ASSESEMENT OF GENETIC DIVERSITY IN FORAGE OAT (AVENA SATIVA L.)

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SUMMARY

The present study was conducted during winter season of 2016-17 with 27 diverse oat genotypes. On the basis of D2 values all the twenty seven genotypes studied were grouped into six clusters. Cluster I with ten genotypes emerged as the largest cluster followed by Cluster II and cluster III with seven genotypes each. Cluster IV, V and VI were solitary clusters. The highest intra cluster distance was observed for the cluster III containing seven genotypes, followed by cluster II containing seven genotypes and cluster I containing ten genotypes. The maximum (%) contribution towards genetic divergence was contributed by green forage yield followed by leaf/stem ratio and leaf length. The superior genotypes identified for hybridization for green forage yield improvement were Phule Surabhi, ROG-15-3, ROG-15-11, ROG-15-19, Phule Harita and ROG-15-24.

Key words : Forage oat, clusters, diversity

Oat (Avena sativa L.) is an important winter cereal in the world. It is mainly cultivated as fodder crop in India. Oat protein has a relatively well balanced amino acid composition. The crop is preferred by the farmers due to its multi-cut nature, high forage yield and good quality nutritious fodder. The genus Avena is large and diverse and contains both wild and cultivated species of polyploidy series. Its stem or culm is composed of a series of nodes and internodes. The nodes are solid the elongated internodes of the mature stem are hollow in the center but during early vegetative stage of development the internodes are solid or show only a slight indication of the breakdown of pith. The position of the leaf on the oat plant and the kinds of plant part produced are similar to those in other grasses. The leaves are solitary, alternate, two ranked and sessile. A completely developed oat leaf consists of terminal portion, the blade, a basal portion, the sheath, and a membranous appendage, the ligule. The blade is elongate, flat, narrow and linear. The margin of blade is entire and its tip is acute. The leaf sheath is an open cylinder. In the young plant the sheaths of the older leaves encloses the stem and younger leaves. Each lateral branch terminates in a single apical spiklete. Other spikelet is born on second or third-order of branches. Each panicle may have 20 to 50 spikelets. The flowers are perfect zygomorphic, bracteates and hypogeous (Bhardwaj, 2012). The genetic diversity is produced due to inherent genetic differences in germplasm lines/varieties/landraces and is of major interest to the plant breeders. The precise information about genetic divergence is crucial for identification of diverse parent for hybridization. Therefore, the present investigation was conducted with twenty four forage oat genotypes along with three checks (Phule Surabhi, Kent and Phule Harita) to study genetic diversity in forage oat.

MATERIAL AND METHODS

The present investigation entitled, 'Assessment of genetic diversity in oat (Avena sativa L.)' was conducted at AICRP on Forage Crops and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra during rabi 2016-17. This zone comes under the semi-arid, sub-tropical and geographically situated between 19º47' to 19º57' north latitude and 74º 32' to 74º 19' east longitude and at altitude of 657 meters above mean sea level. The annual rainfall ranges between 310-620 mm with an average rainfall 520 mm. The distribution of rain is erratic and the number of rainy days varies from 25-45 in different years. Most of the rainfall is received through south west monsoon during June to September. The annual minimum temperature ranges from 8 to 28.5°C and maximum 26.2 to 42.8°C. During the crop period temperature ranged from 8.6 to 29.4^o C, relative humidity from 28 to 68% without rain.

The crop was sown in the third week of December 2016. The experimental material consisted of 27 diverse genotypes of oat (*Avena sativa* L.). Out of which twenty four genotypes were provided by the IGFRI, Jhansi and three national checks from AICRP on FC&U, MPKV, Rahuri. The genotypes were evaluated in randomized block design (Panse and Sukhatme, 1985) with two replications. Each plot consisted of two rows of 3 m length, spaced 30 cm apart. All the recommended agronomical practices were followed to raise the good crop. Observations were recorded on five randomly selected plants in each replication for all the characters viz., plant height at 50 per cent flowering, number of leaves per tiller, leaf length (cm), leaf width (cm), stem thickness (mm), per cent crude protein content (A.O.A.C., 1990), per cent dry matter except number of tillers per meter row length, leaf stem ratio and green forage yield (Kg/m row length. Standard statistical procedures were followed for estimating genetic parameters such as genetic diversity (Mahalanobis 1936).

RESULTS AND DISCUSSION

The twenty seven genotypes of forage oat were grouped into six clusters using Tocher's method presented in Table 1. Among all the clusters, cluster I was the largest cluster having 10 genotypes followed by cluster II and cluster III having 7 genotypes each.

Cluster IV, V and VI were solitary clusters (Fig. 1). Singh and singh (2010) grouped seventy oat genotypes into seven clusters and two ungrouped cluster. The IX cluster showed promise to green forage yield, dry mater yield, per day green fodder productivity, tillers per plant and per cent dry matter. Ahmed et al. (2011) grouped seventy five exotic and indigenous oat germplasm lines into nine clusters suggested more contribution towards genetic divergence was from days to 50% flowering, grain yield, leaf stem ratio and green forage yield. Jaipal and Shekhawat (2016) grouped thirty oat genotypes into four clusters, reported effective characters in section could be leaf: stem ratio, dry matte yield, seed index, green forage yield and grain yield. Kaur and Kapoor (2017) generated dendrogram among 96 oat genotypes for various morpho-agronomical traits collected from various eco-geographical regions found



Fig. 1. Dendrogram showing the clustering pattern of twenty seven oat genotypes by Tocher's method.

six clusters. Maximum inter cluster-distance was recorded between clusters I and VI (9.06) suggesting significant high genetic diversity among genotypes in these clusters.

Average intra and inter-cluster D² values among 27 genotypes are presented in Table 2. In respect of intra cluster distances, cluster III had the highest value (D=7.59) followed by cluster II (7.10) and cluster I (6.54). The inter cluster distance (D) range from 8.49 to 16.66. The maximum inter cluster distance (D = 16.66) was observed between cluster II and cluster V, followed by cluster IV and V (D = 16.06), cluster V and cluster VI (D = 15.18), cluster III and cluster VI (14.35). The minimum inter cluster distance (D= 6.54) was in cluster II and cluster IV. The cluster mean for ten characters studied are presented in Table 3. It was revealed that cluster II ranked first for two traits viz., leaf/stem ratio (0.72) and dry matter content (20.64). Cluster II also ranked second for number of leaves per tiller (6.70). Cluster III exhibited second highest cluster mean for the characters viz., plant height, number of tillers per meter

TABLE	1
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Grouping of twenty seven oat genotypes	nto different clusters by	Tocher's method
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Cluster No.	Number of strains	Genotypes included in the cluster						
	10	ROG-15-9, ROG-15-17, ROG-15-18, Kent, ROG-15-23, ROG-15-14, ROG-15-2, ROG-15-20, ROG-15-6, ROG-15-16						
II	7	ROG-15-4, ROG-15-7, ROG-15-8, ROG-15-21, ROG-15-10, ROG-15-5, ROG-15-22						
III	7	ROG-15-3, ROG-15-11, RO-19, ROG-15-24, ROG-15-12, ROG-15-19, ROG-15-13						
IV	1	ROG-15-15						
V	1	RO-11-1						
VI	1	ROG-15-1						

Clusters	Ι	II	III	IV	V	VI
I	6.54 (42.77)	9.29 (86.30)	8.60 (73.96)	9.16 (83.90)	11.13	9.96 (99.20)
II	(12.77)	7.10	11.62	8.49	16.66	11.00
III		(30.41)	(133.04) 7.59	9.97	10.88	(121.00)
IV			(57.60)	(99.40) 0.00	(118.37) 16.06	(205.92) 13.79
v				(0.00)	(257.92) 0.00	(190.16) 15.18
VI					(0.00)	(230.43) 0.00 (0.00)

 TABLE 2

 Average intra and inter cluster distance

Bold figures denote intra cluster distance. Figures in parenthesis denote D^2 values.

 TABLE 3

 Cluster means for ten characters in twenty seven genotypes of forage oat

Cluster No.	Plant height at 50% flowering cm	No. of tillers/ m. row length	No. of leaves/ tiller	Leaf length (cm)	Leaf width (mm)	Leaf/Stem (L/S) ratio	Stem thickness (mm)	Green forage yield kg/m row length	Dry matter content (%)	Crude protein content (%)
Ι	105.86	91.90	6.45	44.58	2.07	0.48	21.98	1.50	20.14	7.19
II	108.29	71.21	6.70	43.55	2.09	0.72	19.50	1.03	20.64	6.12
III	124.64	104.71	6.41	48.16	2.56	0.61	26.04	2.04	20.50	7.23
IV	133.00	58.00	6.20	52.10	2.61	0.43	31.90	1.59	20.19	6.01
V	118.10	107.50	7.40	37.40	2.27	0.25	25.80	2.59	20.38	7.80
VI	98.50	85.00	4.70	29.00	1.58	0.39	17.50	0.58	19.94	5.80
Population mean	115.23	86.38	6.31	35.20	2.19	0.48	23.78	1.55	20.29	6.69

row length, leaf width, leaf/stem ratio, stem thickness, green forage yield, dry matter content and crude protein content. Cluster IV ranked first for four characters namely, plant height at 50 % flowering (133.00), leaf length (52.10), leaf width (2.61) and stem thickness (31.90). Cluster V recorded highest cluster means for traits viz., number of tillers per meter row length (107.50), number of leaves per tiller (7.40), green forage yield (2.59) and crude protein content (7.80). The maximum (%) contribution towards genetic divergence was contributed by green forage yield followed by leaf/stem ratio and leaf length. The probability of getting desirable segregants and promising recombinations will be more, if crosses are attempted between genotypes belonging to more diverse clusters such as III, IV and V.

In conclusion, based on cluster mean, *per se* performance and inter cluster distance, a tentative hybridization programme for green forage yield improvement in oat is given below. Promising parents for hybridization between Phule Surabhi with ROG-15-3, ROG-15-11, ROG-15-19, Phule Harita and ROG-15-24.

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