

## GENETIC DIVERGENCE IN FODDER OAT (*AVENA SATIVA* L.) FOR YIELD AND QUALITY TRAITS

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(Received : 14 August 2017; Accepted : 10 September 2017)

### SUMMARY

The present investigation was carried out with 92 genotypes of oat maintained in the germplasm of Forage Section, Department of Genetics & Plant Breeding, CCSHAU, Hisar. The Mahalanobis'  $D^2$  statistics for genetic divergence divided 92 oat genotypes into nine clusters indicating presence of substantial genetic diversity in the evaluated germplasm. The average inter-cluster distance was found to be highest between clusters IV and IX followed by clusters I and VIII. The minimum inter-cluster distance was noticed between clusters V and VI. The minimum intra-cluster distance was noticed in cluster I and highest intra-cluster distance was observed in cluster VII. The clusters I, II and IV had higher cluster mean values for most of the characters. Therefore, use of the genotypes viz., JO 1, ALGERIAN, HFO 912, DULO, UPO 212, OS 6, OS 305, HJ 8, OS 403, HFO 879, HFO 878, JHO 2006-4, JHO 851, HFO 832, HFO 409, HFO 831 and FOS 1/29 which fall in these clusters might be considered as potential parents for obtaining high heterotic response and consequently better segregants for dry matter yield in forage oat.

**Key words :** Diversity, oat, clusters, fodder

Genetic diversity is a pre-requisite for any crop improvement programme. Since the genetic variability is fast depleting due to developmental activities of man and continuous use of variability in the on-going crop improvement programmes.

Oat (*Avena sativa* L.) is the most important cereal (graminaceous) forage crop grown during winter season, which is used as food, feed and fodder. Oat fodder is mostly fed as green and surplus is converted into silage or hay for further use during fodder deficit period (Suttie and Reynolds, 2004). It is a preferred feed of all the animals and its straw is soft and superior to wheat and barley. Oat is a self-pollinated allohexaploid crop ( $2n=6x=42$ ) with basic chromosome number  $x=7$  having genomic constitution of AACCCDD (Rines *et al.*, 2006). The genus *Avena* is very large and diverse and includes diploid, tetraploid and hexaploid species.

Fodder oat is used as a multipurpose crop worldwide. They are usually winter sown, grazed prior to stem elongation and taken to maturity for use as feed and/or milling grains. Multiple cuts are usually taken, after which part or all of the crop may be saved for seed. Oat has adequate soluble carbohydrates and fibres (Peterson *et al.*, 2005). Oat provides one of the richest sources of the dietary soluble fibre beta-glucan,

providing 5.0 g (oat meal) to 7.2 g (oat bran) per 100 g serving (Glore *et al.*, 1994). Nutrition experts believe that beta-glucan inhibits cholesterol build up and hence helps in the prevention of heart disease (Whitehead *et al.*, 2014). Oat has assumed considerable importance in India as fodder as well as grain for animal feed particularly calves and young stocks, horses, poultry and sheep. On dairy farms, oat fodder is a must, as it can be fed green and the surplus converted into silage or hay for use during the scarcity period.

The total area, production and productivity of oat during 2015 were about 9.58 million hectares, 22.60 million metric tonnes and 2.36 metric tonnes per hectare, respectively, in the world (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 per cent of total oat produced in the world (FAO, 2015). In India, oat is grown on 100,000 hectares of area with productivity of 35-40 tonnes of green fodder per hectare. In India, it is mainly grown in **rabi** season mostly for fodder in U. P., Punjab, Bihar, Haryana and M. P. (Anonymous, 2014).

### MATERIALS AND METHODS

The experiment was conducted at Forage

Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana, India) during **rabi** 2015-16. The experimental material comprising 92 oat genotypes was evaluated for 24 characters following the recommended agronomical package of practices in a randomized block design with three replications keeping row to row distance 45 cm. The observations were recorded on five randomly selected plants of each genotype in each replication for the 16 morphological characters viz., plant height (cm), number of days to 50 per cent flowering, number of days to maturity, flag leaf length (cm), internode length (cm), number of tillers/plant, peduncle length (cm), axis length (cm), number of spikelets/panicle, seed yield (g), 100-seed weight (g), leaf length (cm), leaf width (cm), green fodder yield (kg), dry matter yield (kg) and number of leaves/plant; and six seed quality parameters viz., germination (%), seedling length (cm), seedling dry weight (mg), seed vigour index I, seed vigour index II and electrical conductivity (mS/cm/seed) and quality characters such as forage crude protein (%) and seed crude protein (%). Estimation of degree of divergence was analyzed by Mahalanobis (1936)  $D^2$  statistics among different pairs of statistics. While method suggested by Rao (1952) was followed for computing  $D^2$  values and for determining group constellations.

## RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences within the population for all the 24 characters studied. This suggested that the genotypes under investigation consisted of sufficient amount of diversity and also indicated that this material

was appropriate for estimation of further analysis. On the basis of  $D^2$  values, the 92 genotypes were grouped into nine clusters following Tocher's method. The clusters IX and VI were the largest ones with 18 and 17 genotypes each, followed by clusters V, III, VII, VIII, II, IV and I with 13, 10, 9, 8, 6, 6 and 5 genotypes, respectively. Significant amount of variability can be inferred from the pattern of group constellation (Table 1). This revealed that pattern of clustering of genotypes did not depend upon their geographical origin. It means that the genotypes from same geographical origin do not group together i. e. genetic constitution of the genotypes is dominant. Dendrogram generated in which nine clusters are clearly distinguished is shown for 92 genotypes in Fig. 1. Bahadur and Choubey (2008), Yadav *et al.* (2011), Ahmed *et al.* (2011), Krishna *et al.* (2014) and Kumar *et al.* (2016) suggested that the cluster with higher number of lines had low genetic diversity among the lines and they were more closely related. The inter-cluster distances were higher than intra-cluster distances suggesting the presence of high genetic diversity between lines of any two clusters than the lines present within the cluster.

The inter- and intra-average distance among nine clusters was computed and presented in Table 2. The highest inter-cluster divergence was observed among genotypes of clusters IV and IX (8.304), clusters I and VIII (8.161) and clusters III and IX (7.741), whereas the lower inter-cluster distance was observed between clusters V and VI (6.243), followed by clusters III and V (6.323). The intra-cluster distance was highest in the cluster VII- (6.512) followed by cluster IX (6.238), cluster II (6.292), cluster VI (5.578), cluster V (5.558), cluster III (5.550), cluster IV (5.483),

TABLE 1  
Clustering of 92 genotypes of oat on the basis of  $D^2$  statistics

Cluster	No. of genotypes	Genotypes
Cluster I	05	JO 1, ALGERIAN, HFO 912, DULO, UPO 212
Cluster II	06	JHO-2006-4, JHO 851, HFO 832, HFO 409, HFO 831, FOS-1/29
Cluster III	10	JHO 822, HFO 906, HFO 504, HFO 883, HFO 914, HFO 913, JHO-99-1, HFO 896, HFO 919, HFO 867
Cluster IV	06	OS 6, HFO 305, HJ 8, OS 403, HFO 879, HFO 878
Cluster V	13	KENT, HFO 704, HFO 505, HFO 508, HFO 502, HFO 910, HFO 78, HFO 603, HFO 885, HFO 865, HFO 851, HFO 893, HFO 852
Cluster VI	17	HFO 60, HFO 920, HFO 707, HFO 904, HFO 902, HFO 845, HFO 909, HFO 603, HFO 611, HFO 715, HFO 605, HFO 924, HFO 114, HFO 703, HFO 610, HFO 908, HFO 905
Cluster VII	09	HFO 267, HFO 975, HFO 575, HFO 921, HFO 614, HFO 69, HFO 706, HFO 864, HFO 58
Cluster VIII	08	HFO 876, HFO 877, HFO 874, HFO 875, HFO 872, HFO 839, HFO 884, HFO 498
Cluster IX	18	OL 125, UPO 212, HFO 865, HFO 885, HFO 414, JHO-2006-2, HFO 836, HFO 863, HFO 841, HFO 433, HFO 880, HFO 870, OL 10, DUNAV, SKO 90, PLP 1, KALOJAN, SUBZAR



TABLE 3  
Cluster mean for 24 characters in oat germplasm

Clusters	PH	DF	DM	FLL	IL	TPL	PL	AL	NOS	SY	SI	LL	LW	GFY	DMY	NOL	CPg	CPf	GP	SL	SDW	SVI	SVII	EC
I	131.87	93	118.53	26.93	20.60	8.99	24.10	23.73	70.60	135.07	3.41	36.00	1.707	1.494	0.309	41.267	11.81	13.45	86.87	30.639	7.93	2660.33	686.870	0.305
II	120.67	96.44	120.89	23.17	17.33	10.3	23.78	19.75	64.50	104.00	3.36	38.00	2.028	1.088	0.199	47.333	11.89	13.20	86.78	32.512	9.54	2823.44	821.67	0.273
III	107.5	92.17	116.53	24.1	16.83	8.8	29.63	24.02	65.87	96.20	3.33	36.50	1.753	0.948	0.203	39.967	13.20	13.50	90.90	34.957	10.17	3173.23	918.9	0.231
IV	121.28	92.78	122.17	26.5	17.89	9.29	28.43	24.31	84.33	144.56	3.92	36.61	1.822	1.277	0.230	45.278	13.57	13.61	89.22	32.890	12.35	2934.61	1097.67	0.214
V	108.59	91.62	114.87	25.95	19.10	8.69	33.28	24.95	67.26	119.74	3.40	36.00	1.277	0.872	0.159	41.974	12.26	13.66	85.95	31.838	11.13	2734.51	952.72	0.230
VI	113.8	94.73	118.73	25.53	17.57	8.71	24.03	24.52	67.22	94.82	3.36	34.00	1.815	1.006	0.206	37.216	12.66	12.96	86.80	31.985	12.52	2772.94	1081.67	0.242
VII	108.78	92.74	114.67	18.85	16.22	8.90	20.17	17.78	73.56	81.44	3.62	31.26	1.537	0.977	0.158	40.222	13.09	12.94	89.15	31.840	9.62	2839.04	853.56	0.237
VIII	96.67	91.13	128.33	19.63	16.42	9.62	25.38	19.40	73.21	83.21	3.44	29.13	1.563	0.624	0.144	44.58	13.01	12.87	83.92	31.127	11.06	2610.5	925.29	0.26
IX	100.65	95.26	121.54	21.65	13.50	9.00	23.00	20.86	62.13	95.72	2.97	31.91	1.822	0.820	0.156	42.481	12.19	13.17	84.94	30.265	9.66	2569.83	815.85	0.365

PH—Plant height (cm), DF—No. of days to 50 per cent flowering, DM—Number of days to maturity, FLL—Flag leaf length (cm), IL—Internode length (cm), TPL—Number of tillers per plant, PL—Peduncle length (cm), AL—Axis length (cm), NOS—Number of spikelets per panicle, SY—Seed yield(g), SI—100-seed weight (g), LL—Leaf length (cm), LW—Leaf width (cm), GFY—Green fodder yield(kg), DMY—Dry matter yield (kg), NOLS—Number of leaves per plant, CPg—Crude protein in grain (%), CPf—Crude protein in forage (%) GP—Germination %, SL—Seedling length (cm), SDW—Seedling dry weight (mg), SVI—Seed vigour index-I, SVII—Seed vigour index-II and EC—Electrical conductivity (mS/cm/seed).

cluster IV (3.92) and the minimum for cluster IX (2.97).

Cluster IV showed the maximum mean value (144.56) for seed yield and cluster VII showed the lowest mean value (81.44). For leaf length, the highest mean value was possessed by cluster II (38.00) and the lowest value was possessed by cluster VIII (29.13). Leaf width was the highest in cluster II (2.028) and the lowest in cluster V (1.280). Cluster II recorded the highest mean value of number of leaves per plant (47.333) and the lowest in cluster VI (37.216).

Cluster I showed the maximum mean value (1.494) for green fodder yield and cluster VIII showed the lowest mean value (0.624). For dry matter yield, the highest mean value was possessed by cluster I (0.309) and the lowest value was possessed by cluster VIII (0.144). Crude protein in grain was the highest in cluster IV (13.57) and the lowest in cluster I (11.81). Cluster V recorded the highest mean value of crude protein in forage (13.67) and the lowest in cluster VIII (12.87). Cluster III revealed the highest mean value for germination per cent (90.90), whereas cluster VIII had the lowest mean value (83.92). Cluster III showed the maximum mean value (34.957) for seedling length and cluster IX showed the minimum mean value (30.265). For seedling dry weight, the highest mean value was possessed by cluster VI (12.52) and the lowest value was possessed by cluster VII (7.93). Seed vigour index I was the highest in cluster III (3173.23) and the lowest in cluster IX (2569.83). Seed vigour index II was recorded minimum for cluster I (686.87) and maximum for cluster IV (1097.67). For electrical conductivity, cluster IX (0.365) had the highest mean value, while cluster IV had the lowest mean value (0.214). Similar findings were also reported by Singh and Singh (2011).

The distribution of mean values in various clusters revealed that the clusters I, II and IV had better cluster means for most of the characters.

Therefore, clusters I, II and IV might be considered desirable for selecting genotypes which may be used as promising parents for hybridization. The genotypes JO 1, ALGERIAN, HFO 912, DULO, UPO 212, OS 6, HFO 305, HJ 8, OS 403, HFO 879, HFO 878, JHO-2006-4, JHO 851, HFO 832, HFO 409, HFO 831 and FOS-1/29 which fall in these clusters could be used in crossing programme to obtain high heterotic response and thus better segregants in subsequent generations for dry matter yield in forage oat.

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