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ACCESSING GENETIC DIVERSITY IN OATS BASED ON MORPHO-AGRONOMIC TRAITS

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SUMMARY

The present study was undertaken to assess the genetic diversity present in the 96 oat (*Avena sativa* L.) germplasm lines representing the collection from various eco-geographical regions of the country. Genetic divergence among 96 accessions was worked out for various morpho-agronomic traits to generate dendrogram based on squared euclidean distance. Maximum inter cluster-distance was recorded between clusters I and VI (9.06) suggesting significant high genetic diversity among genotypes of these clusters. The best 20 genotypes identified on the basis of 10 per cent higher grain yield than the best check OL 10 were 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 and JHO-2009-1.

Key words : Genetic divergence, cluster, oat, germplasm

Oat is a western Mediterranean cereal crop with a moderately agricultural history, since its cultivation had started. Oat is a winter forage crop which is grown worldwide. It is also used as multipurpose crop for grain, pasture and forage. Oats' taxonomic patterns are similar to that of wheat and consists of a polyploid series with seven basic (x=7) chromosomes number, *i.e*. diploid, tetraploid and hexaploid. The genomic constitution of common culivated oat (*A. sativa*) is AACCDD. The genus *Avena* belongs to the Poaceae family. Recently, with the advancement of enlarged dairy industries in India, the oats have enchanted the breeder's attention for its modernization due to its quality fodder with high nutritional quality and grains yield with more net energy gains (Ruwali *et al* 2013).In recent years, oat grain was mainly used as a livestock feed (Nikoloudakis 2016). Oats 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). Oats (*A. 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). . 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.

MATERIALS AND METHODS

The experimental material consists of 96 genotypes of oats collected from diverse eco-geographic regions of the country and maintained at the experimental area of Forage Research Farm, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. These genotypes were analysed in Augmented design where each entry was accommodated in two rows of 2 m length with row to row spacing of 50 cm 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. A total of seventeen morphological traits viz; ?-G% - beta-glucan, PL-Panicle Length, GL-Grain Length, GW-Grain Width, 1000 GW-Thousand Grain Weight, SY-Stover Yield, GY-Grain Yield, NOET- Number of Effective Tillers per meter row length, SNPP-Spikelet Number per Panicle, FNPP- Floret Number per Panicle, GNPP- Grain Number per Panicle, PH - Plant Height, FLL- Flag Leaf Length, FLW-Flag Leaf Width, LL -Leaf Length, LW - Leaf Width, SG - Stem Girth had been evaluated. Statistical analysis for morpho-agronomic traits was carried out using the software SPAD (Rahore

2004) on data recorded for grain traits on three check varieties and 93 test. 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.

RESULTS AND DISCUSSION

The mean square was significant among checks for beta-glucan, GY and SNPP, revealing that the significant differences were present between the three checks (Table 1). Among the test genotypes : 1000-GW, SY, NOET per meter row showed significant mean square values, indicating differences among the test genotypes for these traits. Beta-glucan, PL, 1000 GW, GY, SNPP, FLL, FLW, LW and SG showed significant mean squares suggesting significant differences for test genotypes *vs* controls for these traits.

Analysis of genetic divergence was done by using Minitab software (Barbara *et al.,* 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. The dendrogram representing the genetic diversity among 96 genotypes is presented in Fig. 1. It reflects potential relationship among the genotypes studied.

The cluster III consisting of 51 genotypes was the largest amongst all and was followed by cluster IV with 19 genotypes. Cluster VI was the smallest one consisting of a single genotype, whereas cluster I had 15, II had 7 and V had 3 genotypes (Table 2). The check cultivars OL10, OL 125 and Kent fell in III cluster. 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 and diverse clusters are beneficial for hybridization programme in oat improvement.

The minimum inter cluster distance value (2.78) was observed between clusters III and I, whereas, maximum inter cluster distance value (9.06) was recorded between clusters I and VI indicating that genotypes in these clusters were distant to each other (Table 3). 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

TABLE 1
Statistical analysis using the software SPAD (*P<=0.05; **P<=0.01 Figures in parentheses indicate the P value)

Source	d. f.	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	d. f.	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.

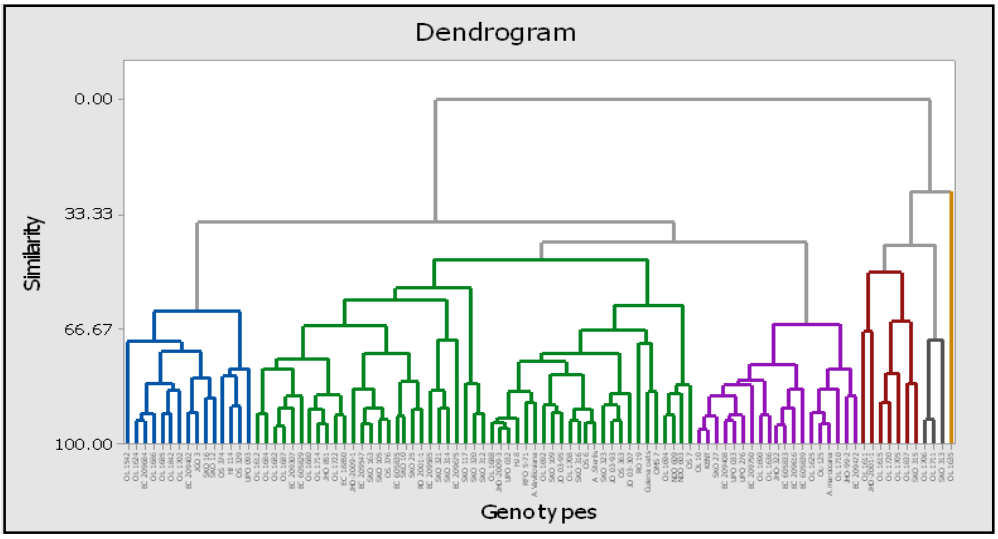

Fig. 1. Dendrogram representing genetic diversity in ninety six genotypes evaluated.

TABLE 2
Clustering pattern in 96 genotypes evaluated

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 3
Average inter-cluster distances in 96 oat genotypes

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

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. If seed yield is not be less than 10% of best check(OL-10), 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 and JHO-2009-1.

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