.90	6.77	5.28	0.76	0.24	90.00	7.90	9.99	0.00
NPPP	8.67	28.73	16.40	6.50	0.78	98.60	8.20	70.12	0.00
SI	1.87	3.04	2.35	0.36	0.06	97.40	4.24	38.87	0.00
SYPP	52.44	345.71	166.70	88.65	4.52	99.70	4.70	384.30	0.00

Heritability is a good indicator of transmission of characters from parents to its progeny. Heritability is classified as low (below 30%), medium (30%-60%), and high (above 60%). High heritability is helpful to the breeders in effectively selecting for a particular character from a diverse genetic population. Heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. In this trial, the broad sense heritability values were manifested to be very high for most of the traits ranging from 82.90% to 99.70% presenting an excellent opportunity for the breeders for direct selection of these traits for yield improvement, except for days to maturity that exhibited a low heritability of about 8.80%. Seed yield per plot and days to 50% flowering exhibit highest heritability (99.7%) among the traits followed by plant height (99.6%), no of pods per plant (98.6%), seed index (97.4%), no. of branches per plant (90.0%) and plant stand percentage (82.9%) (Table- 3). Selection of traits with very high heritability, say 80% or more, should be fairly easy since a close correspondence between the genotypes and phenotypes can be visualized due to the relatively small contribution of the environment effect to the phenotypes. Similar findings have been reported for days to 50% flowering, plant height, number of branches per plant and number of pods per plant by Sakthivel *et al.*<sup>22</sup>. On the other hand, a low estimate of heritability with lowest values of GCV and PCV was observed for days to maturity indicating that phenotypic selection for this trait would be difficult, thereby, indicating a limited possibility of improvement for this trait through selection. These results for the chosen traits with high

heritability imply that a few test locations and years might be sufficient for stable expression of these traits.

*Genetic advance (GA) as per cent of mean:*

Johnson *et al.*<sup>12</sup>, reported that heritability estimates along with genetic gain would be more rewarding than heritability alone in predicting the consequential effect of selection to choose the best individual. High heritability is not always associated with high genetic advance as reported by Yadav *et al.*<sup>28</sup>. Genetic advances can give the information about how much of a gain under selection will actually occur. Genetic advance as percent of mean is classified as; values from 0-10% are low, 10-20% is moderate and 20% and above is high. Based on the above delineation, the genetic advance as per cent of mean was found to be high for most of the traits in this trial, except days to 50% flowering and days to maturity. The genetic advance as per cent of mean was estimated to be highest for seed yield per plot (109.26%), followed by no. of pods per plant (80.48%), plant stand percentage (35.64%), plant height (33.07%), seed index (30.62%) and no. of branches per plant (26.72%). High estimates of heritability for the above traits has also been reported in this study coupled with high genetic advance as per cent of mean which suggested that these characters can be considered as favourable attributes for the improvement through selection. This may be due to predominance of additive gene action for these traits (Panse<sup>18</sup>) and thus, could be improved upon by adapting selection without progeny testing. Chowdhury *et al.*<sup>5</sup>, and Sakthivel *et al.*<sup>22</sup>, found similar results for number of pods per plant and seed yield per plant, respectively.

Table-3. Genetic parameters for 19 lentil genotypes

Variable	GCV	PCV	$h^2_{(bs)}$	GA	GA%M
DF50%	4.05	4.06	99.70	6.82	8.33
DM	2.19	7.39	8.80	1.46	1.34
PH	16.09	16.12	99.60	11.50	33.07
PS%	19.00	20.86	82.90	23.43	35.64
NBPP	13.68	14.42	90.00	1.41	26.72
NPPP	39.35	39.63	98.60	13.20	80.48
SI	15.06	15.26	97.40	0.72	30.63
SYPP	53.11	53.18	99.70	182.15	109.26

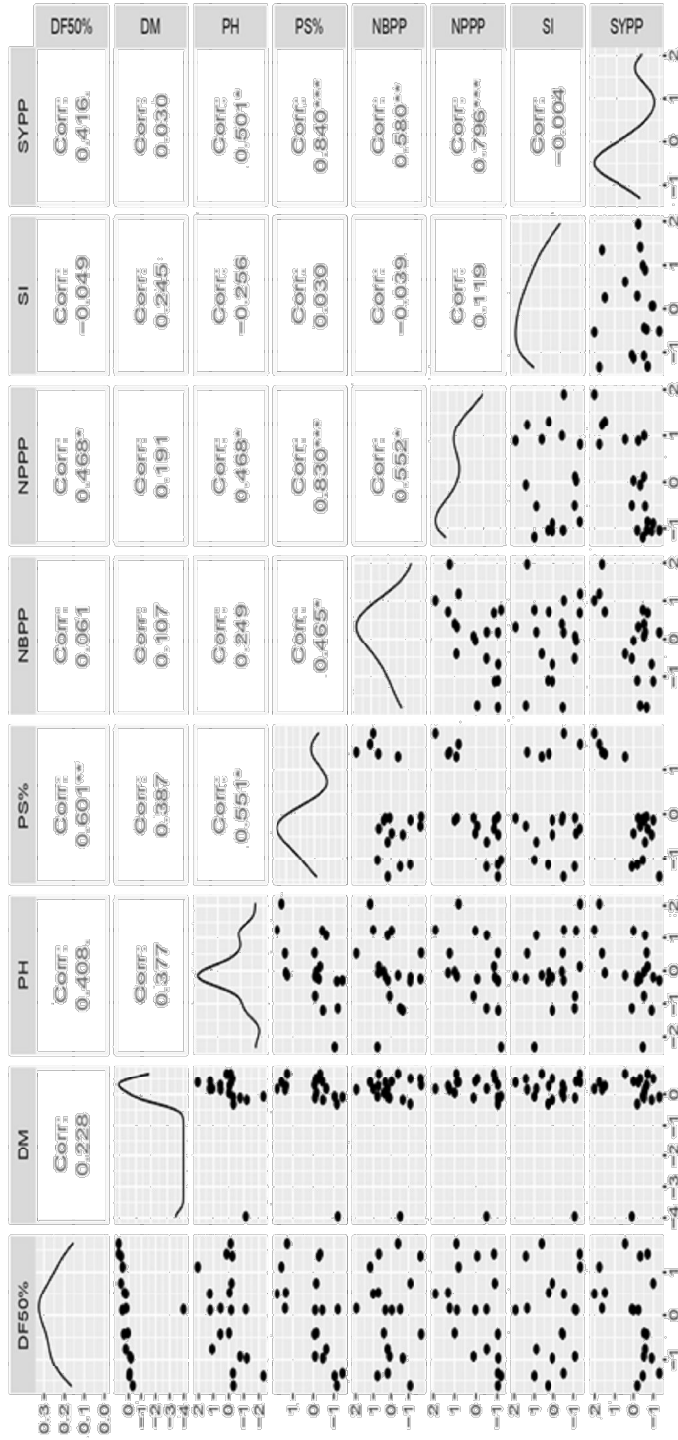
On the other hand, high heritability with low genetic advance as per cent mean (8.32%) was noted for days to 50% flowering, whereas, low heritability and low genetic advance as per cent of mean (1.33%) was revealed for days to maturity indicating that the scope for improving these two traits through selection is much limited. This may be attributed to the non-additive gene action corresponding to these traits<sup>12</sup>. Low genetic advance for days to maturity was also reported by Dugassa *et al.*<sup>7</sup>, and Sakthivel *et al.*<sup>22</sup>.

#### Correlation :

Seed yield is a result of many traits that are interdependent. The desirable traits in a crop have been noticed to be highly associated among them and with seed yield. The analysis of the relationship among these traits and their association with seed yield is essential to establish selection criteria. The link between yield and yield contributing traits in the present study was investigated by correlation analysis. The study revealed phenotypic and genotypic correlation co-efficient among the eight analysed traits of nineteen genotypes

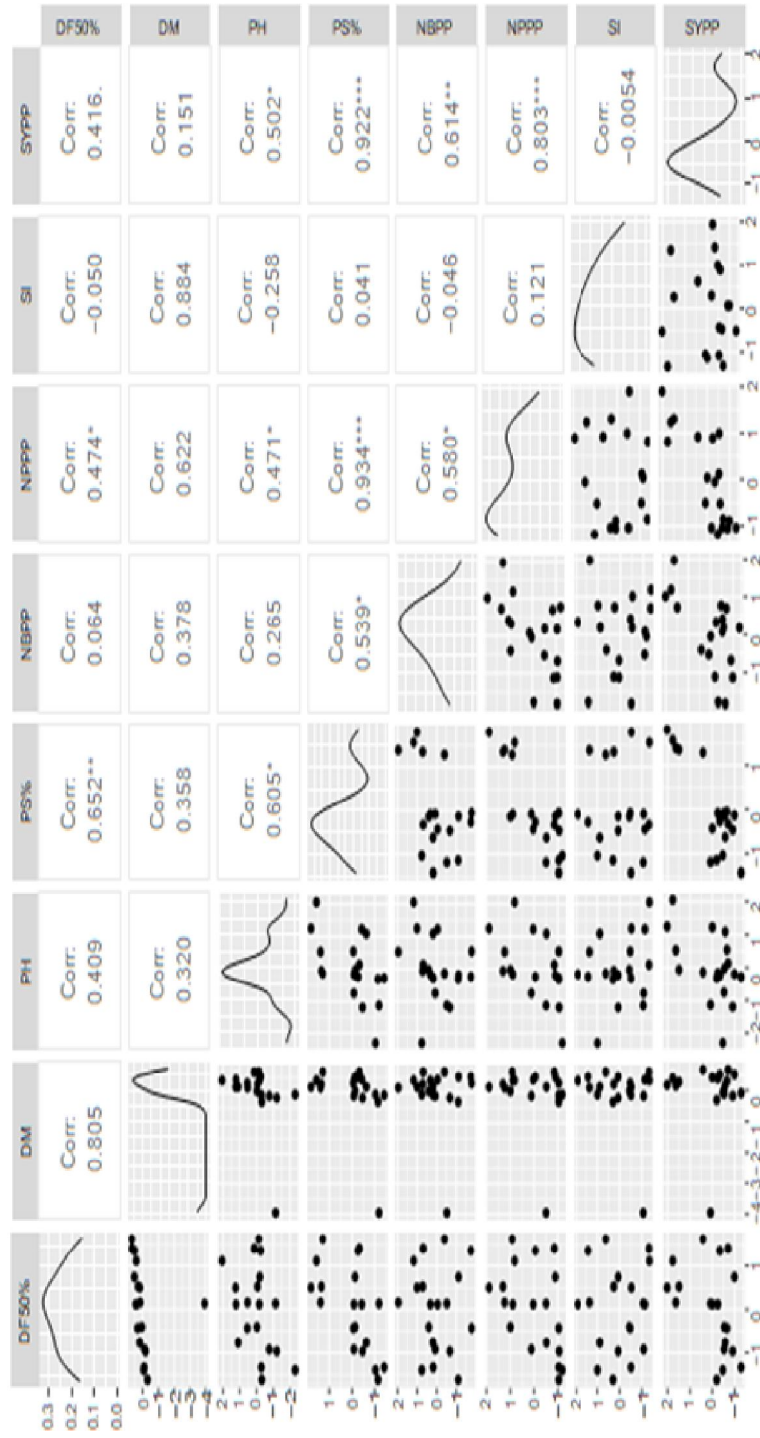
(Table 4 and 5). The seed yield per plot exhibited a positive and significant association with plant height, plant stand percentage, number of branches per plant and number of pods per plant at both phenotypic and genotypic levels. This indicated that accessions with higher plant height, plant stand percentage, number of branches per plant and number of pods per plant are high yielders. Similar positive and significant association of number of pods per plant with seed yield has been reported by a number of researchers like Seifu<sup>23</sup>, Ramigry *et al.*<sup>20</sup>, Zaman *et al.*<sup>29</sup>, Khattab<sup>13</sup>, Bakhs<sup>3</sup>, Esmail<sup>8</sup>, Kumar *et al.*<sup>14</sup>, Singh *et al.*<sup>25</sup>, Abo-Shetaia *et al.*<sup>1</sup>, Chakraborty and Haque<sup>4</sup>, Tadele *et al.*<sup>26</sup>. Dugassa *et al.*<sup>7</sup>, Tigist<sup>27</sup>, and kumar *et al.*<sup>14</sup>, found positive significant correlation of plant height with seed yield. Zaman *et al.*<sup>29</sup>, found positive significant correlation of number of branches per plant with yield. Seed index was found to have a negative association with yield in this study. Generally, positive and significant associations of pair of characters at both phenotypic and genotypic level justify the possibility of correlated response to selection.

Table-4. Phenotypic correlation co-efficient among different quantitative traits in nineteen lentil genotypes



DF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, PS%= Plant Stand percentage, NBPP= No. of branches per plant, NPPP= No. of pods per plant, SI= seed index, SYPP= Seed yield per plot

Table-5. Genotypic correlation co-efficient among different quantitative traits in nineteen lentil genotypes



DF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, PS%= Plant Stand percentage, NBPP= No. of branches per plant, NPPP= No. of pods per plant , SI= seed index, SYPP= Seed yield per plot



Correlation study of the yield and its contributing traits found that the genotypic correlation coefficients were in most cases greater than the phenotypic correlation coefficients, indicating that the link was mostly attributable to genetic factor. This suggested the presence of strong inherent association for the traits studied with yield and hence phenotypic selection may be rewarding. Similar results were reported by Sakthivel *et al.*<sup>22</sup>. Higher magnitude of genotypic correlation helps in selection for genetically controlled characters and gives a better response for seed yield improvement than that would be expected on the basis of phenotypic association alone (Robinson *et al.*<sup>21</sup>).

#### *Path analysis :*

Although correlation coefficient indicates the nature of association among the traits but path coefficient analysis splits the correlation values into direct and indirect effects so as to measure the relative importance of

causal factors involved. Using seed yield per plot as a dependent character and yield components as independent characters, path coefficient analysis was performed at both the phenotypic and genotypic levels. Each component acts in two different ways, directly affecting yield and indirectly affecting component characters—two actions that were not shown by correlation research. Both at phenotypic and genotypic level plant stand percentage, number of branches per plant and number of pods per plant had positive direct effects on seed yield per plot indicating their importance during selection in yield improvement program (table 6 and 7). A similar study by Tadele *et al.*<sup>26</sup>, reported direct positive effect by plant stand percentage and number of pods per plant on seed yield. Number of branches per plant showed direct positive effect on seed yield in an experiment done by Chowdhury *et al.*<sup>5</sup>. Though, plant height showed a positive and significant correlation with seed yield per plot, it was found to have an indirect effect on seed yield through other

Table-6. Phenotypic path co-efficient among different quantitative traits in nineteen lentil genotypes

Variable	DF50%	DM	PH	PS%	NBPP	NPPP	SI	SYPP
DF50%	-0.0897	-0.0205	-0.0366	-0.0539	-0.0054	-0.042	0.0044	0.4158
DM	-0.0939	-0.4108	-0.1548	-0.1592	-0.044	-0.0784	-0.1009	0.03
PH	0.0877	0.081	0.2149	0.1184	0.0535	0.1005	-0.055	0.5011
PS%	0.512	0.3298	0.4688	0.8512	0.3956	0.7064	0.0254	0.8398
NBPP	0.0117	0.0206	0.0478	0.0892	0.192	0.1059	-0.0076	0.5799
NPPP	-0.0055	-0.0023	-0.0055	-0.0098	-0.0065	-0.0118	-0.0014	0.7962
SI	-0.0064	0.0322	-0.0335	0.0039	-0.0052	0.0156	0.131	-0.0041
RESIDUAL EFFECT = 0.3545								

DF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, PS%= Plant Stand percentage, NBPP= No. of branches per plant, NPPP= No. of pods per plant, SI= seed index, SYPP= Seed yield per plot

Table-7. Genotypic path co-efficient among different quantitative traits in nineteen lentil genotypes

Variable	DF50%	DM	PH	PS%	NBPP	NPPP	SI	SYPP
DF50%	-0.1527	-0.123	-0.0626	-0.0997	-0.0098	-0.0725	0.0077	0.4169
DM	0.1962	0.2437	0.3219	0.3311	0.0923	0.1517	0.2155	0.1512
PH	-0.1489	-0.4798	-0.3633	-0.2198	-0.0965	-0.1713	0.094	0.5023
PS%	0.2311	0.4811	0.2142	0.3541	0.1911	0.3308	0.0145	0.9223
NBPP	0.006	0.0356	0.025	0.0508	0.0941	0.0547	-0.0044	0.6146
NPPP	0.2651	0.3479	0.2635	0.5222	0.3247	0.5589	0.068	0.8036
SI	0.0201	-0.3544	0.1037	-0.0164	0.0186	-0.0487	-0.4007	-0.0054
RESIDUAL EFFECT = 0.6112								

DF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, PS%= Plant Stand percentage, NBPP= No. of branches per plant, NPPP= No. of pods per plant , SI= seed index, SYPP= Seed yield per plot

Table-8. Cluster membership summary

Cluster	Members	Genotypes
1	9	LSS21-112, LSS21-113, LSS21-115, LSS21-122, LSS21-123, LSS21-11, LSS21-12, LSS21-13, LSS21-14.
2	4	LSS21-114, LSS21-117, LSS21-120, LSS21-121.
3	3	LSS21-116, LSS21-119, LSS21-15.
4	3	LSS21-111, LSS21-118, LSS21-16.

component characters. This implicated that performing indirect selection for traits like plant height would also prove to be beneficial in yield improvement. Based on path analysis, plant stand percentage, number of branches per plant and number of pods per plant were the most important traits for yield improvement.

The residual effect enables accurate description of the interaction pattern of other potential yield-enhancing factors. In the present study the residual effect was 0.35 and 0.611 at phenotypic and genotypic level, respectively indicating that the traits under

study are not sufficient to account for variability and there might be few or more important characters other than those studied in the present investigation and thus solicits inclusion of some more characters. Inclusion of some physiological characters like LAI, Chlorophyll content, Harvest index etc could be considered important in order to derive a much clear picture of the casual relationship.

#### *K-means clustering :*

The technique of grouping data into clusters based on shared criteria is known as cluster analysis. The goal of K-means clustering

Table-9. Descriptive statistics

Variable	Cluster	Min	Max	Mean	StdDev
DF50.	1	76.53	86.59	80.93	3.61
DF50.	2	82.44	85.6	83.81	1.31
DF50.	3	77.46	84.37	80.17	3.68
DF50.	4	82.3	87.36	84	2.9
DM	1	106.76	114.68	110.72	2.59
DM	2	110.52	112.49	111.29	0.9
DM	3	107.83	113.45	109.94	3.06
DM	4	77.34	114.73	101.59	21.02
PH	1	21.88	40.89	33.51	5.28
PH	2	34.44	46.3	40.07	5.12
PH	3	28.05	33.71	31.64	3.13
PH	4	28.41	41.65	34.69	6.65
PS.	1	50.04	64.93	59.98	5.76
PS.	2	84.26	90.55	86.71	2.87
PS.	3	46.26	63.89	56.51	9.16
PS.	4	49.41	83.38	64.2	17.41
NBPP	1	3.9	5.86	5.09	0.78
NBPP	2	5.82	6.77	6.2	0.41
NBPP	3	4.42	5.41	4.86	0.5
NBPP	4	4.87	5.24	5.03	0.19
NPPP	1	8.67	22.89	14.45	5.43
NPPP	2	21.69	28.73	24.94	2.9
NPPP	3	9.53	10.58	9.91	0.58
NPPP	4	13.11	22.38	17.37	4.68
SI	1	1.87	3.04	2.44	0.41
SI	2	1.87	2.83	2.32	0.41
SI	3	2.16	2.37	2.3	0.12
SI	4	1.94	2.57	2.16	0.36
SYPP	1	104.3	149.61	125.06	15.8
SYPP	2	299.01	345.71	320.03	19.85
SYPP	3	52.44	86.08	72.58	17.78
SYPP	4	166.39	203.8	181.31	19.82

is to divide “n” objects into k clusters, with each object belonging to the cluster with the closest mean. The clustering algorithm K-means is centroid-based. K is an input parameter that denotes the number of clusters. The cluster centre that is closest to each data point in the

collection is given that element’s location. It’s not always evident how to choose the best K value. K-means algorithm’s optimal cluster value discovery is crucial. In this proposed work, elbow approach was used to determine the clusters’ ideal value.

Nineteen lentil genetic resources were divided into four clusters by Non-hierarchical cluster analysis (k-mean) and Elbow method was used to find out the optimum number of clusters. The clustering pattern revealed that the Cluster I included nine accessions that were primarily distinguished by mostly all characters have average mean values. Cluster II had four accessions majority of which all characters have high mean values except days to 50% flowering. Cluster II had four accessions which are characterized by desired mean values and the genotypes belongs to these clusters can be utilized for the future breeding programs. Cluster III comprised of three accessions, which were characterized by all characters have low mean values and Cluster IV have three genotypes which have the average mean values of all traits. Generally, genotypes within a group showed little divergence from each other than from genotypes of different groups, as observed by Sharma *et al.*<sup>24</sup>. Hybridization among genotypes from different clusters or selection of outperforming genotypes can be practiced in crop improvement programs.

#### *Principal component analysis :*

Principal component analysis (PCA) can be used to generate two- or three-dimensional scatter plots of the entities included in the study. In these plots the geometrical distance between any two entities reflects the genetic diversity between them and the grouping of entities reveals the sets of genetically similar entities.

Eigen values of each PC were carried out to determine whether a PC contained pattern and needs to be retained in the data analysis. A PC needs to be retained if its eigen value is greater than one. Here the eigen values of each PC is presented for up to eighth PC

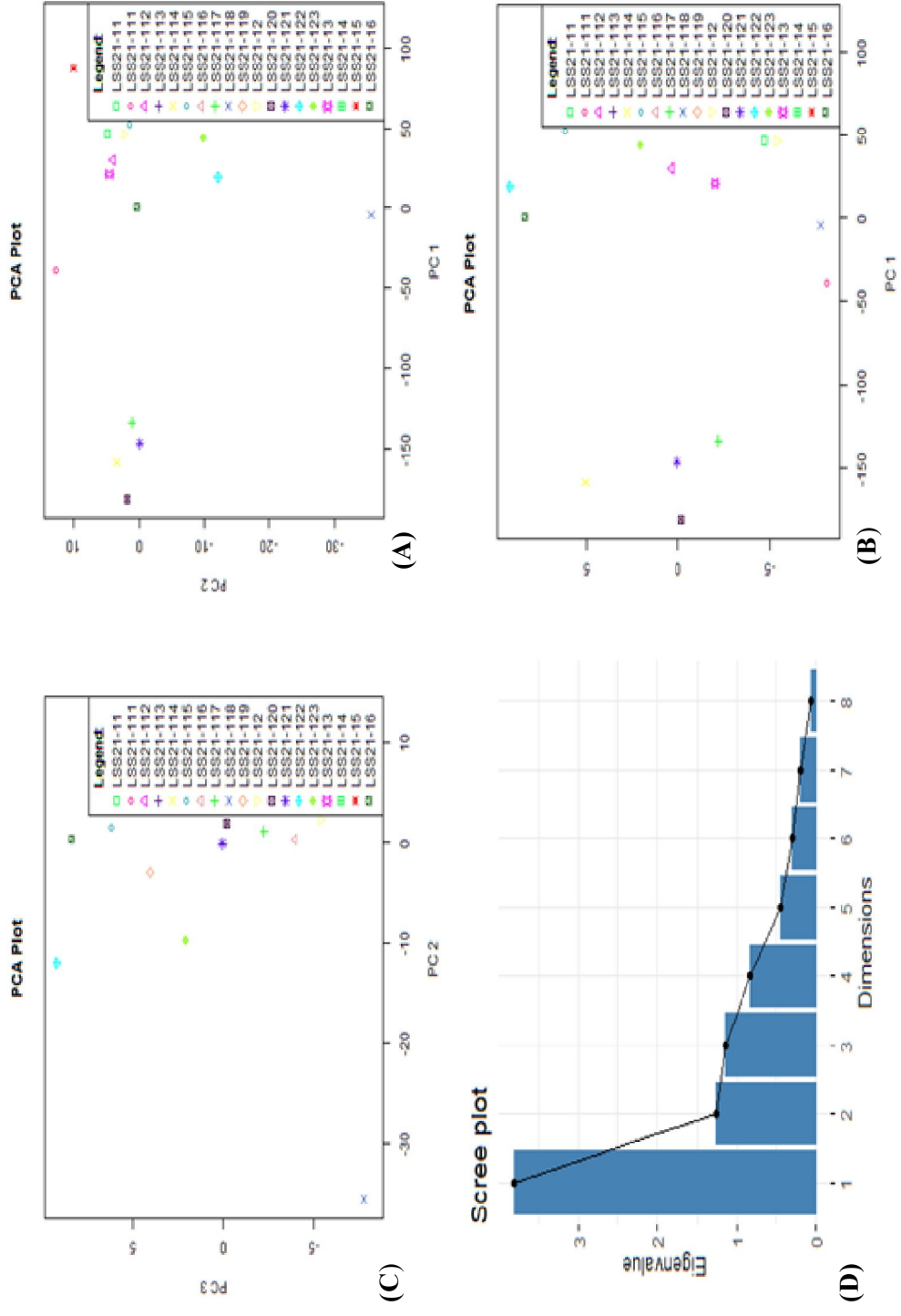
or the maximum number of PCs for the data but eigen values for PC1, PC2 and PC3 are more than one while remain PCs are close zero, so PC1, PC2, and PC3 should be considered in this data set. PC1 had 47.5 % of variation existing in the data set while PC2 had 15.7% and PC3 had 14.3%. Therefore PC1, PC2 and PC3 combined explain the 77.6 % of variation in the data set so this appears to be high goodness of fit to the data. Alam *et al.*<sup>2</sup>, also studies PCA for lentil genotypes that showed about 62% variation about the first two principal coordinates and a cumulative of about 78% with the first three principal coordinates which is in line with our results. A distinct pattern of genotype clustering in the factor plane could be seen in the scatter plot created between PC1 to PC2, PC1 to PC3 and PC2 to PC3.

Table-10. Eigenvalues of Correlation Matrix

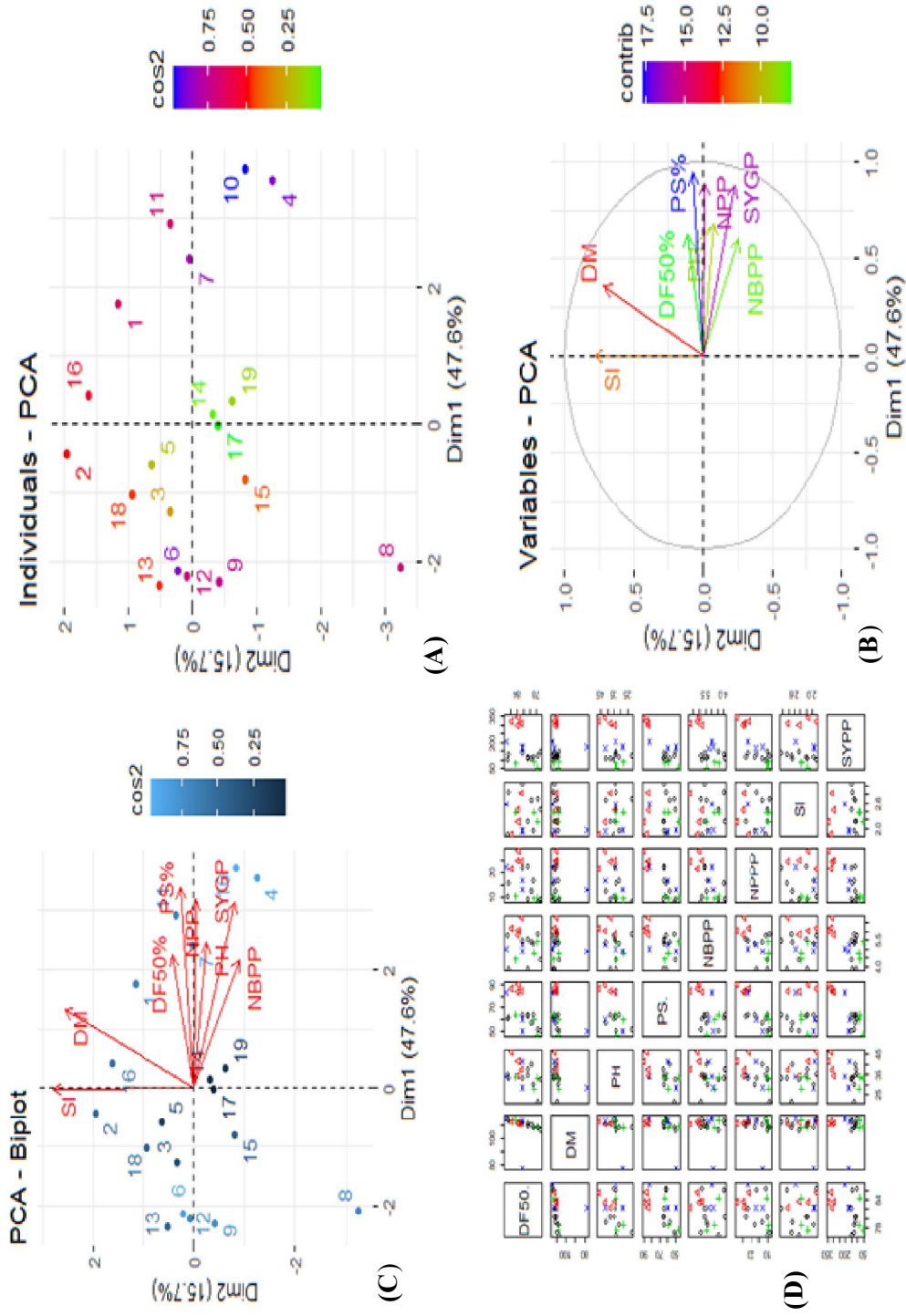
Variable	Eigenvalues	Proportion	Cumulative Proportion
PC1	3.805	0.476	0.476
PC2	1.258	0.157	0.633
PC3	1.145	0.143	0.776
PC4	0.823	0.103	0.879
PC5	0.441	0.055	0.934
PC6	0.287	0.036	0.97
PC7	0.191	0.024	0.994
PC8	0.051	0.006	1

Table 11. Loadings (Eigenvectors) of Correlation Matrix

	PC1	PC2	PC3
DF50%	<b>0.32</b>	0.103	<b>-0.384</b>
DM	0.187	<b>0.64</b>	<b>-0.296</b>
PH	<b>0.351</b>	-0.064	<b>-0.463</b>
PS%	<b>0.484</b>	0.068	-0.003
NBPP	<b>0.308</b>	-0.222	<b>0.447</b>
NPPP	<b>0.456</b>	-0.008	0.224
SI	-0.002	<b>0.694</b>	<b>0.499</b>
SYPP	<b>0.45</b>	-0.2	0.228



(A, B, C) PCA biplots based on genotypes distribution and PC interaction between PC1 to PC2, PC1 to PC3 and PC2 to PC3. (D) Scree plot based on eigenvectors.



(A, C) Distribution and grouping of germplasm lines across first two principal components (B) PCA graph of different traits for first two principal components (D) K-Means plot

The current crop varietal trail came to the conclusion that the quality of the trail can be regarded as considerable because all traits' have significant *F*-values. Most of the traits in the study possessed high to medium estimates of coefficients of variation that highlighted the existence of appreciable amount of genetic variability in the tested genotypes. All traits exhibited low standard errors, hence proved the trail to be of high precession. The genotypes in this trail can further be forwarded to multi environment variety trail.

The traits like days to 50% flowering, plant height, plant stand percentage, number of branches per plant, number of pods per plant, seed index and seed yield per plot showed high heritability indicating low environmental effects. Days to maturity showed low heritability indicating high environmental effects on the phenotype of such trait. High heritability coupled with high genetic advance was recorded for plant height, plant stand percentage, number of branches per plant, number of pods per plant, seed index and seed yield per plot indicating a substantial contribution of additive gene action and hence unveils scope for improvement through selection.

Seed yield per plant was significantly and positively correlated with traits like plant height, plant stand percent, number of branches per plant, and number of pods per plant. Based on path analysis, plant stand percentage, number of pods per plant and number of branches per plant were most important for yield improvement practicing direct selection for these traits. Indirect selection could also be practiced for plant height through other component characters.

The K-mean clustering grouped the nineteen genotypes under study in four distinct clusters. Out-crossing among divergent genotypes of different clusters or selection of outperforming genotypes is suggested for crop improvement. Principal coordinate analysis confirmed the presence of moderate to high genetic diversity in the tested accessions.

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