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Comparative diversity analysis of oat genotypes under multi-cut system

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Abstract
The present investigation was carried out with 92 genotypes of oat maintained in germplasm of Forage Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar. The Mahalanobis' D^2 statistics for genetic divergence classified 92 oat genotypes into eleven and nine clusters in first cut and second cut, respectively in multi-cut system, indicating the presence of substantial genetic diversity in the evaluated germplasm. Average inter-cluster distance in Ist cut was found highest between cluster IX and XI (6.826) followed by cluster IV and VII (6.676). The minimum inter cluster distance was noticed between cluster V and VI (3.508). The minimum intra cluster distance was noticed in cluster VII (2.602) and highest intra-cluster distance was observed in cluster V- (5.098).The clusters II, V, and XI were having higher cluster mean values for most of the characters studied. In 2nd cut, average inter-cluster distance was found highest between cluster II and VII (8.071), followed by cluster III and VI (7.857). The minimum inter cluster distance was noticed between cluster VI and VIII (5.766). The minimum intra cluster distance was noticed in cluster IV (4.899) and highest intra-cluster distance was observed in cluster VII- (6.078).The clusters II, III, IV and IX had higher cluster mean values for most of the characters studied. The genotypes HFO-58, OS-6, KENT, HFO-851, HFO-867, HFO-502, HFO-508 and HFO-880 which performed better in both 1stcut and 2nd cut clusters might prove as potential tool for obtaining high heterotic response and consequently superior segregants for dry matter yield and quality in forage oat under multi-cut system.

Keywords: Clusters, Diversity, Fodder, Multi-cut, Oat genotypes

Introduction

Oat is a self pollinated allohexaploid crop (2n=6x=42) having genomic constitution AACCDD belonging to the very large and diverse genus *Avena* which includes diploid, tetraploid and hexaploid species. Oat is thought to be originated in Asia Minor (Gibson and Benson, 2002).The cultivated hexaploid oat evolved similar to wheat through cycles of interspecific hybridization and polyploidization and combines seven chromosome pairs from each of the three diploid genomes designated AA, CC and DD. Oat domestication occurred very late and in very different way than wheat, probably it evolved in wheat and barley as weed four to five thousand years ago. Domestication of oat is considered to be in two centres: the near east includes Iran, Iraq and Turkey and the western Mediterranean covers the Iberian Peninsula and northwest Africa (Jellen and Beard, 2000).

Oats contain the highest protein level among the cereals, with 12 to 20% protein in the dehulled kernel (Peterson, 1992). Moreover, oat protein is unique and the amino acid profile is more reasonable in oat than cereals having high lysine content (Biel *et al.,* 2009; Varma *et al.,* 2016). In relation to fodder, oat used to be grown mostly as single cut which restricted its availability to shorter period but now it is extensively used as multi-cut leading to prolonged availability of green fodder which has a great role in establishing more productive dairy industry in India. Now the availability of green fodder and dry fodder is deficient by 64.2 and 24.8%, respectively in India (Rawal, 2001). It is not possible to increase the area under fodder crops due to pressure of more remunerative cereal crops like wheat. Therefore, the only way out is to evolve multi-cut varieties which give more tonnage per unit area per unit of time. Generally oat is grown as a sole crop but it can also be taken as intercrop with berseem to give a nutritious fodder. Farmers face the scarcity of fodder during the winter (Dec-Jan) and they have to feed the cattle with dry stalks of pearl millet or wheat straw. Oat fodder is mostly fed as green and surplus is converted into silage or hay for further use during scarcity period. It is preferred feed of all the animals and its straw is soft and superior to wheat and barley.

The total global 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. 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 STAT, 2015). Annual global production during 2013-2017 was 24 million tonnes with Russia, Canada, Australia and Poland being the leading oat producing countries (FAO STAT, 2019). In India, 100,000 hectares of area is under oat cultivation with productivity of 35-40 tonnes of green fodder per hectare and mainly grown in Rabi season primarily for fodder in Uttar Pradesh., Punjab, Bihar, Haryana and Madhya Pradesh (Anonymous, 2014).

Oat has high protein content in 1st cut (12.10-15.63 %) and comparatively low in 2nd cut (9.63 - 13.57%; Poonia and Phogat, 2017). The increasing availability of winter fodder primarily depends on the berseem and oats and due to depletion in land resources, the urgent need arise to develop new varieties having high yield potential with better quality. The variability in berseem is limited so the focus should be more to exploit oat germplasm for fulfilling the fodder requirement during the *Rabi* season. The oat genotypes selected as fodder cultivars should have high regeneration capacity after each cut and with more digestible green fodder for livestock (Stevens *et al.,* 2004), while feed purpose cultivars should have high grain yield and harvest index, free from pests and can withstand adverse environmental forces (Martinez *et al.,* 2010; Chaudhary *et al.,* 2014).

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 ongoing crop improvement programmes. The basic need for a successful crop breeding programme is the nature and magnitude of genetic variability present in the germplasm which serves as most valuable natural resource in providing the required traits to develop new varieties (Ahmed *et al.,* 2011). Genetically diverse genotypes derived from different agro- ecological zones are likely to produce more heterotic effects with desirable segregants in the crossing programme. Therefore, the present investigation was undertaken to estimate the genetic diversity in the genotypes of different agro-ecological origin.

Materials and Methods

***Plant materials and experimental designing*:** The experimental materials were comprised of 92 genotypes of oat collected from seven SAU's/ ICAR institutes of India and three countries including Algeria, Australia and Bulgaria comprising of ten *Avena* species (Table 1). These genotypes were selected from germplasm available in Forage section, Department of Genetics and Plant breeding, CCS Haryana Agricultural University, Hisar, India. The field experiment was conducted during *Rabi* season 2015-2016 at the Farm of Forage Section. Hisar is semi-arid and subtropical with prevailing hot and dry winds during summer months situated at 29°10' N latitude and 75°44' E longitude with an altitude of 228 meters above the mean sea level. The experiment was carried out in random block design with three replications. Each genotype was sown in three rows of 3 m length with a row-to-row distance 25 cm and plant to plant spacing of 10 cm. The recommended cultural and agronomic practices were followed to raise crop. During study the weather parameters were also recorded. The average minimum and maximum temperature (3 to 42 ºC) and relative humidity (55.0-95.0%) exhibited a wide range. The rainfall during the crop growth season occurred in the month of March and April.

***Observations recorded*:** The observations were recorded on five competitive plants randomly selected of each genotype in each replication for the 4 and 11 morphological characters in first cut and second cut of multi-cut system, respectively. The observation recorded for plant height (cm), number of tillers per plant, green fodder yield/meter row length (kg), dry matter yield/meter row length (kg) in first cut. While in second cut, observations were recorded on the characters, namely, plant height (cm), number of days to 50% flowering, number of tillers/plant, internode length (cm) peduncle length (cm), flag leaf length (cm), leaf length (cm), leaf width (cm), green fodder yield/meter row length (kg), dry matter yield/meter row length (kg) and number of leaves/ plant.

The 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) were also recorded. The 100 seeds per replication grown in the germinator at 26 °C for one week and data on 30 seedlings recorded for seedling length and seedling dry weight. The forage crude protein (%) was estimated for first cut at 65 days after sowing and second cut at days to 50% flowering. The seed quality characters were estimated at Seed Quality Laboratory, Department of Seed Science and Technology, while forage crude protein content (%) was determined

Table 1. List of 92 oat genotypes used in the present investigation

Source	No. of genotypes	Name of genotypes with species and genomic constitution
ALGERIA	1 (Hexaploid)	ALGERIAN (A. *sativa* L.-AABBCC)
AUSTRALIA	1 (Hexaploid)	KENT (A. *sativa* L.-AABBCC)
BULGARIA	3 (Hexaploid)	DUNAV, KALOJAN, DULO (A. *sativa* L.-AABBCC)
CSKHPAU, Palampur	1 (Hexaploid)	PLP-1 (A. *sativa* L.-AABBCC)
GBPUAT, Pantnagar	2 (Hexaploid)	UPO-94, UPO-212 (A. *sativa* L.-AABBCC)
IGFRI,Jhansi	5 (Hexaploid)	JHO-2006-4, JHO-822, JHO-851, JHO-99-1, JHO-2006-2 (A. *sativa* L.-AABBCC)
JNKVV, Jabalpur	1 (Hexaploid)	JO-1 (A. *sativa* L.-AABBCC)
PAU, Ludhiana	2 (Hexaploid)	OL-125, 0L-10 (A. *sativa* L.-AABBCC)
SKAUST, Srinagar	2 (Hexaploid)	SABZAR, SKO-90 (A. *sativa* L.-AABBCC)
	2 (Diploid)	HFO-305 (*Avena nuda*-AA) , HFO 864 (*Avena brevis*-AA)
	4 (Tetraploid)	HFO-58 (*A. barbata-AACC)*, HFO-865 (*A. insularis*-AACC), HFO-867(*A. maroccana-AACC)*, HFO-870(*A. vaviloviana-AABB*) HFO-60 (*A.byzantina*), HFO-504 (*A. fatua*), HFO-872 (*A. sterilis*)
CCSHAU, Hisar	68 (Hexaploid)	HFO-267, FOS-1/29, OS-6, HFO-505, HFO-975, HFO-69, HFO-876, HFO-877, HFO-879, HFO-502, HFO-78, HFO-603, HFO-414, HFO-409, HFO-508, HFO-498, HFO-875, HFO-878, HFO-874, HFO-523, HFO-433, HFO-885, HFO896, HFO-839, HFO-836, HFO-863, HFO-884, HFO-841, HFO-851, HFO-880, HFO-893, HFO-852, HFO-862, HFO-845, HFO-883, HFO-831, HFO-114, HFO-603, HFO-832, HFO-605, HFO-611, HFO-704, HFO-715, HFO-610, HFO-706, HFO-703, HFO-575, HFO-614, HFO-707, HFO-905, HFO-908, HFO-914, HFO-909, HFO-904, HFO-910, HFO-913, HFO-921, HFO-924, HFO-919, HFO-906, HFO-912, HFO-902, HFO-920, HJ-8 & OS-403 **(***A. sativa* L.-AABBCC*)*

following Micro-Kjeldahl method (Nelson and Sommers, 1980) of nitrogen estimation at Quality Analysis Laboratory, Forage Section.

***Statistical analysis*:** It was carried out according to estimation of degree of divergence among different pairs of statistics and the data was statistically analyzed as per standard procedure of D^2 to assess genetic diversity (Mahalanobsis, 1936). Genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by (Rao, 1952).

Results and Discussion

The analysis of variance showed highly significant differences within the population for all the characters studied in first cut and second cut of multi-cut oat (Poonia *et al.,* 2018). This suggested that the genotypes under investigation consisted of sufficient amount of variability and also indicated that this material was appropriate for further analysis.

First cut of multi-cut oat

***Genetic divergence*:** The D^2 analysis on agro-morphological, seed and fodder quality traits grouped the ninety two genotypes into eleven different clusters was based on distance ranges. Maximum number of genotypes in single cluster represented that genotypes had less genetic variation among them and are related more closely. The crossing in these clusters will offer less improvement in breeding programme. Clustering pattern revealed that clusters VIII and V were the largest ones with 18 and 14 genotypes followed by cluster I and III, cluster VI and XI, cluster IV and X, cluster II, IX and cluster VII with10,7, 6, 5and 4 genotypes each, respectively (Table 2).

***Intra and inter cluster average D^2 values*:** Highest intra cluster distance was observed for cluster V (5.098) followed by cluster IX (4.013) and cluster IV (3.740), indicating that lines in these clusters were relatively more diverse among themselves. The diversity studied among the clusters based on the inter cluster D^2 values and it ranged between 2.602 to 6.826. The maximum inter cluster distance observed was 6.826 (Table 3) between cluster IX and XI, followed by cluster IV and VII (6.676), and cluster IV and XI (6.604) suggesting significant amount of diversity among lines of these clusters. The lowest inter cluster distance was observed between clusters V and VI (3.508), cluster VII and VIII (3.717), and cluster I and III (3.730.8) showing the narrow genetic

diversity and close relationship for many characters of the genotypes in these clusters. Cluster XI was characterized by genotype having desired prominent characters like high green fodder yield, high dry matter yield and tall plants (Table 4). The prominent traits of individuals in cluster V displayed highest fodder crude protein and high seed vigour index-II, whereas cluster II for highest germination percentage and high seed vigour index-I.

Second cut of multi-cut oat

***Genetic divergence*:** The morphological and quality characters studied in the ninety two genotypes grouped into nine different clusters indicated the presence of a wide genetic diversity in the materials under study. The composition of different clusters varied, containing 2 to 16 genotypes depending upon the similarity in the expression of their genetic divergence (Table 5). Clusters I and II had the largest number *i.e.,* 16 genotypes followed by cluster IX with 14 genotypes, cluster VI with 13 genotypes, cluster VIII with 10 genotypes, clusters IV, V, III and VII with 8, 7, 6 and 2 genotypes, respectively. The reason for grouping the genotypes of same geographic origin into different clusters might be due to the different genetic architecture and wide divergence in features.

Intra and inter cluster average D^2 values: The highest intra cluster D^2 value was observed for cluster VII- (6.078) followed by cluster III (5.588), cluster VIII (5.429), cluster IX (5.131), cluster I (5.011), cluster I (5.002), cluster II (4.919), cluster VI (4.908) and cluster IV (4.899). The cluster VII with highest intra cluster distance showed maximum diversity with two genotypes (HFO-870 and HFO-880), while with eight genotypes (ALGERIAN, FOS-1/29, HFO-69, JHO-2006-4, JHO-851, UPO-94, HFO-878 and HFO-832) the cluster III was least diversed (Table 6).

Table 2. Clustering of 92 oat genotypes in 1st cut of multi-cut system on the basis of D^2 statistics

Cluster	No. of genotypes	Genotypes
Cluster I	10	ALGERIAN, JO-1, HFO-885, HFO-878, HFO-69, UPO-94, SKO-90, JHO-2006-4, JHO-851, HFO-832
Cluster II	05	HFO-913, HFO-914, HFO-870, HFO-906, HFO-267
Cluster III	10	HFO-614, HFO-575, JHO-822, HFO-505, HFO-60, HFO-504, HFO-706, HFO-862, JHO-99-1, HFO-883
Cluster IV	06	KENT, HFO-851, HFO-867, OS-6, HFO-872, HFO-896
Cluster V	14	HFO-305, HFO-879, HFO-919, HFO-908, HFO-893,HFO-902, HFO-910, HFO-904, HFO-610, HFO-920, HFO-909, HFO-852, HJ-8, OS-403
Cluster VI	07	HFO-905,HFO-707, HFO-603, HFO-92, HFO-605, HFO-924, HFO-703
Cluster VII	04	OL-125, 0L-10, SABZAR, DULO
Cluster VIII	18	HFO-603, HFO-975, HFO-498, HFO-704, HFO-715, HFO-433, HFO-864, HFO-78, HFO-409, HFO-414, HFO-523, HFO-841, HFO-865, HFO-114, HFO-611, HFO-836, HFO-863, HFO-884
Cluster IX	05	PLP-1, JHO-2006-2, HFO-880 , KALOJAN, HFO-508
Cluster X	06	DUNAV, HFO-876, HFO-877, HFO-875, HFO-874, HFO-831
Cluster XI	07	HFO-58, HFO-502, UPO-212, FOS-1/29, HFO-912, HFO-839, HFO-845

Table 3. Average intra (diagonal) and inter (above diagonal) cluster D^2 values in ninety two genotypes of oat in 1st cut of multi-cut system

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**2.970**	4.071	3.730	5.151	5.036	4.643	3.969	4.160	5.051	4.704	5.081
II		**3.354**	4.020	4.769	5.330	4.581	5.548	5.463	5.734	6.456	6.544
III			**3.033**	4.813	4.232	4.072	4.784	4.514	5.947	5.941	4.526
IV				**3.740**	4.065	4.381	**6.676**	5.299	5.851	6.349	**6.604**
V					**5.098**	**3.508**	5.845	4.273	5.753	5.758	4.924
VI						**2.609**	5.200	3.997	5.206	5.646	5.423
VII							**2.602**	3.717	4.959	4.959	4.678
VIII								**2.904**	4.375	4.292	4.539
IX									**4.013**	4.722	**6.826**
X										**3.600**	5.859
XI											**3.398**

Table 4. Cluster means for different characters of oat germplasm in 1st cut of multi-cut oat

Clusters	Characters										
	PH (cm)	NOLS	GFY (kg)	DMY (kg)	CP1 (%)	GP (%)	SL (cm)	SDW (mg)	SV-I	SV-II	EC (mS/ cm/seed)
I	52.1	9.13	0.208	0.050	13.99	88.5	32.4	8.30	2867	732	0.273
II	54.5	7.95	0.159	0.039	14.00	**91.0**	34.6	8.24	**3142**	747	0.262
II	58.0	8.11	0.243	0.058	14.24	90.0	33.3	9.43	2991	845	0.241
IV	53.1	8.43	0.169	0.035	14.51	87.9	**34.7**	12.70	3052	1111	0.201
V	56.4	7.92	0.222	0.053	**14.60**	86.7	33.1	**13.29**	2863	**1149**	0.213
VI	59.5	7.51	0.196	0.045	14.16	89.7	31.5	11.89	2823	1063	0.250
VII	62.6	8.63	0.232	0.053	13.42	85.0	29.9	7.77	2537	658	0.374
VIII	54.7	8.34	0.218	0.049	13.97	84.7	29.8	10.83	2521	913	0.287
IX	42.1	8.39	0.141	0.036	14.03	85.2	30.4	10.66	2583	905	**0.403**
X	35.4	**9.33**	0.212	0.051	13.05	83.6	30.5	10.41	2541	867	0.303
XI	**62.9**	8.33	**0.322**	**0.075**	13.87	85.0	31.7	10.47	2689	884	0.257

PH: Plant height; NOLS: Number of leaves per plant; GFY: Green fodder yield; DMY: Dry matter yield; CP1: Crude protein in 1st cut forage: GP: Germination percent; SL: Seedling length; SDW: Seedling dry weight; SVI: Seed vigour index-1; SVII: Seed vigour index-2; EC: Electrical conductivity

Table 5. Clustering of 92 genotypes of oat in 2nd cut of multi-cut on the basis of D^2 statistics

Cluster	No. of genotypes	Genotypes
Cluster I	16	JO-1, HFO-921, HFO-505, HFO-839, HFO-885, HFO-912, HFO-862, HFO-883, HFO-906, HFO-913, HFO-914, HFO-614, HFO-575, JHO-99-1, HFO-267, SKO-90
Cluster II	16	JHO-822, OS-6, HFO-305, KENT, HFO-851, HFO-867, HFO-879, HFO-502, HFO-908, HFO-704, HFO-910, HFO-610, HFO-706, HFO-703, HFO-905, HFO-603
Cluster III	06	HFO-896, HFO-919, HFO-707, HFO-924, HFO-909, HFO-852
Cluster IV	08	ALGERIAN, FOS-1/29, HFO-69, JHO-2006-4, JHO-851, UPO-94, HFO-878, HFO-832
Cluster V	07	PLP-1, SABZAR, DULO, UPO-212, HFO-841, HFO-611, HFO-504
Cluster VI	13	HFO-523, OL-125, HFO-864, HFO-865, HFO-498, HFO-884, HFO-78, HFO-975, 0L-10, DUNAV, HFO-877, HFO-876, HFO-836
Cluster VII	02	HFO-870, HFO-880
Cluster VIII	10	JHO-2006-2, HFO-715, HFO-893, HFO-845, HFO-409, KALOJAN, HFO-831, HFO-872, HFO-875, HFO-874
Cluster IX	14	HFO-58, HFO-60, HFO-508, HFO-433, HFO-603, HFO-863, HFO-114, HFO-414, HFO-904, HFO-902, HFO-920, HFO-605, HJ-8, OS-403

Table 6. Average intra (diagonal) and inter (above diagonal) cluster D^2 values in ninety two genotypes of oat in 2nd cut of multi-cut system

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**5.002**	5.952	6.358	5.813	6.072	6.534	7.046	6.602	6.709
II		**4.919**	6.003	6.300	6.347	6.908	**8.071**	6.306	6.117
III			**5.588**	7.684	7.727	7.857	7.849	7.140	6.783
IV				**4.899**	5.854	6.089	7.458	6.154	6.356
V					**5.011**	6.191	7.309	6.310	6.541
VI						**4.908**	6.981	**5.766**	6.450
VII							**6.078**	7.252	**7.867**
VIII								**5.429**	6.211
IX									**5.131**

Table 7. Cluster mean for different characters of oat germplasm in 2nd cut of multi-cut oat

Clusters	Characters																
	PH (cm)	DF (days)	FLL (cm)	IL (cm)	TPL	PL (cm)	LL (cm)	LW (cm)	GFY (g)	DMY (kg)	NOLS	CP2 (%)	GP (%)	SL	SDW (mg)	SVI	SVII	EC (mS/ cm/ seed)
I	71.9	115.4	22.02	16.65	8.49	25.98	29.50	1.50	0.406	0.107	39.50	**12.62**	89.10	33.59	8.88	2993	788	0.238
II	80.8	118.1	**25.46**	**19.63**	8.65	**29.00**	33.10	1.81	0.431	0.112	39.70	12.22	88.00	31.95	12.29	2811	1077	0.224
III	68.5	114.4	23.50	15.44	7.71	24.08	31.22	1.74	0.433	0.112	34.10	12.23	**88.70**	**34.56**	13.41	**3059**	1182	0.222
IV	75.5	121.5	21.88	17.63	**9.86**	22.00	33.29	1.75	0.486	0.119	**45.00**	11.61	88.30	32.49	8.37	2869	**736**	0.278
V	**85.1**	121.1	23.86	17.91	8.92	22.67	**35.91**	2.01	0.411	0.109	41.00	11.25	85.90	30.29	9.24	2600	791	0.354
VI	68.7	122.5	19.67	13.92	8.99	22.53	26.15	1.47	0.454	0.117	42.30	10.98	84.70	29.14	**9.79**	2467	827	0.305
VII	53.7	113.7	15.83	11.17	8.13	22.42	26.33	**2.17**	0.405	0.106	39.20	12.38	86.80	32.59	9.34	2827	798	0.515
VIII	65.4	**123.3**	21.13	15.53	9.11	25.23	29.07	2.03	0.455	0.118	44.20	11.61	84.00	31.78	11.86	2667	991	0.267
IX	80.4	122.1	22.10	15.92	8.64	21.46	31.33	1.91	**0.661**	**0.161**	38.80	11.83	86.20	31.67	11.69	2729	1004	**0.256**

PH: Plant height; DF: No. of days to50% flowering; FLL: Flag leaf length; IL: Internode length; TPL: Number of tillers per plant; PL: Peduncle length; LL: Leaf length; LW: Leaf width; GFY: Green fodder yield; DMY: Dry matter yield; NOLS: Number of leaves per plant; CP2: Crude protein in 2nd cut forage; GP: Germination percent; SL: Seedling length; SDW: Seedling dry weight; SVI: Seed vigour index-1; SVII: Seed vigour index-2; EC: Electrical conductivity.

When diversity was studied among the clusters based on the inter cluster D^2 values, it showed a range of 4.899 to 8.071. The average inter-cluster distance was highest between cluster II and VII (8.071), followed by cluster III and VI (7.857) and cluster III and VII (7.849). Whereas the lower inter cluster distance was observed between cluster VI and VIII (5.766), followed by cluster IV and V (5.854). The higher inter cluster distance indicated the presence of more diversity among the genotypes included in these clusters. The perusal of the clustering analysis revealed that the individuals within any one cluster were more closely related than the individuals in different clusters (Table 6).

The cluster IX having maximum cluster mean for green fodder yield (0.661 kg) and dry matter yield (0.161kg) was most important for improvement for fodder purpose. The green fodder yield (0.405 kg) and dry matter yield (0.106 kg) were observed with lowest mean values in cluster VII (Table 7). The plant height was observed as lowest in cluster VII (53.7 cm) and highest in cluster V (85.1 cm), which also had longest leaves length (35.91 cm). Cluster II recorded the highest flag leaf length (25.46 cm), internode length (19.63 cm) and peduncle length (29.00 cm). The cluster VII recorded the lowest flag leaf length (15.83) and internode length (11.17), while leaf width (2.17 cm) was highest in cluster VII and the genotypes belonging to this cluster had lowest days to 50 % flowering (113.7 days) indicating early maturing genotypes. For number of tillers/plant, the highest mean value was possessed by cluster IV (9.86) and the lowest by cluster III (7.71). Cluster IV recorded the highest mean value of number of leaves per plant (45.00) and the lowest in cluster III (34.06). Cluster I recorded the highest mean value of crude protein in forage (12.62) and the lowest in cluster VII (10.98). For seed quality characters, cluster III recorded high germination (88.70%), longest seedling length (34.56 cm), highest seed vigour index-I (3059) and seed vigour index-II (1182).

The D^2 analysis revealed that genotypes grouped in different clusters were independent of their geographical origin (Table 2 and 5), where the genotypes from different SAU's/ ICAR institutes were grouped together in same cluster and revealed that the genetic constitution of the genotypes was dominant over the geographical origin. These results were in conformity with the findings of earlier studies (Bahadur and Choubey, 2008; Yadav *et al.,* 2011; Ahmed *et al.,* 2011; Krishna *et al*., 2014; Kumar *et al.,* 2016; Kumari *et al.,* 2019). The seed quality characters were analysed by Verma *et al.* (2014), and

focussed the importance of diversity. The reason for grouping the genotypes of same geographic origin into different clusters might be due to the different genetic architecture and wide divergence in features. The different genetic architecture might be the result of free exchange of materials among different regions of country, either for direct introduction for breeding purposes or for general cultivation. Genetic drift and selection in different environments could be the other important factors contributing towards the divergence. In last 20-30 years comparing to other fodder crops oat productivity has been declined due to both decrease in numbers of grown cultivars and types of oats along with reduction in oats acreage. Both of the factors had negative impact from genetic resource conservation perspective on the farm diversity (Medraoui *et al.,* 2007; Sofalian *et al.*, 2008). Indeed, the presence of remarkable diversity within the germplasm collection appears to be of great importance in providing valuable materials for breeding programmes that are aimed at oat improvement (Veronesi and Falcinelli, 1988).

Conclusion

The narrow genetic diversity present among modern oat cultivars might have consequences both for the vulnerability of crops to new diseases and for their ability to respond to changing climatic conditions. It is thus imperative to exploit the genetic diversity present in available germplasm including wild relatives or landraces to develop new cultivars for broadening the genetic base of commercial oat cultivars. Therefore, the genotypes HFO-58, OS-6, KENT, HFO-851, HFO-867, HFO-502, HFO-508 and HFO-880 which showed high regeneration capacity after first cut and offered maximum diversity in both cuts could be used under multi-cut system and might be considered as potential parents for obtaining high heterotic response and consequently transgressive segregants for dry matter yield and quality in fodder oat. The genetic potential of genotypes studied for both agro-morphological and quality related characters could be useful to ensure the sustainability of quality fodder for longer duration during lean period.

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