

EVALUATION OF AVENA SPECIES FOR YIELD, QUALITY ATTRIBUTES AND DISEASE REACTION

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SUMMARY

Twenty-four genotypes from 16 different *Avena* spp. were studied for yield, quality characters and disease reaction at CCSHAU, Hisar during **rabi** 2010-11. The estimates of GCV, PCV, heritability and GA (as % of mean) were highest for green fodder yield followed by dry fodder yield, seed yield per plant and reducing sugar. *Avena sativa* cv. OS 6 had maximum CP (14.54%) for grain, while *A. barbata* cv. HFO 58 had minimum CP value (11.97%). In case of IVDMD, *A. brevis* cv. HFO 864 had minimum digestibility (41.64%), whereas *A. nuda* cv. HFO 305 had maximum value (64.28%). *A. maroccana* cv. HFO 867 had highest CP (14.51%) for fodder, while *A. barbata* cv. HFO 58 had lowest CP (12.65%). *A. sativa* cv. OS 376 had highest TSS (7.96%) as well as reducing sugar (4.49%) and *A. nuda* cv. HFO 305 had highest fat (9.45%). All the genotypes were found moderately to highly resistant to diseases under study. The desirable genotypes of various *Avena* species either could be used as such or in hybridization programme to transfer the desirable characters to cultivated species.

Key words : *Avena* spp. yield, quality characters and disease reaction

Oat (*Avena sativa* L.) is a constituent of family Gramineae and ranks 6th in world cereal production. Oats both as forage and grain are good source of protein, fibres and minerals. Oats have manifold uses in human food and industrial uses. 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. In India, the oat is 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 undertaken with the chief objective of evaluating some accessions of wild and

cultivated *Avena* species for yield and quality parameters and their reaction to major diseases.

MATERIALS AND METHODS

The present study was conducted at Forage Research Area, Department of Genetics and 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; IGFR, Jhansi; and Forage Section, Department of Genetics & Plant Breeding, CCSHAU, Hisar constituted the experimental material for the present investigations. Brief information regarding 24 accessions belonging to different *Avena* species is given in Table 1. 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 14th Dec. 2009. The observations were recorded on five random and competitive plants/

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

S. No.	Species	Accession No.	Genome	Chromosome No.	Distribution characteristics
Diploid					
1.	<i>Avena nuda</i> L.	HFO 305	AA	2n=14	Marginally cultivated
2.	<i>A. strigosa</i> Schreb.	HFO 869/ IG 03-536-1	AsAs	2n=14	Marginally cultivated
3.	<i>A. brevis</i>	HFO 864/ IG 03-470	AA	2n=14	Marginally cultivated
4.	<i>A. longiglumis</i> Dur.	HFO 871/IG03-480	A A	2n=14	Wild
5.	<i>A. prostrata</i>	HFO 866/EC415008	ApAp	2n=14	Wild
Tetraploid					
6.	<i>A. abyssinica</i> Hochst.	HFO 868/IG 03-456	AABB	2n=28	Marginally cultivated
7.	<i>A. barbata</i> Pott. ex Link.	HFO 58	AABB	2n=28	Wild
8.	<i>A. insularis</i>	HFO 865/EC 425098	AACC	2n=28	Wild
9.	<i>A. murphyi</i>	HFO 873/EC 7120	AACC	2n=28	Wild
10.	<i>A. maroccana</i>	HFO 867/IG 03-482	AACC	2n=28	Wild
11.	<i>A. vaviloviana</i>	HFO 870/EC415201	AABB	2n=28	Wild
Hexaploid					
12.	<i>A. fatua</i> L.	HFO 504	AACCDD	2n=42	Wild
13.	<i>A. sterilis</i> L.	HFO 872/EC4730	AACCDD	2n=42	Wild
14.	<i>A. orientalis</i> Schreb.	HFO 103	AACCDD	2n=42	Marginally cultivated
15.	<i>A. byzantina</i> C. Koch	HFO 60	AACCDD	2n=42	Cultivated
16.	<i>A. sativa</i> 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

genotype/replication for recording the data on fodder and seed yield. The fodder and grain samples were subjected to biochemical analysis for estimating crude protein content by micro-Kjeldahl's method; fat content by Soxhlet method; total soluble sugar by the method of Dubois *et al.* (1956); reducing sugars by the method of Nelson (1944) and the concentration of non-reducing sugars was calculated by subtracting the reducing sugars from the total sugars. *In vitro* dry matter digestibility (IVDMD) in fodder was determined by the method of Tilley and Terry (1963) as modified by Barnes *et al.* (1971). The data for different characters were statistically analyzed on the basis of the model described by Panse and Sukhatme (1985).

RESULTS AND DISCUSSION

The mean sum of squares due to genotypes was highly significant for all the 10 characters studied (Table 2). This indicated the prevalence of enough genetic variability in the materials under study for selection and

improvement and suitability for further statistical analysis for all the characters studied. The results with regard to mean, range, coefficient of variation (PCV and GCV), heritability (broad sense) and genetic advance as per cent of mean are presented in Table 3. Wide range of variability from 60.69 g (*A. fatua*) - 470.13 g (*A. sativa* cv. HJ 8) was recorded for green fodder yield/plant, with a population mean [204.06 g]. Moderate genotypic [GCV=60.48%] and phenotypic coefficients of variation [PCV=61.31%] were recorded along with high heritability (97.3%) and high genetic advance as per cent of mean [122.92%]. Similarly, wide range of variability from 10.66 g (*A. strigosa*)-65.33 g (*A. sativa* cv. OS 346) with a population mean [33.36 g] for dry fodder yield/plant was recorded. Moderate genotypic [GCV=56.42%] and phenotypic coefficients of variation [PCV=57.24%] were recorded along with high heritability (97.1%) and high genetic advance as per cent of mean [114.57%]. Moderate to high estimates of heritability coupled with high genetic advance for most of the traits in oats have been reported by earlier workers

TABLE 2
Analysis of variance for yield and quality parameters in *Avena* species

Source of variation	d. f.	GF/plant (g)	DF/plant (g)	SY/plant (g)	TSS (%)	RS (%)	NRS (%)	IVDMD (F) (%)	CP (Grain) (%)	Fat (%)	CP (F) (%)
Replications	2	605.16	1.09	0.10	0.001	0.007	0.007	15.06	0.43*	0.21	0.35
Genotypes	23	46125.38**	1073.41**	2.70**	2.13**	4.43**	4.43**	92.48**	1.54**	3.93**	0.72*
Error	46	418.59	10.34	0.10	0.0008	0.0008	0.005	17.19	0.23	0.27	0.40
CV	-	10.02	9.64	6.83	1.74	1.74	2.87	7.78	3.57	7.23	4.63

*, **Significant at P=0.05 and P=0.01 levels, respectively.

TABLE 3
Parameters of variability, heritability and genetic advance (as % of mean) for yield and quality traits in *Avena* species

Character	Mean±SE	Range	Coefficient of variation (%)		Heritability broad sense (%)	GA as % of mean
			GCV	PCV		
GFY (g/plant)	204.06±11.56	60.69-470.13	60.48	61.31	97.30	122.92
DMY (g/plant)	33.36±1.81	10.66-65.33	56.42	57.24	97.10	114.57
SY /plant (g)	88.62±3.58	21.00-156.33	42.77	43.37	97.20	86.91
100-SW (g)	4.71±0.18	3.24-6.33	19.74	20.89	89.20	38.42
TSS (%)	4.32±0.04	2.06-7.96	30.29	30.33	99.70	62.30
RS (%)	1.65±0.01	1.03-4.49	50.89	50.92	99.80	104.78
NRS (%)	2.66±0.04	0.09-5.08	45.57	45.66	99.60	93.69
IVDMD (F) (%)	53.23±2.34	41.66-64.27	9.41	12.21	59.30	14.93
CP (G) (%)	13.56±0.27	11.97-14.54	4.86	6.03	64.80	8.06
Fat (%)	7.26±0.29	4.90-9.45	15.18	16.81	81.50	28.24
CP (F) (%)	13.68±0.35	12.65-14.50	2.40	5.21	21.20	2.28

GFY–Green fodder yield, DMY–Dry matter yield, SY–Seed yield, SW–Seed weight, TSS–Total soluble sugars, RS–Reducing sugars, NRS–Non-reducing sugars, IVDMD–*In vitro* dry matter digestibility, CP (G)–Crude protein (grain), CP (F)–Crude protein (fodder).

(Pundir *et al.*, 2008). Travlos and Giannopolitis (2010) reported that several wild *Avena* species were used as donors of valuable character in oat breeding because of presence of variability in *Avena* species. For seed yield/plant also wide range of variability from 21.00 g (*A. maroccana*)-156.33 g (*A. brevis*) with a population mean [88.62 g] was recorded. Moderate genotypic [GCV=42.77%] and phenotypic coefficients of variation [PCV=43.37%] were recorded along with high heritability [broad sense, 97.2%] and high genetic advance as per cent of mean [86.91]. However, Arora and Sangwan (2014) reported variability from 2.80 g (*A. longiglumis*) to 25.57 g (*A. prostrata*), a much lower range as compared to present investigation. In the case of total soluble sugar a wide range of variability from 2.06% (*A. brevis*)-7.96% (*A. sativa* cv. OS 376) was recorded, with a population mean [4.32%]. Moderate

genotypic [GCV=30.29%] and phenotypic coefficients of variation [PCV=30.33%] were recorded along with high heritability [99.7%] and moderate genetic advance as per cent of mean [62.30%]. Genotype OS 376 belonging to cultivated species *A. sativa* had the highest (7.91%) total soluble sugar, which can be utilized in breeding programme. Wide range of variability from 1.03% (*A. strigosa*)-4.49% (*A. sativa* cv. OS 376) was recorded for reducing sugar, with a population mean [1.65%]. Moderate genotypic [GCV=50.89%] and phenotypic coefficients of variation [PCV=50.92%] were recorded along with high heritability [99.8%] and high genetic advance as per cent of mean [104.78%]. Genotype OS 376 (*A. sativa*) having highest reducing sugar (4.49%) can be utilized in breeding programme to improve sugar content in oats. For non-reducing sugar also, a wide range of variability (Table 4) from 0.09%

(*A. brevis*) -5.08% (*A. longiglumis*) was recorded, with a population mean [2.66%]. Moderate genotypic [GCV=45.57%] and phenotypic coefficients of variation [PCV=45.66%] were recorded along with high heritability [99.6%] and high genetic advance as per cent of mean [93.69%]. For IVDMD in fodder, a wide range of variability from 41.66% (*A. brevis*)-64.27% (*A. nuda*) was recorded, with a population mean [53.23%]. Low genotypic [GCV=9.41%] and phenotypic coefficients of variation [PCV=12.21%] were recorded along with moderate heritability [broad sense, 59.3%] and low genetic advance as per cent of mean [14.93%]. Moderate range of variability from 12.65% (*A. barbata*)-14.50% (*A. maroccana*) was recorded for crude protein in fodder, with a population mean [13.68%]. Very low genotypic [GCV=2.40%] and phenotypic coefficients of variation [PCV=5.21%] were recorded along with low heritability [21.2%] and very low genetic advance

as per cent of mean [2.28%] for this trait. For crude protein in grain a moderate range of variability from 11.97% (*A. barbata*) -14.54% (*A. sativa* cv. OS 6) was recorded, with a population mean [13.56%]. Very low genotypic [GCV=4.86%] and phenotypic coefficients of variation [PCV=6.03%] were recorded along with moderate heritability [64.8%] and very low genetic advance as per cent of mean [8.06%]. Mojumdar and Ahmad (1980) reported that *A. weistii*, a diploid species, possessed highest percentage of crude protein, while *A. abyssinica* (4 x) gave highest dry matter percentage with maximum crude protein in seeds. Redaelli *et al.* (2009) evaluated the impact of genotype, environment and rotation on the variability of important bioactive compounds (protein and O-glucan) in the grains of seven naked and two husked oat genotypes. Genetic, agronomic and environmental effects for all the parameters were investigated and significant interactions between

TABLE 4
Mean performance of some *Avena* species for yield and quality traits

Species	GF (g/plant)	DF (g/plant)	SY/ plant (g)	TSS (%)	RS (%)	NRS (%)	IVDMD (F) (%)	CP (Grain) (%)	Fat (%)	CP (F) (%)
<i>A. barbata</i> Pott. ex Link. cv. HFO 58	145.00	20.67	118.67	4.87	1.45	3.43	52.77	11.97	7.47	12.65
<i>A. byzantina</i> C. Koch. cv. HFO 60	203.33	37.67	103.00	3.87	1.09	2.82	48.44	14.42	7.92	13.47
<i>A. orientalis</i> Schreb. cv. HFO 103	96.32	18.67	78.33	4.67	1.12	3.55	48.23	13.51	8.40	13.87
<i>A. sativa</i> L. cv. HFO 267	310.00	58.00	122.00	3.99	1.44	2.55	57.22	14.07	6.51	13.64
<i>Avena nuda</i> L. cv HFO 305	179.27	25.33	54.67	3.65	1.27	2.37	64.28	13.35	9.45	13.66
<i>A. fatua</i> L. cv. HFO 504	60.69	11.33	102.00	2.93	1.16	1.77	60.74	13.33	8.50	14.25
<i>A. brevis</i> cv. HFO 864	124.93	18.00	156.33	2.06	1.97	0.09	41.66	14.52	8.00	14.42
<i>A. insularis</i> cv. HFO 865	75.07	12.67	83.00	3.84	1.15	2.69	52.13	14.40	7.53	13.24
<i>A. prostrata</i> cv. HFO 866	184.60	26.67	81.33	3.74	1.18	2.56	55.21	13.52	5.89	13.04
<i>A. maroccana</i> cv. HFO 867	78.67	13.67	21.00	2.65	2.21	0.44	54.24	12.34	7.53	14.51
<i>A. abyssinica</i> Hochst. cv. HFO 868	135.60	24.33	34.67	3.70	1.16	2.54	56.57	14.41	7.20	13.77
<i>A. strigosa</i> Schreb. cv. HFO 869	62.00	10.67	64.33	4.16	1.03	3.07	47.15	13.60	8.30	13.44
<i>A. vaviloviana</i> cv. HFO 870	115.69	19.67	70.67	6.21	1.16	5.05	47.42	13.63	7.99	13.07
<i>A. longiglumis</i> Dur. cv. HFO 871	67.28	12.33	30.67	6.20	1.12	5.08	55.96	14.35	5.17	14.23
<i>A. sterilis</i> L. cv. HFO 872	110.33	19.33	48.67	3.86	1.35	2.51	58.13	13.28	6.43	13.63
<i>A. murphyi</i> cv. HFO 873	272.00	43.00	45.33	4.45	1.36	3.09	52.84	12.90	5.49	13.35
<i>A. sativa</i> L. cv. OS 6	252.67	47.33	106.00	3.67	1.13	2.54	46.34	14.54	8.40	14.27
<i>A. sativa</i> L. cv. OS 346	430.33	65.33	77.33	6.06	3.06	3.00	54.42	12.71	7.03	14.05
<i>A. sativa</i> L. cv. OS 363	408.67	59.33	116.67	3.19	3.04	0.16	47.48	12.65	7.85	13.30
<i>A. sativa</i> L. cv. OS 374	273.33	47.33	127.00	4.68	2.37	2.31	59.86	13.49	7.69	13.76
<i>A. sativa</i> L. cv. OS 376	322.00	60.67	81.67	7.96	4.49	3.47	56.95	13.35	7.87	14.08
<i>A. sativa</i> L. cv. JHO 2006-2	185.00	33.33	112.33	4.89	1.61	3.28	52.15	13.20	6.53	13.13
<i>A. sativa</i> L. cv. HJ 8	470.13	62.67	144.00	3.30	1.04	2.26	59.70	13.91	6.40	13.49
<i>A. sativa</i> L. cv. NGB 4462	334.67	52.67	147.33	5.13	1.73	3.39	47.73	14.18	4.90	14.22
Mean	204.07	33.36	88.63	4.32	1.66	2.67	53.23	13.57	7.27	13.69
S. Em±	11.81	1.86	3.67	0.04	0.02	0.04	2.39	0.28	0.30	0.37
C. D. (P=0.05)	33.63	5.29	10.44	0.12	0.05	0.13	6.81	0.80	0.86	1.04
C.V. (%)	10.03	9.64	7.17	1.64	1.74	2.87	7.79	3.58	7.23	4.63

variability factors were found. Total dietary fiber (TDF) content was also determined. Moderate range of variability from 4.90% (*A. sativa* cv. NGB 4462) - 9.45% (*A. nuda*) was recorded for fat percentage, with a population mean [7.26%]. Low genotypic [GCV=15.18%] and phenotypic coefficients of variation [PCV=16.81%] were recorded along with high heritability [broad sense, 81.5%] and moderate genetic advance as per cent of mean [28.24%]. While comparing the nutritive value of two varieties viz., HFO 114 and Kent of oat (*Avena sativa*), Gupta *et al.* (1978) reported not much difference in both the varieties for several quality parameters studied. Tian *et al.* (2010) determined the significant correlation among compositions including starch, protein and reducing sugars, free amino acids and phytic acids. A close correlation was also found between colour of malt flour at 50 pC and the length of shoots and rootlets. The results suggested that oat is

good food material and germination can improve their nutritional properties. Zwer (2010) reported that oat is a versatile grain for food, animal feed and non-food products due to its unique grain qualities compared to other cereal grains. Recent research has identified grain quality traits that improve the nutritive value of oats as an animal feed compared to many other cereals.

Disease reaction studies (Table 5) revealed that the genotypes included in the present study were moderately to highly resistant. None of the genotypes was highly susceptible. Genotypes HFO 504 (*A. fatua*) and NGB 4462 (*A. sativa*) were among the most resistant genotypes to all the three diseases. For Leaf Blight NGB 4462 (*A. sativa*); for Yellow Rust HFO 60 (*A. byzantina*), HFO 103 (*A. orientalis*), HFO 305 (*A. nuda*), HFO 504 (*A. fatua*), HFO 864 (*A. brevis*), HFO 869 (*A. strigosa*), HFO 871 (*A. longiglumis*) and NGB 4462 (*A. sativa*) were among highly resistant with score 1 and for

TABLE 5
Screening of oat entries for resistance against leaf blight, yellow rust and powdery mildew diseases

S. No.	Species	Leaf blight	Yellow rust	Powdery mildew
1.	<i>A. barbata</i> Pott. ex Link. cv. HFO 58	3	3	1
2.	<i>A. byzantina</i> C. Koch. cv. HFO 60	3	1	1
3.	<i>A. orientalis</i> Schreb. cv. HFO 103	4	1	1
4.	<i>A. sativa</i> L. cv. HFO 267	5	2	2
5.	<i>Avena nuda</i> L. cv. HFO 305	4	1	3
6.	<i>A. fatua</i> L. cv. HFO 504	2	1	1
7.	<i>A. brevis</i> cv. HFO 864	3	1	1
8.	<i>A. insularis</i> cv. HFO 865	3	3	2
9.	<i>A. prostrata</i> cv. HFO 866	3	3	3
10.	<i>A. maroccana</i> cv. HFO 867	4	2	3
11.	<i>A. abyssinica</i> Hochst. cv. HFO 868	4	3	1
12.	<i>A. strigosa</i> Schreb. cv. HFO 869	3	1	2
13.	<i>A. vaviloviana</i> cv. HFO 870	4	2	2
14.	<i>A. longiglumis</i> Dur. cv. HFO 871	3	1	2
15.	<i>A. sterilis</i> L. cv. HFO 872	3	3	1
16.	<i>A. murphyi</i> cv. HFO 873	3	2	1
17.	<i>A. sativa</i> L. cv. OS 6	4	3	2
18.	<i>A. sativa</i> L. cv. OS 346	3	2	1
19.	<i>A. sativa</i> L. cv. OS 363	4	2	3
20.	<i>A. sativa</i> L. cv. OS 374	5	1	1
21.	<i>A. sativa</i> L. cv. OS 376	2	3	3
22.	<i>A. sativa</i> L. cv. JHO 2006-2	3	3	3
23.	<i>A. sativa</i> L. cv. HJ 8	5	2	1
24.	<i>A. sativa</i> L. cv. NGB 4462	1	1	2

Scale used (1-9) :

1-Highly resistant (No symptoms)

3-Resistant (0.0-10.0% disease intensity)

5-Moderately resistant (10.1-25.0% disease intensity)

7-Susceptible (25.1-50.0% disease intensity)

9-Highly susceptible (More than 50% disease intensity).

Powdery Mildew HFO 58 (*A. barbata*), HFO 60 (*A. byzantina*), HFO 103 (*A. orientalis*), HFO 504 (*A. fatua*), HFO 864 (*A. brevis*), HFO 868 (*A. abyssinica*), HFO 872 (*A. sterilis*) and HFO 873 (*A. murphyi*). OS 346, OS 374 and HJ 8 (all belonging to *A. sativa*) had score 1 i. e. were highly resistant. These genotypes can be successfully utilized to incorporate resistance in elite genetic backgrounds. Availability of several genotypes for particular diseases is also beneficial for plant breeder as he has option to choose the one which is having good specific combining ability if it is to be utilized in hybrid breeding programme in future.

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