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VARIABILITY STUDIES FOR QUALITATIVE AND QUANTITATIVE TRAITS IN ADVANCED LINES OF OAT (*Avena sativa* L.)

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ABSTRACT

Genetic variability was estimated among thirty four genotypes of oat during *rabi* 2010 at the All India Co-ordinated Research Project on Forage crops, Seed Breeding Farm, JNKVV, Jabalpur(MP). Observations were recorded on days to harvest, plant height (cm), internode length (cm), peduncle length (cm), panicle length (cm), panicle weight (g), spikelets panicle^{-1}, chlorophyll content (µg cm^{-2}), total dry matter yield (kg), total green fodder yield (kg), awn nature and awn colour. Analysis of variance indicated highly significant differences among the genotypes for all the characters studied. The materials for the present study comprises of genotypes which were selected on the basis of performance for fodder yield and yield contributing characters in the previous generation and were derived from genotypes Kent and JO-1 subjected to doses of gamma rays which were grown in M_6 generation. In JO-1 population, the genotype JMO-187 had recorded maximum total green fodder yield while in Kent population the genotype JMO-429 recorded maximum total green fodder yield. The genotype JMO-448 had recorded highest panicle length and maximum number of spikelets panicle^{-1} in JO-1 population while in Kent population the genotype JMO-425 had recorded highest panicle length and maximum spikelets panicle^{-1}. High values of phenotypic and genotypic coefficient of variation was recorded for chlorophyll content followed by spikelets panicle^{-1}, total dry matter yield and total green fodder yield which indicated the presence of ample amount of variation for these characters. High values of heritability coupled with high expected genetic advance was observed for the characters viz., chlorophyll content and spikelets panicle^{-1} suggesting the presence of additive gene action, thus there is scope for selection.Significant diversity for some qualitative traits was recorded during this investigation for awn nature and awn colour. The superior genotypes identified from these variability studies are JMO-187, JMO-448, JMO-425 and JMO-429.

(Key words: Oat, variability, PCV, GCV, heritability)

INTRODUCTION

Oat (*Avena sativa* L.) is an important forage annual crop of *rabi* season belongs to family Poaceae. The genus *Avena* incorporates diploid, tetraploid and hexaploid species based on a basic chromosome number of x = 7. *Avena sativa* L. and *Avena byzantina* K. Koch are the main species grown for fodder and grain. The cultivated oat *Avena sativa (*L.*)* (2n = 6x = 42), a natural allohexaploid, together with wild weedy hexaploid species like *A.sterilis* and *A.fatua*, have evolved through repeated cycles of introgression, hybridization and polyploidization, combining three distinct diploid genomes (AACCDD). The crop ranks sixth in world cereal production and is widely cultivated for fodder (as hay and silage) and feed for several years and accounts for at least 60 per cent of the total world production. The total world area under oat is approximately 26.8 m ha. Most of the oat grain worldwide is consumed as animal feed and is principally fed to dairy cattle, horses, mules and turkeys.The nutritive value of oat forage is high and dry matter digestibility is in excess of 75 per cent when fed to dairy cattle (Burgess *et al.,* 1972). The cereal straws have almost similar chemical composition but oat straws has more digestible organic matter and metabolizable energy (Cuddeford, 1995).In India, the oat is widely grown in Uttar Pradesh, Madhya Pradesh, Haryana, Punjab, Himachal Pradesh, Rajasthan, Bihar, Gujarat, Andhra Pradesh and hilly tracts of southern plateau.

Yield is a complex character which mainly depends upon several component characters, so that selection of genotypes based on yield component is not effective but based on component character is more effective. Thus, variability in genotypes for yield and yield contributing characters forms the basic factor to be considered while making selection of parents since estimate of genetic parameters are useful to breeder for designing an effective breeding programme. Hence, present investigation was undertaken to know the GCV, PCV, heritability and genetic advance for various yield contributing characters.

MATERIALS AND METHODS

The present investigation was conducted at All India Co-ordinated Research Project on Forage Crops, Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during the *rabi*

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2010–2011.Thirty four varieties of oat were treated with different doses(150,200,300 and 400 Gy) of gamma rays at Gamma chamber JNKVV, Jabalpur(MP) and response to the different doses of gamma rays in M_1 and onward generations were recorded. Seeds harvested in M_5 generation from the gamma rays treated populations and seeds of different mutants selected from the same generation were used as experimental materials for study in M_6 generation along with untreated population of same variety. The total treatments are mentioned below:

Treatments (M_6 population)

Sr.no.	Treatments	Variety	Mutagenic treatment	Sr. No.	Treatments	Variety	Mutagenic treatment
1	T_1	JO–1	Control	18	T_{18}	JMO–448	200
2	T_2	JMO–220	300	19	T_{19}	JMO–189	300
3	T_3	JMO–222	300	20	T_{20}	JMO–193	300
4	T_4	JMO–14	300	21	T_{21}	JMO–194	300
5	T_5	JMO–41	300	22	T_{22}	JMO–197	300
6	T_6	JMO–42	300	23	T_{23}	JMO–199	300
7	T_7	JMO–54	200	24	T_{24}	Kent	Control
8	T_8	JMO–56	200	25	T_{25}	JMO–425	300
9	T_9	JMO–71	200	26	T_{26}	JMO–424	300
10	T_{10}	JMO–75	200	27	T_{27}	JMO–421	300
11	T_{11}	JMO–79	200	28	T_{28}	JMO–419	300
12	T_{12}	JMO–131	200	29	T_{29}	JMO–415	300
13	T_{13}	JMO–139	200	30	T_{30}	JMO–413	300
14	T_{14}	JMO–149	400	31	T_{31}	JMO–407	300
15	T_{15}	JMO–159	300	32	T_{32}	JMO–404	300
16	T_{16}	JMO–158	300	33	T_{33}	JMO–401	300
17	T_{17}	JMO–187	300	34	T_{34}	JMO–429	300

Thirty four treatments as mentioned earlier including treated and untreated populations were sown in Randomized Complete Block Design with three replications. The sowing of experimental materials was done on 13.11.10. Each plot was maintained of size 3x10 m^2 and having three rows for each treatment in each replication. The distance between rows 30 cm and plants 5 cm was maintained. The following observations were recorded on five tagged plants in M_6 generation. Days to harvest, plant height (cm), internode length(cm), peduncle length (cm), panicle length (cm), panicle weight (g), spikelets panicle^{-1}, chlorophyll content (μg cm^{-2}), total dry matter yield (kg), total green fodder yield (kg), awn nature and awn colour. The relative chlorophyll content was assessed with a hand held chlorophyll meter. The analysis of variance for the experimental design was analyzed by the method given by Panse and Sukhatme (1954), heritability in broad sense was calculated by using the formula suggested by Hanson *et al.* (1956) and genetic advance as per Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences for all characters suggesting the presence of high genetic variability among the genotype assessed (Table 1). These results are in conformity with the findings of Bibi *et al.* (2012) who reported that all genotypes differ significantly with respect to days to harvest, plant height, internode length, total dry matter yield and total green fodder yield.

The genotypes were selected on the basis of mean performance of genotypes for different quantitative characters i.e. days to harvest, the range for days to harvest for JO–1 population was from 98.14 to 109.00 days, the genotype JMO–42 (98.14) was early maturing and late maturing variety was JMO–448 (109.00) while in Kent population for days to harvest ranged from 103.54 to 107.61 days, the genotype JMO–404 (103.54) was early maturing and late maturing variety was JMO–415 (107.61), for plant height the genotypes JMO–448 (119.24 cm) andJMO–220 (98.80 cm) were recorded maximum and minimum plant height in JO–1 population while in Kent population the genotypes JMO–415 (117.98 cm) and JMO–424 (103.25 cm) recorded maximum and minimum plant height, for internode length in

JO–1 population, highest value of internode length was recorded in genotype JMO–131(15.40 cm) while lowest internode length was observed in the genotype JMO–193(11.40 cm) while in Kent population maximum internode length was observed in the genotype JMO–429 (14.00 cm) and minimum internode length in the genotype JMO–424(12.60 cm), for peduncle length in JO–1 population maximum length was recorded in the genotype JMO–448(42.00 cm) while minimum in the genotype JMO–41 (34.03 cm), while in Kent population genotypes JMO–429(39.22 cm) and JMO–404 (36.76 cm) were recorded maximum and minimum peduncle length respectively (Table 2).

For panicle length in JO–1 population genotype JMO–448(24.67 cm), had maximum panicle length while minimum was observed in the genotype JMO–424(18.40 cm), while in Kent population genotypes JMO–425(23.75 cm) and JMO–424 (18.40 cm) were recorded maximum and minimum panicle length. The genotypes JMO–448 (12.60g) and JMO–149(6.70g) were recorded maximum and minimum panicle weight in JO–1 population, while in Kent population genotype JMO–425 (12.50g) recorded maximum whereas genotype JMO–429(7.90g) recorded minimum panicle weight, for spikelets panicle^{-1} in JO–1 population maximum number of spikelets panicle^{-1} was counted in JMO–448 (197.21) and minimum was recorded in JMO–159 (82.05), while in Kent population genotypes JMO–425 (198.53) and JMO–424 (82.05) showed maximum and minimum number of spikelets panicle^{-1}, for chlorophyll content in JO–1 population, maximum amount of chlorophyll content was recorded in genotype JMO–448(34.31 μg cm^{-2}) and minimum was recorded in genotype JMO–54(12.81 μg cm^{-2}), while in Kent population genotypes JMO–425(39.35 μg cm^{-2}) and JMO–424 (10.47 μg cm^{-2}) showed maximum and minimum amount of chlorophyll content. The genotypes JMO–448 (8.25 kg) and JMO–54 (3.55 kg) were recorded maximum and minimum total dry matter yield in JO–1 population, while genotypes JMO–413(8.23 kg) and JMO–424 (3.25 kg) were recorded maximum and minimum total dry matter yield in Kent population, for total green fodder yield in JO–1 population highest quantity fodder yield produced was recorded in the genotype JMO–187(39.55 kg) while least was observed in JMO–54(22.65kg), while in Kent population JMO–429(43.66kg) recorded maximum and JMO–425(21.45kg) recorded minimum total green fodder yield (Table 2).

Phenotypic coefficient of variation (PCV) was higher in magnitude than that of genotypic coefficient of variation (GCV) for chlorophyll content (35.48 and 30.86) followed by spikelets panicle^{-1} (31.44 and 26.11), total dry matter yield (23.44 and 19.41) and total green fodder yield (21.24 and 15.38) indicating the substantial modifying effect of environment in the expression of these traits (Table 3). Similar to these results Krishna *et al.* (2013) also observed that estimates of GCV was smaller than that of PCV suggesting influence of environment on them and Bibi *et al.* (2012) recorded that PCV was slightly greater than GCV for days to harvest, plant height and internode length indicating influence of environment on them. Sangwan and Arora (2011) also reported similar results for plant height and dry matter yield in fodder oat.

Heritability is the index of transmissibility of characters from parents; need to be studied in order to determine the extent to which the observed variation is inherited. High heritability estimates were observed for chlorophyll content(86.90), panicle length(84.40), panicle weight(83.10) and spikelets panicle^{-1}(83.00), such characters are governed by additive gene effects thus, there is scope for improvement through individual plant selection. Similar results were reported by Bahadur *et al.* (2008) who observed high heritability for panicle length and panicle weight in oat.

Chlorophyll content and spikelets panicle^{-1} showed high estimates of heritability with high genetic advance indicated the role of additive gene effects in the inheritance of these traits. These results are in conformity with the findings of Krishna *et al.* (2013) who observed that high heritability with high genetic advance for spikelets panicle^{-1}, plant height and green fodder yield which indicated the role of additive gene effects in the inheritance of these traits. Singh and Singh (2010) also recorded that, the heritability and genetic advance were high for characters like plant height, green fodder yield and dry matter yield indicating the involvement of additive type of gene action in controlling these characters (Table 3).

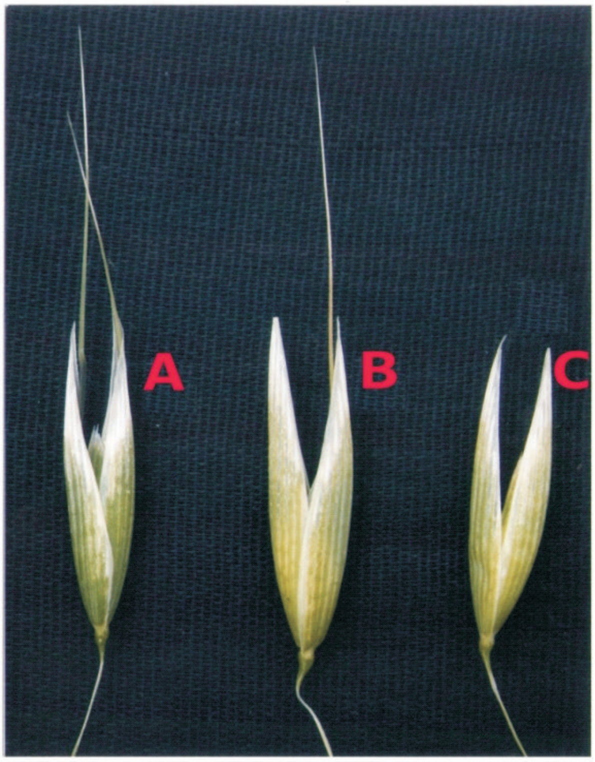

Fig.1. Presence of awn

A- Double awned, B-Single awened, c- Awnless

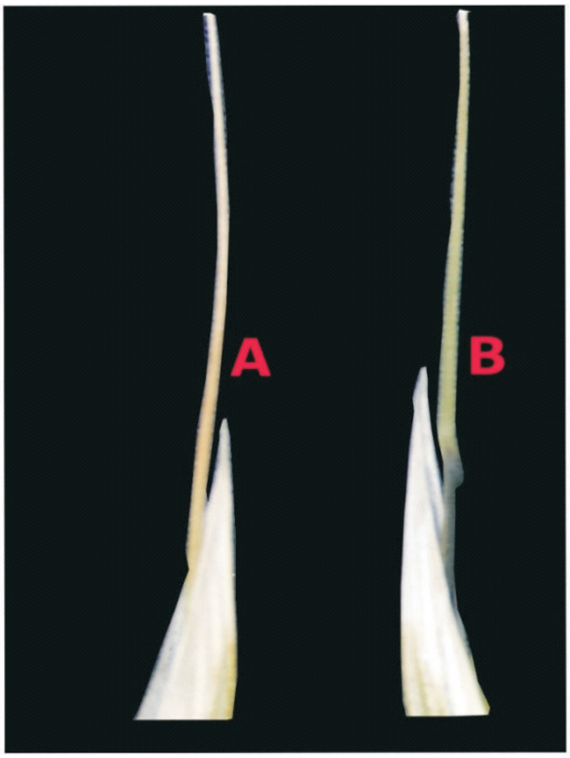

Fig.2. Awn colour

A-White colour awn, B-Black colour awn

Table 1. Analysis of variance for fodder yield and its components in oat

Source of Variation	d.f.	Days to harvest	Plant height (cm)	(cm)	Peduncle length (cm)	Panicle length (cm)
Replication	2	4.941	5.926	00.575	00.421	900.33
Genotype	33	17.996**	840.584**	200.383**	100.075**	80.556**
Error	66	10.296	00.555	0.682	0.742	00.495

Source of Variation	d.f.	Panicle weight (g)	Spikelets panicle $^{-1}$	Chlorophyll content (µg cm^{-2})	Total dry matter yield (k g)	Total green fodder yield (k g)
Replication	2	00.000098	20.1615	000.369	1100.382	170.582
Genotype	33	70.247**	316100.337**	1280.043**	50.161**	680.516**
Error	66	10.566	0.692	00.095	0.685	00.489

***,** Significant at 5% and 1% level respectively.**

Table 2. Mean values of thirty four genotypes for different characters in oat

Sr. No.	Genotypes	Days to harvest	Plant height	Internode length	Peduncle length (cm)	Panicle Length (cm)	Panicle weight (g)	Spikelets panicle^{-1}	Chlorophyll content (µg cm^{-2})	Total dry matter yield (k g)	Total green fodder yield (kg)
1	JO-1	102.00	99.20	12.4	34.67	21.5	9.2	101.44	17.15	6.25	30.45
2	JMO-220	102.00	98.80	13.2	39.43	23.62	9.5	106.24	26.92	6.45	34.95
3	JMO-222	104.24	110.00	13.6	36.55	18.95	7.8	105.45	28.23	5.35	32.25
4	JMO-14	103.33	108.45	12.5	39.00	21.35	7.6	93.17	16.65	4.75	25.66
5	JMO-41	99.24	112.24	12.1	34.33	19.45	7.1	98.95	18.99	5.25	29.44
6	JMO-42	98.14	111.87	12.0	37.84	20.56	7.4	95.05	17.04	3.56	26.26
7	JMO-54	104.56	110.26	11.7	35.44	21.44	8.1	93.46	12.82	3.55	22.65
8	JMO-56	106.26	111.43	14.0	36.00	21.65	9.8	123.56	21.56	7.76	32.96
9	JMO-71	105.44	109.45	13.6	36.17	22.45	9.2	103.64	19.39	8.05	31.75
10	JMO-75	101.20	110.46	13.0	37.12	21.67	8.9	105.44	15.75	6.05	27.50
11	JMO-79	100.26	108.90	13.7	38.23	22.14	9.0	106.25	21.71	5.95	32.15
12	JMO-131	106.76	113.46	15.4	37.33	18.89	7.3	104.44	21.01	5.55	31.85
13	JMO-139	102.64	105.66	13.5	36.83	19.69	7.6	105.65	28.89	6.75	34.35
14	JMO-149	103.24	103.45	11.8	34.78	18.79	6.7	83.25	13.70	4.25	24.65
15	JMO-159	104.00	105.45	12.3	35.74	18.89	6.9	85.45	14.50	4.84	25.26
16	JMO-158	104.28	114.24	11.9	37.98	23.75	8.2	135.35	17.85	5.65	27.25
17	JMO-187	108.69	118.20	12.6	40.14	24.56	12.4	194.45	32.25	7.84	38.55
18	JMO-448	109.00	119.24	13.2	42.00	24.67	12.6	197.55	34.45	8.25	39.26
19	JMO-189	106.53	104.25	12.3	39.78	22.35	8.5	145	17.53	5.75	26.95
20	JMO-193	101.26	102.35	11.4	36.00	22.46	9.2	136.54	18.95	6.55	31.65
21	JMO-194	103.00	109.46	12.34	37.45	21.23	8.4	143.44	26.03	6.35	35.21
22	JMO-197	102.45	103.06	12.6	34.98	21.56	8.8	139.65	20.28	6.49	29.45
23	JMO-199	102.66	102.88	12.7	36.46	21.78	7.8	109.55	15.64	6.25	28.35
24	Kent	105.00	110.86	14.0	39.22	19.66	7.9	116.04	23.43	6.75	34.44
25	JMO-425	104.48	113.00	13.3	38.77	23.75	12.5	198.20	39.76	8.23	43.66
26	JMO-424	103.66	103.25	12.6	38.48	18.40	7.1	82.05	10.77	3.25	21.45
27	JMO-421	104.46	110.48	13.2	37.64	21.46	9.4	141.53	19.38	7.15	30.98
28	JMO-419	106.45	114.44	13.0	36.89	21.00	8.0	123.26	21.95	6.95	32.96
29	JMO-415	107.61	117.98	13.5	39.77	22.47	8.7	131.43	23.13	6.85	33.25
30	JMO-413	104.39	114.21	12.7	37.44	22.43	11.4	178.77	31.95	8.27	38.75
31	JMO-407	106.00	115.00	15.0	38.82	23.2	10	155.56	22.58	7.75	33.27
32	JMO-404	103.56	106.56	13.7	36.76	21.73	10.4	162.33	19.19	7.20	30.85
33	JMO-401	104.39	115.28	13.2	39.42	23.21	8.9	110.05	16.03	6.15	27.46
34	JMO-429	103.97	107.48	13.9	39.58	21.89	8.3	113.75	15.70	6.23	29.95

Table 3. Genetic parameters of variation for fodder yield and its components in oat

Characters	Range		Mean	Variances			Co-var.		Heritability broad sense (%)	Genetic advance as % of mean
	Min.	Max.		Phenotypic	Genotypic	Environment	GCV	PCV		
Days to harvest	98.14	109.00	141.51	2.982	2307	10.296	2.22	2.87	77.30	40.21
Plant height (cm)	98.80	119.24	600.112	28.565	28.009	00.555	6.23	8.54	72.90	9.86
Internode length (cm)	11.40	15.40	15.23	10.249	00.566	0.682	5.78	8.58	45.30	80.02
Peduncle length (cm)	34.03	42.00	37.55	3.853	30.111	0.742	4.69	5.22	80.70	19.55
Panicle length (cm)	18.40	24.67	21.55	30.182	2.687	00.497	7.60	8.27	84.40	29.05
Panicle weight (g)	6.70	12.60	8.84	20.4316	20.4019	00.023	15.25	18.35	83.10	35.97
Spikelets panicle^{-1}	82.05	198.53	124.27	1054.241	1053.241	0.6927	2611	31.44	83.00	41.06
Chlorophyll content (μgcm^{-2})	10.67	39.35	21.15	42.744	42.649	00.095	30.86	35.48	86.90	44.15
Total dry matter yield (k g)	3.0.25	80.27	60.29	20.177	10.492	0.685	19.41	23.44	68.50	33.10
Total Green fodder yield (k g)	21.45	43.66	30.95	23.165	22.675	00.489	15.38	21.24	72.40	31.35

Significant diversity for some qualitative traits was recorded during this investigation for awn nature and awn colour (Fig. 1 and 2). The genotypes JMO-159 and JMO-158 were double awned, JMO-56, JMO-71, JMO-75 and JMO-139 were single awned genotypes, while control JO-1 and JMO-187 were awnless genotype. Variation in awn colour was observed among the genotypes, straight type of awn was observed in JMO-75 and JO-1 (control) with white colour awn, while JMO-424 was with twisted and black coloured awns. These results are in conformity with the findings of Yu *et al*. (2007) who observed variation in awn colour and awn nature.

Above results indicated that a large amount of variation within accessions existed and such variation is helpful for plant breeder to exploit for the improvement of oat crop plants. Genetic variability was observed among the mutants for quantitative and qualitative traits which may increase the existing gene pool and the expression of heritability and genetic advance was found greatly influenced by gamma rays treatments. Such changes can be exploited in the improvement of desirable traits such as total green fodder yield, total dry matter yield, spikelets panicle^{-1} and plant height. Heritability estimates are of great importance to plant breeder primarily as a measure of the value of selection for particular characters in various types of progenies and a special tool for more accurate separation of variability due to inheritance. On the basis of mean performance of these characters superior genotypes JMO-187, JMO-448, JMO-425 and JMO-429 were identified.

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