

Research Article

Study on lentil (*Lens culinaris* Medikus) genotypes for its yield and attributing characters and DUS characterization under Terai Region of West Bengal

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Abstract

Lentil (*Lens culinaris* M.) is one of the important rabi pulse crops in India. Despite high-yielding varieties, there is a lack of resources available to respond to malnutrition in developing countries. Therefore, the present investigation was carried out on 40 diversified lentil genotypes to determine the most suitable genotypes based on the studied characters. Under the present investigation, the forty genotypes, including two checks viz., WBL77 and IPL220 was, laid in an alpha lattice design during *rabi* season of 2019-20 and 2020-21 at the instructional farm of Uttar Banga Krishi Viswavidyalaya, Coochbehar, West Bengal. To access the divergence cluster, an analysis was carried out using tocher values using Mahalanobish D^2 distances. On the contrary, the Distinctness, Uniformity, and Stability (DUS) characterization were done after PPV&FR guidelines on lentil. A study on correlation revealed that seed zinc showed a significantly negative (-0.216*) association with yield plant⁻¹. The forty lentil genotypes formed six clusters, with cluster I consisting of the highest 15 genotypes and cluster VI monogenotypic, with maximum inter-cluster distance found between cluster III and VI (317.77) and seed protein content showed the highest contribution towards total divergence (40.8%). A study on flowering habits revealed that one genotype was found to be a determinate type and the rest were indeterminate. The association study revealed a significant positive correlation between seed cooking time and seed sizes (0.433**) and the cooking score showed a significant negative (-0.278*) correlation with seed size. However, IC614827 was found to have the most suitable genotypes than others in the field due to its notable performance.

Keywords: Correlation, Divergence, Genotypic coefficient of variances (GCV), Lentil, Phenotypic coefficient of variances (PCV)

INTRODUCTION

Globally, lentil (*Lens culinaris* Medikus.) is one of the most significant pulse crops, occupying 5.57 million hectares of land and yielding over 6.82 million tons annually with an average yield of about 1225 kg ha⁻¹ (FAOSTAT, 2022). In India, the crop is grown over a total area of 1.42 million hectares; the overall production stands at about 1.28 million tonnes with an average yield of about 904 kg ha⁻¹ (DAC&FW, 2022). It is one of India's most nutritious *rabi* pulse crops and is mostly consumed by the Indians as dal. *Lens culinaris* is divided into two subspecies viz., macrosperma and microsperma (Barulina, 1930) and in the Indian subcontinent, mainly the microsperma types are found having smaller sized seeds (< 25 gm per 1000 seed weight) with red, orange and yellow cotyledons. The protein content in the lentil seeds varies from 22-34.6%, and the seed contains a significant level of lysine, which is considered the limiting amino acid in cereals. However, the seeds lack amino acids like tryptophan, methionine and cystine (Adsule et al., 1989; Hang et al., 2022). Micronutrient malnutrition affects more than half of the world population, particularly in developing countries and over one billion people in Southeast Asia and sub-Saharan Africa suffer from micronutrient malnutrition, often used synonymously with the term "hidden hunger" (Mayer et al., 2008, Kumar et al. (2023). The hidden hunger problem can be partially addressed by developing and consuming Fe and Zn-rich varieties. Lentil, with a formidable mineral content, can be the crop of choice in this situation of malnutrition (Altaf et al., 2024). In India, the average productivity of lentils is very low compared to the world average, primarily due to agroecological and management constraints. Therefore, the present investigation aimed to identify the genotypes of the lentil variety, which have the potential to yield high and be concomitantly enriched with other quality parameters such as protein content and micronutrients like iron and zinc.

MATERIALS AND METHODS

Experimental area

The present experiment on lentils was conducted in Uttar Banga Krishi Viswavidyalaya, Pundibari, during the *Boro* season of 2018-19 and 2019-20 in lentil. The experimental site is located in *Terai* region of West Bengal in Pundibari, Coochbehar, above 43 m altitude from mean sea level. The soil is well drained and sandy loam in texture with soil pH around 5.74. The experimental materials consisted of forty genotypes of lentil, including two checks WBL77 and IPL 220 (*Lens culinaris* Medikus), which were collected from the National Bureau of Plant Genetic Resources (NBPGR), New Delhi and the International Centre for Agricultural Research in Dry Areas (ICARDA), Bhopal centre, Madhya Pradesh. The genotypes collected and included in the

experiment are given in Table 1. Genotypes 1 to 32 obtained from NBPGR, New Delhi and 33 to 40 from ICARDA, Bhopal, were included in the experiment (Table 1).

Experimental inputs

Observations were recorded on five plants selected at random from each replication for various morphological characters. The experimental design used an alpha lattice design followed by three replications. Plot size was maintained at 2m × 1.5m with plant-to-plant spacing 10 cm and row-to-row spacing of 30 cm. Fertilizer was applied from time to time in the field with a basal dose of 20 kg N, 40 kg P₂O₅, 20 kg K₂O and 20 kg of S to raise good crops (Kumar et al., 2018). Intercultural operation was conducted as and when required.

Studied characters

The quality and yield attributed Distinctness, Uniformity, and Stability (DUS) characteristics parameters under study consisted of leaflet size, plant growth habit, flower colour, cotyledon colour, seed size, flowering habit, seed cooking time, seed iron and zinc content presented in the supplementary file (Singh et al., 2005). Seed digestion using a 9:4 di-acid mixture (HNO₃:HClO₄), the absorbance was read against the blank in an Atomic absorption spectrophotometer, Model PinAAcle 900F, PerkinElmer, Singapore (Kumar et al., 2013 and Zarcinas et al., 1987). Seed protein content was estimated after Lowry et al., 1951, which measured colorimetrically against the blank using a spectrophotometer model UV-1900I Shimadzu, Japan. Apart from this, seed yield was also estimated and variance was performed on the above characters (Alvarado et al., 2020).

Data analysis

Genotypic variance, phenotypic variance, heritability (broad sense) and, genetic advance as a percentage (GAM), character association study and genetic divergence study were carried out. Among the techniques employed were Panse and Sukhatme's (1985) analysis of variance (ANOVA), Burton's (1952) phenotypic and genotypic coefficients of variance (PCV and GCV), Johnson et al. (1955) simple correlation, and genetic divergence following Mahalanobis (1936). Only the pooled data was used to compute the correlation and divergence analysis and to calculate the genetic parameters (GCV, PCV, broad sense heritability, and genetic advance as a percentage of the mean). The statistical analysis tools that were utilized were R studio v 4.1.1.

RESULTS AND DISCUSSION

Analysis of variance for yield and attributing traits

Any plant breeding program's essential premise is the existence of genetic variation. Crops' overall improvement in genotype depends critically on sufficient varia-

Table 1. Detail of the accessions of lentil (*Lens culinaris* Medikus) genotypes

Sl. No.	Genotypes	Place of collection	Details	Sl. No.	Genotypes	Place of collection	Parents
1	IC241067	Unknown	Unknown	21	IC199779	Unknown	Unknown
2	IC241090	Unknown	Unknown	22	IC78486	Unknown	Unknown
3	IC241119	Unknown	Unknown	23	EC225484		
4	IC241072	Unknown	Unknown	24	IC241071	Unknown	Unknown
5	IC565035	Murshidabad, W.B	WBL-185	25	IC78513	Sirmaur, H.P	Unknown
6	IC241082	Unknown	Unknown	26	IC610426	Kanpur, U.P	KLB 2008
7	IC78535	Unknown	Unknown	27	IC241097	Unknown	Unknown
8	IC78531	Unknown	Unknown	28	IC241061	Unknown	Unknown
9	EC16391	Switzerland	Unknown	29	IC620839	Unknown	RKL 607
10	IC78545	Solan, H.P	Unknown	30	IC544556	Champaran, Bihar	Unknown
11	IC78540	Unknown	Unknown	31	IC614827	Udham singh nagar, Uttarakhand	PL 098
12	EC223188	Syria	Unknown	32	IC201778	Bahraich, U.P	Unknown
13	IC78518	Unknown	Unknown	33	EC223219	Syria	FLIP88-45L 6469
14	IC78547	Solan, H.P	Unknown	34	EC267544	Syria	ILL 6829
15	WBL77 (c)	Unknown	Maitree	35	EC267563	Syria	ILL 6464
16	IC78454	Unknown	Unknown	36	EC267598	Syria	X 87553
17	IC78462	Solan, H.P	Unknown	37	EC267604	Syria	X 87531
18	EC33920	Australia	CPI 32813	38	EC267636	Syria	LISN E 89
19	EC223244	Syria	1939 Morocco	39	IC78408	Unknown	Unknown
20	EC225486	Syria	Pant L 406	40	IPL220 (c)	Unknown	Unknown

Table 2. Analysis of variance for yield and attributing characters in lentil germplasm

Year	Sources of variation	d.f	Character			
			Seed iron (mg kg ⁻¹)	Seed zinc (mg kg ⁻¹)	Seed protein (g 100 g ⁻¹)	Yield plant ⁻¹ (g)
I (2019-20)	Genotypes	39	783.6**	405.4**	30.10**	29.49**
	Replication	2	313.0**	16.6	0.32	0.09
	Block (Replication)	9	37.7	8.0	0.24	0.76
	Error	69	28.8	10.4	0.54	4.56
II (2020-21)	Genotypes	39	1089.0**	464.2**	33.75**	0.93**
	Replication	2	946.4**	332.2**	4.93*	0.02
	Block (Replication)	9	104.2	25.7	0.51	0.04
	Error	69	123.0	21.4	1.19	0.04
Pooled	Year	1	3499.0**	355.8**	22.02**	0.19
	Genotype	39	1800.0**	741.5**	62.53**	1.58**
	Rep (Year)	4	630.0**	174.6**	2.62*	0.03
	Year×Genotype	39	72.0	128.1**	1.32*	0.11**
	Block (year×rep)	18	71.0	16.9	0.38	0.06
	Error	138	76.0	15.9	0.86	0.05

*, ** Significant at 5% and 1% levels of probability, respectively.

Table 3. Mean, range, GCV, PCV, heritability (bs) and genetic advance in lentil

Sl. No.	Character	Mean	Range	GCV (%)	PCV (%)	Heritability % (broad sense)	Genetic advance as percent of mean
1	Seed iron (mg kg ⁻¹)	103.74	61.00-156.00	23.00	24.80	95.77	43.91
2	Seed zinc (mg kg ⁻¹)	59.06	33.00-93.80	25.88	28.05	97.85	49.17
3	Seed protein (g 100g ⁻¹)	23.10	17.23-33.61	19.60	20.09	98.62	39.41
4	Yield plant ⁻¹ (g)	1.51	0.41-2.76	47.01	49.92	96.68	91.20

Table 4. Genotypic correlation between yield and attributing characters in lentil

Character	Seed zinc (mg kg ⁻¹)	Seed protein (g 100g ⁻¹)	Yield plant ⁻¹ (g)
Seed iron (mg kg ⁻¹)	0.222*	0.025	0.017
Seed zinc (mg kg ⁻¹)		-0.130	-0.216*
Seed protein (g 100g ⁻¹)			-0.150

**, * Significant at 1% and 5% probability level

bility in quality and yield attributes (Begna and Teressa, 2024). The present study was carried out to evaluate the present population of *L. culinaris* Medikus and make further improvements. The study on analysis of variance (Table 2) revealed significant variation in the set of genotypes on studied characters (seed iron, seed zinc, seed protein and seed yield plant⁻¹) for both seasons and pooled analysis data showed that genotypes differed significantly for all the studied yield and yield ascribing traits indicates the presence of adequate genetic variation thus, provide an opportunities for selection of suitable genotypes in the given environment. Vanave *et al.* (2019) reported significant variation in lentils (*L. culinaris* Medic.) for the studied characters, namely, days to initiation of flowering, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of pod plant⁻¹, number of seed pod⁻¹, 100 seed weight, straw yield plant⁻¹, harvest index and seed yield plant⁻¹ which was similar to the present study for one parameter namely seed yield plant⁻¹.

Genetic parameter analysis

Successful selection depends on the extent of variability in a given population, particularly regarding the traits for which improvement is sought. The present study revealed that, in the environment, all the studied characters differ significantly except for seed yield plant⁻¹. The magnitude of the genotypic coefficient of variation (GCV) ranged from 19.60% to 47.01% and the phenotypic coefficient of variation (PCV) range was between 20.09% to 49.92%. All the characters in the current experiment displayed high levels of PCV and GCV. The range of different GCV and PCV values for different characters was classified as suggested by Sivasubramanian and Madhavamenon (1973), which comprised low (<10%), moderate (10–20%), and high (>20%).

There were very few variations between the GCV and PCV levels noted for seed iron (23.00% and 24.80%), respectively and seed protein content (19.60% and 20.09%) signify that the apparent variance results from both the influence of the environment and the genes. Characters with high phenotypic coefficients of variation showed environmental influence; hence, care must be taken throughout the selection process because environmental variations are unexpected and could mislead the results. Similar observation was also reported by Gupta *et al.* (2021) for the characters, namely seed protein and zinc content in lentil for the species of *L. culinaris* Medik. The broad sense heritability was high for all of the characteristics that contributed to the yield attributing traits under investigation (Table 3). Classification of heritability values as proposed by Johnson *et al.* (1955) which comprised with moderate (30–60%), high (>60%), and low (<30%). However, because it combined the results of both additive and non-additive gene action, heritability estimation by itself was insufficient to provide any definitive results. Thus, in addition to the heredity effect, genetic advancement as a percentage of the mean (GAM) was a key factor in selection. Johnson *et al.* (1955) classified the magnitude of GAM values as low (< 10%), moderate (10-20%) and high (> 20%). The assessment of high heritability⁽¹⁾ coupled with high GAM⁽²⁾ was recorded for all the studied characters like seed iron (95.77⁽¹⁾, 43.91⁽²⁾), seed zinc (97.85⁽¹⁾, 49.17⁽²⁾), seed protein (98.62⁽¹⁾, 39.41⁽²⁾) and seed yield (96.68⁽¹⁾, 91.20⁽²⁾). Studies on heritability and genetic advancement revealed that simple selection among germplasm accessions can significantly improve these traits as heritability and genetic advancement were high. A similar observation was reported by Dugassa *et al.* (2015) for the characters, namely, the number of pods plant⁻¹ and grain yield with local variety of Horo Guduru Wollega Zone of Oromia Regional

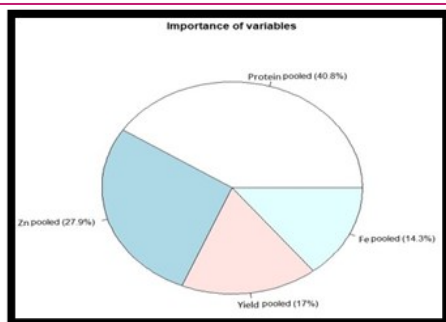


Fig. 1. Contribution of different variable towards total divergence

State of Ethiopia in lentil for *L. culinaris* Medic.

Character association study between yield and attributing traits

As different morphological and quality parameters play a pivotal role in the selection and development of improved varieties, a study on the association of these characters among themselves and with yield will enable a breeder to select a desirable genotype for further crop improvement programme. The genotypic correlation coefficient among four yields and its attribute ascribing characters showed a varying degree of genotypic relationship between the characteristics (Table 4). A significant negative correlation was revealed by seed zinc with seed yield plant⁻¹ (-0.216*). And seed iron revealed a significant positive correlation with seed zinc content (0.222). Greater magnitude of genotypic correlation aids in the selection of genetically controlled traits and increases the likelihood of improving seed yield more than would be predicted based only on phenotypic connection (Rabinson *et al.*, 1951). In confirmation

with the present study, Gautam *et al.* (2018) revealed a significant negative correlation between seed protein content and 100 seed weight in lentils (*L. culinaris* Medik.), which indicated that improving quality attributes will reduce the yield or yield attributing traits.

Genetic divergence study

A direct correlation exists between the success of hybridization in creating new types and genetic diversity. Forty genotypes of lentils were grouped using Mahalanobis D₂ statistics which gives six clusters (Table 5) with cluster I consisting of highest number of genotypes 15 followed by cluster II with 8 genotypes, whereas, cluster V (6 genotypes) and cluster IV and V consisting with 5 number of genotypes in each cluster while the cluster VI consist of only one genotype (EC267598). The average intra and inter-cluster distance revealed that cluster V had maximum intra-cluster distance (113.74) followed by cluster IV (57.14), cluster III (56.44), cluster II (36.79), cluster I (27.43) and cluster VI (0.00) being mono genotypic presented in Table 6. The maximum inter-cluster distance was found between clusters III and VI (317.77) followed by clusters V and VI (264.03) and clusters I and VI (219.92). Thus, the genotypes belonging to distant clusters are likely to yield maximum genetic advantages when put in hybridization, being genetically diverse. The cluster means for different yield attributing traits revealed variable values for different characters, with seed protein contributing the maximum (40.80%), followed by seed zinc (27.90) presented in Fig. 1. Cluster mean (Table 7) of various traits showed that cluster VI was superior for character seed protein content

Table 5. Clustering of lentil genotypes for yield and attributing traits

Cluster No.	Total No. of genotypes	Name of genotypes
I	15	IC241067, IC78540, IC241119, IC78545, IC78547, EC225486, EC267544, IC241097, IC78454, EC16391, EC225484, IC610426, EC223188, IC199779, IC241072
II	8	IC201778, EC267604, IC78408, IC78531, EC267604, IC78462, EC33920, IC241061
III	5	IC78436, IC614827, EC223244, IC241082, IC241090
IV	5	IC241071, IC544556, IC565035, IC620839, EC223219
V	6	IC78513, EC267563, IC78535, IPL220, IC78518, WBL77
VI	1	EC267598

Table 6. Inter and Intra cluster distance of lentil germplasm for yield and attributing traits

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	27.43	90.12	60.31	98.57	65.15	219.92
Cluster II		36.79	146.57	108.81	133.87	65.01
Cluster III			56.44	133.54	113.66	317.77
Cluster IV				57.14	152.47	173.58
Cluster V					113.74	264.03
Cluster VI						0.00

Table 7. Cluster means of lentil germplasm for yield and attributing traits

Cluster	Seed iron (mg kg ⁻¹)	Seed zinc (mg kg ⁻¹)	Seed protein (g 100g ⁻¹)	Yield plant ⁻¹ (g)
Cluster I	105.85	58.57	21.40	1.44
Cluster II	97.46	51.33	26.66	1.48
Cluster III	102.14	59.20	20.33	2.30
Cluster IV	117.89	74.13	25.98	1.54
Cluster V	96.53	59.43	21.09	1.13
Cluster VI	102.85	49.95	31.49	1.05
Contribution (%)	14.30	27.90	40.80	17.00

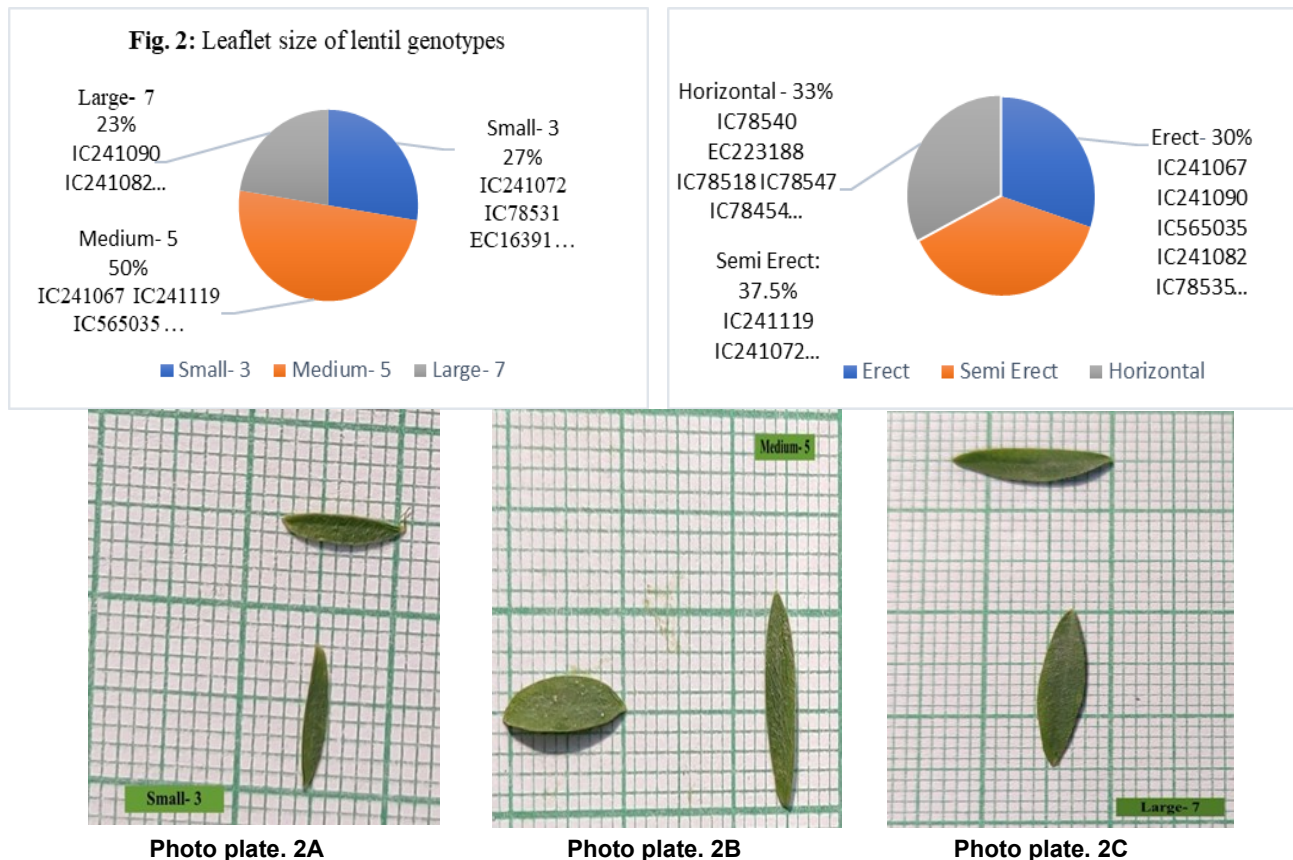
(31.49). Cluster III was superior for yield plant⁻¹(2.30). The two clusters, being the most distant (317.77), thus could favourably be used to identify the divergent genotypes and the association between the characters of importance. Additionally, these clusters would further enable genetic diversity by crossings between the genotypes of divergent clusters, which should be made for varietal development instead of considering those clusters with the smallest genetic distances.

Furthermore, rather than depending on a small number of wild species, it is necessary to promote interspecific hybridization to generate variability and develop the variety of many divergent lineages. Genetic drift and selection in different environments could cause greater diversity than geographical distance (Moll *et al.*, 1962). Kumar *et al.* (2004) conducted an experiment on diver-

gence study with 44 lentil (*L. culinaris* Medik.) genotypes comprising ten clusters. Tenth cluster was identified with promising parents for hybridization in lentil. Cluster V showed the highest intra-cluster distances. On the other hand, clusters III and VI showed the highest inter-cluster distances, which could be exploited to generate superior transgressive segregants.

DUS characterization for qualitative characters

A study on qualitative parameters recorded after PPV&FRA descriptors list characters such as plant leaflet size was recorded over both the experiment years, 2019-20 and 2020-21. It was found that 23% of the genotypes fell under large leaflet size and denominated as 7, 50% fell under medium (5) and 27% fell under small (3) leaflet size presented in Fig.2. The

**Fig. 2.** Leaflet size 2A, 2B and 2C showing small, medium and large leaflet size of lentil respectively

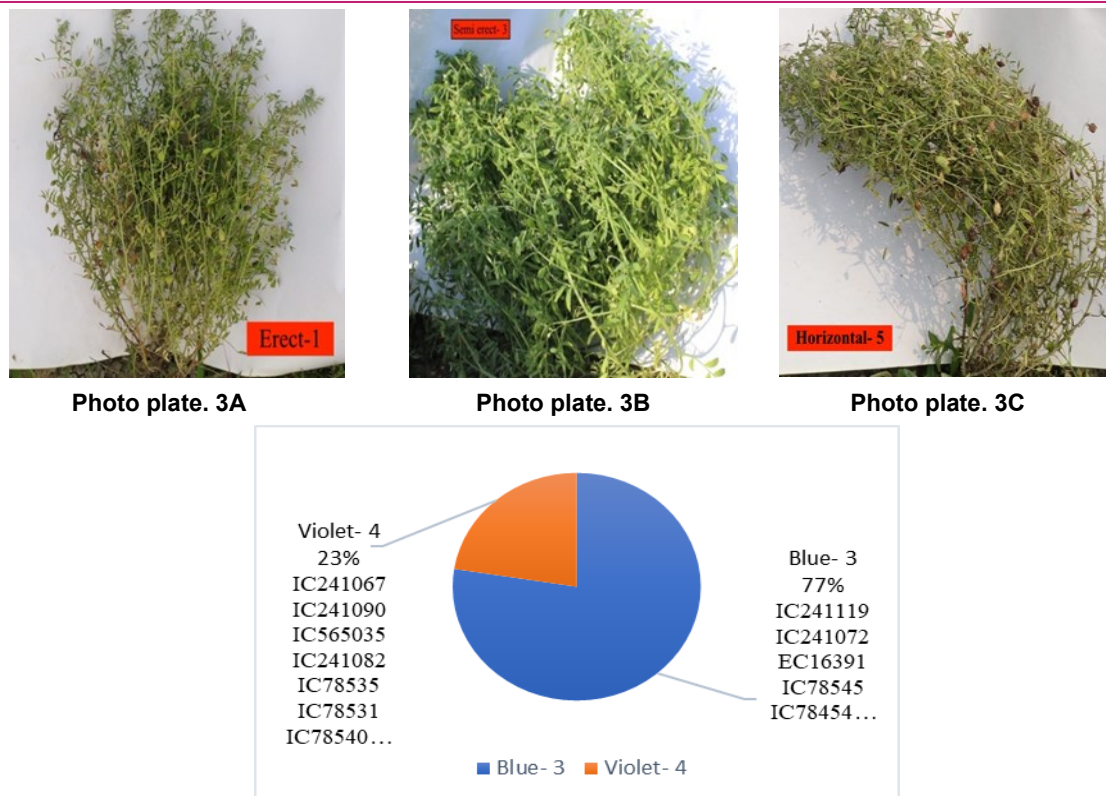


Fig. 3. Plant growth habit in lentil genotype; 3A, 3B and 3C showing erect, semi erect and horizontal plant growth habit of lentil respectively

study on plant growth habit (Fig. 3) revealed 30% were erect type (1) of appearances, 37.5% genotypes shows semi-erect (3) type and remaining 33% genotypes revealed horizontal type (5) of appearances. 77% of the studied genotypes show blue (3) coloured and the remaining 23% identified as violet type (4) over the years of experiment (Fig. 4). Two types of cotyledon colour were identified where 18% of the genotypes found with orange colour (3) and rest 82% of the genotypes were yellow in colour (1) (Fig. 5). Lentil seed sized (Fig. 6) were categorized as large (7), medium (5) and small (3). The weight of 100 seeds, if less than 2.0 g, was termed small types under present investigation, which was 65% of the total number of genotypes. Similarly, 100 seeds weighing between 2.0-2.5 g were named as medium types, which was 30% under study, and the weight of 100 seeds, if marked more than 2.5 g, was termed as large seed, which was 5%. Choudhary *et al.* (2017) studied the lentil species *L. culinaris* Medikus for qualitative trait characterization. The study revealed all the genotypes found with orange cotyledon colour ex-

cept one which has yellow. Further study on plant growth habits revealed 29%, 65% and 6% genotypes were classified into erect, semi-spreading and spreading, respectively. Reddy *et al.* (2024) studied DUS characterization in lentil genotype species *L. culinaris* Medik. The study exhibited all the genotypes that showed orange-coloured cotyledon except for one. Seed size showed tetramorphic variation, leaflet size showed trimorphic variation, while plant growth habit and flower colour showed dimorphic variation.

Study on flowering habits and cooking quality

Apart from the above characteristics, such as flowering habit, which was either determinate or indeterminate in nature, lentils were an indeterminate type of crop. Under the present investigation, it was revealed that all the 39 genotypes were recorded as indeterminate except IC620839, which showed the determinate type presented in Fig. 7. A study on characters association study was carried out with the characters like seeds cooking time, cooking score and seed size presented in Table 8 which showed seed cooking time significantly and positively correlated with seed size (0.433**) and on other hand cooking score showed significant negative correlation (-0.278*) with seed size which signify if seed sizes increase cooking time will also increase. Similar observation was also reported by Santos *et al.* (2018) in pulse germplasm, including lentil (*L. culinaris* Medik.). Ford *et al.* (2007) study on lentil (*L. culinaris* Medikus) exhibited that genotypes branching and flow-

Table 8. Correlation between seed cooking time, cooking score and seed size

Character	Cooking score	Seed size
Seed cooking time	0.203	0.433**
Cooking Score		-0.278*

**, *Significant at 1% and 5% probability level



Photo Plate. 4A



Photo plate 4B

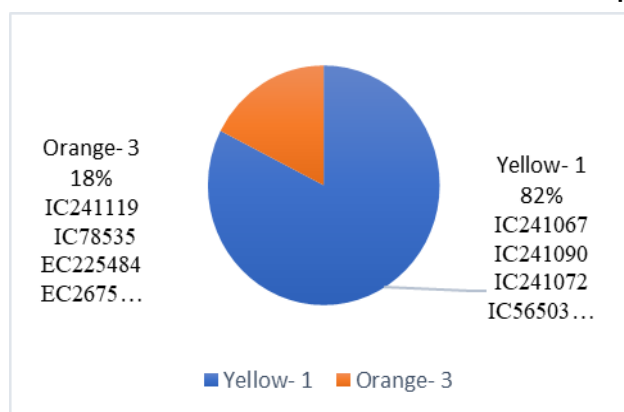


Fig. 4. Flower colour in lentil genotype; 4A and 4B showing blue and violet flower colour of lentil respectively



Photo plate. 5A

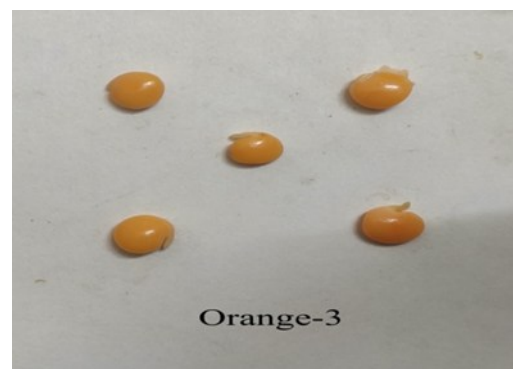


Photo plate. 5B

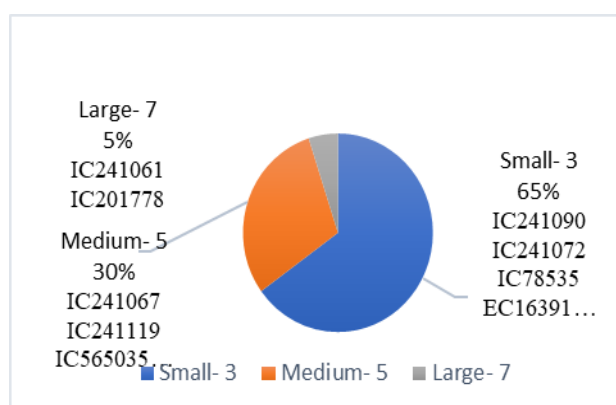


Fig. 5. Cotyledon colour in lentil genotypes. Photo plate 5A and 5B showing yellow and Orange cotyledon colour of lentil respectively



Fig. 6. Seed sizes in lentil genotypes; Photo plate 6A, 6B and 6C showing small, medium and large seed sizes of lentil respectively

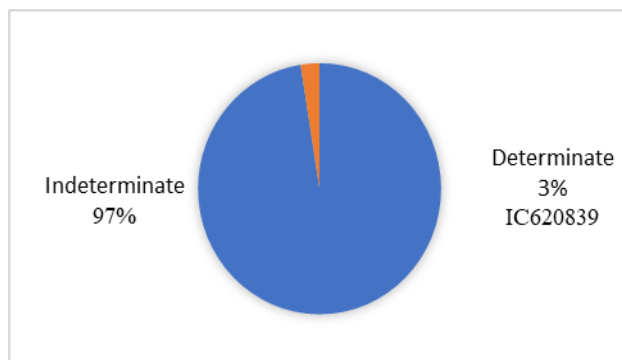


Fig. 7. Flowering habit in lentil genotypes

ering habits were indeterminate. Erskine *et al.* (1985) study on lentil (*L. culinaris* Medik.) revealed a significant positive correlation between cooking time and seed size, which also helps to predict cooking quality. The present study encompasses the characterization of cooking quality and DUS-attributing traits. The significant variation in the variation analysis for all the genotypes encouraged further investigation, especially what type of gene action for these cooking qualities governed by tapping the same helps the breeder choose suitable breeding methods for further improvement of crop genetic background. The character association study among yield and cooking attributing traits highlights an inversely proportional relation between quality, such as seed zinc content and yield attributes, which indicates improving the quality aspect may reduce the quantitative traits dominance, such as yield. With the help of a visual assessment of five different traits, the DUS characterisation is useful for varietal protection before entering the active seed multiplication chain. Further study on flowering habit revealed most of the studied genotypes were indeterminate types except IC620839, which exhibited a determinate flowering habit and could be further exploited for hybridization as a desirable qualitative trait. Characters association study on seed size and cooking time revealed the smaller size of seeds proportionate to less cooking time. Therefore, microsperma types of lentil seeds are desirable for further selection and hybridization programmes.

Conclusion

The present study revealed significant variation among the *L. culinaris* Medikus genotypes for yield and attributing traits in pooled analysis. The correlation study established that seed zinc had a significant negative correlation with seed yield, and seed iron revealed a significant positive correlation with seed zinc, suggesting that further selection of desirable genotypes leads to the improvement of the traits. Study on genetic diversity provides comprehensive strategies for improving the set of traits under study. Clustering based on genetic distance revealed six clusters followed after Mahalanobis D^2 analysis, which emphasizes opportunities of hybridization between genetically divergent genotypes viz; IC78436, IC614827, EC223244, IC241082, IC241090 and EC267598. Traits such as seed protein content and seed zinc have markedly contributed to divergence among the clusters. A study of seed cooking time and seed size revealed a significant positive association and a cooking score revealed a significant negative association with seed size, indicating that the time taken to cook will be longer for lentils with an increase in seed size.

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Conflict of interest

The authors declare that they have no conflict of interest.

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