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GENETIC DIVERGENCE, PRINCIPAL COMPONENT ANALYSIS AND CLUSTER ANALYSIS FOR YIELD, YIELD COMPONENTS AND NUTRITIONAL QUALITY TRAITS IN LENTIL (*Lens culinaris* MEDIK.)

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ABSTRACT

Lentil is an important food legume valued for its high protein content and nutritional quality. Effective genetic improvement of yield and quality traits depends on the availability of genetic variability and the identification of divergent parental material. Multivariate approaches such as principal component and cluster analyses facilitate the characterization of genetic diversity and identification of traits contributing most strongly to divergence, thereby supporting the selection of promising parents for breeding programmes. The present investigation was carried out to assess genetic divergence using principal component analysis (PCA) and cluster analysis among 51 lentil entries comprising 15 parental genotypes (12 lines and 3 testers) and 36 F_1 hybrids for 15 morpho-agronomic and nutritional quality traits. The field experiment also included 36 F_2 populations, giving 87 treatments in total; however, the F_2 populations were not included in the PCA and cluster analyses. The experiment was conducted in a randomized complete block design during *Rabi* 2025–26 at the Student Instructional Farm, C. S. Azad University of Agriculture and Technology, Kanpur. Significant genetic variability was observed for all traits. PCA revealed that the first five principal components accounted for 85.34% of the total variation. PC1 (33.72%) was primarily associated with seed yield per plant, days to maturity, days to 50% flowering, protein content and number of pods per cluster, while PC2 (21.96%) was dominated by seeds per pod and number of primary branches. Hierarchical clustering grouped the entries into ten distinct clusters. The maximum inter-cluster distance was observed between Cluster III and Cluster X (627.97), indicating wide genetic divergence. Biological yield per plant made the greatest contribution (33.98%) to total genetic divergence, followed by the number of primary branches (11.74%) and the number of secondary branches (10.86%). Cluster I exhibited desirable mean performance for seed yield, biological yield and protein content, while Cluster VIII recorded the highest harvest index and methionine content. Hybridization between genotypes belonging to distant clusters (particularly Cluster III × Cluster X and Cluster I × Cluster VI) is recommended for generating superior recombinants with improved yield and nutritional quality in lentil breeding programmes.

Key words : *Lens culinaris*, Genetic divergence, Principal component Analysis, Cluster analysis, Protein content, Methionine, Line × tester.

Introduction

The genus Lens belongs to the legume tribe Vicieae, which also includes the major pulse crops of classical Mediterranean civilizations faba bean (*Vicia faba*) and pea (*Pisum sativum*). Lens is a small Mediterranean genus comprising the cultivated lentil (*Lens culinaris* Medikus subsp. culinaris) and six closely related wild taxa (Ferguson *et al*., 2000). Lentil is a diploid (2n = 2x = 14), predominantly autogamous species and ranks among the oldest domesticated crops, with its origin traced to the Near East (Zohary, 1972; Zohary, 1999).

Lentil is highly valued as a nutritious food legume owing to its high protein concentration (approximately 24–26%) and favourable nutritional profile that includes

appreciable quantities of minerals, carbohydrates and dietary fibre (Sarker *et al*., 2004 and Johnson *et al*., 2020). Beyond grain nutrition, lentil contributes to soil fertility through symbiotic biological nitrogen fixation and fits well into cereal–pulse cropping systems because of its relatively short duration and adaptation to residual soil moisture (Erskine *et al*., 2016). Two cultivated varietal groups are conventionally distinguished on the basis of seed size: microsperma (seed diameter < 6 mm) and macrosperma (seed diameter > 6 mm) (Barulina, 1930).

Protein concentration alone does not fully determine the nutritional quality of lentil; amino-acid composition is equally critical. Methionine, an essential sulphur-containing amino acid, is relatively limiting in lentil protein. Substantial genetic and environmental variation has been documented for protein and methionine content, indicating realistic opportunities for genetic improvement of nutritional quality (Kumar *et al*., 2016; Johnson *et al*., 2020, 2024; Wright *et al*., 2025).

Lentil breeding has a comparatively short history relative to the major cereals (Materne and McNeil, 2007). Modern breeding programmes typically employ bulk-population methods followed by single-plant selection at advanced generations, with emphasis on high seed and straw yields. Simultaneous improvement of seed yield and quality traits depends on the availability of sufficient genetic variation and on the identification of genetically divergent parents. Multivariate techniques such as principal component analysis (PCA) and hierarchical cluster analysis are powerful tools for quantifying genetic divergence, identifying the relative contribution of individual traits and grouping genotypes into homogeneous clusters. Such information is indispensable for the rational selection of parents in hybridization programmes aimed at developing high-yielding, nutritionally superior lentil cultivars.

The present study was therefore undertaken to (i) estimate the extent of genetic variability for yield, yield components and nutritional quality traits, (ii) perform principal component analysis to identify the major sources of variation, (iii) group genotypes into genetically distinct clusters and (iv) quantify the relative contribution of different traits towards total genetic divergence among a set of lentil lines, testers and their hybrid progenies.

Materials and Methods

Experimental material and Crossing Programme

Fifteen genetically diverse lentil genotypes comprising twelve lines and three testers were selected on the basis of their geographic origin, adaptability, earliness, yield potential and disease reaction. The genotypes were obtained from the Legume Section, Department of Genetics and Plant Breeding, C.S. Azad University of Agriculture and Technology (CSAUA&T), Kanpur, U.P., India. Detailed pedigree and key morphological features of the parental genotypes are presented in Table 1.

A line × tester mating design was adopted. Controlled pollinations were performed during the preceding Rabi season to generate 36 F_1 hybrids (12 lines × 3 testers). The F_1 plants were selfed under isolation to produce the corresponding F_2 populations. The final evaluation trial therefore consisted of 87 treatments (15 parents + 36 F_1s + 36 F_2s). For the multivariate analyses reported in the present study, only 51 entries comprising the 15 parents

Table 1 : Details of parental genotypes used in the line × tester experiment.

S. no.	Genotype	Pedigree / Source	Institution	Salient Features
1	KLS 1445	Germplasm	CSAUA&T, Kanpur	High biomass, early, high yield
2	KLS 1447	Germplasm	CSAUA&T, Kanpur	Small seed, early under late sowing
3	KLS 1449	Germplasm	CSAUA&T, Kanpur	High biomass, wilt resistance
4	KLS 1451	Germplasm	CSAUA&T, Kanpur	Small seed, early, wilt & rust resistant
5	KLS 1453	Germplasm	CSAUA&T, Kanpur	Early maturity, higher yield
6	PL 318	Germplasm	GBPUA&T, Pantnagar	Small seed, more clusters, high yield
7	PL 342	Germplasm	GBPUA&T, Pantnagar	Medium bold, high biomass, more clusters
8	IPL 24-3	Germplasm	ICAR-IIPR, Kanpur	Medium bold, early, multiple resistance
9	IPL 244	Germplasm	ICAR-IIPR, Kanpur	Small seed, early, high biomass
10	VL 161	Germplasm	ICAR-VPKAS, Almora	Medium bold, high biomass, wilt & rust resistant
11	NDL 2018	Germplasm	ANDUA&T, Ayodhya	Large seed, high yield, rust resistant
12	VL 162	Germplasm	ICAR-VPKAS, Almora	Large seed, high biomass, rust resistant
13	KLS 218	KLS 5133 / L 9362	CSAUA&T, Kanpur	Resistant to rust and wilt (Tester)
14	KL 320	PL 406 / P 237	CSAUA&T, Kanpur	Moderately resistant to wilt & rust (Tester)
15	PL 639	L-9 / Type 8	GBPUA&T, Pantnagar	Small seeded, susceptible to wilt (Tester)

and 36 F_1 hybrids were included; the 36 segregating F_2 populations were not included in the PCA or cluster analysis.

Field Experiment and observations

The field trial was laid out in a randomized complete block design (RCBD) with three replications during the Rabi season of 2025–26 at the Student Instructional Farm (SIF), C.S. Azad University of Agriculture and Technology, Kanpur (26.45° N, 80.32° E; 125.9 m above mean sea level). Each parent and F_1 entry was sown in a single-row plot of 3 m length, while each F_2 population was accommodated in a double-row plot of the same length. Row-to-row and plant-to-plant spacing were maintained at 30 cm and 10 cm, respectively. Recommended package of agronomic practices for lentil was followed to raise a healthy crop.

Observations were recorded on five randomly selected competitive plants per plot for the following fifteen traits: days to 50% flowering (DFF), days to maturity (DM), plant height (PH, cm), number of primary branches per plant (NPB), number of secondary branches per plant (NSB), number of clusters per plant (NCP), number of pods per cluster (NPC), total number of pods per plant (TPP), seeds per pod (SPD), 100-seed weight (HSW, g), biological yield per plant (BY, g), seed yield per plant (SYP, g), harvest index (HI, %), protein content (PC, %) and methionine content (MC, %). Protein content was estimated by the micro-Kjeldahl method and methionine content by the spectrophotometric method of Horn *et al*. (1946).

Statistical analyses

Mean values of the 15 traits were subjected to descriptive statistical analysis. Principal component analysis was performed on the correlation matrix of the standardized data to extract orthogonal components that capture the major axes of variation. Eigenvalues greater than unity were considered for interpretation of principal components. Hierarchical cluster analysis was carried out using Euclidean distance and Ward's minimum-variance method to classify the genotypes into homogeneous groups. Intra- and inter-cluster distances were calculated following Mahalanobis D^2 statistics. The relative contribution of each trait towards total genetic divergence was estimated according to the method of Singh (1981). All analyses were performed using standard statistical packages (R software and SPSS).

Results and Discussion

Descriptive Statistics and variability

Wide ranges of variation were observed for all the fifteen traits under study (Table 2). Days to 50% flowering ranged from 44.67 to 59.67 days (mean 50.70), while days to maturity varied from 115.67 to 135.21 days (mean 120.24). Plant height exhibited a range of 37.09–51.77 cm. Number of secondary branches (12.33–27.13), total pods per plant (47.27–87.92) and seed yield per plant (2.61–4.61 g) showed particularly high coefficients of variation, indicating ample scope for selection. Protein

Table 2 : Descriptive statistics for 15 morpho-agronomic and quality traits in lentil.

Trait	Min	Max	Range	Mean	SE	SD	CV (%)	Median
DFF	44.67	59.67	15.00	50.70	0.44	3.19	6.29	50.33
DM	115.67	135.21	19.54	120.24	0.48	3.42	2.85	119.83
PH	37.09	51.77	14.68	45.75	0.48	3.45	7.53	45.79
NPB	2.80	5.13	2.33	3.84	0.08	0.59	15.40	3.87
NSB	12.33	27.13	14.80	20.02	0.48	3.48	17.38	19.50
NCP	16.93	29.13	12.20	24.70	0.29	2.06	8.35	24.60
NPC	1.93	3.60	1.67	2.92	0.05	0.38	12.93	3.00
TPP	47.27	87.92	40.65	71.57	1.21	8.70	12.16	71.72
SPD	1.20	1.93	0.73	1.66	0.03	0.19	11.48	1.67
HSW	2.51	3.56	1.05	3.18	0.03	0.21	6.73	3.21
BY	7.54	11.69	4.15	9.72	0.13	0.96	9.92	9.69
SYP	2.61	4.61	2.00	3.72	0.06	0.46	12.33	3.80
HI	33.67	45.99	12.32	38.34	0.37	2.64	6.88	37.87
PC	22.17	28.97	6.80	25.87	0.22	1.57	6.06	25.93
MC	0.22	0.34	0.12	0.278	0.004	0.027	9.76	0.280

DFF = days to 50% flowering; DM = days to maturity; PH = plant height (cm); NPB = primary branches; NSB = secondary branches; NCP = clusters/plant; NPC = pods/cluster; TPP = total pods/plant; SPD = seeds/pod; HSW = 100-seed weight (g); BY = biological yield (g); SYP = seed yield/plant (g); HI = harvest index (%); PC = protein content (%); MC = methionine content (%).

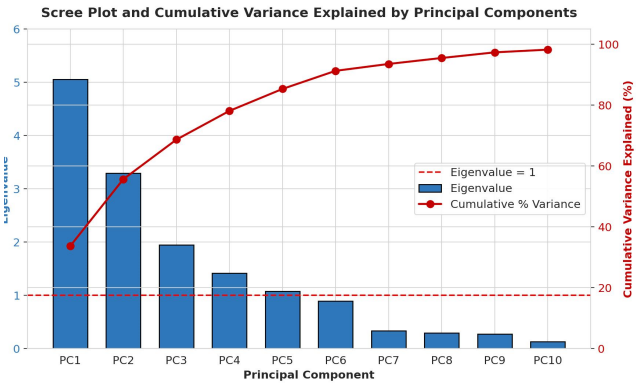


Fig. 1 : Scree plot showing eigenvalues and cumulative percentage of variance explained by the principal components.

Table 3 : Eigenvalues, percentage of variance and cumulative variance of principal components.

PC1	5.058	33.72	33.72
PC2	3.293	21.96	55.68
PC3	1.951	13.01	68.68
PC4	1.417	9.44	78.13
PC5	1.081	7.21	85.34
PC6	0.893	5.96	91.29
PC7–PC15	< 0.34	8.71	100.00

content ranged from 22.17 to 28.97% (mean 25.87%) and methionine content from 0.22 to 0.34% (mean 0.278%). The relatively lower coefficients of variation for protein and methionine suggest that these quality traits are under stronger genetic control and may respond well to hybridization between extreme genotypes.

Principal Component analysis

Principal component analysis reduced the fifteen correlated traits into a smaller set of uncorrelated principal components. The first five principal components possessed eigenvalues greater than 1.0 and together explained 85.34% of the total phenotypic variation (Table 3; Fig. 1). PC1 alone accounted for 33.72% of the variation and was heavily loaded by seed yield per plant (11.18%), days to maturity (10.38%), days to 50% flowering (10.10%), protein content (9.70%), number of pods per cluster (9.68%) and total pods per plant (9.62%). Thus, PC1 essentially represents a "yield–earliness–protein" axis. PC2 explained an additional 21.96% of variation and was dominated by seeds per pod (21.39%), number of primary branches (12.32%), biological yield (10.60%) and methionine content (9.83%) (Table 4; Fig. 2). The cumulative contribution of the first three components reached 68.68%, indicating that a substantial proportion of the total variation can be visualized in a reduced PCA space (Fig. 7).

Cluster analysis and Genetic divergence

Hierarchical cluster analysis based on Euclidean distance and Ward's method grouped the genotypes into ten distinct clusters (Table 5; Fig. 4). Cluster I was the largest, containing 29 genotypes (mostly F_1 and F_2 hybrids involving the tester KLS 218 and several lines). Cluster II comprised eight genotypes, while Clusters III–VII each contained two or three genotypes. Clusters VIII, IX and X were monogenotypic, represented by IPL 244, PL 639 and VL 162, respectively. The presence of monogenotypic clusters indicates that these genotypes are genetically distinct from the remaining material and may serve as valuable sources of unique alleles.

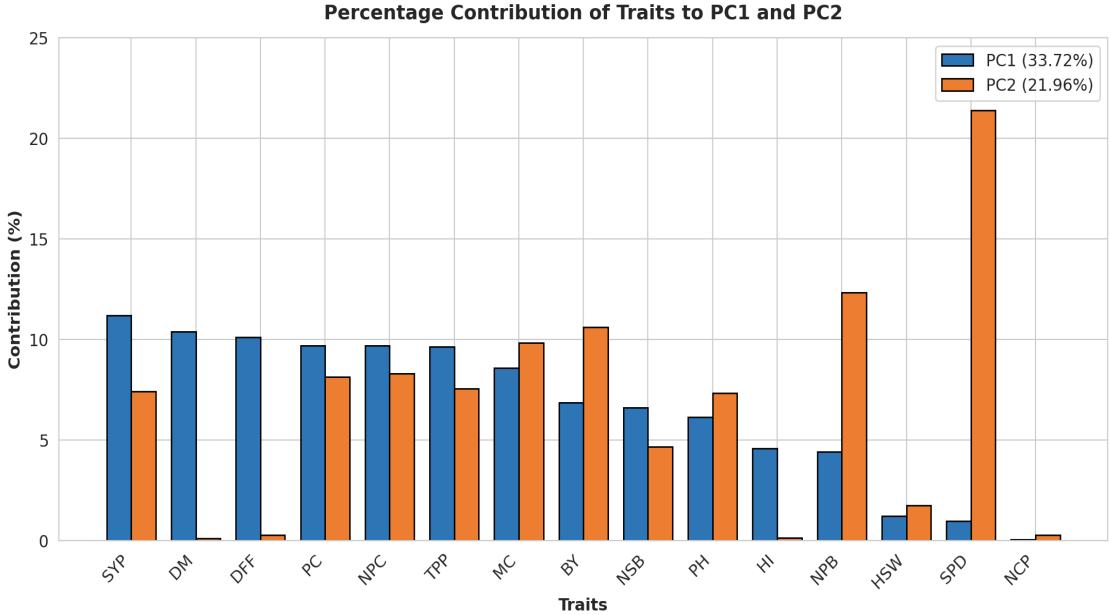


Fig. 2 : Percentage contribution of individual traits to the first two principal components (PC1 and PC2).

Table 4 : Percentage contribution of individual traits to the first eight principal components.

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DFF	10.10	0.28	2.93	5.56	7.69	18.96	7.35	4.31
DM	10.38	0.11	0.00	0.22	18.31	12.21	41.00	0.40
PH	6.14	7.33	10.03	0.33	0.04	11.23	9.23	5.78
NPB	4.42	12.32	7.37	0.21	3.35	8.81	9.95	3.42
NSB	6.59	4.65	11.94	2.74	0.26	13.35	12.92	12.49
NCP	0.06	0.27	11.44	41.98	12.40	0.23	2.66	0.70
NPC	9.68	8.30	2.74	0.78	10.99	0.01	2.32	5.96
TPP	9.62	7.55	0.28	8.59	4.91	0.58	1.18	20.12
SPD	0.97	21.39	0.09	3.22	4.45	1.50	0.99	0.54
HSW	1.21	1.73	21.98	1.15	25.15	8.02	0.35	19.21
BY	6.84	10.60	0.09	14.01	5.48	0.40	0.00	0.07
SYP	11.18	7.40	7.27	0.69	0.55	0.15	0.01	0.90
HI	4.57	0.12	19.82	19.77	1.33	0.29	10.67	7.56
PC	9.70	8.12	0.78	0.24	2.93	13.28	0.02	15.05
MC	8.58	9.83	3.24	0.52	2.17	11.01	1.35	3.50

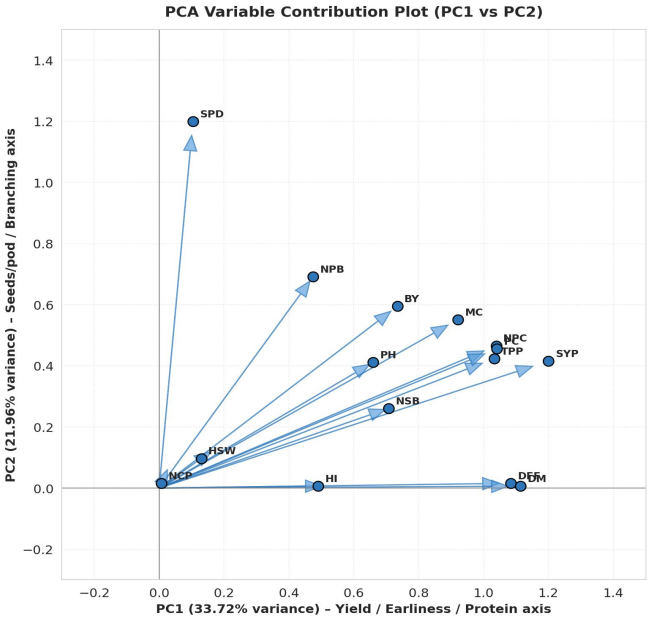


Fig. 3 : PCA variable contribution plot (PC1 vs PC2) showing the relative influence of traits on the major axes of variation.

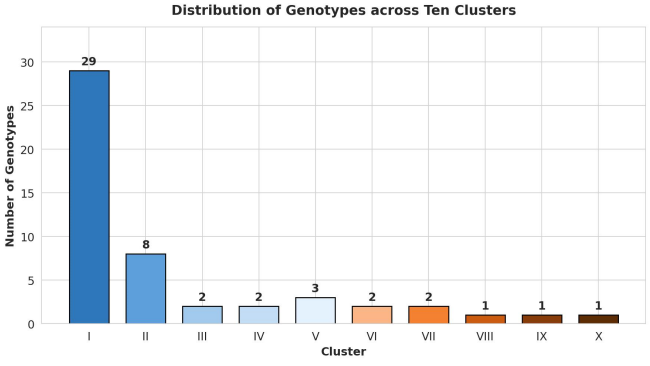


Fig. 4 : Distribution of genotypes across the ten clusters obtained by hierarchical clustering.

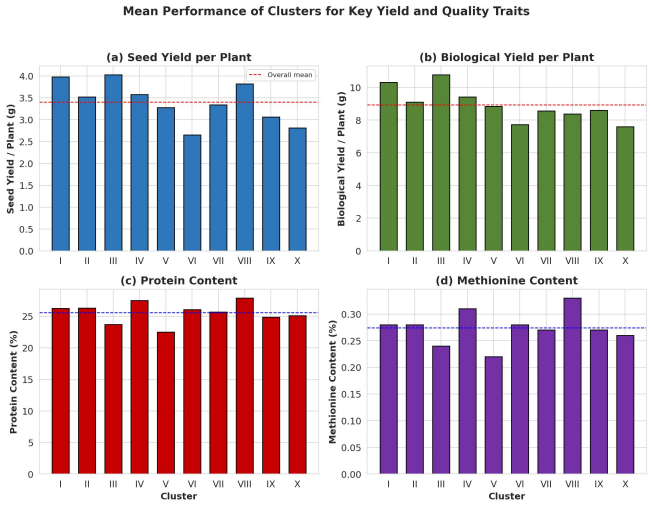


Fig. 5 : Mean performance of the ten clusters for seed yield, biological yield, protein content and methionine content. Dashed lines indicate overall means.

Cluster mean values for the fifteen traits (Table 6; Fig. 5) revealed clear differentiation among groups. Cluster I recorded the highest mean seed yield (3.98 g), biological yield (10.31 g) and a favourable combination of secondary branches and pods per plant, making it the most productive cluster. Cluster III possessed the tallest plants and the highest number of clusters per plant together with good seed yield. Cluster IV was characterized by the highest number of secondary branches, pods per cluster and total pods, along with elevated protein (27.50%) and methionine (0.31%). Cluster VIII (IPL 244) stood out for the highest harvest index (45.62%), protein content (27.87%) and methionine content (0.33%). Cluster IX (PL 639) was the latest-maturing and shortest genotype, while Cluster X (VL 162)

Table 5 : Composition of clusters formed by hierarchical clustering of lentil genotypes.

Cluster	No.	Genotypes included
I	29	KLS 1453×KLS 218, NDL 2018×KLS 218, KLS 1449×KLS 218, KLS 1447×KLS 218, IPL 24-3×KLS 218, IPL 244×KLS 218, VL 161×KLS 218, KLS 1445×KLS 218, PL 318×KLS 218, VL 162×KLS 218, KLS 1445×KL 320, KLS 1447×PL 639, PL 342×KLS 218, KLS 1447, NDL 2018×KL 320, NDL 2018×PL 639, KLS 1453×KL 320, KLS 1453×PL 639, KLS 1445×PL 639, IPL 24-3×PL 639, KLS 1449×KL 320, VL 161×KL 320, IPL 24-3×KL 320, KLS 1447×KL 320, PL 318×KL 320, VL 162×KL 320, KLS 1451×KL 320, IPL 244×KL 320, KLS 1449×PL 639
II	8	KLS 1453, VL 162×PL 639, PL 318×PL 639, VL 161×PL 639, KLS 1451×PL 639, PL 342×PL 639, IPL 244×PL 639, IPL 24-3
III	2	KLS 1451×KLS 218, KLS 218
IV	2	KL 320, PL 342×KL 320
V	3	KLS 1449, KLS 1451, NDL 2018
VI	2	PL 318, PL 342
VII	2	KLS 1445, VL 161
VIII	1	IPL 244
IX	1	PL 639
X	1	VL 162

Table 6 : Mean performance of clusters for morpho-agronomic traits in lentil.

Cl.	DFF	DM	PH	NPB	NSB	NCP	NPC	TPP	SPD	HSW
I	49.57	118.56	47.19	4.10	21.10	24.71	3.05	74.66	1.71	3.22
II	52.21	121.25	44.31	3.58	19.23	23.95	2.97	70.24	1.57	3.22
III	51.83	122.33	48.42	4.40	17.70	28.33	2.23	63.24	1.87	3.25
IV	48.33	118.00	43.89	3.40	26.13	25.37	3.43	85.37	1.37	3.14
V	51.56	121.11	41.33	2.98	16.00	26.33	2.07	54.38	1.76	3.14
VI	54.00	123.17	41.72	2.87	19.93	26.77	2.83	75.10	1.23	2.55
VII	55.67	123.33	45.51	4.07	12.67	25.57	2.43	60.53	1.77	3.13
VIII	49.67	121.67	44.23	2.80	15.87	23.93	2.80	66.47	1.73	3.35
IX	59.67	129.33	37.09	2.87	17.67	23.13	2.73	66.60	1.27	3.32
X	46.33	121.00	45.23	4.40	20.20	16.93	3.20	54.60	1.93	2.71

Table 6 (contd.) : Mean performance of clusters for yield and quality traits.

Cluster	BY (g)	SYP (g)	HI (%)	PC (%)	MC (%)
I	10.31	3.98	38.60	26.21	0.28
II	9.11	3.52	38.60	26.30	0.28
III	10.78	4.03	37.45	23.66	0.24
IV	9.43	3.58	37.84	27.50	0.31
V	8.85	3.28	37.14	22.49	0.22
VI	7.73	2.65	34.36	26.03	0.28
VII	8.56	3.34	39.12	25.63	0.27
VIII	8.38	3.82	45.62	27.87	0.33
IX	8.60	3.06	35.61	24.84	0.27

combined early flowering with high seeds per pod but low biological yield.

Inter-cluster distances (Table 7; Fig. 6) were substantially larger than intra-cluster distances, confirming the existence of genuine genetic divergence among the groups. The maximum inter-cluster distance was recorded between Cluster III and Cluster X (627.97), followed by Cluster I and Cluster X (437.82) and Cluster I and Cluster VI (435.01). The minimum inter-cluster distance occurred between Cluster II and Cluster IX (133.99). Intra-cluster distances were highest for Cluster I (91.56) and Cluster V (92.27), reflecting moderate heterogeneity within these larger groups, while monogenotypic clusters necessarily had zero intra-cluster distance.

Relative contribution of Traits to Genetic divergence

The relative contribution of individual traits towards total genetic divergence (Table 8; Fig. 7) indicated that biological yield per plant was by far the most important contributor (33.98%), followed by number of primary

Table 7 : Intra- (diagonal) and inter-cluster distances among ten clusters of lentil genotypes.

Cl.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	91.6	151.6	169.1	147.8	343.1	435.0	296.7	319.7	325.1	437.8
II	151.6	78.4	259.9	132.1	181.2	189.5	146.4	136.0	134.0	222.6
III	169.1	259.9	30.5	373.3	307.1	579.7	281.5	496.8	349.5	628.0
IV	147.8	132.1	373.3	33.6	358.2	262.6	375.1	257.9	275.0	370.4
V	343.1	181.2	307.1	358.2	92.3	204.4	151.5	221.6	135.8	281.6
VI	435.0	189.5	579.7	262.6	204.4	69.9	222.0	202.1	133.4	201.6
VII	296.7	146.4	281.5	375.1	151.5	222.0	78.2	172.6	151.2	216.8
VIII	319.7	136.0	496.8	257.9	221.6	202.1	172.6	0.0	181.5	232.4
IX	325.1	134.0	349.5	275.0	135.8	133.4	151.2	181.5	0.0	280.0
X	437.8	222.6	628.0	370.4	281.6	201.6	216.8	232.4	280.0	0.0

Table 8 : Relative contribution of different traits towards total genetic divergence.

Trait	Contribution (%)
Biological yield per plant (BY)	33.98
Number of primary branches (NPB)	11.74
Number of secondary branches (NSB)	10.86
Number of pods per cluster (NPC)	6.84
Days to maturity (DM)	5.50
Total pods per plant (TPP)	5.36
Number of clusters per plant (NCP)	3.70
Methionine content (MC)	3.69
Protein content (PC)	3.60
Harvest index (HI)	3.48
Plant height (PH)	3.15
Seed yield per plant (SYP)	2.59
100-seed weight (HSW)	2.18
Seeds per pod (SPD)	1.82
Days to 50% flowering (DFF)	1.51

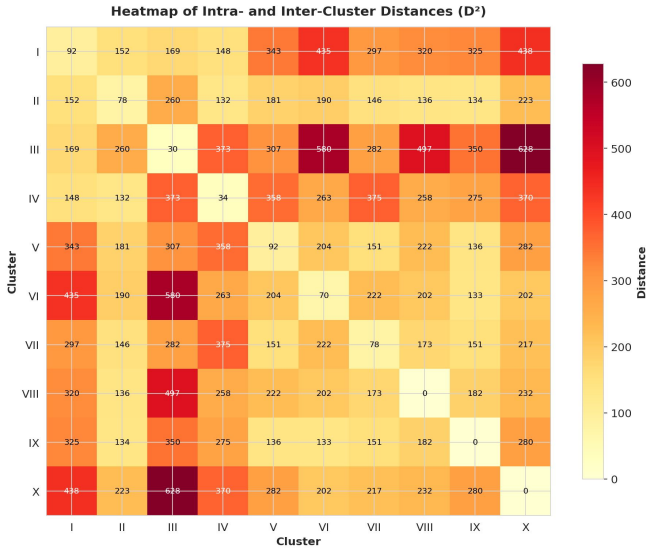


Fig. 6 : Heatmap of intra- and inter-cluster distances (Mahalanobis D²). Darker colours indicate greater genetic divergence.

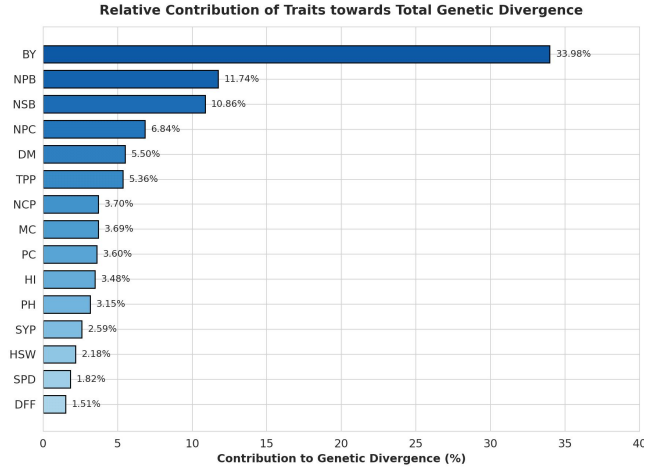


Fig. 7 : Relative contribution (%) of individual traits towards total genetic divergence among the lentil genotypes.

branches (11.74%), number of secondary branches (10.86%), number of pods per cluster (6.84%), days to maturity (5.50%) and total pods per plant (5.36%). Protein content and methionine content contributed 3.60% and 3.69%, respectively. Days to 50% flowering and seeds per pod made the least contribution. These results underscore the predominant role of biomass and branching traits in differentiating the genotypes and suggest that selection for biological yield and branching habit would simultaneously capture a large fraction of the existing genetic diversity.

Overall, the multivariate analyses demonstrated the existence of substantial genetic diversity among the studied lentil genotypes and their hybrid derivatives. The identification of divergent clusters and the quantification of trait contributions provide a sound basis for the rational selection of parents. Hybridization between genotypes of Cluster III (high yield and biomass) and Cluster X (early flowering and high seeds per pod), or between Cluster I and Cluster VI, is expected to generate transgressive segregants for both productivity and

nutritional quality. Genotypes belonging to Cluster VIII (IPL 244) offer an excellent source of high harvest index, protein and methionine and should be utilized in quality-breeding programmes.

Conclusion

The present study revealed considerable genetic variability for yield, yield-contributing and nutritional quality traits among 15 lentil parents and their 72 hybrid progenies. Principal component analysis showed that the first five components explained more than 85% of the total variation, with PC1 representing a combined yield–earliness–protein axis. Hierarchical clustering distributed the genotypes into ten clusters of varying size and genetic distance. The largest inter-cluster distances were observed between Cluster III and Cluster X and between Cluster I and Cluster VI, indicating these combinations as the most promising for hybridization. Biological yield, primary branches and secondary branches were the major contributors to genetic divergence. Cluster I combined high seed and biological yield with good protein content, while Cluster VIII (IPL 244) was outstanding for harvest index, protein and methionine. Strategic crossing among genetically distant clusters is recommended for the simultaneous improvement of productivity and nutritional quality in future lentil breeding programmes.

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