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Assessing Genetic Diversity in Dual Purpose Oat (*Avena sativa* L.) Cultivars Based on Morphological and Quality Traits

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A B S T R A C T

The present study was undertaken to assess the genetic diversity present in the ninety six oat (*Avena sativa* L.) germplasm lines representing the collection from various eco-geographical regions of the country. On the basis of mean performance of the genotypes for fodder traits; OL 10 for plant height (60.09cm), OL 1636 for leaf length (53.55cm) and JO 03-95 for leaf width (1.86 cm), OS 7 for GFY (3.38kg/plot) and JHO-2001-1 for DMY (0.61 kg/plot) were found to be superior. Similarly, on basis of mean performance of the genotypes for grain traits; OS 7 for beta-glucan (4.35%), JHO-2009-1 for grain length (15 mm), OL 1542, OL 1611, OL 1615, OL 1636, OL 1635, JHO 851, EC 605839, EC 605833, EC 209750, EC 209472, EC 209408, SKO 315, SKO 312, and RO-2001-1 for grain width (3.3 mm) and UPO-093 for grain yield (426.91 g/plot) were found to be superior. Genetic divergence among 96 accessions was worked out for fodder and grain traits and then for dual purpose to generate dendrogram based on complete linkage and squared euclidean distance. All the 96 accessions were grouped into 6 clusters. Maximum inter cluster distance for fodder, grain and dual purpose was recorded between clusters VI and III (9.99), clusters I and VI (9.06), clusters IV and V (11.24) respectively, suggesting significant high genetic diversity between genotypes of these clusters. According to criteria followed by *Proceedings of AICRP* (FCU 2015), the 14 best dual purpose genotypes evaluated are: UPO 093, OL 1611, JHO-2001-1, HJ 114, JHO 851, OL 1635, OS 329, SKO 27, HJ 8, OS 363, OL 1714, OS 376, EC 605833 and JHO-2009-1.

Introduction

Oat is regarded as most important cereal crop throughout the world and used as an important source of essential nutrients for human consumption (Boczkoswka and Tarczyk, 2013). Oat (*Avena sativa* L.) is a highly important and economic crop and in world, it ranks sixth in cereal production after wheat, rice, maize, barley and sorghum (FAO, 2012).

The genus *Avena* belongs to the Poaceae family. 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. For oats to classify as a dual purpose crop, it should have high green fodder and grain yield harvested from the same crop where the first cut is taken for fodder and subsequently the crop is harvested at the time of grain maturity.

Increased oat consumption is often enhanced due to nutritional attributes including antioxidants and high soluble fiber (Rasane *et al.*, 2015). Oats is good source of antioxidants like avenanthramides, alpha- tocopherol, alpha-tocotrienol and also total dietary fiber including beta-glucans (Oliver *et al.*, 2010). Latest research have analyzed the oat consumption effects on health and benefits on health are beyond reducing cardio vascular risk like diabetes, controls blood-pressure levels, lowers blood cholesterol concentrations, controls and maintains weight and gastro-intestinal health (Clemens, 2014).

Morphological evaluation of a germplasm collection is useful to describe its genetic diversity and to identify agronomically significant variation. Such an assessment involves characterization of variations for various morphological traits.

Before embarking on a breeding programme, assessment of germplasm collection for key agronomic traits, seed quality and defensive traits, flowering, maturity, plant height, protein content, oil content, primary branches, number of capsules, resistances to pests and diseases, drought and cold tolerances and other worthwhile traits is important (Krull and Berlaug, 1970).

Morphological traits are associated with a relatively small number of loci, thus the potential difference could be lost in the analysis of large amounts of molecular data (Diederichsen, 2009).

Materials and Methods

Plant material

The experimental material consists of 96 genotypes from diverse eco-geographic regions of the country maintained at the experimental area of Forage Research Farm, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. The names and origin of the plant material used in the present investigation has been given in Table 1. Ninety-six *Avena sativa* accessions were morphologically analysed by Augmented Design. Each entry was accommodated in two rows of 2m length and three checks viz., OL 125 (zonal check), OL-10 (state check) and Kent (national check) were repeated randomly among each block to obtain an estimate of the error. To raise the healthy crop, recommended agronomic practices were followed. Oat germplasm lines were analysed during *Rabi* 2014-15 for various morpho- agronomic traits.

Morphological analysis

Data on five randomly tagged plants of each entry per genotype was recorded. Data for some of the morpho-agronomic traits viz; days to flowering, days to maturity, green fodder yield, dry matter yield, stover yield were taken on the plot basis and rest of the data for other characters were recorded from tagged plants only. A total of 34 morphological traits viz., PH 1-Plant Height in first cut, NOL/plant -No. of Leaves per Plant, LL 1-Leaf Length in first cut, LW 1-Leaf Width in first cut, NOT-No. of Tillers per Plant, SG 1-Stem Girth in first cut, GFY (kg/plot)-Green Fodder Yield, DMY (kg/plot)-Dry Matter Yield, RG %-Regeneration Percentage, LSR-Leaf Stem Ratio, DF-Days to Flowering, DM-Days to Maturity, LAI-Leaf Area Index, ADF %-Acid Detergent Fibre (%), NDF%-Neutral Detergent Fibre (%), IVDMD%-In-Vitro Dry Matter Digestibility Percentage, CP%-Crude

Protein, β- G%- beta-glucan, PL-Panicle Length, GL-Grain Length, GW-Grain Width, 1000 GW-Thousand Grain Weight, SY-Stover Yield, GY-Grain Yield, NOET per meter row-No. of Effective Tillers per Meter Row Length, SNPP-Spikelet No. per Panicle, FNPP-Floret No. per Panicle, GNPP-Grain No. per Panicle, PH 2-Plant Height in second cut, FLL-Flag Leaf Length, FLW-Flag Leaf Width, LL2-Leaf Length in second cut, LW 2-Leaf Width in second cut, SG 2-Stem Girth in second cut.

Results and Discussion

Analysis of variance (ANOVA)

The analysis was carried out using the software SPAD (Rahore *et al.,* 2004). Data with respect to check varieties were subjected to analysis of variance as per Augmented design (Federer, 1956) to obtain adjusted trait values for 3 checks as well as for 93 test genotypes.

Analysis of genetic divergence

The analysis of genetic divergence was done by using Minitab software (Barbara 1972). Cluster analysis is a multivariate technique which aims to classify a sample on basis of a set of measured variables into a number of different groups such that similar subjects are placed in same group. It provides a way for scientists to discover potential relationships and assists to construct systematic structures in large number of variables and observations. Clustering methods includes analysis of characterizing data on genotypes from which the core collection is to be selected (Hintum and Knupffer, 1995).

The analyses of variances (Table 2) were carried out using data recorded for morpho-agronomic traits on three check varieties and 93 test genotypes sown in augmented block design for dual purpose during *Rabi* 2014-15. The mean square for blocks (adjusted) were significant for ADF% for fodder and 1000 GW, GY, NOET per meter row, FLL, FLW, GNPP, FNPP for grain related traits indicating the low heterogeneity among the blocks. The mean square for treatments (Adjusted) were found significant for PH 1, LL 1, LW 1, GFY, DMY, RG%, DM, DF, LAI, ADF, CP for fodder and beta glucan, PL, GL, GY, SY, 1000 GW, SNPP, FLL, FLW, SG, LL 2 indicating that the significant differences were present between the genotypes for these traits. Contrast analysis was computed to examine the experimental material in terms of variation present among the checks (controls), among the test genotypes (treatments) and test genotypes *vs* checks. The mean square for PH 1 (cm), GFY (kg/plot), DMY (kg/plot), DF was significant among checks for fodder traits and beta glucan, GY, SNPP for grain traits, revealing that the significant differences were present between the three checks. Among the test genotypes most of the traits viz; PH 1 (cm), LW 1 (cm), RG%, DF, DM, LAI, ADF%, CP% for fodder and 1000GW, SY, NOET per meter row for grain traits showed significant mean square values, indicating differences among the test genotypes for these traits. PH 1 (cm), LW 1 (cm), GFY (kg/plot), DMY (kg/plot), LSR, DF, DM, LAI and CP% for fodder and beta glucan, PL, 1000GW, GY, SNPP, FLL, FLW, LW 2 and SG 2 for grain showed significant mean square suggesting significant differences for test genotypes *vs* controls for these traits.

Distribution of accessions into different clusters

Genetic divergence among 96 accessions (93 test genotypes and 3 checks) of oats was worked out for fodder and grain traits and then for dual data, to generate dendrogram based on complete linkage, Squared Euclidean Distance (Fig. 1–3).

Fig.1 Dendrogram for fodder traits

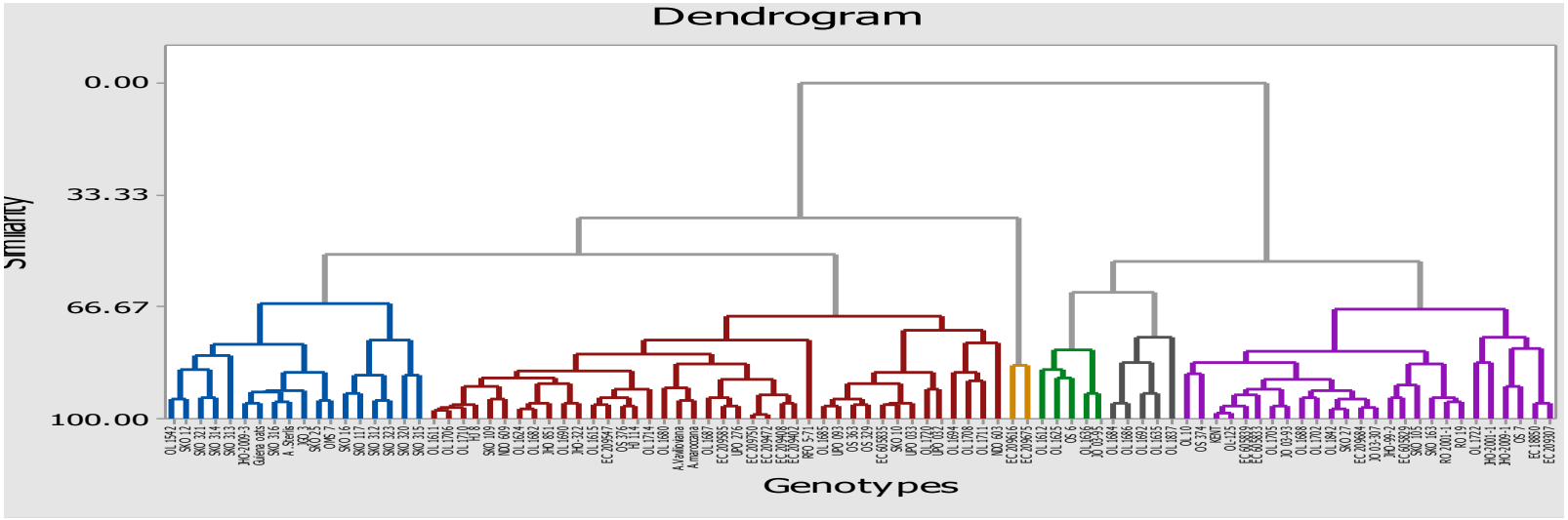

Fig.2 Dendrogram for grain traits

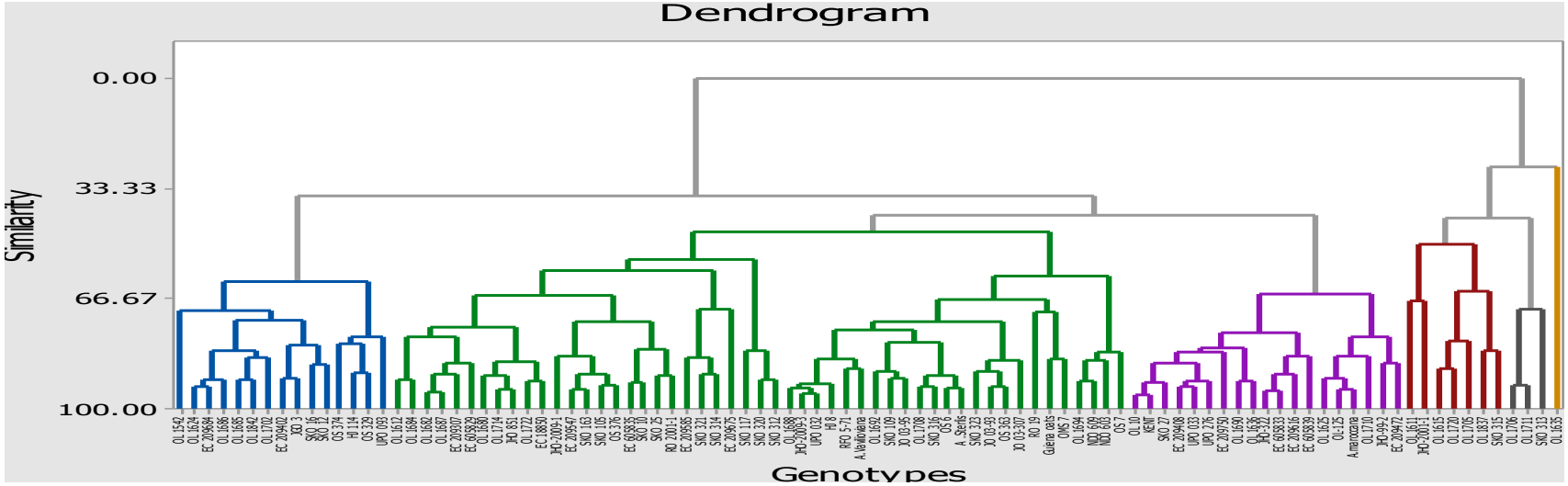

Fig.3 Dendrogram for dual purpose

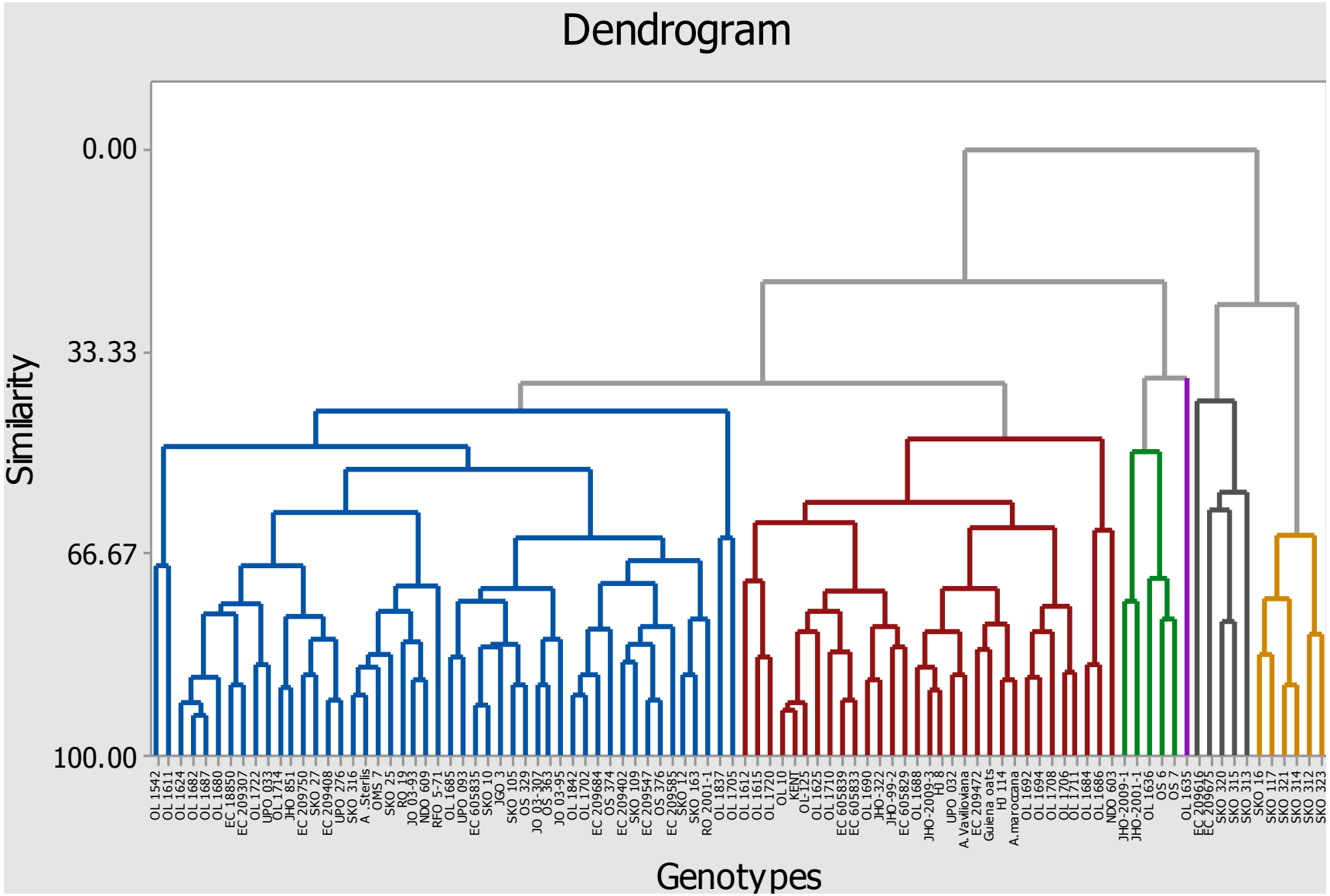

Table.1 List of source germplasm evaluated in present study

S. No.	Genotype	Origin	S. No.	Genotype	Origin	S. No.	Genotype	Origin	S. No.	Genotype	Origin
1	OL 1542	Ludhiana	25	OL 1710	Ludhiana	49	EC 605835	Exotic collection	73	RO 19	Rahori
2	OL 1611	Ludhiana	26	OL 1711	Ludhiana	50	EC 18850	Exotic collection	74	RFO 5-71	Rahori
3	OL 1612	Ludhiana	27	OL 1714	Ludhiana	51	EC 209684	Exotic collection	75	JO 03-93	Jabalpur
4	OL 10	Ludhiana	28	OL 1720	Ludhiana	52	EC 209307	Exotic collection	76	JO 03-307	Jabalpur
5	OL 1615	Ludhiana	29	OL 1722	Ludhiana	53	EC 209675	Exotic collection	77	JO 03-95	Jabalpur
6	OL 1624	Ludhiana	30	JHO-2009-1	Jhansi	54	EC 209547	Exotic collection	78	OS 376	Hisar
7	OL 1625	Ludhiana	31	JHO-2001-1	Jhansi	55	SKO 109	J&K	79	OS 6	Hisar
8	Kent	Ludhiana	32	JHO-99-2	Jhansi	56	SKO 10	J&K	80	OS 363	Hisar
9	OL 1680	Ludhiana	33	JHO-322	Jhansi	57	SKO 105	J&K	81	OS 7	Hisar
10	OL 1682	Ludhiana	34	JHO-2009-3	Jhansi	58	SKO 16	J&K	82	UPO 032	Pantnagar
11	OL 1684	Ludhiana	35	OL 1636	Ludhiana	59	SKO 117	J&K	83	UPO 276	Pantnagar
12	OL 1685	Ludhiana	36	OL 1635	Ludhiana	60	SKO 12	J&K	84	UPO 033	Pantnagar
13	OL 1606	Ludhiana	37	JHO 851	Jhansi	61	SKO 321	J&K	85	UPO 093	Pantnagar
14	OL 1687	Ludhiana	38	EC 605839	Exotic collection	62	SKO 314	J&K	86	HJ 8	Hisar
15	OL 1688	Ludhiana	39	EC 605833	Exotic collection	63	SKO 320	J&K	87	HJ 114	Hisar
16	OL 1690	Ludhiana	40	OL-125	Ludhiana	64	SKO 315	J&K	88	NDO 603	Faizabad
17	OL 1692	Ludhiana	41	EC 605829	Exotic collection	65	SKO 313	J&K	89	NDO 609	Faizabad
18	OL 1694	Ludhiana	42	EC 209750	Exotic collection	66	SKO 312	J&K	90	OS 329	Hisar
19	OL 1837	Ludhiana	43	EC 209472	Exotic collection	67	SKO 316	J&K	91	*A. vavilioviana*	Wild
20	OL 1842	Ludhiana	44	EC 209616	Exotic collection	68	SKO 323	J&K	92	*A. maroccana*	Wild
21	OL 1702	Ludhiana	45	EC 209408	Exotic collection	69	SKO 27	J&K	93	*A. sterlis*	Wild
22	OL 1705	Ludhiana	46	EC 209402	Exotic collection	70	SKO 163	J&K	94	*Guinea oats*	Wild
23	OL 1706	Ludhiana	47	OS 374	Hisar	71	SKO 25	J&K	95	OMS 7	Hisar
24	OL 1708	Ludhiana	48	EC 209585	Exotic collection	72	RO 2001-1	Rahori	96	JGO 3	Jabalpur

Table.2 Analysis of variance (ANOVA) for the morpho-agronomic traits in oats

For Fodder

Source	d.f.	PH 1 (cm)	NOL/plant	LL 1(cm)	LW 1(cm)	NOT	SG 1 (mm)	GFY(kg/plot)	DMY(kg/plot)	RG%
Block (Adj.)	10	3.85 (0.5830)	131.29 (0.457006)	1.53 (0.999529)	0.01 (0.361819)	6.48 (0.457006)	0.26 (0.862048)	0.05 (0.718466)	0.005 (0.345153)	48.03 (0.103707)
Treatments (Adj.)	95	26.92 (0.000018)**	207.54 (0.108101)	40.94 (0.004459)**	0.02 (0.007778)**	10.25 (0.108101)	7.63 (0.143081)	0.16 (0.039158)*	0.008 (0.030309)*	74.42 (0.003663)*
Error	20	4.48	127.93	14.21	0.008	6.32	0.50	0.084	0.004	25.07
Contrast Analysis										
(i) Among control	2	225.86 (0.000010)**	329.52 (0.101076)	41.98 (0.075115)	0.01 (0.179735)	16.27 (0.101076)	0.61 (0.315170)	0.35 (0.031226)*	0.02 (0.013130)*	15.90 (0.540568)
(ii) Among test genotypes	92	9.33 (0.031982)*	205.72 (0.112719)	38.36 (0.006845)	0.01 (0.023351)*	10.16 (0.112719)	0.74 (0.157136)	0.12 (0.156725)	0.006 (0.119525)	75.45 (0.003377)**
(iii) Test-*vs* control	1	1283.99 (0.000010)**	121.48 (0.341461)	279.43 (0.000255)	0.39 (0.000010)**	5.99 (0.341461)	2.69 (0.031169)	3.89 (0.000010)**	0.18 (0.000010)**	76.45 (0.096130)

Source	d.f.	LSR	DF	DM	LAI	ADF%	NDF%	IVDMD%	CP%
Block (Adj.)	10	0.01 (0.091557)	13.42 (0.562430)	19.74 (0.452105)	3.19 (0.352500)	39.82 (0.000550)**	43.98 (0.709081)	3.97 (0.4631)	0.33 (0.867649)
Treatments (Adj.)	95	0.01 (0.612544)	37.48 (0.011797)*	37.89 (0.040851)*	10.86 (0.000409)**	15.80 (0.022389)*	46.77 (0.822612)	1.79 (0.972121)	1.62 (0.012715)*
Error	20	0.01	15.18	19.10	2.68	7.13	62.32	3.75	0.664936
Contrast Analysis									
(i) Among control	2	0.01 (0.491179)	78.56 (0.015431)*	15.64 (0.455318)	0.21 (0.921790)	4.10 (0.571664)	8.34 (0.875475)	0.29 (0.783601)	1.96 (0.075094)
(ii) Among test genotypes	92	0.01 (0.706931)	35.99 (0.015155)*	37.59 (0.042858)*	8.54 (0.002315)**	16.22 (0.019465)*	47.58 (0.807760)	1.82 (0.969016)	1.60 (0.013833)*
(iii) Test vs control	1	0.046 (0.008258)**	95.50 (0.020852)*	113.35 (0.024329)*	255.27 (0.000010)**	0.33 (0.831756)	52.43 (0.369965)	0.45 (0.736104)	2.94 (0.048121)*

For Grain

Source	df	β- G%	PL	GL	GW	1000 GW	SY	GY	NOET/m Row	SNPP
Block (Adj.)	10	0.09 (0.067344)	1603.80 (0.544656)	0.002 (0.398929)	0.01 (0.942286)	35.88 (0.019526)*	0.08 (0.278879)	2600.73 (0.005329)**	620.56 (0.025712)*	8797.28 (0.546932)
Treatments (Adj.)	95	0.13 (0.002694)**	6366.74 (0.000958)**	0.005 (0.012889)*	0.01 (0.862295)	45.66 (0.000745)**	0.14 (0.017202)*	5694.22 (0.000010)**	167.71 (0.828459)	56227.46 (0.000025)**
Error	20	0.04	1767.72	0.002	0.01	12.25	0.06	684.08	225.16	9727.87
Contrast Analysis										
(i)Among control	2	0.59 (0.000170)**	1699.49 (0.399336)	0.002 (0.339969)	0.01 (0.690446)	16.90 (0.274409)	0.01 (0.852351)	7441.55 (0.000635)**	194.03 (0.437529)	8622.04 (0.427748)
(ii) Among test genotypes	92	0.12 (0.005129)**	5695.39 (0.002124)**	0.005 (0.012395)*	0.01 (0.847481)	43.76 (0.001027)**	0.14 (0.014734)*	5246.77 (0.000010)**	168.91 (0.821943)	50403.66 (0.000061)**
(iii) Test-*vs* control	1	0.38 (0.007355)**	79943.36 (0.000010)**	0.007 (0.089089)	0.01 (0.857798)	265.98 (0.000151)**	0.03 (0.513141)	46711.55 (0.000010)**`	1.52 (0.935253)	707440.72 (0.000010)**

Source	df	FNPP	GNPP	PH	FLL	FLW	LL	LW	SG
Block(Adj.)	10	2482.25 (0.025712)*	2482.25 (0.025712)*	90.29 (0.290880)	39874.80 (0.019527)*	70890.46 (0.019519)*	13.95 (0.612605)	0.02 (0.896346)	1.27 (0.428152)
Treatments (Adj.)	95	949.91 (0.470122)	949.91 (0.470122)	78.83 (0.382095)	50743.02 (0.000745)**	90208.87 (0.000745)**	29.13 (0.083577)	0.07 (0.045886)*	1.13 (0.589938)
Error	20	900.65	900.65	68.98	13608.79	24191.83	16.97	0.04	1.19
Contrast Analysis									
(i) Among control	2	776.12 (0.437529)	776.13 (0.437529)	119.09 (0.203410)	18787.88 (0.274385)	33404.70 (0.274323)	32.19 (0.175978)	0.01 (0.896079)	0.75 (0.539710)
(ii) Among test genotypes	92	963.27 (0.454313)	963.27 (0.454313)	77.77 (0.396640)	48622.82 (0.001027)**	86439.48 (0.001027)**	29.36 (0.080961)	0.07 (0.046239)*	1.01 (0.705962)
(iii) Test-*vs* control	1	34.79 (0.846172)	34.79 (0.846172)	105.46 (0.230614)	295471.04 (0.000151)**	525286.81 (0.000151)**	2.17 (0.724118)	0.19 (0.034825)*	12.59 (0.003991)**

(*P<=0.05; **P<=0.01 Figures in parentheses indicate the P value)

Table.3 Clustering pattern obtained by analysis for fodder traits

Cluster	No. of genotypes	Genotypes
I	18	OL 1542, JHO-2009-3, SKO 16, SKO 117, SKO 12, SKO 321, SKO 314, SKO 320, SKO 315, SKO 313, SKO 312, SKO 316, SKO 323, SKO 25, *A. sterlis*, *Guinea oats*, OMS 7, JGO
II	40	OL 1611, OL 1615, OL 1624, OL 1680, OL 1682, OL 1685, OL 1687, OL 1690, OL 1694, OL 1706, OL 1708, OL 1710, OL 1711, OL 1714, OL 1720, JHO-322, JHO 851, EC 209750, EC 209472, EC 209408, EC 209402, EC 209585, EC 605835, EC 209547, SKO 109, SKO 10, RFO 5-71, OS 376, OS 363, UPO 032, UPO 276, UPO 033, UPO 093, HJ 8, HJ 114, NDO 603, NDO 609, OS 329, *A. vavilioviana*, *A. maroccana*,
III	5	OL 1612, OL 1625, OL 1636, JO 03-95, OS 6
IV	26	OL 10, Kent, OL 1688, OL 1842, OL 1702, OL 1705, OL 1722, JHO-2009-1, JHO-2001-1, JHO-99-2, EC 605839, EC 605833, OL 125, EC 605829, OS 374, EC 18850, EC 209684, EC 209307, SKO 105, SKO 27, SKO 163, RO 2001-1, RO 19, JO 03-93, JO 03-307, OS 7,
V	5	OL 1684, OL 1686, OL 1692, OL 1635, OL 1837
VI	2	EC 209616, EC 209675

Table.4 Clustering pattern obtained by analysis for grain traits

Cluster	No. of genotypes	Genotypes
I	15	OL 1542, OL 1624, EC 209684, OL 1686, OL 1685, OL 1842, OL 1702, EC 209402, JGO 3, SKO 16, SKO 12, OS 374, HJ 114, OS 329, UPO 093
II	7	OL 1611, JHO 2001-1, OL 1615, OL 1720, OL 1705, OL 1837, SKO 315
III	51	OL 1612, OL 1684, OL 1682, OL 1687, EC 209307, EC 605829, OL 1680, OL 1714, JHO 851, OL 1722, EC 18850, JHO 2009-1, EC 209547, SKO 163, SKO 105, OS 376, EC 605836, SKO 10, SKO 25, RO 2001-1, EC 209585, SKO 321, SKO 314, EC 209675, SKO 117, SKO 320, SKO 312, OL 1688, JHO 2009-3, UPO 032, HJ 8, RFO 5-71, *A. vavilioviana*, OL 1692, SKO 109, JO 03-95, OL 1708, SKO 316, OS 6, *A. sterlis*, SKO 323, JO 03-93, OS 363, JO 03-307, RO 19, *Guinea oats*, OMS 7, OL 1694, NDO 609, NDO 603, OS 7
IV	19	OL 10, Kent, SKO 27, EC 209403, UPO 033, UPO 276, EC 209750, OL 1690, OL 1636, JHO 322, EC 605833, EC 209616, EC 605839, OL 1625, OL 125, *A. maroccana*, OL 1710, JHO 99-2, EC 209472
V	3	OL 1705, OL 1711, SKO 313
VI	1	OL 1635

Table.5 Clustering pattern obtained for dual purpose

Cluster	No. of genotypes	Genotypes
I	48	OL 1542, OL 1611, OL 1624, OL 1682, OL 1687, OL 1680, EC 18850, EC 209307, OL 1722, UPO 033, OL 1714, JHO 851, EC 209750, SKO 27, EC 209750, EC 209408, UPO 276, SKO 316, *A. sterlis*, OMS 7, SKO 25, RO 19, JO 03-93, NDO 609, RFO 5-71, OL 1685, UPO 093, EC 605835, SKO 10, JGO 3, SKO 105, OS 329, JO 03-307, OS 363, JO 03-95, OL 1842, OL 1702, EC 209684, OS 374, EC 209547, OS 376, EC 209585, SKO 12, SKO 163, RO 2001-1, OL 1837, OL 1705
II	31	OL 1612, OL 10, OL 1615, OL 1625, Kent, OL 1684, OL 1686, OL 1688, OL 1690, OL 1692, OL 1694, OL 1706, OL 1708, OL 1710, OL 1711, OL 1720, JHO-99-2, JHO-322, JHO-2009-3, EC 605839, EC 605833, OL 125, EC 605829, EC 209472, UPO 032, HJ 8, HJ 114, NDO 603, *A. vavilioviana*, *A. maroccana*, *Guinea oats*
III	5	JHO 2009-1, JHO 2001-1, OL 1636, OS 6, OS 7
IV	1	OL 1635
V	5	EC 209616, EC 209675, SKO 320, SKO 315, SKO 313
VI	6	SKO 16, SKO 117, SKO 321, SKO 314, SKO 312, SKO 323

Table.6 Average inter-cluster distances in 96 oat accessions for fodder

Cluster	I	II	III	IV	V	VI
I	0.00	3.33	5.67	4.41	5.87	6.78
II		0.00	4.16	2.31	3.66	7.67
III			0.00	3.66	4.31	9.99
IV				0.00	3.95	9.43
V					0.00	9.61
VI						0.00

Table.7 Average inter-cluster distances in 96 oat accessions for grain

Cluster	I	II	III	IV	V	VI
I	0.00	4.86	2.78	3.90	6.22	9.06
II		0.00	3.98	3.89	4.81	6.93
III			0.00	2.80	4.21	8.02
IV				0.00	4.68	7.13
V					0.00	8.19
VI						0.00

Table.8 Average inter-cluster distances in 96 oat accessions for dual purpose

Cluster	I	II	III	IV	V	VI
I	0.00	2.59	4.51	9.37	7.45	5.46
II		0.00	4.77	8.37	7.30	5.91
III			0.00	9.01	10.18	8.75
IV				0.00	11.24	11.11
V					0.00	5.88
VI						0.00

All the 96 accessions were grouped into six clusters. The critical examination of clusters indicated the presence of high level of genetic diversity in the germplasm collection. The clustering pattern of accessions in each of the six clusters is presented in Table 3, 4 and 5.

Large number of genotypes in a single cluster depicts that these genotypes are more closely related and had less genetic variation among them. It further implies that hybridization programme employing these genotypes inhabiting a common cluster will be of little use programme and diverse clusters are beneficial for hybridization programme in oat improvement.

Identification of diverse and desirable accessions

In addition to grouping of accessions to different clusters, hierarchical clustering based on squared Euclidean distance was also used to identify the diverse and desirable accessions in terms of inter cluster distance.

The inter-cluster distances were larger than the intra-cluster distances indicating wider genetic diversity between genotypes of the clusters with respect to the traits considered. Therefore, combinations with high heterotic response and superior recombinants may be obtained through hybridizations between genotypes across the

clusters (Murty and Arunachalam, 1996). Low levels of intra-cluster distances were pinpointing of narrow genetic variation within a cluster (Table 6–8).

According to criteria followed by *Proceedings of AICRP* (FCU, 2015) a dual purpose crop should have higher green fodder yield than best check and seed yield should not be less than 10% of best check. Following this criteria, the best check is OL 10. The 70 genotypes having higher fodder yield than best check (OL 10) are OS 7, JHO-2001-1, OS 6, OL 1636, OL 1722, JHO-2009-1, SKO 10, JO 03-95, UPO 033, OL 1612, JO 03-307, JHO-322, EC 209684, SKO 27, JHO-99-2, OL 1635, EC 209307, UPO 093, JO 03-93, OS 329, OL 1625, OMS 7, OL 1624, OL 1611, OL 1692, OL 1686, SKO 314, OL 1688, OL 1705, OL 1720, EC 605835, RFO 5-71, OL 1702, JHO-2009-3, OL 1690, JHO 851, OL 1615, OL 1684, OL 1687, OL 1706, JGO 3, OL 1685, EC 18850, OL 1842, *A. vavilioviana*, EC 605829, OL 1714, OL 1694, OS 363, EC 605833, SKO 320, SKO 105, NDO 609, OL 1682, UPO 032, OL 1837, OL 1680, EC 605839, RO 19, HJ 114, SKO 16, HJ 8, SKO 316, SKO 109, EC 209585, UPO 276, EC 209547, OS 376, SKO 163, RO 2001-1 and these are the best 20 genotypes for grain yield are UPO 093, OL 1611, JHO-2001-1, HJ 114, OS 374, OL 1542, *A. maroccana*, JHO 851, OL 1635, OS 329, SKO 27, HJ 8, OS 363, EC 209408, EC 209402, OL 1714, OL 1685, OS 376, EC 605833, JHO-2009-1.

A total of 14 genotypes viz; UPO 093, OL 1611, JHO-2001-1, HJ 114, JHO 851, OL 1635, OS 329, SKO 27, HJ 8, OS 363, OL 1714, OS 376, EC 605833, JHO-2009-1 were adjudged superior after evaluating the accessions by following this criterion.

Some of these genotypes fell in different clusters and some lied in same the clusters for fodder, grain and dual purpose. For fodder, OL 1611, JHO 851, OS 363, UPO 093, HJ 8, HJ (114, OS 329 fell in cluster II, implies that they have less genetic differences. Similarly, JHO-2009-1, JHO-2001-1, EC 605833, SKO 27 fell in cluster IV and OL 1635 in cluster V. It implies that genotypes in cluster II, IV and V have genetic differences. The best check OL 10 fell in cluster IV. Similarly, for grain purpose HJ 114, OS 329, UPO 093 lied in cluster I, HJ 114, OS 329, UPO 093 fell in cluster II, OL 1714, JHO 851, JHO 2009-1, OS 376, HJ 8, OS 363 fell in cluster III, SKO 27, EC 605833 in cluster IV and OL 1635 in cluster VI. The best check OL 10 lies in cluster IV. For dual purpose, OL 1611, OL 1714, JHO 851, SKO 27, UPO 093, OS 329, OS 363, OS 376 fell in cluster I, EC 605833, HJ 8, HJ 114 fell in cluster II, JHO 2009-1, JHO 2001-1 in cluster III and OL 1635 in cluster IV and OL 10 fell in cluster II. As beta-glucan is very important quality trait, these are the 11 genotypes having higher beta-glucan content than best check (OL 10): OS 7, NDO 603, NDO 609, OS 374, HJ 114, OS 6, OL 1611, OL 1636, OL 1706, RO 19, OS 329, HJ 114 and OS 29 were also evaluated as best dual purpose lines.

Agronomic traits and morphological analysis has been repeatedly used when characterizing large data sets of Avena taxa in gene banks (Diederichsen, 2008, 2009), or smaller sets of oat species, cultivars and landraces (Souza and Sorrells 1991; Sheikhehpour *et al.,* 2014; Boczkowska *et al.,* 2014). As a result, morphological description has become a valuable source of information for breeding and agronomic research programs (Boczkowska *et al.,* 2014). Even though morphological traits are generally employed in order to estimate genetic variation since their measurements are not laborious, still, diversity estimation based on morphology alone has limitations. Unfortunately, traits are heavily influenced by the environment, are limited in number and possibly unintentional selection for traits with agronomical value (Nikoloudakis *et al.,* 2016).

So convincingly in the present study, lot of variation has been observed for most of the traits under consideration; therefore, many of these accessions may be included in a core group constituted for association mapping of important traits for dual oat improvement.

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