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Genetic Divergence among Oat (*Avena sativa* L.) Genotypes under Dual purpose and Seed Yield related Systems

Priyanka, V.K. Sood, Amit Rana* and Sawan Kumar
Department of Genetics and Plant Breeding,
CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, (Himachal Pradesh), India.

(Corresponding author: Amit Rana)*

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ABSTRACT: The present study was conducted during *Rabi* season 2018-19 with 58 diverse oat genotypes in order to study genetic diversity for different agro-morphological and quality traits among dual purpose and seed yield purpose systems separately. Based on D^2 statistic, genotypes were grouped into 12 clusters in case of dual purpose system whereas 11 clusters in seed related system. The inter-cluster distances were observed to be higher than intra-cluster. Cluster I emerged as the largest cluster followed by Cluster II under both the systems. Among both the systems, β- glucan content contributed maximum towards genetic divergence followed by crude protein content of seed while the lowest by leaf: stem ratio and harvest index under dual purpose and seed yield purpose systems, respectively. Genotypes IG-03-205, EC-528883 and OS-6 were found more diverse under both the systems which can be utilized in future hybridization programmes.

Keywords: Oat; genetic diversity; hybridization; nutritional quality.

INTRODUCTION

Oat (*Avena sativa* L.) is one amongst the foremost vital forage and feed crops of the world. The genus *Avena* is massive and numerous containing both wild and cultivated polyploidy species with basic chromosome number of n=7. It is a vital forage crop of winter in numerous parts of the world and additionally developed as multipurpose crop for fodder and grain. Green fodder contains approximately 10 to 13% protein and 30 to 35% dry matter. In spite of being tall fed fodder crop, it is presently picking up significance due to its unique and imperative quality characteristics, particularly the lipid and protein in grains. Contrasting from other cereal grains such as wheat and barley it is rich within the cancer preventing agents α-tocotrienol, α-tocopherol, and avenanthramides, and he reduce obesity, lowering bad cholesterol compound β-glucan (Oliver *et al.,* 2010). Oat within the regions of Himalayas incorporates a more extensive flexibility, since of its great developing environment, speedy re-growth and superior wholesome esteem (Sood *et al.,* 2016). Oat can tolerate acidic soils better than other small grain cereals showing that the plant has the potential to be grown in varied environments (Chen *et al.,* 2007). The protein substance of the hull-less oat (groat) ranges from 12 to 24 per cent, which is the most elevated among cereals (Lasztity, 1999). Oats contain more protein, fatty acids, iron, magnesium, phosphorus, and zinc than wheat, maize, barley, and rice.

Assessment of germplasm is of colossal importance in genetic enhancement of the crop. Genetic diversity examination helps in interpreting the hereditary background and breeding esteem of the germplasm. Genetic diversity is a key aspect of the improvement of germplasm which is directly related to crop production (Ali *et al.,* 2021). It was too said that a much less diverse genetic pool utilized by plant breeders than the all-inclusive accessible genetic diversity confined by the crop (Joshi *et al.,* 2012). Among the different strategies identified/developed to consider the genetic diversity within the genotypes, the Mahalanobis D^2 statistics approach is solid and most frequently. The optimum genetic divergence available between the parents is a critical pre-requisite for victory of any plant breeding programmes, since crosses between genetically divergent parents have been found to supply superior transgressive isolates within the segregating eras (Mahalanobis, 1928). Hence, evaluation of genetic diversity existing within the breeding materials is a fundamental prerequisite for any breeding programme. So, the present investigation was undertaken with fifty eight oat germplasm lines, amongst which PLP-1, OS-6 and KENT were utilized as checks.

MATERIALS AND METHODS

A. Experimental site and material

The experiment was conducted during *Rabi* 2018-19 at Experimental Farm of the Fodder Section, CSK HPKV, Palampur which is situated at 32°6′N latitude, 76°3′E longitude at an elevation of 1290.8 m (a.m.s.l.). Agro climatically the location represents the mid-hill zone of Himachal Pradesh (Zone-II) and is characterized by humid sub-temperate climate with high rainfall (2500 mm). The present investigation consisted of 58 diverse genotypes of oat, which were evaluated in randomized block design (Panse and Sukhatme, 1985) with three replications and 25 cm × 15 cm crop geometry (Table 1).

Table 1: List of oat germplasm (*Avena sativa* L.) accessions used in the present study.

Sr. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	Sr. No.	Genotypes
1.	ADG-214	16.	HJ-8	31.	JPO-25	46.	SNTM-90
2.	ALGERIAN	17.	IG-03-203	32.	JPO-28	47.	PLP-11
3.	AVE-3018	18.	IG-03-205	33.	JPO-29	48.	PLP-12
4.	EC-528390	19.	IG-03-208	34.	JPO-30	49.	PLP-13
5	EC-528865	20.	JHO-862	35.	JPO-31	50.	PLP-14
6.	EC-528883	21.	JPO-36	36.	JPO-40	51.	PLP-15
7.	EC-528889	22.	JPO-38	37.	JPO-41	52.	PLP-16
8.	EC-528890	23.	JPO-14	38.	JPO-44	53.	PLP-17
9.	EC-528894	24.	JPO- 17	39.	JPO-45	54.	PLP-18
10.	EC-528895	25.	JPO-18	40.	JPO-46	55.	PLP-19
11.	EC-528896	26.	JPO-19	41.	K-353	56.	KENT (C)
12.	HFO-52	27.	JPO-20	42.	KKR-AK-15	57.	OS-6 (C)
13.	HFO-102	28.	JPO- 21	43.	KKR-AK-26	58.	PLP-1 (C)
14.	HFO-114	29.	JPO-22	44.	OATS-79		
15.	HFO-163	30.	JPO-24	45.	OATS-80		

B. Field study and data evaluation

Two experiments were conducted on same genotypes for recording observations for dual purpose and seed purpose separately. In case of dual purpose system the plants were harvested 70 days after sowing (DAS and 5-6 cm stubble was left in the field to allow the crop to regenerate to see the effect of cutting on yield and quality traits, whereas, in case of sole seed yield related system all the traits were recorded without cut in order to compare yield and quality characters of sole seed yield purpose system with dual-purpose system.

Data were recorded for different fodder traits *viz*., plant height at 90 DAS (cm), regeneration (%), leaves per plant, tillers per plant, leaf stem ratio, green fodder yield per plant (g), dry matter (%), dry matter yield per plant (g), crude protein content of fodder (%), crude protein yield per plant (g), ADF (%) and NDF (%) and seed yield related traits *viz*., days to 50 % flowering, plant height at maturity (cm), days to 75% maturity, biological yield per plant (g), seed yield per plant (g), harvest index (%), 100-seed weight (g), crude protein content of seed (%) and β-glucan content (%). Quality traits such as ADF (%) and NDF (%) were determined by the method given by Van Soest (1991) and Van Soest and Snifftn (1984) respectively. The crude protein content for each genotype was analyzed following Micro-Kjeldhal Method (AOAC 1970) and Beta glucan content (%) was estimated by alkali extraction with Congo Red (CR) estimation method (Wood *et al.*, 1977; Semedo *et al.*, 2015).

Keeping these focuses in mind, the present study based on genetic divergence was assessed by utilizing D^2 statistics recommended by (Mahalanobis, 1928), which is based on multivariate investigation of quantitative characteristics. The gathering of genotypes into distinctive clusters is done by following Tocher's strategy as depicted by (Rao, 1952).

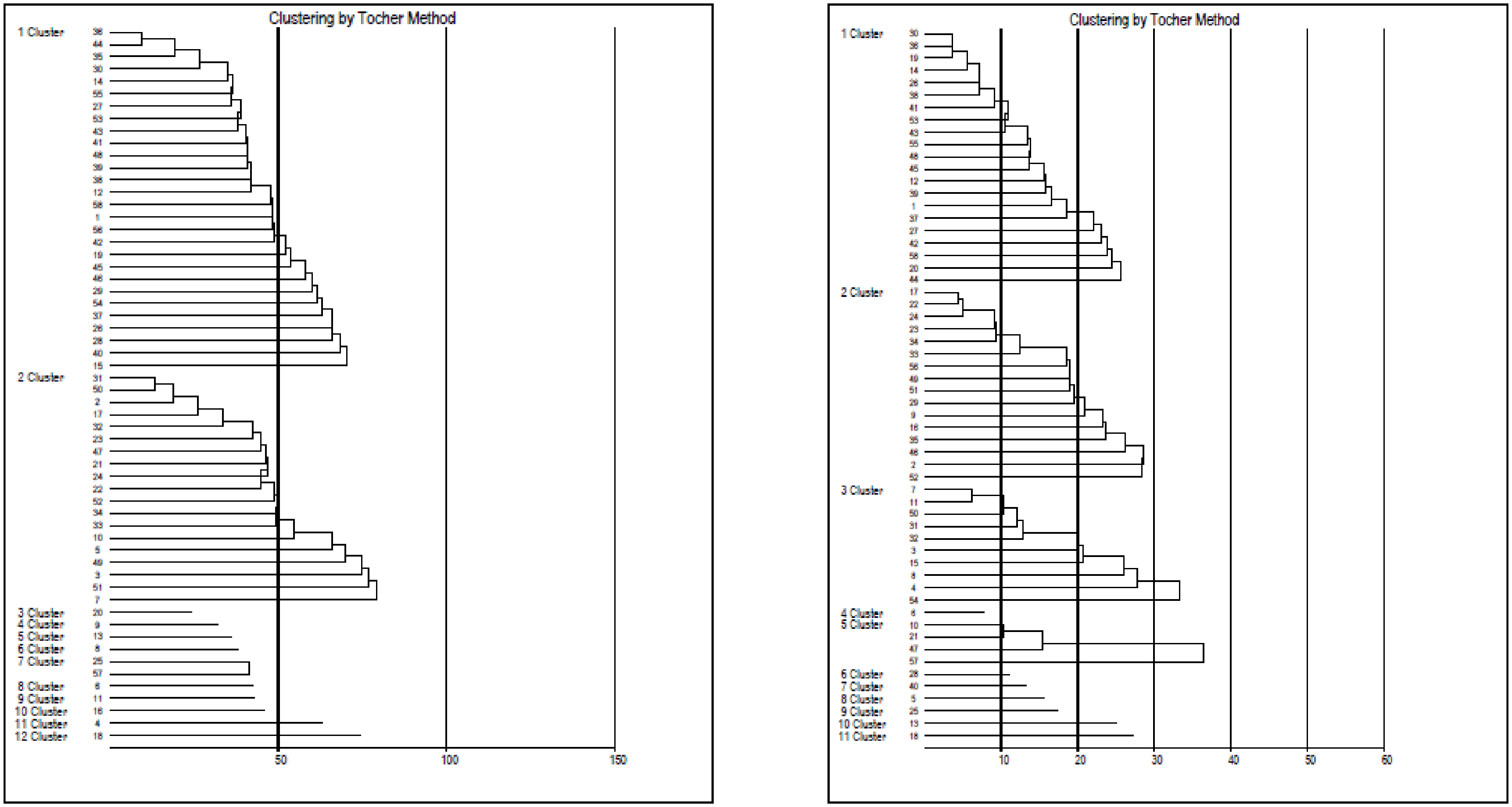
RESULTS AND DISCUSSION

A. Clustering

In the present study, 58 genotypes grouped into twelve clusters in case of dual purpose system (Fig. 1a) whereas in seed related system, genotypes were clustered into 11 groups (Fig. 1b). Cluster I, II, VII consisted of 28, 19 and 2 genotypes, respectively and remaining clusters *i.e*. III, IV, V, VI, VIII, IX, X, XI, and XII consisted of one genotype each (Table 2).

Table 2: Distribution of 58 dual purpose related oat genotypes among clusters on the basis of D^2-analysis.

Cluster No.	No. of Genotypes	Genotypes
I	28	ADG-214, HFO-52, HFO-114, HFO-163, IG-03-208, JPO-19, JPO-20, JPO-21, JPO-22, JPO-24, JPO- 31, JPO-40, JPO-41, JPO-44, JPO-45, JPO-46, K-353, KRR-AK-15, KRR-AK-26, OATS-79, OATS-80, SNTM-90, PLP-12, PLP- 17, PLP-18, PLP- 19, PLP-13, KENT
II	19	JPO-25, PLP-14, ALGERIAN, IG-03-203, JPO-28, JPO-14, PLP-11, JPO-36, JPO-17, JPO-38, PLP-16, JPO-30, JPO-29, EC-528895, EC-528865, , PLP-1, AVE-3018, PLP-15, EC-528889
III	1	JHO-862
IV	1	EC-528894
V	1	HFO-102
VI	1	EC-528890
VII	2	JPO-18, OS-6
VIII	1	EC-528883
IX	1	EC-528896
X	1	HJ-8
XI	1	EC-523890
XII	1	IG-03-205



(a) Dual purpose system (b) Seed yield related system

Fig. 1. Clustering of the oat genotypes (Tocher's Method).

In the case of seed yield related system, Cluster I, II, III, V and VII consisted of 21, 16, 10, 4 and 2 genotypes, respectively and remaining clusters i.e. IV, VI, VIII, IX, X and XI consisted of one genotype each (Table 3). Genetic divergence study also supported by numerous researchers earlier (Bahadur and Choubey 2007; Mut, 2015; Jaipal and Shekhawat 2016; Kaur and Kapoor 2017). More diverse the parents within its overall limits of fitness, the more prominent are the chances of heterotic expression in F1's and a broad spectrum of variability in segregating generations (Arunachalam, 1981).

Table 3: Distribution of 58 seed yield related oat genotypes among clusters on the basis of D2-analysis.

Cluster No.	No. of genotypes	Genotypes
I	21	JPO-24, JPO-40, IG-03-208, HFO-114, JPO-19, JPO-44, K-353, PLP-17, KRR-AK-26, PLP-19, PLP-12, OATS-80, HFO-52, JPO-45, ADG-214, JPO-41, JPO-20, KRR-AK-15, KENT, JHO-862, OATS-79
II	16	IG-03-203, JPO-38, JPO-17, JPO-14, JPO-30, JPO-29, PLP-13, PLP-15, JPO-22, EC-528894, HJ-8, JPO-31, SNTM-90, ALGERIAN, PLP-1, PLP-16
III	10	EC-528889, EC-528896, PLP-14, JPO-25, JPO-28, AVE-3018, HFO-163, EC-528890, EC-523890, PLP-18
IV	1	EC-528883
V	4	EC-528895, JPO-36, PLP-11, OS-6
VI	1	JPO-21
VII	1	JPO-46
VIII	1	EC-528865
IX	1	JPO-14
X	1	HFO-102
XI	1	IG-03-205

B. Average intra and inter-cluster distances

Among dual purpose system, the highest intra-cluster distance was observed in cluster II (28.37) followed by cluster V and XII with an average intra-cluster distance of 25.85and 25.80respectively (Table 4). The highest inter-cluster distance was observed between cluster IX and V (44.49) followed by cluster IV and III (44.27) and cluster XII and I (41.76).

Among seed yield related traits, the highest intra-cluster distance was observed in cluster III (15.18) followed by cluster I and II with an average intra-cluster distance of 14.39and 13.91 respectively (Table 5). The highest inter-cluster distance was observed between cluster IV and III (37.63) followed by cluster VII and I (36.02) and cluster VIII and II (35.84).

Table 4: Average intra and inter-cluster distance among 58 dual purpose related oat genotypes in different environments.

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**18.89**											
II	20.89	**28.37**										
III	27.56	32.094	**0.00**									
IV	23.78	28.76	44.27	**0.00**								
V	23.89	44.61	26.70	34.81	**25.85**							
VI	23.30	34.13	37.18	13.31	48.10	**0.00**						
VII	25.52	23.57	39.60	30.49	27.88	26.79	**0.00**					
VIII	26.78	29.86	41.33	32.68	28.61	30.16	27.44	**0.00**				
IX	21.61	36.86	29.52	30.81	44.49	36.76	31.31	27.23	**0.00**			
X	34.01	29.53	31.85	28.22	30.11	29.49	15.55	24.72	26.86	**0.00**		
XI	21.64	28.21	34.41	16.93	26.13	24.52	20.47	18.11	24.63	20.55	**0.00**	
XII	41.76	32.25	16.43	25.51	27.90	18.50	26.30	30.31	28.10	35.68	26.45	**25.80**

Table 5: Average intra and inter-cluster distance among 58 seed yield related oat genotypes indifferent environments.

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**14.39**										
II	27.06	**13.91**									
III	17.77	28.32	**15.18**								
IV	25.53	28.36	37.63	**0**							
V	28.58	37.04	17.38	33.59	**5.81**						
VI	26.59	29.51	37.67	18.18	25.28	**0**					
VII	36.02	20.07	27.94	16.57	29.83	24.54	**0**				
VIII	27.87	35.84	26.66	17.6	37.68	12.45	15.13	**0**			
IX	26.55	29.14	19.06	27.83	18.15	26.75	16.68	14.01	**0**		
X	28.07	39.75	29.85	25.01	13.32	12.57	19.42	28.96	21.91	**0**	
XI	27.16	16.05	19.73	27.49	18.59	27.28	15.89	13.07	26.58	30.59	**0**

C. Cluster mean and contribution of individual character towards divergence

Among dual purpose traits, Cluster III exhibited the highest cluster mean for plant height 90 DAS, cluster V for 100-seed weight, cluster VIII for days to 50 % flowering and biological yield per plant, cluster IX for leaf stem ratio, cluster X for tillers per plant, regeneration, harvest index, seed yield per plant and crude protein content of seed, Cluster XI exhibited the highest cluster mean for leaves per plant, fresh fodder yield per plant, dry matter, dry matter yield and plant height at maturity. Cluster IV was found best for three traits *viz.*, the crude protein content of fodder (%), crude protein yield per plant and ADF content (Table 6). Among dual purpose traits, β- glucan content contributed maximum towards genetic divergence (31.68%) followed by crude protein content of seed (18.06%) and lowest by leaf stem ratio (0.06%) (Table 8).

Among seed yield related system, Cluster IV exhibited highest cluster mean for days to 50 % flowering, cluster VIII for biological yield per plant, cluster IX for plant height, cluster X for tillers per plant, seed yield per plant, harvest index, 100 seed weight and crude protein content and cluster XI for leaves per plant and β-glucan content. Lowest cluster mean for days to 50 % flowering, tillers per plant, days to 75 % maturity and crude protein content found in cluster VI (Table 7). Among seed yield related traits, β-glucan content contributed maximum towards genetic divergence (31.80%) followed by crude protein content of seed (21.48%) and lowest by harvest index (0.84%) (Table 9).

The clustering pattern showed the presence of sufficient genetic diversity among different genotypes of oat. The highest inter-cluster distance among dual purpose traits was observed between cluster IX and V (44.49) followed by cluster IV and III (44.27) while, among seed yield related traits it was observed between cluster IV and III (37.63) followed by cluster VII and I (36.02) exhibiting wide genetic diversity among its genotypes.

Table 6: Cluster means values for fodder yield, its component and quality traits of dual purpose related oat genotypes in different environments.

Traits	I	I	III	IV	V	VI	VII	VIII	IX	X	XI	XII	MEAN	MIN	MAX
Plant height 90 DAS (cm)	39.66	38.36	43.44**	41.52	42.80	43.21	41.09	36.58*	42.07	40.25	39.96	40.08	40.90	36.58	43.44
Leaves per plant	29.09	31.03	36.17	29.50	26.63*	30.37	27.73	31.67	27.73	40.93	43.00**	30.50	31.47	26.63	43.00
Tillers per plant	9.41	8.62	11.53	10.11	10.77	7.57*	9.58	8.57	9.53	13.00**	9.70	10.13	9.79	7.57	13.00
Leaf Stem ratio	0.28	0.27	0.32	0.26	0.25*	0.32	0.33	0.31	0.40**	0.32	0.30	0.26	0.29	0.25	0.40
Fresh Fodder Yield per plant (g)	107.57	111.86	102.86	105.44	104.88	113.22	112.20	111.28	100.30*	137.60	138.1**	108.00	111.49	100.30	138.10
Dry Matter (%)	21.52	21.37	26.00	21.130	21.10	21.49	21.06	21.30	19.20*	22.620	23.4**	21.14	21.87	19.20	23.40
Dry Matter Yield per plant (g)	23.29	24.05	26.70	22.350	22.11	24.35	23.75	23.72	19.27*	31.130	32.31**	22.84	24.42	19.27	32.31
Crude protein content of fodder (%)	10.08	9.98	8.64*	11.86**	10.65	10.45	9.28	8.92	11.79	10.68	9.70	10.18	10.17	8.64	11.86
Crude protein yield per plant (g)	14.20	14.50	12.43*	18.34**	16.37	14.90	14.19	14.21	18.24	14.77	14.68	15.06	15.11	12.43	18.34
ADF (%)	33.00	31.91	35.74	39.55**	31.88	39.12	30.24	33.63	38.70	31.99	26.02*	27.18	33.34	26.02	39.55
NDF (%)	32.04	31.19	32.18	32.00	32.03	36.57	31.96	31.02	33.08	32.07	27.75*	41.1**	32.41	27.75	41.10
Regeneration (%)	80.030	79.420	64.17*	88.42	80.53	89.92	77.22	57.87	86.750	90.5**	85.180	85.600	81.094	64.17	90.500
Days to 50% flowering	140.92	145.42	144.00	154.67	153.67	142.67	151.83	159.3**	154.67	138.33*	151.33	148.00	148.71	138.33	159.33
Plant height at maturity (cm)	108.14	113.21	124.7	106.93	118.50	100.34*	115.78	105.23	111.93	106.61	129.5**	116.16	112.72	100.34	129.52
Days to 75% maturity	178.39	181.32	183.00	177.33	181.00	177.33	184.83*	180.00	184.67	179.33	163.33*	179.00	180.13	163.33	184.83
Biological Yield per plant (g)	93.55	95.80	96.61	99.94	89.41	101.13	87.27*	103.2**	89.11	89.63	98.40	90.23	94.38	87.27	103.27
Harvest Index(%)	24.81	25.84	24.53	23.17	28.86	26.03	20.98*	25.23	23.86	30.85**	25.56	28.50	25.64	20.98	30.85
Seed Yield per plant(g)	26.63	27.11	25.42	23.28*	32.27	25.76	24.01	24.40	26.74	34.42**	25.99	31.58	26.99	23.28	34.42
100 Seed Weight (g)	3.38	3.45	3.11	3.40	4.28**	4.19	2.87*	3.89	3.86	3.18	3.98	3.17	3.56	2.87	4.19
Crude protein content of Seed (%)	10.19	9.53*	11.81	11.74	11.94	9.73	8.75	10.59	7.82	11.85**	8.42	9.92	10.09	9.53	11.85
Beta Glucan content (%)	4.10	2.72	4.07	3.03	4.37	3.67	4.33	4.63	2.99	2.83*	3.78	5.92**	3.77	2.83	5.92

*minimum values; **maximum values

Table 7: Cluster means values for seed yield, its component and quality traits of seed yield related oat genotypes.

Traits	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	MEAN	MIN	MAX
Days to 50% flowering	138.05	142.35	141.67	156.3**	139.08	127.00*	130.67	149.00	160.67	150.67	145.00	144.13	127.00	156.33
Plant Height (cm)	113.12	112.99	114.64	116.63	107.91	105.54	103.93	91.39*	120.2**	102.53	115.22	110.28	91.39	120.26
Days to 75 % maturity	175.37	176.81	175.93	177.00	179.08	165.67*	178.33	183.33	184.0**	178.00	176.00	177.76	165.67	13.00
Biological yield per plant (g)	96.16	97.45	99.86	106.01	100.00	100.56	88.52*	111.7**	92.69	92.14	92.96	97.54	88.52	111.73
Seed yield per plant (g)	27.68	29.75	29.04	26.02*	26.21	30.44	29.52	18.62	26.03	33.91**	33.23	27.84	26.02	33.91
Harvest Index	26.49	28.95	28.94	27.63	26.13	30.66	26.01	20.8*	24.13	31.27**	30.90	27.76	20.80	31.27
100 Seed Weight (g)	3.37	3.35	3.80	3.90	3.05	3.23	3.59	3.73	2.94*	4.29**	3.18	3.47	2.94	4.29
Crude protein % (Seed)	10.38	10.56	8.75	10.58	8.65	8.25*	8.81	10.54	8.91	11.98**	9.92	9.68	8.25	11.98
Beta Glucan (%)	4.25	2.79*	3.32	4.633	2.83	4.52	5.08	2.84	4.67	4.37	5.92**	4.06	2.79	5.92

*minimum values; **maximum values

Table 8: Contribution of individual characters toward divergence among 58 dual purpose related genotypes of oat.

Sr. No.	Source	Contribution %	Times Ranked 1st
1.	Plant Height 90 DAS (cm)	0.48	8.00
2.	Leaves per plant	0.24	4.00
3.	Tillers Per Plant	0.12	2.00
4.	Leaf Stem Ratio	0.06*	1.00
5.	Fresh Fodder Yield per plant (g)	0.97	16.00
6.	Dry Matter (%)	0.48	8.00
7.	Dry Matter Yield per plant (g)	2.12	35.00
8.	Crude Protein content of Fodder (%)	6.78	112.00
9.	Crude Protein Yield per plant	0.42	7.00
10.	ADF (%) and	3.39	56.00
11.	NDF (%)	4.42	73.00
12.	Regeneration (%)	2.24	37.00
13.	Days to 50% flowering	9.42	157.00
14.	Plant height at maturity(cm)	0.12	2.00
15.	Days to 75% maturity	0.91	15.00
16.	Biological Yield per plant (g)	1.56*	26.00
17.	Seed Yield per plant (g)	0.36	6.00
18.	Harvest Index	1.80	30.00
19.	100 Seed Weight (g)	13.85	229.00
20.	Crude Protein content of seed (%)	18.06**	301.00
21.	Beta Glucan content (%)	31.68**	528.00

*minimum values; **maximum values

Table 9: Contribution of individual characters toward divergence among 58 seed purpose related genotypes of oat.

Sr. No.	Source	Contribution %	Times Ranked 1st
1.	Days to 50% flowering	16.56	276.00
2.	Plant height (cm)	2.88	48.00
3.	Days to 75% maturity	3.84	64.00
4.	Biological Yield per plant (g)	4.56	76.00
5.	Seed Yield per plant (g)	1.86	31.00
6.	Harvest Index (%)	0.84*	14.00
7.	100 Seed Weight (g)	15.36	256.00
8.	Crude Protein % (Seed)	21.48**	358.00
9.	Beta Glucan content (%)	31.80**	530.00

*minimum values; **maximum values

CONCLUSION

Overall it can be concluded that D^2-statistic helped in grouping different genotypes into 12 clusters in case of dual purpose traits while in case of seed yield related traits genotypes were grouped into 11 clusters. Cluster I contain maximum genotypes followed by cluster II. Inter and intra-cluster distances clearly indicated that there is a wide genetic diversity in the population under study. The highest inter-cluster distance was found between Cluster IX and cluster V among dual purpose related traits while among seed yield related traits it was observed between cluster IV and III. Overall, genotypes IG-03-205, EC-528883 and OS-6 were found to be more diverse. On the basis of high inter-cluster values, hybridization between genotypes EC-528883 and JPO-28; IG-03-205 and JPO-46; EC-528865 and JPO-38 can be performed in order to exploit heterosis and genotypes in these clusters can be used as parents in future hybridization programmes. Mut *et al.*, (2015) also grouped 100 genotypes into seven clusters each of which had 17, 21, 13, 12, 20, 12 and 5 genotypes. Also Poonia and Phogat (2017) used the Mahalanobis D^2 statistics for studying the genetic divergence and divided 92 oat genotypes into nine clusters indicating the presence of substantial genetic diversity in the evaluated germplasm.

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Conflict of Interest. None.

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