Original Research Article

Genetic Diversity Studies in Forage Oat (*Avena sativa* L.) Genotypes

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A B S T R A C T

Forty four genotypes of forage oat were evaluated during *Rabi* 2018-19 in a RBD designs with three replications. The observations were recorded on yield and yield contributing traits *viz.,* days to 50 % flowering, plant height (cm), number of leaves /tiller, number of internodes / tiller, leaf length (cm), leaf breadth (cm), stem girth (cm), L/S ratio, dry matter content , crude protein content and green forage yield (kg/net plot). The D^2 statistics showed that there was adequate diversity among the genotypes. The D^2 values, forty four genotypes were grouped into six clusters. Genotypes of the same geographic origin were classified under different clusters, indicating that the grouping pattern did not show a significant relationship between genetic diversity and geographical diversity. Plant height contributed maximum for divergence followed by days to 50 % flowering leaf length leaf: stem ratio green forage yield and leaf width. On the basis of per se performance, inter cluster distance and cluster mean the genotypes viz., RO-19, RO-11-1, OS-6, HFO-611, OS-432, UPO-16-4, JO-05-7 and JO-10-501 could be used for future breeding programme

Introduction

Oat (*Avena sativa* L.) 2n = 6x = 42, is a winter forage crop which is grown worldwide. It is also used as multipurpose crop for grain, pasture and forage. It is considered to be one of the best dual purpose cereal crops that fit well into the platter of human and cattle as well. Recently, with the advancement of enlarged dairy industries in India, the oats have enchanted the breeder's attention for its modernization due to its quality fodder with high nutrition and grains with more net energy gains (Ruwali *et al.,* 2013).

In India, oat is grown as fodder crop during *rabi* season in north-western and the central parts and now its cultivation is extending to eastern region as well. The total area of about 500,000 hectare is covered under oat cultivation in the country. The production and productivity of Indian livestock remains less due to insufficient and nutritionally unbalanced supply of fodder and feed. Presently, India faces a net deficit of 63 per cent green fodder, 24 per cent dry crop residues and 64 per cent feeds.

There is need of fodder improvement by promotion of integrated technology and

processes for enhancing the availability of fodder throughout the year; fodder crop improvement requires a long term and multidisciplinary approach.

Generally diverse individuals are likely to produce more heterotic effects during the crossing programme and desirable segregants are also produced. Genetic diversity depicts the heritable variation within and between populations of a species.

Materials and Methods

The present investigation was conducted at AICRP on Forage Crops and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra during *rabi* 2018-19. The experimental material consisted of forty four oat genotypes collected from different AICRP centers on Forage Crops and Utilization in India. The list of forty four genotypes is given in Table 1. The experiment was laid out in randomized block design (RBD) with two replications having thirty eight genotypes with six checks. The observations were recorded on five randomly selected plants in each replication for all the characters except leaf stem ratio and green forage yield (Kg/net plot). The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1936) as described by Rao (1952).

Results and Discussion

Test with Wilks criterion and analysis of variance for dispersion of genotypes

Significant differences between genotypes based on the pooled effects of all the traits were tested by Wilks 'λ' (Statistics) criterion. The significance of 'λ' (Statistics) values was tested by 'χ^2' at 473 degrees of freedom. The 'λ' (Statistics) value was 2121.36. This value was significant indicating that the genotypes

differed significantly when all characters were considered simultaneously. The analysis of variance of dispersion of forty four genotypes is presented in Table 2.

Mahalanobis's D^2 values

The mean values of forty four genotypes [(X1) – (X2)] were transformed into standardized uncorrelated mean values [(Y1) – (Y2)]. The D2 values were computed for all possible combination that is 44 (44-1)/2 =946 pairs of genotypes.

Cluster pattern

The aim of cluster formation and measuring inter and intra cluster divergence is to provide the basis for selection of parents for hybridization programme. The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to the different clusters and will not give expected desired heterotic response and segregants in further generations.

The cluster formation was done by following Tocher's method, as described by Rao (1952). All the forty four genotypes studied were grouped into six clusters (Table 3). Cluster I with nineteen genotypes emerged as the largest cluster followed by Cluster IV, Cluster III and cluster II with ten, nine and four genotypes respectively. Cluster V and VI were solitary clusters.

Earlier workers Prasad *et al.,* (2003) grouped 247 oat germplasms into six clusters, Kumar *et al.,* (2005) grouped 100 oat germplasms into nine clusters Mall and Vishwakarma (2006) grouped 48 oat genotypes into seven clusters, Bahadur and Chaubey (2008) grouped 50 oat germplasms into nine clusters, Ahmed *et al.,* (2011) grouped 75 oat

germplasms into nine clusters, Krishna *et al.,* (2014) grouped 50 oat genotypes into ten clusters, Jaipal and Shekhawat (2016) grouped 30 oat genotypes into four clusters and Kumari *et al.,* (2019) grouped 50 oat genotypes into six clusters

Genotypes of the same geographic origin were classified under different clusters, indicating that the grouping pattern did not show a significant relationship between genetic diversity and geographical diversity.

Similar findings were also reported by Mall and Vishwakarma (2006) and Bahadur and Chaubey (2008) in forage oat genotypes.

Intra and inter cluster distance

The average intra and inter cluster D and D^2 values are presented in Table 4. In respect of intra cluster distances, cluster IV had the highest value (D=8.68) followed by cluster II (6.68) and cluster I (5.98).

The inter cluster distance (D) range from 9.28 to 17.21. The maximum inter cluster distance (D =17.21) was observed between cluster III and cluster IV, followed by cluster II and cluster IV (D = 16.00), cluster III and cluster VI (D = 15.50). The minimum inter cluster distance (D= 9.28) was in cluster I and cluster V.

Table.1 List of forty four forage oat genotypes

S.N.	Genotype	Origin	S.N.	Genotype	Origin
1	OL-1861-1	Ludhiana	23	HFO-225	Hisar
2	OL-1802	Ludhiana	24	HFO-417	Hisar
3	OL-1842	Ludhiana	25	OL-1866	Ludhiana
4	HFO-619	Hisar	26	UPO-16-4	Pantnagar
5	NDO-1102	Faizabad	27	HFO-514	Hisar
6	OS-377	Hisar	28	OL-1873	Ludhiana
7	JO-10-501	Jabalpur	29	OL-1804-1	Ludhiana
8	OL-1769	Ludhiana	30	SKO-229	Srinagar
9	OL-1876	Ludhiana	31	JO-04-19	Jabalpur
10	JO-05-7	Jabalpur	32	HFO-607	Hisar
11	OL-1869	Ludhiana	33	JO-4-321	Jabalpur
12	OL-1871	Ludhiana	34	OL-1862	Ludhiana
13	OL-1766-1	Ludhiana	35	OL-1769-1	Ludhiana
14	OL-1861-1	Ludhiana	36	OS-424	Hisar
15	HFO-611	Hisar	37	RSO-8	Rahuri
16	JO-05-301	Jabalpur	38	RSO-60	Rahuri
17	HFO-609	Hisar	39	JHO-822 (Ch)	Jhansi
18	SKO-225	Srinagar	40	OS-6(Ch)	Hisar
19	OS-432	Hisar	41	UPO-212 (Ch)	Pantnagar
20	HFO-610	Hisar	42	Kent (Ch)	Hisar
21	UPO-10-3	Pantnagar	43	RO-19 (Ch)	Rahuri
22	PLP-18	Palampur	44	RO-11-1 (Ch)	Rahuri

Table.2 Analysis of variance for dispersion in forty four oat genotypes

Source of variation	Degree of freedom (df)	Mean sum of squares
Genotype	43	1.9922E03**
Error	85	6.8589E-07
Total	128	6.6925E02

** Significant at 1% level

Table.3 Grouping of forty four oat genotypes based on D^2 analysis

Cluster No.	Number of genotypes	Name of Genotypes	Origin
CL-I	19	HFO- 417	Hisar
		Kent	Hisar
		HFO- 610	Hisar
		UPO-212	Pantnagar
		SKO- 225	Srinagar
		HFO-607	Hisar
		RSO-8	Rahuri
		OL-1871	Ludhiana
		OL-1861-1	Ludhiana
		HFO-609	Hisar
		HFO-619	Hisar
		OL-1862	Ludhiana
		OS-377	Hisar
		JHO-822	Jhansi
		HFO-225	Hisar
		OL-1866	Ludhiana
		OL-1869	Ludhiana
		UPO-10-3	Pantnagar
		HFO-514	Hisar
CL-II	4	RO-19	Rahuri
		RO-11-1	Rahuri
		OL-1769	Ludhiana
		OS-6	Hisar
. CL-III	9	HFO-611	Hisar
		OS-424	Hisar
		OS-432	Hisar
		OL-1861-1	Ludhiana
		OL-1876	Ludhiana
		OL-1766-1	Ludhiana
		RSO-60	Rahuri
		OL-1769-1	Ludhiana
		NDO-1102	Faizabad

Table.4 Average intra (bold) and inter cluster distance (D) values for six clusters in forty four oat genotypes

| Clusters	I	II	III	IV	V	VI
I	**5.98**	9.97	10.42	10.34	9.28	**9.91**
II		**6.68**	10.63	16.00	12.59	**12.11**
III			**5.53**	17.21	11.07	**15.50**
IV				**8.68**	12.88	**11.01**
V					**0.00**	**12.16**
VI						**0.00**

Bold figures denote intra cluster distance

Table.5 Mean values of the six clusters for eleven characters in forty four oat genotypes

Cluster No.	Days to 50 % flowering	Plant height (cm)	No. of leaves / tiller	No. of internodes / tiller	Leaf length (cm)	Leaf width (cm)	Stem girth (cm)	Leaf: stem ratio	Dry matter (%)	Crude protein (%)	Green forage yield /(kg /net plot)
CL-I	77.33	86.39	5.39	4.82	33.61	1.16	2.01	0.67	18.80	9.95	2.43
CL-II	85.33	106.13	6.57	5.82	35.01	1.33	2.60	0.56	19.37	10.14	3.09
CL-III	67.52	104.13	5.84	5.19	36.61	1.03	2.55	0.72	20.60	9.54	2.98
CL-IV	80.87	67.73	5.17	4.67	36.19	1.47	1.83	0.75	17.80	10.14	1.70
CL-V	75.33	85.40	4.40	4.00	52.05	1.08	2.70	0.77	18.28	9.55	3.34
CL-VI	86.00	83.63	5.67	5.07	37.39	2.02	2.11	1.63	17.34	11.09	2.49

Table.6 Per cent contribution of eleven different characters of oat genotype for divergence

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50 % flowering	153	16.17 %
2	Plant height (cm)	509	53.81 %
3	No. of leaves/tiller	7	0.74 %
4	No. of internodes/tiller	7	0.74 %
5	Leaf length (cm)	61	6.45 %
6	Leaf width (cm)	14	1.48 %
7	Stem girth (cm)	61	6.45 %
8	Leaf: stem ratio	48	5.07 %
9	Dry matter (%)	22	2.33 %
10	Crude Protein (%)	48	5.07 %
11	Green forage yield (kg/net plot)	16	1.69
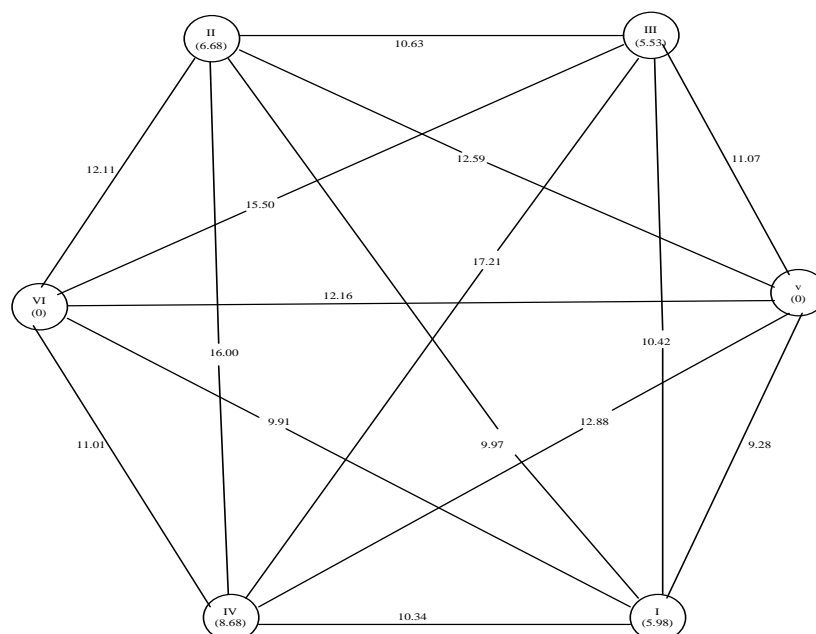
Cluster mean

A comparison of the mean value of eleven characters of different clusters is presented in the Table 5. Considerable differences in cluster mean values were evident for all the characters.

1. Days to 50 % flowering: The cluster mean for days to 50 % flowering was found to be highest in cluster VI (86.50 days) whereas minimum cluster mean was found in clusters III (67.52 days)

2. Plant height (cm): The cluster mean for plant height was found to be highest in cluster II (106.13 cm) followed by cluster III (104.13 cm), whereas minimum cluster mean was found in clusters IV (67.73 days)

3. Number of leaves per tiller: The cluster mean for number of leaves per tiller was found to be highest in cluster II (6.87) followed by cluster III (5.84), whereas minimum cluster mean was found in

clusters V (4.40)

4. Number of internodes per tiller: Maximum mean number of internodes/tiller was observed for cluster II (5.82) and minimum for cluster V (4.0).

5. Leaf length (cm): Maximum mean leaf length was observed for cluster V (52.05 cm) and minimum for cluster I (33.61cm).

6. Leaf width (cm): The genotypes grouped in cluster VI had maximum mean leaf width (2.02 cm) and cluster III had minimum (1.03 cm)

7. Stem girth (cm): Mean stem girth of the genotypes was maximum in cluster V (2.70 cm) and the lowest in the case of genotypes included in cluster IV (1.83 cm).

8. Leaf: Stem ratio (L/S): The genotypes of cluster VI (1.63) and II (0.56) had the maximum minimum mean leaf: stem ratio, respectively.

9. Dry matter content (%): The genotypes of

cluster III (20.60 %) had the maximum dry matter content followed by cluster II (19.37%) and minimum dry matter content was observed in cluster VI (17.34%).

10. Crude protein content (%): The genotypes of cluster VI (11.09 %) had the maximum crude protein content while minimum was observed in cluster III (9.54%).

11. Green forage yield (kg/net plot): The cluster mean for green forage yield was found to be highest in cluster V (3.34) followed by cluster II (3.09), whereas minimum cluster mean was found in clusters IV (1.70 kg).

Per cent contribution of various characters for divergence

The utility of D^2 analysis, which is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The selection and choice of parents mainly depends upon contribution of characters towards divergence. The more the number of times that each of the eleven characters appeared in first rank the more it contributed towards diversity. The per cent contribution of twelve characters on genetic divergence is presented in Table 6.

Plant height contributed maximum (53.81 %) for divergence followed by days to 50 % flowering (16.17 %), leaf length (6.45 %), leaf: stem ratio (5.07 %), green forage yield (1.69 %) and leaf width (1.48 %).

This result was in accordance with Mall and Viswakarma (2006) reported high contribution to the divergence by green forage yield, contribution due to days to 50 % flowering, leaf: stem ratio and green forage

yield was reported by Ahmed *et al.,* (2011) and high contribution to the divergence due to leaf length and green forage yield was reported by Kumari *et al.,* (2019).

Identification of diverse genotypes for future hybridization programme

Considering the inter-cluster distance, cluster means and per se performance of genotypes, the genotypes *viz.,* RO-19, RO-11-1, OS-6, HFO-611, OS-432, UPO-16-4, JO-05-7 and JO-10-501 could be utilized in future breeding programme for creating maximum spectrum of variability for different forage yield contributing characters which will facilitate to develop superior genotypes with respect to more than one characters and also possible to improve more than one character simultaneously.

In conclusion forty four genotypes of oat were grouped into six clusters. Based on cluster mean, per se performance and inter cluster distance, the eight genotypes *viz.,* RO-19, RO-11-1, OS-6, HFO-611, OS-432, UPO-16-4, JO-05-7 and JO-10-501 were identified to be superior and hence suggested to be utilized these genotypes for hybridization programme for green forage yield improvement in oat.

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