World Journal of Pharmaceutical and Life Sciences
WJPLS
www.wjpls.org
SJIF Impact Factor: 6.129

GENETIC DIVERGENCE STUDY IN FORAGE OAT (AVENA SATIVA L.) FOR GREEN FODDER YIELD

Yogendra Prasad[1], Kamleshwar Kumar[2], Ravi Kumar3, Sunil Kumar[4] and Sanjay Kumar[5]*

[1,2,3]Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand 834 006, India
[4]Department of Plant Breeding and Genetics, Veer Kunwar Singh College of Agriculture, Dumraon (Buxar), Bihar Agricultural University, Bihar 802136, India.
[5]Department of Plant Breeding and Genetics, MBAC, Agwanpur, Saharsa-852201, Bihar, India.

Corresponding Author: Sanjay Kumar
Department of Plant Breeding and Genetics, MBAC, Agwanpur, Saharsa-852201, Bihar, India.

Article Received on 27/01/2021 **Article Revised on 17/02/2021** **Article Accepted on 07/03/2021**

ABSTRACT

Oat (Avena sativa L.) is a multi-purpose winter cereal forage crop grown in many parts of the world. In India, it is used as green fodder, hay and silage for animals. The experimental material for present study consisted of 14 diverse for the presence genotype of oat. Observations were recorded on seven quantitative traits to assess the variability and diversity analysis using D2 analysis during Rabi 2018-19 at RVC Farm, BAU, Kanke (Jharkhand). Estimates of high heritability (broad sense) were obtained for all the characters. The magnitude of PCV was greater than the corresponding GCV for all the characters indicating importance of environment in the expression of characters on the basis of result. Out of seven characters studied, days to 50 % flowering, plant height (cm), dry matter yield per plot, dry matter yield (%), green fodder yield (kg/plot), Leaf/Stem ratio and Crude Protein (%) showed high GCV and heritability coupled with high genetic advance as percent of mean which revealed that these traits might be under control of additive gene effects and therefore, they are more reliable for effective selection. Clustering pattern grouped the germplasm lines into six different clusters. Cluster VI is characterized by lines having prominent traits like high green fodder yield and tall plants. Contribution percentage towards genetic divergence was more for days to 50% flowering (40.66), Crude Protein % (23.08), Plant height (13.19 cm), Green fodder yield (13.19 kg/ha) and Leaf/Stem ratio (6.59). So the direct selection for these traits would be helpful in the selection of diverse for the presence genotype. This study gave an insight into the variability pattern of advanced oat lines which will be helpful for further utilisation.

KEYWORDS: Cluster, Diversity, genetic advance, heritability.

INTRODUCTION

The genus Avena belongs to the grass family Poaceae. Oat (*Avena sativa* L.) is an economically important crop and ranks sixth in world cereal production after wheat, rice, maize, barley and sorghum (FAO, 2012). It is mainly cultivated as fodder crop in India. For a successful crop breeding programme, nature and amount of genetic variability available in the germplasm is the basic requirement. The germplasm collected from different regions serves as the most valuable natural resource in providing the required traits to develop new varieties. Genetically diverse individuals are likely to produce more heterotic effects during the crossing programme and produce desirable segregants. As a dual purpose crop, multi-cut nature, high forage yield and good source of protein, fiber and minerals. It is used as green crop, hay and silage for animals. Differing from other cereal grains such as wheat and barley, it is rich in the antioxidants α-tocotrienol, α-tocopherol, and avenanthramides, as well as total dietary fibre including the soluble fibre β-glucan (Oliver *et al.*, 2010).

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 the 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).

MATERIALS AND METHODS

The experimental material for the presence study consisted of 14 diverse genotypes of oat. Observations were recorded on seven quantitative traits to assess the variability and diversity analysis using D^2 analysis during Rabi 2018-19 in Forage crops, RVC Farm, BAU, Kanke (Jharkhand).

The observations were recorded on five randomly selected plants in each genotype for the following 14 quantitative traits viz., days to 50% flowering, plant height (cm), green fodder yield (kg/ha), dry matter yield (g/plot), dry matter yield (%), leaf stem ratio and crude protein (%). All the recorded data was averaged and the means of all the accessions were analyzed for simple.

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.

Table 1: Analysis of variance for seven characters in Fodder Oat.

Sl. No.	Characters	Mean sum of Squares		
		Replication (df=2)	Treatments (df=14)	Error (df=28)
1.	Days to 50 % Flowering	4.00	1191.14	14.00
2.	Plant height (cm)	36.24	5637.38	198.31
3.	GFY (Kg/plot)	94.70	1435.62	60.58
4.	DMY (g/plot)	23.05	1239.14	96.28
5.	DMY (%)	23.22	309.71	33.00
6.	Leaf/Stem ratio	0.001	0.098	0.006
7.	CP (%)	1.40	67.86	2.35

Table 2: Range and mean of 7 characters in Forage Oat.

Sl. No.	Characters	Range	Mean	CV (%)
1.	Days to 50 % Flowering	79.33 - 97.67	88.86	0.83
2.	Plant height (cm)	96.63 – 140.87	131.80	2.09
3.	GFY (Kg/plot)	20.10 – 40.50	30.07	5.08
4.	DMY (g/plot)	31.33 – 52.33	43.48	4.43
5.	DMY (%)	15.67 – 26.17	21.74	5.18
6.	Leaf/Stem ratio	0.26 – 0.42	6.84	4.40
7.	CP (%)	4.90 -10.10	0.33	4.44

Table-3: Estimation of genetic parameters of seven characters of Forage Oat.

Sl. No.	Characters	σ2 p	σ2 g	PCV	GCV	Heritability (Broad sense)	Genetic Advanced as % of mean (5%)
1.	Days to 50 % Flowering	30.54	30.36	6.22	6.20	99	12.74
2.	Plant height (cm)	144.55	142.01	9.12	9.04	98	18.46
3.	GFY (Kg/plot)	36.81	36.03	20.17	19.96	97	40.68
4.	DMY (g/plot)	31.77	30.54	12.97	12.71	96	25.67
5.	DMY (%)	7.94	7.52	12.96	12.61	95	25.28
6.	Leaf/Stem ratio	1.74	1.71	19.29	19.12	98	39.05
7.	CP (%)	0.003	0.002	15.16	14.95	97	30.35

Table-4: Cluster mean for 7 characters in Forage Oat.

Sl. No.	Character	Days to 50% Flowering	Plant ht. (cm)	GFY (Kg/plot)	DMY (g/plot)	DMY (%)	Leaf stem ratio	CP (%)
1.	**Cluster-I**	*88.83*	*134.68*	*30.12*	*42.54*	*21.27*	*0.32*	*6.38*
2.	**Cluster-II**	*80.33*	*139.23*	*25.18*	*51.83*	*25.92*	*0.31*	*7.40*
3.	**Cluster-III**	*96.00*	*135.67*	*33.90*	*41.33*	*20.67*	*0.39*	*8.20*
4.	**Cluster-IV**	*94.67*	*116.13*	*24.13*	*45.33*	*22.67*	*0.32*	*5.40*
5.	**Clster-V**	*97.67*	*140.87*	*34.60*	*31.33*	*15.67*	*0.42*	*10.10*
6.	**Clster-VI**	*84.33*	*96.63*	*37.10*	*46.67*	*23.33*	*0.35*	*6.20*

Table- 5: Mean table for 7characters in Forage Oat.

Sl. No.	Character	Days to 50 % Flowering	Plant height (cm)	GFY (Kg/plot)	DMY (g/plot)	DMY (%)	Leaf/Stem Ratio	CP (%)
1.	HFO-806	94.67	116.13	24.13	45.33	22.67	0.32	5.40
2.	OL-1874-1	96.00	135.67	33.90	41.33	20.67	0.39	8.20
3.	HFO-818	90.00	134.77	29.33	42.67	21.33	0.31	5.70
4.	JO-06-23	84.33	136.87	31.97	39.33	19.67	0.31	7.10
5.	OS-6 (NC)	81.33	139.27	23.03	52.33	26.17	0.34	6.80
6.	NDO-1802	79.33	139.20	27.33	51.33	25.67	0.27	8.00
7.	UPO-18-1	90.67	138.20	35.93	42.00	21.00	0.30	7.00
8.	Kent (NC)	87.67	138.00	22.77	47.00	23.50	0.27	5.90
9.	OL-1876-1	91.67	135.57	40.50	38.00	19.00	0.41	7.20
10.	JHO-18-1	93.33	125.00	31.07	38.33	19.17	0.34	6.77
11.	OS-403	97.67	140.87	34.60	31.33	15.67	0.42	10.10
12.	SKO-241	84.33	96.63	37.10	46.67	23.33	0.35	6.20
13.	RO-11-1-3	85.67	134.33	29.27	46.67	23.33	0.26	4.90
14.	RO-11-1-2	87.33	134.73	20.10	46.33	23.17	0.34	6.47
	Mean	**88.86**	**131.80**	**30.07**	**43.48**	**21.74**	**0.33**	**6.84**

Table- 6: Number and name of genotypes in different cluster.

Cluster	No. of genotypes	Genotype
I	8	Kent, RO-11-1-2, HFO-818, RO-11-1-3, JO-06-23, UPO-18-1, OL-1876-1.
II	2	OS-6, NDO-1802
III	1	OL-1874-1
IV	1	HFO-806
V	1	OS-403
VI	1	SKO-241

Table- 7: Inter and Intra Cluster Distance.

Cluster	I	II	III	IV	V	VI
I	12.42	18.58	16.64	16.49	24.79	16.99
II	18.58	7.96	27.10	26.67	35.27	20.25
III	16.64	27.10	0.00	17.26	11.68	23.01
IV	16.49	26.67	17.26	0.00	26.53	16.96
V	24.79	35.27	11.68	26.53	0.00	31.78
VI	16.99	20.25	23.01	16.96	31.78	0.00

Table- 8: Independent character contribution towards divergence.

Sl. No.	Source	Times Ranked1st	Contribution (%)
1.	Days to 50 % Flowering	37	40.66
2.	Plant height (cm)	12	13.19
3.	GFY (Kg/plot)	12	13.19
4.	DMY (g/plot)	0	0.00
5.	DMY (%)	3	3.30
6.	Leaf/Stem Ratio	0	6.59
7.	CP (%)	21	23.08

RESULTS AND DISCUSSIONS

The analysis of variance revealed significant differences among the genotypes for all the characters under study. The result indicates that there is a plenty scope for the improvement of germplasm through selection and heterosis breeding. The results clearly indicate that all the fourteen genotypes of oat studied shows high variability for green fodder yield, dry matter yield and its component traits. The earlier workers Singh and Singh (2011) and Bind *et al.* (2016) 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 under study.

The D^2 analysis on morphological traits grouped the fourteen lines into six clusters, on the basis of relative magnitude of cluster distances. Cluster pattern revealed that, Cluster I was the largest group consisting of 8 genotypes followed by cluster II having two genotypes. Cluster III, IV, V and VI each had one genotype (Table 6).

The intra and inter cluster distances among fourteen genotypes are given in Table 7. 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 II (35.27) followed by cluster V (31.78), cluster III (27.10), cluster IV (26.67), cluster V (26.53) and cluster I (24.79). 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 7.96 to 35.27. The average inter-cluster distance was found to be highest between cluster II and V (35.27) followed by cluster V and VI (31.78) and cluster II and III (27.10) whereas, the lowest inter-cluster distance was observed between cluster III and V (11.68). The higher inter-cluster distance indicated the presence of more diversity among the genotypes included among these clusters.

The cluster means for the seven quantitative traits studied in fourteen 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. Cluster II has shows the highest characters mean for DMY (g/plot) and DMY (%). Cluster V exhibited highest character mean for plant height (cm), leaf stem ratio and CP (%) whereas, Cluster-VI exhibited highest character mean for GFY (kg/plot), Hence, it is obvious from the result obtained that, Cluster V may be used as one of the parent in crossing programme to enhance the more plant height (cm), leaf stem ratio and CP %, genotype belong to Cluster VI may be used as the parent for enhancing the GFY.

In addition to classify the genotype in to Cluster based on the genetic divergence, the amount of contribution made by 7 traits towards divergence was also Estimated. The maximum contribution towards divergence was observed by Days to 50 % flowering (40.66 %) followed by CP % (23.08), plant height (13.19 %), GFY (13.19 %), Leaf stem ratio (6.59 %) and DMY % (3.30 %) as evident from the Table-8. Hence, the present study clearly indicated the influence of the character and their habit in the clustering pattern. Similar result was also obtained by Wagh *et al.*, 2019.

REFERENCES

1. Bind, H.; Bharti, B.; Pandey, M. K.; Kumar, S.; Vishwanath and Kerkhi, S. A. Genetic variability, heritability and genetic advance studies for different characters on green fodder yield in oat (*Avena sativa* L.). *Agricultural Science Digest*, 2016; 36(2): 88-91.
2. FAO Production Statistics. *Food and Agriculture Organisation, Rome*, 2012.
3. Frey, R. J. Improving crop yields through plant breeding in moving of yield plateau. *American Society of Agronomy*, 1971.
4. Oliver, R. E.; Obert, D. E.; Hu, G.; Bonman, J. M. and Jackson, E. W. Development of Oat based Markers from Barley and Wheat Microsatellites. Genome, 2010; 6: 458-71.
5. Rao, C. R. Advanced biometrical methods in biometric research. *John Wiley and Sons Inc., New York*, 1952; 357–363.
6. Mahalanobis, P. C. Study on the generalized distance in statistics. Proceedings of the National Institute of Sciences of India, 1936; 2: 49- 55.
7. Singh, S. B. and Singh, A. K. Genetic Variability and Divergence Analysis in Oat (*Avena sativa L.*) under Rainfed Environment of Intermediate Himalayan Hills. *Indian Journal of Plant Genetic Resources*, 2011; 24(1): 56–61.
8. Wagh, V. R; Sonone, A. H. and Damame, S. V. Assesement of genetic divesity in Forage Oat (*Avena sativa* L.). *Forage Res.*, 2019; 45(3): 203-205.