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Research Article

Genetic diversity and variability analysis in oats (*Avena sp*) genotypes

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Abstract
Fifty oat genotypes belonging to eight different *Avena* species were evaluated to assess the genetic diversity and genetic divergence. The observations were recorded on five randomly selected plants in each genotype for quantitative traits. The Non-hierarchical Euclidean cluster analysis grouped oat genotypes into six clusters indicating presence of substantial genetic diversity in the evaluated germplasm. The highest intra-cluster distance which was observed in cluster VI followed by cluster I, cluster II, cluster V, cluster IV and cluster III. A maximum inter cluster distance showed between cluster II and cluster III followed by between cluster III and cluster IV. The minimum inter cluster distance was noticed between cluster V and cluster IV. Cluster II and III had better cluster means for many characters, so genotypes from these clusters can be used as parents for future breeding programmes. A total of eight principal components were extracted on the basis of eigen values (>1) and these components explained total of 75% variability. Varimax rotation enabled loading of all the traits on different principal factors. The first principal factor (PF) showed high loading for flag leaf length, dry fodder yield per plant and green fodder yield per plant. The second factor was composed of some of trait like high dry fodder yield, dry matter *per cent*, leaf length and leaf width. It is clear that both of the first three factors which would express the combined effect of flag leaf length, leaf length, leaf width, high dry matter *per cent*, high green fodder yield per plant were most closely associated with dry fodder yield per plant whereas, last three factors were associated with seed yield.

Keywords
Oats, Genetic Diversity, Genetic Variability Parameters, Cluster Analysis, Principal Component Analysis.

Introduction

Oat is basically a European and North American crop. It is best grown in temperate regions of the world as they are winter hardy in nature. Oat requires cool and moist climate. It is an important winter season cereal fodder crop which is rich in energy, protein, vitamin B, phosphorus and iron (Mehra, 1978). The total area, production and productivity are about 9.58 million hectares, 22.60 million metric tonnes and 2.36 metric tonnes per hectare, respectively in the world (Foreign Agriculture Service, USDA, 2016). European Union is the largest producer of oat followed by Russian Federation, Canada, USA and Australia (USDA, 2016). Europe accounts for 64.2% of total oat produced in the world (FAO, 2015). In India, oat is grown on 1, 00,000 hectares of area with productivity of 35-40 tonnes green fodder per hectare (Anonymous, 2014). It is mainly grown in North-western, Central and Hilly parts of India due to congenial climate. It is capable of giving green fodder yield of 333.0-558.0 q/ha under the single cut system, whereas it gives 408.0-416.0 q/ha under multicut system in the North west zone of the country.)

Genetic diversity arises due to geographical separation or due to genetic barriers to crossability or due to different patterns of evolution. Several workers have emphasized the need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations. To measure this extent of diversity, D^2 statistics was used to measure group distance based on multiple characters. It has become one of the important techniques to assess genetic divergence on the basis of multiple traits. Rao (1952) suggested the application of these techniques for the assessment of genetic diversity in plant breeding. The importance of genetic divergence for improving yield potential through hybridization has been emphasized and reviewed by Frey (1971).

The climate of Hisar is semi-arid and subtropical with hot and dry winds during summer months. Warm humid in monsoon and cold dry weather in winter are the general features of this region. Both, winter and summer are usually harsh to bear upon. The mean minimum and maximum temperature exhibit wide variations. A maximum temperature zooming 44ºC to 48ºC during summer and temperature dipping as low as to freezing point accompanied with chill frost in winter is of common occurrence.

Materials and Methods

The present investigation was conducted at Forage Research Area, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana

Agricultural University, Hisar (Haryana, India) during *rabi* 2015-16. The experiment was conducted in Randomized block design with three replications and two row plot of three metre each. Standard recommended agronomical package of practices were followed.

The experimental material comprised of 50 oat genotypes, belonging to eight different *Avena species*, from oat germplasm. These genotypes included released varieties, advanced breeding lines and genetic stocks *etc* collected from IGFRI, different agricultural universities and from European countries (Table 1).

The observations were recorded on five randomly selected plants in each genotype for the following 22 quantitative traits *viz*., plant height at fodder stage (PHF) in cm, number of days to 50% flowering (DF), number of leaves per plant (LPP), flag leaf width (FLW) in cm, flag leaf length (FLL) in cm, leaf length (LL) in cm, leaf width (LW) in cm, culm diameter/ stem girth (CD) in mm, number of nodes on the main culm (NODES), number of days to maturity (DM), plant height at maturity (PHM) in cm, number of tillers per plant (TPP), peduncle length (PL) in cm, axis length (AL) in cm, axis node number (ANN), green fodder yield per plant (GFY/P) in g, dry fodder yield per plant (DFY/P) in g, dry matter (%) DM %), seed yield per plant (SY) in g, 100 seed weight (HSW) in g, seed length (SL) in mm and seed width (SW) in mm.

The genetic divergence was studied by employing Mahalanobis' D^2 statistics (1936) as described by Rao (1952). The genotypes were grouped into different clusters on the basis of Ward's minimum variance method.

Results and Discussion

The analysis of variance investigated during the study indicated significant differences among the genotypes for all the characters studied. These results indicate that there is a plenty of scope for the improvement of germplasm through selection and heterosis breeding. The results clearly indicate that all the studied oat genotypes show high variability for grain and fodder yield and its component traits. The earlier workers Singh and Singh (2011); Shehzad *et al*. (2011); Bibi *et al*. (2012); Hisir *et al*. (2012); Bind *et al*. (2016) also suggested a large and exploitable variation in different oat germplasm, it could be stated that there is ample scope of variation in these traits that could be utilized for improvement through selection for the traits investigated in the present material.

The D^2 analysis on morphological traits grouped the fifty lines into six clusters, on the basis of relative magnitude of cluster distances. Cluster pattern revealed that, cluster V was the largest group consisting of 15 genotypes followed by cluster I and cluster IV (13 genotypes each). Cluster II and VI each had four genotypes whereas cluster III had only one genotype (Table 2).

The intra and inter cluster distances among 50 genotypes are given in Table 3 and the same has been represented by the Figure 1. The results show that inter cluster distances are more than intra cluster distances for all the clusters which indicates the presence of narrow genetic variation within a cluster. The highest intra cluster distance was observed for cluster VI (6.02) followed by cluster I (5.78), cluster II (5.53), cluster V (5.43), cluster IV (5.41) and cluster III (0.00) as this cluster contains only one genotype. The narrow intra cluster distance showed that the genotypes are genetically related.

When diversity was studied among the clusters based on the inter cluster distance, it showed a range of 6.16 to 9.81. The average inter cluster distance was found to be highest between cluster II and III (9.81) followed by cluster III and VI (9.78) and cluster II and VI (9.34) whereas the lowest inter cluster distance was observed between cluster I and IV (6.16). The higher inter cluster distance indicated the presence of more diversity among the genotypes included among these clusters.

Dendrogram showed the clustering pattern in 50 oat genotypes using Ward's minimum variance method of Non- hierarchical Euclidean cluster analysis (Figure 2).

The cluster means for the 22 quantitative traits studied in genotypes of oat revealed considerable differences among the entire clusters. Cluster wise mean and over all cluster mean for the characters are presented in Table 4.

The cluster means for the 22 quantitative traits studied in genotypes of oat revealed considerable differences among all the clusters. Cluster I having 13 genotypes and had highest cluster mean value for height at fodder stage (109.60) and number of nodes (5.97). Cluster II had four genotypes and was associated with characters like leaf per plant (42.15), flag leaf width (2.25), flag leaf length (41.04), culm diameter (6.45), peduncle length (33.97), axis node number (7.08), green fodder yield per plant (203.72). Cluster III had only one genotype with highest leaf length (51.66), leaf width (3.03), tillers per plant (7.57), dry fodder yield per plant (32.42) and seed yield (151.66).

Cluster IV, with 13 genotypes, had highest mean for axis length (32.68) and dry matter percentage (19.62). Cluster V had highest height at maturity (128.11) whereas cluster VI had highest days to maturity (122.50). Comparative evaluation of cluster means suggested that for improving specific character, the genotypes should be taken from the cluster having high mean value for that character. This comparison indicated that clusters II and III had better cluster means for most of the characters; therefore, these clusters might be considered better for selecting genotypes. Results of the present investigation are also in agreement with previous studies carried out on oat by several workers Singh and Singh (2009); Krishna *et al*. (2014); Bind *et al.* (2016).

This comparison indicates that cluster II and III had higher cluster means for most of the characters. Therefore, cluster II and III might be considered better for selecting genotypes.

Another important finding that emerged from the present study is indicative of homeologous nature of different species of oat. Clustering of *Avena sativa, A. nuda, A. vaviloviana, A. byzantina, A. barbata, A. brevis* and *A. orientalisis* a single cluster (Table 4.12) indicates their genomic homeology. It signifies their co-evolution and probability of having common ancestory in past. Similarly, Lokustav (2005) analysed diversity and found phylogenetic relationships and co-evolution in 26 *Avena* species.

Principal component analysis (PCA) is important for the reflection of the highest contributor to the total variation at each axis of differentiation Sharma *et al*. (1998). It is basically a data reduction technique, initially given by Pearson (1901) and later developed by Hotelling (1933) offers solution to the complex problem of large and unmanageable data by transforming the original set of variables into a smaller set of linear combinations that account for most of the variability of the original set. The first principal component absorbs and accounts for maximum proportion of total variability in the set of all variables and remaining components account for progressively lesser and lesser amount of variation. Same trend was observed in the present study. The 8 principal components, having eigen values greater than one altogether explained 74.95% of the total variation and were retained for further studies. The first principal component explained 18.12 % of the total variation. Table 5 The second, third, fourth, fifth, sixth, seventh and eighth principal components explained 14.73%, 10.97%, 7.59%, 6.85%, 6.08%, 5.91% and 4.64% of the total variance, respectively. Vaisi *et al*. (2013) and Krishna *et al*. (2014) who conducted principal component analysis in oat and transferred many correlated variables into a few independent principal components explaining much of the variability of the original set. Further, principal factor analysis was carried out, because the PCA does not assume a definite model. In principal factor analysis each observed variable is expressed linearly in terms of a common factor and a unique factor. The common factors account for the correlation among the variables. While each unique factor accounts for the remaining variance (including error) of that variable. Moreover, in PCA, the total variation contained in a set of variables is considered, whereas, in factor analysis interest centres on that part of variance which is shared by the common factors. Also in contrast to PCA, here the variables axes are allowed to interact resulting in distortion of mutual orthogonality.

The principal factor analysis carried out without any rotation did not derive the clear picture of interaction among the characters .It could not provide a clear picture regarding the idea of character association with respective principal factor as some factors had very high loading of variable and some have negligible. This indicated the next alternative of factor analysis *i.e*. rotation method Kaiser (1958) was used. To select the relevant characters in various principal factors, the correlation values (> ±0.6) were considered as relevant for that principal factor. The factor analysis divided the 22 traits into eight groups or principal factors and the varimax orthogonal rotation was subjected to the matrix of factor loadings after the first extraction of factor loadings. This rotation accentuated the larger loadings in the extracted factors and suppressed the minor loadings thus improving the opportunity of achieving meaningful interpretation of factors (Table 6).

It is clear that both of the first three factors expressing the combined effect of leaves per plant, height at maturity, days to maturity, tillers per plant, green fodder yield per plant, height at fodder stage, dry fodder yield per plant, leaf length, leaf width and dry matter *per cent* age, flag leaf length are regarded as fodder yield factors. PF-4 was associated with axis length and axis node number, hence can be considered as axis factor. Similarly, PF-6, PF-7 and PF-8 can be regarded as seed yield factor collectively.

Such a clear grouping of similar type of variables having loaded on common principal factor elaborates the successful transformation of 22 interrelated variables into eight independent principal factors explaining 74.95% of the variability of the original set.

References

Anonymous. 2014. Forage crops and grasses, Handbook of Agriculture. ICAR.

Bibi, A., Shahzad, A.N., Sadaqat, H. A., Tahir, M. H. and Fatima, B. 2012. Genetic characterization and inheritance studies of oats (*Avena sativa* L.) for green fodder yield. *International journal of Biology, Pharmacy and Allied Sciences.* **1**(4): 450-460.

Bind, H., Bharti, B., Pandey, M.K., Kumar, S.,Vishwanath. and Kerkhi, S.A. 2016. Genetic variability, heritability and genetic advance studies for different characters on green fodder yield in oat (*Avena sativa* L.). *Agricultural Science Digest*. **36** (2): 88-91.

FAO, 2015. *FAOSTAT*. Food and Agriculture Organization of the United Nations. *http://faostat.fao.org/default.aspx*.

Frey, R. J. (1971). Improving crop yields through plant breeding in moving of yield plateau. *American Society of Agronomy*. **20**: 15-58.

Hisir, Y., Kara, Y. and Dokuyucu, T. 2012. Evaluation of oat (*Avena sativa* L.) genotypes for grain yield and physiological traits. *Zemdirbyste-Agriculture.* **99**(1): 55-60.

Hotelling, H. 1933. Analysis of complex statistical variables into principal components. *Journal of Educational Psychology.* **24**: 417.

Kaiser, H.F. 1958. The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, **23**:187

Krishna, A., Ahmed, S., Pandey, H.C. and Kumar, V. 2014. Correlation, path and diversity analysis of oat (*Avena sativa* L.) genotypes for grain and fodder yield. *Journal of Plant Science &Research.* **1:** 1-9.

Mahalanobis, P.C. 1936. Study on the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India*. **2**: 49-55.

Mehra, K.L. 1978. Technical Bulletin, ICAR, New Delhi

Pearson, K. 1901. On lines and planes of closest fit to systems of points in space. *Philosophical Magazine.* **2**: 559.

Rao, C.R. 1952. Advanced biometrical methods in biometric research. John Wiley and Sons Inc., New York, 357–363.

Sharma, J. R., Gupta P. K. and Balyan. 1998. Genetic divergence in a large collection of wheat (*Triticum* sp.). *Indian Journal of Genetics and Plant Breeding* **58** (3):271-278.

Shehzad, M., Ayub.M., Nadeem, M.A., Pervez, M., Nadeem, M. and Sarwar, N. 2011. Comparative study on forage yield and quality of different oat (*Avena sativa* L.) varieties under agroecological conditions. *African Journal of Agricultural Research*. **6** (14) : 3388-3391.

Singh S.B. and Singh, A.K. 2009 Genetic variability, character association and path analysis for green fodder yield and its component characters in oat (*Avena sativa*). *Progressive Research.* **4:**159–162.

Singh, S.B. and Singh, A.K. 2011.Genetic Variability and Divergence Analysis in Oat (*Avena sativa*) under Rainfed Environment of Intermediate Himalayan Hills. *Indian Journal of Plant Genetic Resources.* **24** (1): 56–61.

Vaisi, H., Golparvar, A.R., Resaie, A. and Bahraminejad, S. 2013. Factor analysis of some **3**(3):62-65.

USDA, Foreign Agriculture Service. September, 2016. World agriculture production, Circular Series

Table 1. List of oat genotypes used in the study

Sr. No.	Genotype	Species	Sr. No.	Genotype	Species
1.	HFO 33	*Avena sativa*	26.	HFO 503	*Avena sativa*
2.	HFO 41	*Avena sativa*	27.	HFO 512	*Avena sativa*
3.	HFO 47	*Avena sativa*	28.	HFO 513	*Avena sativa*
4.	HFO 49	*Avena sativa*	29.	HFO 681	*Avena sativa*
5.	HFO 50	*Avena sativa*	30.	HFO 682	*Avena sativa*
6.	HFO 52	*Avena sativa*	31.	HFO 684	*Avena sativa*
7.	HFO 53	*Avena sativa*	32.	HFO 685	*Avena sativa*
8.	HFO 55	*Avena sativa*	33.	HFO 716	*Avena sativa*
9.	HFO 56	*Avena sativa*	34.	HFO 833	*Avena sativa*
10.	HFO 58	*Avena barbata*	35.	HFO 834	*Avena sativa*
11.	HFO 59	*Avena sativa*	36.	HFO 864	*Avena brevis*
12.	HFO 60	*Avena byzantina*	37.	HFO 867	*Avena maroccana*
13.	HFO 103	*Avena orientalis*	38.	HFO 868	*Avena sativa*
14.	HFO 114	*Avena sativa*	39.	HFO 870	*Avena vaviloviana*
15.	HFO 233	*Avena sativa*	40.	ALGERIAN	*Avena sativa*
16.	HFO 239	*Avena sativa*	41.	JHO 851	*Avena sativa*
17.	HFO 305	*Avena nuda*	42.	JO 1	*Avena sativa*
18.	HFO 306	*Avena sativa*	43.	PLP 1	*Avena sativa*
19.	HFO 307	*Avena sativa*	44.	UPO 212	*Avena sativa*
20.	HFO 346	*Avena sativa*	45.	KENT	*Avena sativa*
21.	HFO 476	*Avena sativa*	46.	OS 6	*Avena sativa*
22.	HFO 488	*Avena sativa*	47.	OS 7	*Avena sativa*
23.	HFO 489	*Avena sativa*	48.	OS 377	*Avena sativa*
24.	HFO 490	*Avena sativa*	49.	OS 403	*Avena sativa*
25.	HFO 502	*Avena sativa*	50.	HJ 8	*Avena sativa*

Table 2. Clustering pattern analysis of 50 lines of oat based on D^2 statistics

Clusters	Genotypes	Number of genotypes
Cluster I	HFO 33, HFO 59, HFO 114, HFO 307, HFO 476, HFO 512, HFO 834, HFO 868, OS 377, Algerian (*Avena sativa*) HFO 305 (*Avena nuda*), HFO 870 (*Avena vaviloviana*)	13
Cluster II	HFO 47, HFO 306, HFO 346, HJ 8 (*Avena sativa*)	4
Cluster III	HFO 867 (*Avena maroccana*)	1
Cluster IV	HFO 50, HFO 833, UPO 212, Kent, HFO 684, HFO 685, HFO 233, HFO 488, HFO 502, HFO 503, HFO 681, HFO 682, HFO 490 (*Avena sativa*)	13
Cluster V	HFO 41 JO 1, HFO 49, OS 6, OS 7, HFO 55, JHO 851, HFO 239, HFO 489, HFO 56, HFO 52 (*Avena sativa*) HFO 60 (*Avena byzantina*) HFO 864(*Avena brevis)* HFO 58*(Avena barbata)* HFO 103*(Avena orientalis)*	15
Cluster VI	HFO 53, PLP 1, HFO 513, HFO 716 (*Avena sativa*)	4

Table 3. Intra and Inter cluster distances of 50 oat genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**5.78**	6.56	8.64	**6.16**	6.55	8.06
Cluster II		**5.53**	**9.81**	6.71	7.09	9.34
Cluster III			**0**	8.78	8.96	9.78
Cluster IV				**5.41**	6.49	7.70
Cluster V					**5.43**	7.19
Cluster VI						**6.02**

Table 4. Cluster means of different yield attributing traits in 50 genotypes of oat

Clusters	PHF	DF	LPP	FLW	FLL	LL	LW	CD	NODES	DM	PHM
1	**109.60**	**91.94**	39.72	2.23	38.91	50.20	2.41	6.22	**5.97**	119.33	123.63
II	111.61	92.08	**42.15**	**2.25**	**41.04**	49.75	2.30	**6.45**	5.83	**117.33**	120.75
III	102.92	103.00	39.52	1.40	38.34	**51.66**	**3.03**	4.98	5.77	121.00	116.33
IV	97.75	92.02	39.29	1.91	38.06	49.74	2.19	6.21	5.37	119.20	115.19
V	108.82	95.40	38.32	1.98	34.61	44.11	2.18	6.20	5.64	121.55	**128.11**
VI	79.42	93.58	37.69	2.00	35.14	39.33	1.95	6.07	5.55	122.50	101.47
Mean	**103.90**	**93.37**	**39.22**	**2.04**	**37.25**	**47.38**	**2.25**	**6.19**	**5.67**	**120.09**	**120.63**

Clusters	T/P	PL	AL	ANN	GFY/P	DFY/P	DM%	SY	HSW	SL	SW
1	6.40	25.79	29.48	6.47	180.84	32.00	20.23	99.82	3.06	15.00	2.36
II	5.45	**33.97**	32.11	**7.08**	**203.72**	31.68	15.60	71.33	3.82	14.66	1.94
III	**7.75**	18.55	23.78	5.22	195.38	**32.42**	18.17	**151.66**	**4.50**	15.00	**2.83**
IV	6.48	30.88	**32.68**	7.07	176.16	31.38	**19.62**	138.28	3.52	**16.46**	2.70
V	5.88	29.11	31.62	6.96	172.33	29.23	16.94	83.75	3.11	14.91	2.23
VI	5.98	22.61	24.88	5.97	155.03	26.76	18.63	77.41	3.02	14.83	2.60
Mean	**6.18**	**28.36**	**30.68**	**6.75**	**177.12**	**30.57**	**18.55**	**101.96**	**3.28**	**15.31**	**2.41**

PHF: plant height at fodder stage, DF: days to 50% flowering, LPP: leaves per plant, FLW: flag leaf width, FLL: flag leaf length, LL: leaf length, LW: leaf width, CD: culm diameter, NODES: number of nodes on the main tiller, DM: days to maturity, PHM: plant height at maturity, TPP: tiller per plant, PL: peduncle length, AL: axis length, ANN: axis node number, GFY/P: green fodder yield per plant, DFY/P: dry fodder yield per plant, DrM%:dry matter *per cent*age, SY: seed yield, HSW: hundred seed weight, SL: seed length, SW: seed width

Table 5. Total variance explained by different principal components in oat genotypes

Principal components	Eigen value	Variation explained (%)	Cumulative variation explained (%)
1	3.988	18.13	18.13
2	3.246	14.75	32.88
3	2.414	10.97	43.85
4	1.671	7.59	51.45
5	1.508	6.86	58.30
6	1.340	6.09	64.39
7	1.301	5.91	70.31
8	1.022	4.64	74.95

Table 6. Factor loading of different characters with respect to different principal factor (Varimax rotation)

Characters	PF-1	PF-2	PF-3	PF-4	PF-5	PF-6	PF-7	PF8
LPP	**.697***	.002	.083	.094	-.097	-.003	-.237	.524
HM	**.845***	.085	-.109	.192	.192	.036	-.126	-.146
DM	**-.817***	-.047	.489	.112	-.152	-.154	.011	-.045
TPP	**.672***	-.002	.012	-.163	.036	.064	-.166	.070
GFY/P	**.748***	-.011	.313	.154	.049	-.200	.291	.112
HF	**.851***	-.034	.248	.321	.090	-.011	-.101	.003
DFY/P	**.679***	.630	.087	.109	.069	-.080	.105	.307
LL	.302	**.670***	.014	.289	.199	.045	.325	.070
LW	.194	**.630***	.254	-.163	-.298	-.207	.253	.116
DM%	.041	**.668***	-.414	.004	-.099	.347	-.091	-.046
FLL	.250	.309	**.678***	.203	-.041	.143	.110	-.332
FLW	.108	-.041	.133	**.859***	-.149	.141	-.028	-.101
NODES	.101	-.084	.283	**.610***	-.403	.071	.164	-.093
CD	-.075	-.021	.107	**.790***	.346	-.155	-.036	.104
AL	.061	.014	.242	.046	**.826***	.083	.099	-.070
ANN	.130	-.037	-.017	-.065	**.802***	-.255	.107	-.032
SL	.098	.100	.056	-.005	-.046	**.887***	.058	.038
SW	-.101	-.033	-.141	.164	-.247	**.681***	.152	.581
HSW	.136	.014	-.113	-.003	.131	.106	**.913***	.032
SY	.017	.239	-.218	-.210	.076	.056	.132	**.672***
DF	-.342	-.244	.332	-.327	-.332	.006	.238	-124
PL	.431	.383	.144	-.109	.044	.104	-.288	.152

***Higher loading**

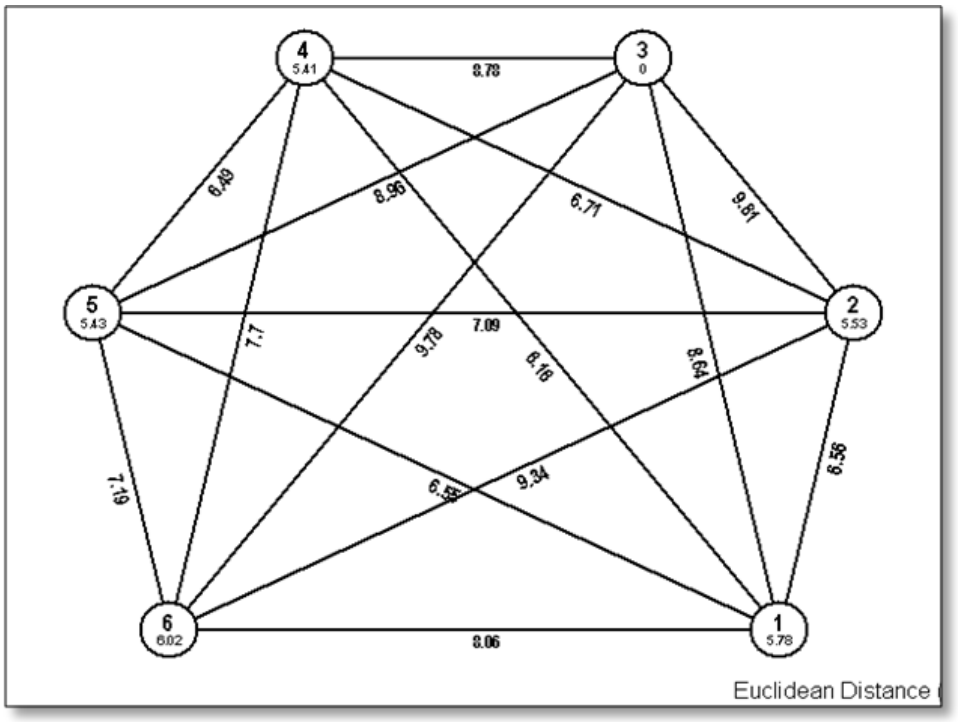


Fig. 1

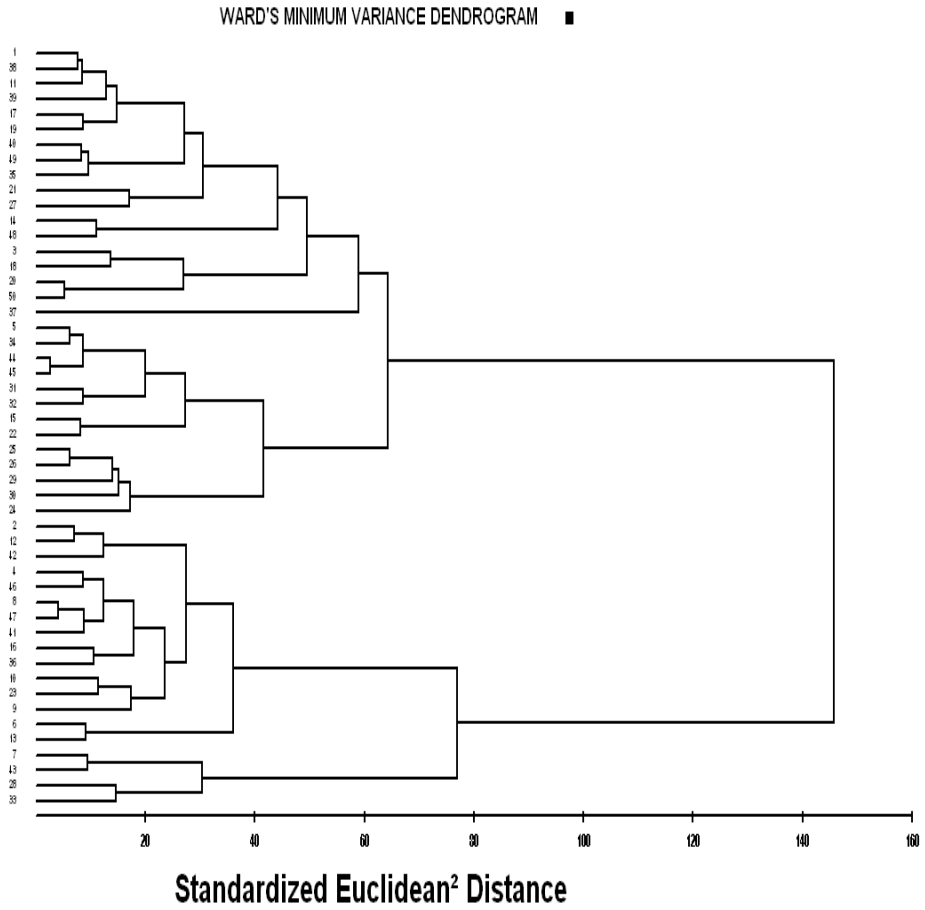
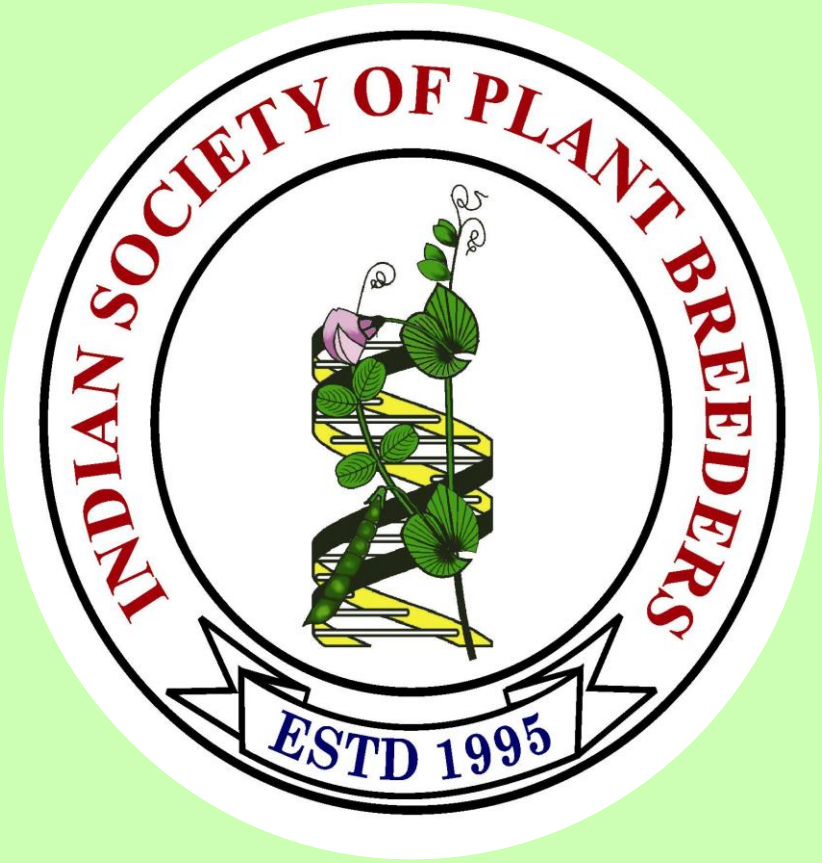


Fig. 2. Dendrogram showing the clustering pattern of fifty genotypes of oat



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