

Genetic Divergence Studies in Lettuce (*Lactuca sativa* L.) Under Protected Conditions in Mid Hills of Himachal Pradesh

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Abstract – Twenty-eight genotypes of lettuce including check cultivars (Simpson Black Seeded and Great Lakes) were evaluated for genetic divergence studies under protected conditions. The present investigation entitled “Genetic evaluation of lettuce (*Lactuca sativa* L.) germplasm under protected conditions” was carried out at experimental farm of Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan (HP) during 2011-12 and 2012-13. The experiment was laid out in a RCBD with three replications. Analysis of variance showed highly significant differences among genotypes for all the characters under study. By multivariate analysis (Mahalanobis D^2 technique), the genetic divergence among the genotypes were quantitatively measured. The genotypes were grouped into five clusters by this technique and more number of genotypes were grouped into cluster V. There was no relationship between clustering pattern and eco-geographical distribution. The effect of genetic divergence on the choice of genetic divergence on the choice of clusters accommodating the parental stock for further breeding programmes is also discussed.

Keywords – *Lactuca sativa* L., Lettuce, Cluster Analysis, D^2 Analysis.

I. INTRODUCTION

Lettuce (*Lactuca sativa* L.) is one of the important leafy vegetable used as salad and also marketed as fresh vegetable. Genus *Lactuca* has more than 100 species and six types. Different types of lettuce are Romaine (Cos), Crisp head (Ice berg), Butter head, Stem (Asparagus), Leaf (Cutting) and Oil-seed lettuce (Mousavi *et al.*, 2013). It is commercially grown in Asia, North and Central America and Europe. The major lettuce growing countries in the world are China, US, Spain, Italy, India and Japan (Dolma *et al.*, 2010). The world production of lettuce and chicory is 24.32 million tonnes over total area of approximately 1.11 million hectares. In India these are cultivated over an area of 0.16 million hectare with production of 1.05 million tonnes. Productivity of lettuce in India is quite low being 6.33 MT/ha as compare to the world average of 21.89 MT/ha (FAO, 2011). There is an increasing demand by the consumers for safe and nutritious foods that improve physical performance, reduce the risks of diseases and increase the life span (Ogden *et al.*, 2007). It is rich in vitamin A and C and minerals like calcium, iron, magnesium, potassium and sodium. However, vitamin-C is lost if it is over cooked. It is grown for its tender leaves and head, which are chopped and used as salad with salt and vinegar. Lettuce is also known to be a sedative, diuretic and expectorant. In India,

it is gaining popularity with the change in food habit and health consciousness among the people (Kaushal and Kumar, 2010). Variation in lettuce is mostly found in vegetative characters like leaf length, shape, colour, texture, size, and heading types. Information on genetic diversity are used to identify the promising diverse genotypes, which may be used in further breeding programme. To enhance productivity, genetic restructuring of lettuce, germplasm is needed to identify high yielding varieties/hybrids. The usefulness of selection depends on amount of genetic variation present. Availability of large germplasm which represent diverse genetic variation is important for the progress of crop breeding and invaluable source of parental strains for hybridization and development of improved varieties (Kaushal and Kumar, 2010).

The profitability of vegetable production depends upon the productivity, quality and timing of growing the crop. Moreover, increasing awareness for quality and healthy food has also led to the rapid increase in demand of vegetables. By bringing more and more area under vegetable cultivation, improved agro-techniques and quality seeds have not yielded satisfactorily to fully meet the ever growing demand of vegetables. Thus, the alternative lies in the promotion and perfection of some advanced technologies like greenhouse technology or protected cultivation. Polyhouse cultivation is an alternate over the traditional cultivation, as it ensures high productivity per unit area with the genetic potentiality of the crop being fully exploited, raising of off-season healthy nursery, production of good quality produce free from any blemishes and finally it is easy to protect the crop against pests and diseases as well as extreme climatic conditions. Most of the farmers of the state are installing polyhouses for off-season vegetable production and for intensive use of their small land holdings (Anonymous, 1999). Round the year occupancy of polyhouses with high value cash crops *viz.* tomato, capsicum and cucumber during summer and lettuce, spinach and coriander during winters is very important for maximizing cropping intensity in one hand and ensuring remunerative returns to the small and marginal farmers of the state on the other hand. Normally, the polyhouses remain occupied during summer, but most of them remained unutilized during winter months due to lack of awareness amongst the farmers to use the appropriate crop in winter months. This practice of keeping polyhouses fallow during winters is highly uneconomical and undesirable as the cost involved in erecting these structure is very high.

Various methods have been employed in analysis of variation in many crop species. The value of genetic diversity by multivariate analysis has been demonstrated in choosing the parental stocks for hybridization by various workers. This technique measures the forces of differentiation at intra - cluster and inter - cluster level and D^2 statistics groups a set of better parents on the basis of genetic divergence with the assumption that the best parents may be those showing the maximum genetic divergence. Genotypes from the same centre used to place in separate cluster indicating wide diversity among genotypes originating from the same geographic region. The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters (Kaushal and Kumar, 2010).

However, very little work has been done on evaluation of lettuce germplasm under protected conditions during winter months. The old cultivars were mostly pointed, non-heading with narrow leaves. Butter and crisp head types were developed latter. Both types need to be exploited for identification of superior one which may further be released for commercial cultivation in HP under protected conditions.

II. MATERIALS AND METHODS

Experiment Environment and Materials

The experiment was carried out in naturally ventilated polyhouse at Experimental Farm of the Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan (HP) during 2011-12 and 2012-13. The experimental site is located at Nauni, about 14 km away from Solan city at an altitude of 1270 metres above mean sea level lying between 35.5° North latitude and 77.8° East longitude. The farm area falls in the mid hill zone of Himachal Pradesh. This particular district is also famous for the production of off-season vegetables. Amongst various district, Solan is popularly known for the quality vegetable and seed production. Solan city that falls in the mid-hills of Himachal Pradesh is also known as mushroom city. Annual precipitation is 0.00-65.90 mm and 3.50-184.30 mm during both the year respectively. Twenty eight genotypes of heading type and leafy type lettuce including check cultivars Simpson Black Seeded and Great Lakes were evaluated in naturally ventilated polyhouses. Seeds were sown in rows spaced 5 cm apart in raised nursery beds sized $3\text{m} \times 1\text{m} \times 15\text{cm}$. The experiment was laid out in a randomized complete block design with three replications in $1.50\text{m} \times 1.20\text{m}$ plots.

One month old seedlings were transplanted to the field with a spacing of $30 \times 30\text{cm}$ between and within rows, respectively, accommodating 20 plants/ plot. Ten plants were randomly selected to record observations on days to marketable maturity, leaf color, number of non-wrapper leaves, gross head weight, net head weight (gross head weight means total weight of head including non-wrapper leaves and stalk weight; net head weight excludes the weight of non-wrapper leaves and stalk weight), heading percentage, yield per plot, β -carotene contents, calcium

contents, iron contents, seed germination percentage, seed vigor index I and II, 1000-seeds weight, head shape index and incidence of diseases. Seed vigor indices I and II were determined by the formula of Abdul-Baki and Anderson (1973). Non-wrapper leaves were removed from heads that were weighed for yield and head shape index determined (Odland and Noll, 1954). Contents of β -carotene and iron were determined according to methods of Ranganna (1995). Observations were subjected to statistical analysis.

Analysis of variance was done on mean values of each plot and others statistical parameters, like mean and standard deviation was computed by the method suggested by Panse and Sukhatme (1985). The analysis of genetic divergence using Mahalanobis's (1936) D^2 statistics was carried out as described by Rao (1952). On the basis of magnitude of generalized statistical distance D ($D = \sqrt{D^2}$) values, the genotypes were grouped into different clusters as suggested by Tocher (Rao, 1952).

III. RESULTS AND DISCUSSION

Mean Performance of Genotypes

Genetic variability is the basic fundamental need for any breeding programme. Genetic improvement can be brought about by manipulating the genetic makeup of the plant for desirable characters or to get rid of the undesirable genes which retard or inhibit certain pathways. The information was obtained regarding nature and extent of variability, heritability, genetic advance and genetic gain, so as to have guidelines for selection of desirable traits.

The analysis of variance indicated highly significant differences among the genotypes for all the traits studied which revealed the existence of good deal of variability in the germplasm. Among horticultural traits, comparatively wide range was observed for gross head weight (299.22-602.02g), net head weight (175.72-537.05g), number of non-wrapper leaves (6.38-12.28), heading percentage (58.27-77.41%), β -carotene contents (2.95-7.21 $\mu\text{g}/100\text{g}$), seed vigour index-II (0.264-0.735) and yield per plot (2.58-10.21kg) under protected conditions.

Wide range of variation for head weight in different genotypes of heading lettuce and yield had also been reported by other workers in lettuce (Thakur *et al.*, 1997; Kaushal and Kumar, 2010 and Dolma *et al.* 2010) and in cabbage for gross head weight, net head weight and heading percentage (Swarup and Sharma, 1965; Jamwal *et al.* 1995; Bhardwaj, 1996; Kumar, 1998; Sharma, 2001; Kumar, 2004 and Dutt, 2006). Amongst various genotypes, UHF Sel.-06 gave maximum yield of 10.21 kg per plot over both the check Simpson Black Seeded and Great Lakes. This genotype also performed well for other characters like number of non-wrapper leaves, gross head weight, net head weight, heading percentage, seed germination, seed vigour index-I & II and 1000-seeds weight. Majority of the genotypes including both the check cultivars had light green coloured leaves, which are in general preferred by consumers.

Besides UHF Sel.-06, five genotypes *viz.*, UHF-Sel.-03, UHF-Sel.-01, CGN-05167, CGN-10944 and CGN-14629 for yield per plot and five genotypes namely UHF Sel.-06, UHF Sel.-03, CGN-10944, CGN-05167 and CGN-14629 performed better for heading percentage over the check Great Lakes.

Co-efficients of variability

The estimates of co-efficients of variability (phenotypic and genotypic) gave a clear picture of amount of variability present in the available germplasm. For all the characters studied, phenotypic co-efficients of variability were higher in magnitude than genotypic co-efficients of variability, though difference was very less in majority of the cases.

Thus, showing that these traits are less influenced by environmental factors. Co-efficients of variability varied in magnitude from character to character (either low or moderate or high). Therefore, it indicated that there was a great diversity in the experimental material used. The characters under study *viz.* gross head weight, net head weight, heading percentage, yield, β -carotene content and incidence of sclerotinia rot recorded wide range of variation and have better scope for improvement through selection.

Moderate to high PCV and GCV were observed for gross head weight, net head weight, non-wrapper leaves, β -carotene and incidence of gray mould diseases. These findings are in contradiction to the findings of other workers in lettuce (Thakur *et al.*, 1997; Jamwal, *et al.*, 1995; Kumar, 1998; Sharma, 2001; Kumar, 2004 and Dutt, 2006). They had reported low co-efficients of variability for non-wrapper leaves in different genotypes of cabbage while high co-efficients of variability for net head weight in lettuce (Thakur *et al.* 1997) and cabbage (Kumar, 2004). Moderate co-efficients of variability for non-wrapper leaves and net head weight (Arumgam *et al.*, 1978; Bhardwaj, 1996 and Sharma, 2001) and various other traits in lettuce (Meglic and Vozlic, 2000 and Kaushal and Kumar, 2010) have also reported moderate to high genotypic co-efficient of variation for gross head weight, net head weight, yield per plot and β -carotene with wider range of values.

Phenotypic performance would be good index for selection in lettuce for characters like gross head, net head weight, heading percentage, yield per plots and incidence of sclerotinia rot, and for quality characters *viz.*, β -carotene and iron contents.

GENETIC DIVERGENCE

In self pollinating crops like lettuce, germplasm is available in the form of a multitude of homozygous lines which can be released as genetically improved cultivars in the specific ecological regions. However, for a long term crop improvement programme, a large and diverse germplasm collection is an invaluable source of parental strains for hybridization and subsequent development of improved varieties. In this respect, various methods have been employed in the analysis of genetic variation in many crop species. The value of D statistic has been demonstrated in choosing parental stocks for cross

breeding. On the basis of D analysis, all the genotypes (28) were grouped into five clusters.

Cluster pattern:

The clustering pattern of 28 genotypes of lettuce on various characters has been presented in table-4. All the genotypes (28) were grouped into five clusters. Maximum numbers of genotypes (10) were accommodated in cluster - V followed by cluster - III (8), cluster - IV (5), cluster - I (3) and cluster - II (2).

Inter and intra cluster divergence:

Average inter and intra cluster divergence (D^2) values are presented in table-4. The diagonal figures in the table represent the intra cluster distances. Maximum intra cluster distance was reported in cluster-I (2.821) while it was minimum in cluster-IV (1.45) whereas highest inter cluster distance (9.512) was recorded between cluster-I and IV followed by lowest (3.251) was observed between cluster-III and V.

Mean intra and inter cluster distance:

The cluster means of the various horticultural traits are presented in table 5. Minimum mean was recorded in cluster-II (59.82) for days to marketable maturity followed by cluster-III (63.24), cluster-I (66.42), cluster-V (67.30) and cluster-IV (73.69). Minimum mean for number of non-wrapper leaves was recorded in cluster-I (6.99) followed by cluster-III (8.53), cluster-V (10.25), cluster-II (10.32) and cluster-IV (11.62). Maximum gross head weight (551.6g) was observed in cluster-I followed by cluster-III (424.17), cluster-II (379.29), cluster-V (371.03) and cluster-IV (330.68). Similarly, maximum net head weight mean was observed in cluster-I (480.1) followed by cluster-III (337.90), cluster-II (275.34), cluster-V (268.04) and cluster-IV (213.78).

Maximum heading percentage was observed in cluster-III (88.58) followed by cluster-V (80.10), cluster-IV (73.98), cluster-I (62.88) and cluster-II (0.00). Maximum yield per plot was observed in cluster-I (9.10) followed by cluster-III (6.04), cluster-II (4.5), cluster-V (4.35) and cluster-IV (3.21). Highest β -carotene contents were recorded in cluster-II (5.6) followed by cluster-V (5.34), cluster-I (5.00), cluster-IV (4.56) and cluster-III (4.55). Cluster-III recorded maximum mean value for calcium contents (10.19) followed by cluster-IV, II, I, and V. Iron contents mean value maximum (1.57) in cluster-II, followed by cluster-I (1.49), cluster-V (1.46), cluster-III (1.38) and cluster-IV (1.17). Maximum seed germination was observed in cluster-I (97.00) followed by cluster-III (96.06), cluster-V (94.10) cluster-II (63.64) and Cluster-IV (91.91). The maximum seed vigour index-I was recorded in cluster-I (1265.3) followed by cluster-III (1195.40), cluster-V (1082.30), cluster-II (1080.30) and cluster-IV (970.97). Similarly, seed vigour index-II was also maximum in cluster-I (0.71) followed by cluster-III (0.55), cluster II (0.47), cluster-V (0.44) and cluster-IV (0.39). However for incidence of sclerotinia rot cluster-II (7.69) exhibited minimum value followed by cluster-V (23.94), cluster-III (28.36), cluster (28.78) and cluster-IV (52.89). The incidence of gray mould was minimum in cluster-I (0.00) followed by cluster-II (8.94), cluster-III (9.28), cluster-V (10.16) and cluster-II (13.80).

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among the genotypes. Based on the relative magnitude of values, all the genotypes grouped into different clusters. Information on genetic diversity was also used to identify the promising diverse genotypes, which may be used in further breeding programme. Genotypes from the same centre were placed in separate cluster indicating wide diversity among genotypes originating from the same geographic region. This may be due to frequent exchange of germplasm between different geographical regions. The genetic divergence in the present study observed among 28 genotypes of lettuce, showed low quantum of divergence and was grouped into five clusters. Amongst the all, cluster-V had large genotypes (10), cluster-III had 8 genotypes, cluster-IV had 5 genotypes, cluster-I had 3 genotypes and cluster-II had 2 genotypes. The resultant five clusters showed the genetic diversity. Similar results were also obtained by Katule *et al.* (1992).

The average maximum intra cluster distance was 2.821 and minimum was 1.450. Theoretically, crossing of genotypes belonging to the same cluster will not expected to yield superior hybrids or transgressive segregants. Maximum inter cluster distance was found between cluster-I and IV (9.512). Such diverse genotypes characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, will have genes with different magnitude of effects. In such cases, chances to obtain favourable transgressive segregants are more on the basis of results obtained.

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters. The data of cluster mean for different characters under study indicated that difference between intra cluster mean was wide for net head weight, heading percentage and yield per plot, which might be responsible for large intra cluster distances. Cluster - I showed maximum mean value for gross head weight, net head weight, seed germination, seed vigour-I, seed vigour index-II, 1000-seeds weight and yield per plot. Cluster-II had maximum value for β -carotene and iron contents. Cluster-III showed minimum value for heading percentage and calcium contents. Crossing between the genotypes of maximum two clusters appeared to be most promising to combine the desirable characters and indicated the significance of genetic divergence Jones *et al.*, 1982; Fedorovo *et al.*, 1999; Oliveria *et al.*, 2004, Langton *et al.*, 2004; Kushwah *et al.*, 2005 and Lakshmiddevamma *et al.*, 2006.

IV. CONCLUSION

In the present studies it can be concluded that genotypes UHF Sel.-06 gave more yield over both the checks and also performed better for majority of characters like number of non-wrapper leaves, gross and net head weight, heading percentage, seed germination, seed vigour index-I & II and 1000-seeds weight. Genotype UHF-Sel.-07 gave

higher content of both β -carotene and Iron whereas genotype CGN-19009 was high in calcium contents. The genotypes Sol. Let.-I, CGN-20721, CGN-05167 and CGN-14651 showed field resistance against the incidence of sclerotinia rot and gray mould diseases under protected conditions. These genotypes can be used in further breeding programmes for the improvement of lettuce. Genetic divergence in 28 genotypes of lettuce was grouped in five clusters. The resultant five clusters showed wider genetic diversity and maximum number of genotypes was accommodated in cluster-V. The maximum inter cluster distance was recorded between cluster-I and IV. Such diverse genotypes characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, chances to obtain favourable transgressive segregants are more on the basis of results obtained. Cluster-I performed better for majority of traits *viz.*, non-wrapper leaves, gross and net head weight, seed germination, seed vigour-I & II, 1000-seeds weight, head shape index, yield per plot and incidence of gray mould under protected conditions (Naturally Ventilated Polyhouse)

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Table 1: Mean Performance different genotypes of lettuce for important traits (Pooled data of two years)

S. No.	Genotypes	Leaf Colour	Gross head weight (g)	Net head weight (g)	Number of non wrapper leaves	Heading Percentage (%)	β- carotene content	Yield per plot (kg)
1.	CGN-04508	*LG	427.87	340.87	8.60	88.00 (70.24)	2.95	6.04
2.	CGN-04543	LG	329.15	212.32	11.62	73.50 (59.12)	5.28	3.16
3.	CGN-04933	LG	327.12	209.12	11.73	72.58 (58.53)	4.42	3.07
4.	CGN-04934	LG	346.97	233.47	11.30	75.42 (60.43)	4.75	3.56
5.	CGN-04987	LG	350.97	238.28	11.17	76.25 (60.98)	3.79	3.67
6.	CGN-04990	LG	356.72	251.22	10.52	78.58 (62.65)	4.53	3.99
7.	CGN-05167	LG	434.93	356.27	7.80	91.87 (74.23)	3.61	6.57
8.	CGN-05169	LG	361.35	257.35	10.33	79.17 (63.05)	3.60	4.12
9.	CGN-05198	LG	401.40	305.90	9.48	83.95 (66.80)	5.85	5.17
10.	CGN-09373	LG	299.22	175.72	12.28	72.17 (58.27)	4.58	2.58
11.	CGN-10944	LG	443.52	366.02	7.65	92.25 (74.35)	6.76	6.78
12.	CGN-11358	LG	410.00	316.00	9.30	85.80 (68.30)	3.67	5.47
13.	CGN-14629	LG	432.27	349.27	8.18	90.80 (73.66)	5.33	6.38
14.	CGN-14651	LG	393.57	297.57	9.53	83.18 (66.17)	4.76	4.99
15.	CGN-19009	LG	422.07	333.57	8.75	87.53 (69.88)	5.60	5.89
16.	CGN-19088	LG	379.42	277.42	10.12	81.70 (65.03)	4.80	4.57
17.	CGN-20721	LG	375.83	273.33	10.20	80.33 (63.97)	4.45	4.43
18.	UHF-Sel.-01	LG	554.13	480.63	7.20	0.00 (0.00)	3.71	9.10
19.	UHF-Sel.-02	LG	352.55	244.05	10.80	77.58 (61.94)	6.88	3.83
20.	UHF-Sel.-03	LG	499.13	424.13	7.38	93.65 (75.85)	5.84	7.97
21.	UHF-Sel.-04	**DG	342.58	227.58	11.43	0.00 (0.00)	5.14	3.37
22.	UHF-Sel.-05	***RG	387.38	289.38	9.78	82.18 (65.35)	6.84	4.79
23.	UHF-Sel.-06	LG	602.02	537.05	6.38	95.00 (77.41)	5.46	10.21
24.	UHF-Sel.-07	DG	389.45	291.97	9.72	82.50 (65.58)	7.21	4.85
25.	Sol. Let-I	LG	351.58	242.58	10.85	76.83 (61.37)	3.63	3.77
26.	Sol. Let-II	LG	354.65	247.15	10.67	0.00 (0.00)	5.61	3.91
27.	Simpson Black Seeded	LG	416.00	323.10	9.20	0.00 (0.00)	6.07	5.63
28.	Great Lakes	LG	429.15	343.65	8.42	89.23 (71.84)	3.71	6.18

*LG- Light Green, **DG- Dark Green, ***RG- Reddish Green,

Table 2: Estimates of phenotypic and genotypic co-efficient of variability for different traits in lettuce

Characters	Range	Mean ± SE	Co-efficients of variability (%)	
			Phenotypic	Genotypic
Days to marketable maturity	52.82-81.82	66.65±3.27	13.35	11.93
Non wrapper leaves	6.38-12.28	9.66±0.54	16.91	15.45
Gross head weight (g)	299.22-602.02	398.96±36.78	19.16	15.49
Net head weight (g)	175.72-537.05	301.61±36.77	29.64	25.61
Heading percentage (%)	71.07-95.00	73.87±5.12	37.00	36.01
β- Carotene (µg/100g)	2.58-10.21	4.96±0.72	27.56	21.00
Calcium content (%)	4.88-11.47	8.73±1.18	25.58	19.49
Iron content (mg/100g)	0.99-1.83	1.40±0.11	16.25	13.02
Seed germination (%)	90.55-97.00	94.57±0.75	2.09	1.85
Seed vigour index-I	932.72-1277.18	1114.18±26.82	9.49	9.02
Seed vigour index-II	0.264-0.735	0.49±0.03	23.38	21.80
1000 seed weight (g)	0.83-1.02	0.91±0.04	7.15	4.70
Head shape index	0.96-1.29	1.02±0.06	36.91	36.09
Incidence of sclerotinia rot (%)	0.00-67.92	29.73±3.86	63.49	61.47
Incidence of gray mould (%)	0.00-35.17	11.87±1.85	90.13	88.08
Yield per plot (kg)	2.58-10.21	5.14±0.91	39.55	33.09

Table 3: Clustering pattern of 28 genotypes of lettuce on the basis of genetic divergence

Cluster	Number of genotypes	Genotypes
I	3	UHF-Sel.-01, UHF-Sel.-03, UHF-Sel.-06
II	2	UHF-Sel.-04, Simpson Black Seeded
III	8	CGN-04508, CGN-05167, CGN-10944, CGN-11358, CGN-14629, CGN-14651, CGN-19009, Great Lakes
IV	5	CGN-04543, CGN-04933, CGN-04934, CGN-04987, CGN-09373
V	10	CGN-04990, CGN-05169, CGN-05198, Sol. Let-I, Sol.Let-II, CGN-19088, CGN-20721, UHF-Sel.-02, UHF-Sel.-05, UHF-Sel.-07

Table 4: Average intra and inter cluster distance (D^2)

Cluster	I	II	III	IV	V
I	2.821				
II	7.113	2.176			
III	4.309	5.534	2.167		
IV	9.512	6.469	5.908	1.45	
V	6.692	4.580	3.251	3.83	2.293

Table 5: Cluster means for different characters of lettuce among 28 genotypes

Characters	Clusters				
	I	II	III	IV	V
Days to marketable maturity	66.41	59.82	63.24	73.69	67.3
Non wrapper leaves	6.99	10.32	8.53	11.62	10.25
Gross head weight (g)	551.6	379.29	424.17	330.68	371.03
Net head weight (g)	480.1	275.34	337.90	213.78	268.04
Heading percentage (%)	62.88	0.00	88.58	73.98	80.10
B-carotene (µg/100g)	5.00	5.60	4.55	4.56	5.34
Calcium content (%)	7.94	8.41	10.19	9.06	7.69
Iron content (mg/100g)	1.49	1.57	1.38	1.17	1.46
Seed germination (%)	97.00	93.94	96.06	91.91	94.10
Seed vigour index-I	1265.3	1080.3	1195.40	970.97	1082.3
Seed vigour index-II	0.71	0.47	0.55	0.39	0.44
1000 seed weight (g)	1.00	0.88	0.94	0.84	0.89
Head shape index	0.64	0.00	1.07	1.27	1.17
Incidence of sclerotinia rot (%)	28.78	7.69	28.36	52.89	23.94
Incidence of gray mould (%)	0.00	8.94	9.28	27.74	10.16
Yield per plot (kg)	9.10	4.50	6.04	3.21	4.35