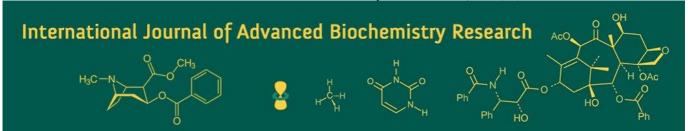
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Exploring genetic variability and trait heritability for yield enhancement in lettuce (*Lactuca sativa* L.)

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Abstract

The present study, titled "Variability Studies in Lettuce (Lactuca sativa L.)", was conducted during the Rabi season of 2024-25 at the Instructional-cum-Research Farm, Department of Horticulture, College of Agriculture, Latur (VNMKV, Parbhani). Ten different genotypes (varieties) of lettuce were evaluated using a Randomized Block Design (RBD) with two replications. Transplanting was done on 31st December 2024 with a spacing of 45 cm \times 30 cm. Each treatment included 20 plants per genotype per replication. Observations were recorded on 22 different characters from five randomly selected plants in each plot. The results showed that there was a wide range of differences among the genotypes for all the traits studied. High values of both genotypic and phenotypic variation were observed for head weight, yield per plant, and total yield. High heritability was found in traits like yield per plant, iron content, dry leaves weight, head weight, total yield, marketable yield, leaf breadth, leaf area, number of leaves, chlorophyll content, dry matter, plant height, and leaf length. These traits also showed high genetic advance, suggesting they can be improved through selection. Among the genotypes, 'Padma', 'Argula', 'Iceberg Lettuce', 'Oakleaf Lettuce', 'Coral Lettuce', and 'Great Lakes' performed better for yield and growth traits. For quality traits, 'Padma', 'Argula', and 'Romaine Lettuce' were found superior. These genotypes are suitable for commercial cultivation and future breeding programme.

Keywords: Variability, heritability, genetic advance, lettuce

Introduction

A member of the Compositae family, lettuce (*Lactuca sativa* L.) is an annual leaf vegetable. Though occasionally grown for its seeds and stems, it is primarily planted as a green vegetable. The king of green salads, lettuce may be used in a variety of dishes, including burgers, soups, and sandwiches. The natural range of lettuce extended from the Mediterranean to Siberia. 2n=18 is its chromosomal number. Plants typically measure 15 to 30 cm in height and spread.

There are six kinds and over 100 species in the genus *Lactuca*. There are several varieties of lettuce, including oil-seed lettuce, romaine (Cos), butterhead, stem (asparagus), crisp head (ice berg), and leaf (cutting) (Mousavi *et al.*, 2013) ^[18]. Asia, North and Central America, and Europe are the regions where it is commercially farmed. China, US, Spain, Italy, India, and Japan are the world's top lettuce-growing nations. (Dolma *et al.*, 2010) ^[2].

One of the most commercially significant leafy vegetable crops in the world is lettuce (*Lactuca sativa* L.). Out of all the salad crops grown worldwide, it takes up the most production space, and its output keeps rising annually. In 2019, China topped the global lettuce production rankings, with the US and India coming in second and third, respectively (FAO, 2019) [4]. Over 1.31 million hectares of lettuce were harvested worldwide, with a total production of over 29.13 million tons (FAO, 2019) [4]. Over 1.76 million hectares, or 1.12 million tons of lettuce were produced in India (FAO, 2020) [5].

Vegetative characteristics such as leaf length, colour, texture, size, and heading types are where lettuce varies most. The prospective diverse genotypes that could be employed in future breeding programs are found using genetic diversity data. Genetic remodeling of lettuce is required to find high-yielding types and hybrids in order to increase production. The degree of genetic variety determines how useful selection is. The advancement of crop breeding depends on the availability of substantial germplasm that represents a variety of

genetic variation. This is also a crucial source of parental strains for hybridization and the creation of improved varieties (Kaushal and Kumar, 2010) [11].

In addition to lowering cholesterol, lettuce contains anti-inflammatory, antioxidant, antibacterial, and anti-cancer qualities. It also helps with insomnia and anxiety management (Khare, 2004) [13]. The presence of bioactive terpenoids and polyphenols, including flavonoids, phenolic acids, and carotenoids, has been linked to the health benefits of leafy lettuce. As people's eating habits change and their awareness of their health grows, it is becoming more and more popular in India Other names for lettuce include expectorant, sedative, diuretic, and anodyne (Kallo, 1986) [12].

2. Materials and Methods

2.1 Testing Location and Layout of Experiment

An experiment was conducted with 10 genotypes of lettuce during Rabi-2024 at Instructional-Cum-Research Farm, at Department of Horticulture, College of Agriculture, Latur. The material under study was constituted of 10 genotypes of Lettuce (Lactuca Sativa L.) which were collected from various places. The sources of these genotypes are Gultekdi market yard, Pune, Sangali local market and ZARS Pune. The trial was carried in Randomized block design with two replications having 45cm × 30cm spacing. The observations were recorded on plant height (cm), number of leaves per plant, leaf area (cm²), head weight (g), stalk weight (g), leaf length (cm), leaf breadth (cm), fresh leaves weight per plant (g), dry leaves weight per plant (g), dry matter content (%), chlorophyll content (mg/100 g), iron content (%), yield per plant (g), yield per plot (kg), marketable yield (q ha⁻¹), total yield(q ha⁻¹), leaf shape, leaf colour, type of leaf, leaf blistering, percent incidence of pest and diseases.

2.2 Experimental Materials

The experiment was conducted using 10 lettuce genotypes namely; Argula, Iceberg Lettuce, Oakleaf lettuce, Romaine Lettuce, Endive, Coral Lettuce, Black seeded Simpson, Butterhead Lettuce, Great Lakes and Padma.

3. Results and Discussion

The improvement of the crop relies heavily on genetic variability. A key factor in successful breeding programs is understanding the type and extent of genetic variation within each crop species. A comprehensive understanding of this variation is essential for its effective application in crop improvement as genetic variation forms the basis for plant breeding, where selection is used to develop enhanced genotypes. The study of genetic advance is crucial as it measures the genetic gain resulting from selection for a specific trait. Therefore, examining heritability, genetic variability and genetic advance is essential for any crop improvement program that involves selection or hybridization.

3.1 Analysis of Variance

Analysis of variance for randomized block design was carried out to assess the variation for all the characters The significance was marked by applying 'F' test. Analysis of variance for sixteen characters consisting of replication mean squares, treatment mean squares and error mean squares is given in (Table 1). The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied viz., plant height,

number of leaves per plant, leaf area, head weight, stalk weight, leaf length, leaf breadth, fresh leaves weight per plant, dry leaves weight per plant, dry matter content, chlorophyll content, iron content, yield per plant, yield per plot, marketable yield and total yield are given in (Table 1) indicating the presence of genetic variability in the existing material. Similar findings reported by Singh *et al.* (2000) [3, 20], Santamaria *et al.* (2000) [21], Ledo *et al.* (2001) [17], Figueiredo *et al.* (2004) [6], Jang *et al.* (2004) [9], Yuri *et al.* (2005) [27], Ijoyah and Koutatouka (2007) [8], Kumar *et al.* (2010) [14], Thakur *et al.* (2013) [24], Ragheb (2015) [19], Kumar *et al.* (2015) [15] and Saha *et al.* (2018) [22]

Table 1: Analysis of variance for different characters studied in the genotypes of lettuce

Sr.	Characters	Mean sum of squares					
No.	Characters	Replication	Treatment	Error			
1.	Plant height (cm)	0.3976	23.106**	3.623			
2.	No. of leaves per plant	0.1824	4.474**	0.457			
3.	Leaf area (cm ²)	0.1280	6.644**	0.519			
4.	Head weight (g)	36.450	14216.82**	241.45			
5.	Stalk weight (g)	6.3056	74.933**	23.018			
6.	Leaf length (cm)	1.1520	16.276**	2.943			
7.	Leaf breadth (cm)	0.3864	9.045**	0.617			
8.	Fresh leaves weight per plant (g)	81.204	732.46**	165.14			
9.	Dry leaves weight per plant (g)	0.3892	15.397**	0.201			
10.	Dry matter content (%)	0.1620	1.593**	0.212			
11.	Chlorophyll content (mg/100 g)	0.0180	1.146**	0.352			
12.	Iron content (%)	0.0005	1.848**	0.021			
13.	Yield per plant (g)	25.200	6475.04**	23.458			
14.	Yield per plot (kg)	0.0320	0.5342**	0.0320			
15.	Marketable yield (q ha ⁻¹)	88.199	954.75**	39.088			
16.	Total yield (q ha ⁻¹)	0.1125	12127.82**	43.652			

3.2 Mean Performance

The mean performance of genotypes for different characters indicated that, higher yield per plant in gram exhibited for the genotypes Padma followed by Argula, Iceberg lettuce, oakleaf lettuce, coral lettuce and great lakes. The mean of genotypes, Padma, Argula, Iceberg, Great lakes and Romaine

Lettuce showed better performance for the traits head weight, stalk weight, fresh leaves weight per plant, marketable yield, yield per plant in kilogram and total yield. Genotypes like Endive, Black seeded Simpson and Butterhead Lettuce were promising for short plant height, number of leaves per plant, leaf area, leaf length, leaf breadth, dry leaves weight per plant, dry matter content, chlorophyll content and iron content respectively.

3.3. Genotypic and Phenotypic coefficient of variation

The amounts of differences in characteristics are measured and expressed as a variance. The total quantity of observed variation or phenotypic variation in character does not accurately represent variation that can be fixed in subsequent generations, whereas genotypic variation is the number of fixable differences from one generation to the next. The environmental variance changes from one location to another and so cannot be fixed.

In general (Table 2), the phenotypic variance was greater than the genotypic variances for the characters viz., plant height (cm), number of leaves per plant, leaf area (cm2), head weight (g), stalk weight (g), leaf length (cm), leaf breadth (cm), fresh leaves weight per plant (g), dry leaves

weight per plant (g), dry matter content (%), chlorophyll content (mg/100 g), iron content (%), yield per plant (g), yield per plot (kg), marketable yield (q ha⁻¹) and total yield (q ha⁻¹).

The data revealed from the (Table 2), the genotypic coefficients of variation varied from 6.06% for dry leaves weight per plant to 36.93% for total yield. The genotypic coefficient of variations was highest for characters viz., head weight (32.26%), yield per plant (27.52%) and total yield (36.93%). The high values of GCV suggested greater phenotypic genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. The moderate variability recorded in the characters, chlorophyll content (18.21%), leaf breadth (17.26%), iron content (13.35%), dry matter content (11.73%), leaf length (11.61%), plant height (11.28%), yield per plot (11.03%), leaf area (11.00%). The lowest genotypic coefficients of variation were found in the dry leaves weight per plant (6.06%), fresh leaves weight per plant (6.58%), stalk weight (8.00%), number of leaves per plant (9.86%) and marketable yield (10.11%). Similar finding reported by Kaushal (2009) [16], Thakur (2013) [24] and Shoaib et al. (2016) [16]. The phenotypic coefficient of variation ranged from 6.10% for dry leaves weight per plant to 37.00% for total yield. The phenotypic coefficient of variations was highest for characters viz., total yield (37.00%), head weight (32.54%), yield per plant (27.57%) and chlorophyll content (21.88%) are given in (Table 2). It indicates that these characters would respond to selection. The rest of the characters such as leaf breadth (17.89%), iron content (13.43%), leaf length (12.82%), dry matter content (12.60%), plant height (12.28%), leaf area (11.46%), yield per plot (11.38%), number of leaves per plant (10.40%) and marketable yield (10.32%) exhibited moderate phenotypic coefficient of variation. The lowest phenotypic coefficients of variation were found in the dry leaves weight per plant (6.10%), fresh leaves weight per plant (7.48%), and stalk weight (9.61%). Similar finding reported by Kaushal (2009) [16], Thakur (2013) [24] and Shoaib *et al.* (2016) [16].

The estimates of phenotypic and genotypic coefficients of variation (Fig.1) were recorded high for head weight, yield per plant in gram and total yield. Whereas, medium values for the characters plant height, leaf area, leaf length, leaf breadth, dry matter content, chlorophyll content, iron content and yield per plot in kilogram. Also, lower values for the characters number of leaves per plant, stalk weight, fresh leaves weight per plant, dry leaves weight per plant, and marketable yield.

Table 2: Mean, range, GCV, PCV, heritability, genetic advance and percent mean of genetic advance in lettuce

Sr. No.	Name of the Character	Mean	Dongo	Genotypic	Phenotypic	GCV	PCV	\mathbf{h}^2	GA	CAM (9/1)
Sr. No.	Name of the Character	Mean	Range	variance	variance	(%)	(%)	(Broad sense)	(%)	GAM (%)
1.	Plant height (cm)	27.66	22.22-33.10	9.74	11.55	11.28	12.28	84.3	5.90	21.33
2.	No. of leaves per plant	14.37	11.97-16.63	2.09	2.23	9.86	10.40	89.8	2.76	19.24
3.	Leaf area (cm ²)	15.90	13.10-18.70	3.06	3.32	11.00	11.46	92.2	3.46	21.77
4.	Head weight (g)	259.05	154.00-360.50	6987.68	7108.41	32.26	32.54	98.3	66.73	36.35
5.	Stalk weight (g)	63.67	57.00-73.10	25.95	37.46	8.00	9.61	69.3	8.73	13.72
6.	Leaf length (cm)	22.24	16.60-27.30	6.66	8.13	11.61	12.82	81.9	4.81	21.64
7.	Leaf breadth (cm)	11.88	8.72-14.89	4.21	4.52	17.26	17.89	93.2	4.08	34.33
8.	Fresh leaves weight per plant (g)	255.74	216.60-285.60	283.66	366.23	6.58	7.48	77.5	30.53	11.93
9.	Dry leaves weight per plant (g)	45.43	41.01-49.83	7.59	7.69	6.06	6.10	98.7	5.64	12.41
10.	Dry matter content (%)	7.08	5.25-8.25	0.69	0.79	11.73	12.60	86.7	1.59	22.51
11.	Chlorophyll content (mg/100 g)	3.46	2.70-5.20	0.39	0.57	18.21	21.88	89.3	1.08	31.21
12.	Iron content (%)	7.15	6.10-8.50	0.91	0.92	13.35	13.43	98.8	1.95	27.35
13.	Yield per plant (g)	206.34	162.20-304.50	3225.79	3237.52	27.52	27.57	99.6	1.18	39.26
14.	Yield per plot (kg)	4.54	3.70-5.30	0.25	0.26	11.03	11.38	94	1.00	22.04
15.	Marketable yield (q ha ⁻¹)	211.60	195.00-252.00	457.83	477.37	10.11	10.32	95.9	43.16	20.40
16.	Total yield (q ha ⁻¹)	210.46	132.30-362.70	6042.08	6063.91	36.93	37.00	96.3	2.70	38.47

Where, GCV-Genotypic coefficients of variation (%), PCV-Phenotypic coefficients of variation (%), h²-Heritability (%), GA-Genetic advance (%), GAM-Genetic advance as percent of mean

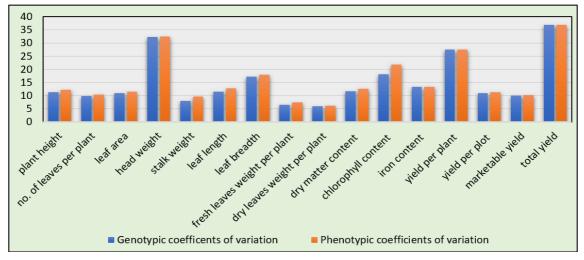


Fig 1: Genotypic and phenotypic coefficient of variation for sixteen characters in lettuce

3.4 Heritability and Genetic Advance as Percent of Mean

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. Heritability in broad sense estimates were highest for (Table 2.) yield per plant (99.6%), iron content (98.8%), dry leaves weight per plant (98.7%), head weight (98.3%), total yield (96.3%), marketable yield (95.9%), yield per plot (94%), leaf breadth (93.2%), leaf area (92.2%), number of leaves per plant (89.8%), chlorophyll content (89.3%), dry matter content (86.7%), plant height (84.3%) and leaf length (81.9%). It indicated that characters were less influenced by environmental effect. This variation is due to total genetic variance. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable. The estimates of heritability were moderate for fresh leaves weight per plant (77.5%) and stalk weight (69.3%). It indicated that character was moderately influenced by environmental effect. This indicated that selection based on phenotypic performance would be effective. These results are in consonance with the findings of Gupta et al. (2008) [7], Tashi et al. (2010) [25], Cassetari et al. (2015) [1], Ragheb et al. (2015) [19] and Thakur et al. $(2016)^{[26]}$.

Genetic advance as percent of mean ranged between 11.93% for fresh leaves weight per plant to 39.26% for yield per plant. The highest estimate of genetic advance as percent of mean was recorded for (Table 2.) yield per plant (39.26%),

total yield (38.47%), head weight (36.35%), leaf breadth (34.33%), chlorophyll content (31.21%), iron content (27.35%), dry matter content (22.51%), yield per plot (22.04%), leaf area (21.77%), leaf length (21.64%), plant height (21.33%), marketable yield (20.40%). Whereas, moderate genetic advance as percent of mean ranged for number of leaves per plant (19.24%), stalk weight (13.72%), dry leaves weight per plant (12.41%) and fresh leaves weight per plant (11.93%). This indicated that, these characters were governed by additive gene action and selection of this trait is more effective. Similar results were also reported by Gupta *et al.*, (2008) [7] and Kumar *et al.* (2010) [14].

Heritability however indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic advance are more effective and reliable in predicting the improvement through selection (Johnson *et al.*, 1955) [10].

High heritability coupled with high genetic advance were observed for head weight, leaf breadth, chlorophyll content, yield per plant and total yield (Fig 2). The results suggested the importance of additive gene action for the inheritance of these characters and improvement could be brought about by phenotypic selection. Moderate heritability along with moderate genetic gain was observed for the characters iron content, dry matter content, yield per plot, leaf area, leaf length, plant height, marketable yield, number of leaves per plant, stalk weight, dry leaves weight per plant and fresh leaves weight per plant. The result suggested the importance of additive gene action for the inheritance of this character and improvement could be brought about by phenotypic selection. Similar finding reported by Shoaib *et al.* (2016) [16] and Thakur *et al.* (2016) [26].

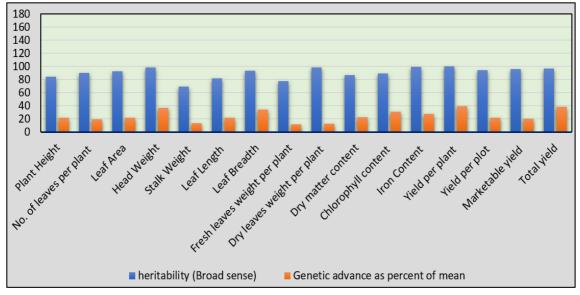


Fig 2: Heritability in Broad sense (%) and genetic advance as percent of mean (%) for sixteen characters in lettuce

4. Conclusion

The analysis of variance indicated highly significant differences among the genotypes for all fifteen traits. It states that all genotypes under investigation were genetically differed. On the basis of mean performances, the genotypes Padma, Argula, Iceberg Lettuce, Oakleaf Lettuce, Coral Lettuce and Great Lakes can be exploited for developing as high yielding genotypes. Genetic variability study

demonstrated that the material used in the current research had significant variability which provided a suitable basis for selection. Higher values of phenotypic coefficient of variation than genotypic coefficient of variation for a trait indicate that the traits are influenced by their environment. While there was a close correspondence between GCV and PCV for the majority of the characters, environmental factors had less influence on the appearance of these

characters. The lowest values of GCV and PCV was recorded for number of leaves per plant, stalk weight, fresh leaves weight per plant and dry leaves weight per plant. The GCV and PCV were reported to be high for head weight, yield per plant and total yield indicate the good scope for genetic improvement of these characters by selection. High heritability with high genetic advance as percent of mean expressed for the characters head weight, leaf breadth, chlorophyll content, yield per plant and total yield are most likely governed by additive genes suggesting that simple selection may effectively improve them. Thus, the genotypes viz., Padma, Argula, Iceberg Lettuce, Oakleaf Lettuce, Coral Lettuce and Great Lakes were found superior for all yield, yield contributing characters and for commercial cultivation and it can be utilized for further improvement of breeding programme.

References

- 1. Cassetari LS, Gomes MS, Santos DC, Santiago WD, Andrade J. Beta carotene and chlorophyll levels in cultivars and breeding lines of lettuce. Acta Hortic 2015;1083;469-473.
- 2. Dolma T, Gupta AJ, Ahmed N. Variability, heritability and genetic advance in lettuce (*Lactuca sativa* L.). Indian J Hortic 2010;67:193-196.
- 3. Singh D, Atwal AK, Bajaj KL. Evaluation of some promising type lettuce (*Lactuca sativa* L.) cultivars for leaf and quality characters. Vegetable Sci 2000;27(1):92-93.
- 4. FAO. Production Year Book. Rome: Food and Agriculture Organization of the United Nations; 2019.
- 5. FAO. FAOSTAT [Internet]. 2020. Available from: http://www.fao.org/faostat/site/default.aspx
- 6. Figueiredo EB-de, Malkeiros EB, Braz LT. Interaction genotype × environment of lettuce cultivars in Jaboticabal, Brazil. Hortic Bras 2004;22(1):66-71.
- 7. Gupta AJ, Dolma T, Chattoo MA, Yasmin S. Estimation of genetic variability and heritability in lettuce (*Lactuca sativa* L.). Indian J Plant Genet Resour 2008;2:138-140.
- 8. Ijoyah MO, Koutatouka M. Yield performance of four lettuce (*Lactuca sativa* L.) varieties compared with the local variety under open field conditions at Anse Boileau, Seychelles. J Sustain Agric Environ 2007;9:146-152.
- 9. Jang S, Kim W, Kwon Y, Ryu S. A high yielding and high quality romaine type lettuce cultivar, Mansang. Korean J Breed 2004;36(3):169-170.
- 10. Johnson. Genetic advance analysis in pea (*Pisum sativum* L.). Madras Agric J 1955;6(7):387-390.
- 11. Kaushal S, Kumar R. Genetic divergence studies in newly introduced genotype of lettuce (*Lactuca sativa* L.). Afr J Basic Appl Sci 2010;2(1-2):18-24.
- Kallo. Lettuce. In: Bose TK, Som MG, editors. Vegetable crops in India Calcutta: Naya Prokash; 1986. p. 692-708.
- 13. Khare CP. Indian herbal remedies: Rational western therapy, ayurvedic, and other traditional usage, Botany. Berlin: Springer Science & Business Media; 2004.
- 14. Kumar R, Kaushal S, Shukla YR. Variability, correlation, and path analysis studies in lettuce (*Lactuca sativa* L.). Int J Vegetable Sci 2010;2(4):299-315.
- 15. Kumar P, Pathania NK, Sharma P, Singh N. Evaluation of lettuce genotypes for yield and quality under

- protected conditions of North-western Himalayas. Himachal J Agric Res 2015;4:184-188.
- 16. Kaushal S. Genetic evaluation of newly introduced genotypes of lettuce (*Lactuca sativa* L.) [MSc thesis]. Solan (HP): Dr. YS Parmar University of Horticulture and Forestry, Nauni; 2009. 58 p.
- 17. Ledo FJ-da-S, Casali VWD, Curz CD, Ledo CA-da-S. Genetic analysis in a lettuce (*Lactuca sativa* L.) diallel. Pesqui Agropecu Bras 2001;36(3):493-499.
- 18. Mousavi SH, Hassandokht MR, Choukan R, Sepahvand N, Khosrowchali M. Cytological study of chromosome and genome composition of Iranian lettuce (*Lactuca sativa* L.) accessions. Eur J Exp Biol 2013;3(1):303-311.
- 19. Ragheb EIM. Mass selection and individual plant selection as two breeding methods for improving lettuce (*Lactuca sativa* L.). Alexandria J Agric Res 2015;60:213-220.
- 20. Singh D, Atwal AK, Bajaj KL. Evaluation of some promising type lettuce cultivars for leaf and quality characters. Vegetable Sci 2000;27:92-93.
- 21. Santamaria P, Generoso C, Gonnella M, Elia A. Yield and nitrate contents of lettuce cultivars. Colture Protette 2000;29:71-77.
- 22. Saha S, Kalia P, Sarkar SK. Evaluation of lettuce genotypes for mineral content. Indian J Hortic 2018;75:613-618.
- 23. Shoaib RM, Abdel NS, Ramadan WA, Ibrahim MM, Aboud KA. Elucidation of some genetic parameters among selected genotypes of prickly oil lettuce (*Lactuca serriola* L.) in Egypt, using morphoagronomic traits and RAPD markers. Res J Pharm Biol Chem Sci 2016;7:1255-1264.
- 24. Thakur M. Genetic evaluation of lettuce (*Lactuca sativa* L.) germplasm under protected conditions [MSc thesis]. Solan (HP): YSP Univ of Horticulture and Forestry, Nauni; 2013. 65 p.
- 25. Tashi D, Gupta AJ, Ahmed N. Variability, heritability and genetic advance in lettuce. Indian J Hortic 2010;67:193-196.
- 26. Thakur M, Kumar R, Kumar S. Studies on genetic variability, correlation and path analysis in lettuce (*Lactuca sativa* L.) under protected conditions. J Appl Nat Sci 2016;8:1924-1930.
- 27. Yuri JE, Souza RJ, Resende GM, Mota JH. Evaluation of crisphead lettuce cultivars in Santo Antonio do Amparo, Brazil. Hortic Bras 2005;23:870-874.