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ASSESSMENT OF RELATIVE VARIABILITY AND ITS DISTRIBUTION PATTERN IN SOME *AVENA* SPECIES[1]

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SUMMARY

Twenty-four genotypes comprising 16 *Avena* spp. were studied for assessing variability and its distribution pattern for 12 morphological characters at Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India during **rabi** 2010-11. Duncan multiple range test reflected relative genotypic variability for each trait among 24 genotypes and distribution pattern for variability suggested six distinct groups for green fodder yield, three groups for seed yield/plant and flag leaf width; two groups each for number of leaves on main culm, tillers per plant, axis node, 100-seed weight, leaf width and height at fodder stage, five distinct groups each for dry fodder yield and spikelets/panicle. Genotype HJ 8 was found to have significant differences between all pairs of genotypes for the characters like axis node, spikelets/panicle, green fodder yield and leaf width. Similarly, genotype NGB 4462 was found to have significant differences between all pairs of genotypes for the particular characters flag leaf width and dry fodder yield.

Key words : *Avena* spp., morphological characters, variability, distribution pattern, Duncan multiple range test

Oat (*Avena sativa* L.) is a constituent of family Gramineae, ranks 6th in world cereal production. Oats both as forage and grain are good source of protein, fibres and minerals. It is used as green crop and silage for animals. Most of the oat grain worldwide is consumed as animal feed. It is principally fed to dairy cattle, horses, mules and turkeys with lesser quantities fed to hogs, beef cattle and sheep. Oat hulls, a food processing by-product, are used as an animal feed, fuel for power plants and in chemical industry. Nutrition experts believe that beta glucans, the water soluble fibres present in oat bran, inhibit cholesterol, which helps in preventing heart disease. They recommend increased daily intake of fibre, such as that in oat bran, because it assists in regulating gastrointestinal function. Several breakfast cereals and bread products are made from oat flour and rolled oat products. In India, the oats are widely grown during **rabi** season in U. P., M. P., Haryana, Punjab, H. P., Rajasthan, Bihar, Gujarat, A. P. and hilly tracts of southern plateau. It has gained importance due to its multi-cut nature with quick regeneration habit which ensures regular supply of green fodder over a long period of time. Keeping in mind the emerging importance of oats, the present study was carried out with the chief objective of estimating the relative variability and distribution pattern of variability in some *Avena* species.

MATERIALS AND METHODS

The present study was carried out at Forage Research Area, Department of Genetics & Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar, during **rabi** 2010-11. Twenty-four genotypes belonging to 16 different species of genus *Avena* obtained from NBPGR, New Delhi; IGFRI, Jhansi; and Forage Section, Department of Genetics & Plant Breeding CCS HAU., Hisar constituted the experimental material for the present investigations. Brief information regarding 24 accessions belonging to 16 *Avena* species is given in Table 1.

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TABLE 1
Brief description of 16 *Avena* species used in the present study

S. No	Species	Accession No.	Genome	Chromosome No.	Distribution characteristics
	Diploid				
1.	*Avena nuda* L.	HFO 305	A A	2n = 14	Marginally cultivated
2.	*A. strigosa* Schreb.	HFO 869/ IG 03-536-1	AsAs	2n = 14	Marginally cultivated
3.	*A. brevis*	HFO 864 / IG 03-470	AA	2n = 14	Marginally cultivated
4.	*A. longiglumis* Dur.	HFO 871/IG03-480	A|A|	2n = 14	Wild
5.	*A. prostrata*	HFO 866 / EC415008	ApAp	2n = 14	Wild
	Tetraploid				
6.	*A. abyssinica* Hochst.	HFO 868 / IG 03-456	AABB	2n = 28	Marginally cultivated
7.	*A. barbata* Pott. ex Link.	HFO 58	AABB	2n = 28	Wild
8.	*A. insularis*	HFO 865 / EC 425098	AACC	2n = 28	Wild
9.	*A. murphyii*	HFO 873 / EC 7120	AACC	2n = 28	Wild
10.	*A. maroccana*	HFO 867 / IG 03-482	AACC	2n = 28	Wild
11.	*A. vaviloviana*	HFO 870 / EC415201	AABB	2n = 28	Wild
	Hexaploid				
12.	*A. fatua* L.	HFO 504	AACCDD	2n = 42	Wild
13.	*A. sterilis* L.	HFO 872 / EC4730	AACCDD	2n = 42	Wild
14.	*A. orientalis* Schreb.	HFO 103	AACCDD	2n = 42	Marginally cultivated
15.	*A. byzantina* C. Koch	HFO 60	AACCDD	2n = 42	Cultivated
16.	*A.sativa* L.	OS 6	AACCDD	2n = 42	Cultivated, Single-cut Variety (National check)
17.	-do-	HJ 8	-do-	2n = 42	Multicut variety (local check)
18.	-do-	OS 346	-do-	2n = 42	Single Cut Variety
19.	-do-	OS 363	-do-	2n = 42	Elite Line
20.	-do-	OS 374	-do-	2n = 42	Elite Line
21.	-do-	OS 376	-do-	2n = 42	Single Cut, Variety identified for release
22.	-do-	NGB 4462	-do-	2n = 42	Elite Line (salinity tolerant)
23.	-do-	JHO 2006-2	-do-	2n = 42	Variety
24.	-do-	HFO 267	-do-	2n = 42	Elite Line

The genotypes were grown in randomized block design (RBD) with three replications, each genotype having single row of three metre length with 15 cm plant to plant distance and 45 cm row to row spacing. The experiment was planted on 14 December 2009. The observations on 11 morphological characters such as number of leaves/plant, number of tillers per plant, number of axis nodes/panicle, number of spikelets/ panicle, seed yield/plant (g), 100-seed weight (g), green fodder yield/plant (g), dry fodder yield/plant (g), flag leaf width (cm), leaf width (cm) and plant height at fodder harvest (cm) were recorded on five random and competitive plants /genotype/replication.

The data for different morphological characters were statistically analyzed on the basis of the model described by Panse and Sukhatme (1985). The mean sums of squares due to genotypes were significant for all the 11 characters studied (Table 2). This indicated the prevalence of enough genetic variability in the material under study for further statistical analysis for all the 11 characters studied.

Duncan's Multiple Range Test

In statistics, Duncan's multiple range test (MRT) is a multiple comparison procedure developed by Duncan (1955). Duncan's MRT belongs to the general class of multiple comparison procedures that use the studentized range statistic qr to compare sets of means. Duncan's new multiple range test (MRT) is a variant of the Student-Newman-Keuls method that uses increasing alpha levels to calculate the critical values in each step of the Newman-Keuls procedure. Duncan's MRT attempts to control family-wise error rate (FWE) at $\alpha_{ew}=1-(1-\alpha\acute{a}_{pc})^{k/2}$ when comparing *k*, where *k* is the number of groups. This results in higher FWE than

TABLE 2
Analysis of variance for various morphological characters in Oats

Source of variation	d. f.	No. of leaves/ plant	No. of tillers/ plant	No. of axis nodes/ panicle	100-SW (g)	No. of spikelets/ panicle	Seed yield/ plant (g)	Green fodder yield/plant (g)	Dry fodder yield/plant (g)	Flag leaf width (cm)	Leaf width (cm)	Plant height at fodder harvest (cm)
Replications	2	126.04	5.26	252.63**	0.004	130.79**	0.10	605.16	1.09	0.075**	0.01	369.67**
Genotypes	23	1949.82**	99.43**	8714.02**	5.14**	4352.53**	2.70**	46125.38**	1073.41**	1.39**	0.59**	818.94**
Error	46	80.22	4.79	84.33	0.005	40.32	0.10	418.59	10.34	0.01	0.02	38.47

unmodified Newman-Keuls procedure which has FWE of $\alpha_{ew}=1-(1-\alpha\acute{a}_{pc})^{k/2}$.

David B. Duncan developed this test as a modification of the Student-Newman-Keuls method that would have greater power. Duncan's MRT is especially protective against false negative (Type II) error at the expense of having a greater risk of making false positive (Type I) errors. Duncan's test is commonly used in agronomy and other agricultural research. This test required computation of a series of values each corresponding to a specific set of pair comprises unlike a single value for all pair wise comparisons in case of LSD. Rank was given for all the genotype means and was arranged in decreasing order based on the preference of the characters under study; the observed differences between means were tested, beginning with largest versus smallest, observed differences which were greater than the corresponding least significant range.

RESULTS AND DISCUSSION

The estimates of mean values and range in variation for 11 morphological characters are given in Table 3. The results obtained from the analysis of Duncan multiple range test are depicted in Table 4. For the character**,** number of leaves, 24 genotypes were grouped into two groups; HFO 871 (*A. longiglumis*) and HFO 873 (*A. murphyii*) were at par and differed significantly with the remaining genotypes. For the trait tillers per plant, 24 genotypes were again grouped into two groups where HFO 873 (*A. murphyii*) and HFO 869 (*A. strigosa*) were at par and differed significantly with rest of the genotypes. Twenty-four genotypes were grouped into two groups for the character axis node; here HJ 8 (*A. sativa*) differed significantly with all the other 23 genotypes. For the character 100-seed weight, 24 genotypes were grouped into two groups, OS 6 (*A. sativa*), HFO 305 (*Avena nuda*), HFO 872 (*A. sterilis*), HFO 866 (*A. prostrata*), OS 346, HFO 867 (*A. maroccana*), HJ 8 (*A. sativa*), and HFO 873 (*A. murphyii*) all were at par and significantly differed with rest of the genotypes. For the trait spikelet/panicle, 24 genotypes were grouped into 4 groups; HJ 8 differed significantly with all the genotypes, also HFO 867 (*A. maroccana*) differed significantly with all the genotypes. Genotypes NGB 4462 (*A. sativa*) and HFO 864 (*A.*

TABLE 3
Mean performance and range in variation for some morphological characters in *Avena* species

S. No.	Characters	Mean±SE	Range
1.	No. of leaves/plant	99.70±5.06	61.66-156.40
2.	No. of tillers/plant	18.7±1.23	11.33-31.93
3.	No. of axis nodes/panicle	5.37±0.22	3.53-6.66
4.	100-SW (g)	4.71±0.18	3.24-6.33
5.	No. of spikelets/panicle	105.10±5.19	15.60-249.53
6.	Seed yield/plant (g)	88.62±3.58	21.00-156.33
7.	Green fodder yield (g)	204.06±11.56	60.69-470.13
8.	Dry fodder (g)	33.36±1.81	10.66-65.33
9.	Flag leaf width (cm)	1.76±0.07	0.54-3.00
10.	Leaf width (cm)	1.82±0.09	0.96-2.68
11.	Plant height at fodder harvest stage	67.66±3.50	38.26-105.80

brevis) were at par, also HFO 305 (*Avena nuda*), HFO 872 (*A. sterilis*), HFO 873 (*A. murphyii*), HFO 865 (*A. insularis*), HFO 871(*A. longiglumis*) were at par. For seed yield per plant, three groups were formed among 24 genotypes, genotypes HFO 864 (*A. brevis*), NGB 4462 and HJ 8 (*A. sativa*) were at par, and differed significantly with others. Among 24 genotypes, for green fodder yield six groups were formed, HJ 8 (*A. sativa*) differed significantly with all the genotypes, OS 346, OS 363 (*A. sativa*) were at par, similarly NGB 4462, OS 376 and HFO 267 (*A. sativa*) are at par. For dry fodder yield, five groups were made NGB 4462 (*A. sativa*) differed significantly with rest of the genotypes. For flag leaf width, three groups were formed and again NGB 4462 (*A. sativa*) differed significantly with rest of the genotypes. For leaf width, two groups were formed among 24 genotypes and genotype HJ 8 differed significantly with others and rest 23 genotypes were at par. For the trait height at fodder stage two groups were formed. Genotypes HJ 8, OS 6 (*A. sativa*) and HFO 864 (*A. brevis*) were at par and rest all were under same bar and were at par.

Loskutov (2005) analyzed the specific diversity of 26 *Avena* species. Morphological and agronomic traits based on characterization and evaluation data in computerized data bases revised phylogenetic relationships and the pathway of specific evolution of the genus *Avena*, improved species classification and selected wild species accession with valuable characters for use in oat breeding. Ma-yanming *et al*. (2006) observed diversity of 35 oat landraces in following characters like branch number, spikelet number, ear length, plant height and growth duration. The results of cluster analysis with sum of squares for the nine traits showed that 35 oat cultivars could be divided into six groups with different characteristics, which could be used in oat breeding.

Kumar *et al*. (2006) studied the pattern of diversity in 100 germplasm lines of oat was analyzed using the principal components method of factor analysis. The genotypes HFO 604, HFO 566, HFO 305, HFO 644 and HFO 552 were the best for green fodder yield and HFO 717, HFO 244 and HFO 264 were best for seed yield. The results provided confirmatory evidence of diversity in oat. Abbas *et al.* (2008) reported that straw of oat was used as animal bedding and sometimes as animal feed. To improve yield and quality of oat, presence of sufficient genetic diversity in the germplasm is an important pre-requisite. This study provided a new trend in research that oat could be used as cultivated crop varieties and it had sufficient diversity for improvement like other major crops.

Qi-Bingjie *et al.* (2008) investigated the genetic diversity in 11 biological characters of 71 oat germplasm. The study showed abundant genetic diversity for all the biological characters. Travlos and Giannopolitis (2010)

TABLE 4
Analysis of Duncan Multilple Range Test for some moprhological traits in *Avena* species

Character	*Avena* species (Serial numbers, key given below)
No. of leaves/plant	14,16, 12,8,5,1,13,2,10,18,4,21,7,17,3,6,19,20,24,9,23,11,22,15
No. of Tillers/plant	16,12, 10,8,13, 5, 4,14,1,7,3,2,18,6,11,17,19,22,21,9,24,23,15,20
No. of Axis Node/panicle	23, 19,20,7,12,18,21,1,2,14,9,24,13,17,5,8,16,4,6,22,15,3,11,10
100-SW (g)	17, 5, 15, 9, 18, 10, 12, 23, 16, 13,20,2,19,21,14,8,6,22,3,1,4,11,7,24
No. of Spikelets/panicle	23, 24,7, 1,20,19,17,2,11,22,9,4,21,13,18,6,3,12, 5,15,16,814, 10
Seed Yield/plant (g)	7,24,23, 20,4,1,19,22,17,2,6, 11,21,9,3,18,13,12,5,15,16,8,14,10
Green Fodder Yield (g)	23, 18,19, 24,21,4, 20,16,17, 2,22,9,5 1,8,7,13,15,3,10,11,14,12,6
Dry Fodder Yield (g)	18,23,21,19,4, 24, 17,20,16, 2,22, 9,5,8,1,13,15,3,7,10,11,14,6,12
Flag Leaf Width (cm)	24, 23,19,22,18,17,15,6,2,3,9,5,1,21,20,4, 16,11,8,13,12,7,10,14
Leaf Width (cm)	23, 24,18,9,6,17,15,19,22,1,2,21,20,3,4,5,8,16,7,10,12,11,13,14
Plant height at fodder harvest stage	23,17,7, 19,3,20,1,14,2,2,18,6,15,13,21,12,5,11,9,8,16,4,10,22,24

S. No. and Key for the genotypes

1. HFO 58 (*A. barbata*), 2. HFO 60 (*A. byzantina*), 3. HFO 103 (*A. orientalis*), 4. HFO 267 (*A.sativa*), 5. HFO 305 (*Avena nuda*), 6. HFO 504 (*A. fatua*), 7. HFO 864 (*A. brevis*), 8. HFO 865 (*A. insularis*), 9. HFO 866 (*A. prostrata*), 10. HFO 867 (*A. maroccana*), 11. HFO 868 (*A. abyssinica*), 12. HFO 869 (*A. strigosa*), 13. HFO 870 (*A. vaviloviana*), 14. HFO 871 (*A. longiglumis*), 15. HFO 872 (*A. sterilis*), 16. HFO 873 (*A. murphyii*), 17. OS 6 (*A. sativa*), 18. OS 346 (*A. sativa*), 19. OS 363 (*A. sativa*), 20. OS 374 (*A. sativa*), 21. OS 376 (*A. sativa*), 22. JHO 2006-2 (*A. sativa*), 23. HJ 8 (*A. sativa*), 24. NGB 4462 (*A. sativa*).

reported that several wild *Avena* species were used as donors of valuable character in oat breeding.

CONCLUSIONS

Duncan multiple range test involved the computation of numerical boundaries that were allowed for classification of the difference between any two genotypes as significant or non- significant. Based upon this, it was concluded that the pairs of means in the study were significantly different. The genotypes that were having significant differences between all pairs of genotypes were kept in one group and those means that were not significantly different were underlined (Table 2). The underlined genotypes were at par, genotype HJ 8 had significant differences for axis node, spikelets/ panicle, green fodder yield and leaf width. Similarly, genotype NGB 4462 (*A.* sativa) was found to have significant difference between all pairs of genotypes for the particular characters flag leaf width and dry fodder yield. Also genotype HFO 867 (*A. maroccana*) had significantly different spikelets/panicle. Genotype HJ 8 (*A. sativa*) was found to have significant differences between all pairs of genotypes for the characters axis node, spikelets/panicle, green fodder yield and leaf width. Similarly, genotype NGB 4462 (*A. sativa*) was found to have significant difference between all pairs of genotypes for the particular characters flag leaf width and dry fodder yield. It was also found that genotypes belonging to different species were at par which signified their co-evolution and probability of having common ancestory in the past.

REFERENCES

Abbas, S. J., S. R. U. Shah, Rasool Ghulam, and Munir Iqbal. 2008 : *Pakistan J. Weed Sci. and Res.,* **14 :** 33-41.

Duncan, D. B. 1955 : *Biometrics,* **11** : 1-42.

Kumar, Y., B. S. Jhorar, and O. Sangwan. 2006 : *Haryana agric. Univ. J. Res.,* **36** : 17-22.

Loskutov, I. 2005 : *Cereal Genet. Resour. (Europe).* pp. 84-90.

Ma Yanming, Zhiyong Liu, Tuting Bai, Wei Wang, and Hao Wang. 2006 : *Xinjiang Agric. Sci.,* **43 :** 510-513.

Panse V. G., and P. V. Sukhatme. 1985 : *Statistical Methods for Agricultural Workers, 4th edn.* Indian Council of Agricultural Research, New Delhi.

Qi Bingjie, Jinghui Liu, Zhiyong Zhang, Julin Gao, and Ruiying Chen. 2008 : *J. Triticeae Crops,* **28** : 594-599.

Travlos, I. S., and C. N. Giannopolitis. 2010 : *Genet. Resour. Crop Evol.,* **57** : 337-341.