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Estimation of genetic variability, heritability and genetic advance for seed yield and its components in Oat (*Avena sativa* L.)

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Abstract

A trial was conducted at Student's Instructional Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *rabi* season 2021-22 in Uttar Pradesh, India. The experimental material comprised of twenty-four genotypes. The genotypes were tested in Randomized Block Design with three replications in three different environments to study the genetic variability, heritability and genetic advance of different characters amongst various genotypes over different environments. Significant differences for various traits in all the environments indicated that ample variability existed among the genotypes. The estimates of heritability were high for all the characters, whereas moderate to high genetic advance was observed for all the characters. High heritability coupled with high genetic advance was observed for number of reproductive tillers per plant, number of nodes per plant, number of leaves per plant, 1000 seeds weight, L:S ratio, green fodder yield, dry matter yield and seed yield per plant on pooled basis.

Keywords: Oat, genetic variability, heritability, genetic advance

Introduction

Oat ranks sixth in the world in cereal production following wheat, maize, rice, barley and sorghum. The amount of oats used for human consumption has increased because of nutritional attributes. Oat (*Avena sativa* L.) are a whole-grain cereal which are a very good source of fiber, especially beta Glucan, and are high in vitamins, minerals, and antioxidants. Avenanthramides, a unique group of antioxidants believed to protect against heart disease is found in oat. The nutritional facts for 3.5 ounces (100 grams) of raw oats are Calories: 389, Water: 8%, Protein: 16.9 grams, Carbs: 66.3 grams, Fiber: 10.6 grams, Fat: 6.9 grams and Carbs make up approximately 66% of oats by dry weight out of which nearly 11% of the carbs is fiber and 85% is starch. Oats are very low in sugar, with only 1% coming from sucrose. Oats are rich in beta Glucans, a unique soluble fiber which helps in lowering cholesterol levels, increase bile acid production, reduce blood sugar and insulin levels, reduces risk of heart diseases. Oats are high in many vitamins and minerals including manganese, phosphorus, copper, iron, selenium, magnesium and zinc. Oats are rich in antioxidants like ferulic acid and phytic acid. The knowledge of genetic variability, heritability and genetic advance helps a breeder to choose appropriate selection method along with the prediction of any gains from that selection. It also allows to know the magnitude of genetic effects. High heritability is associated with additive gene effect whereas low heritability is due to dominance and epistasis.

Material and Methods

A trial was conducted at Student's Instructional Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *rabi* season 2021-22 in Uttar Pradesh, India. The experimental material for present investigation comprised of twenty-four genotypes of Oat (*Avena sativa* L.) developed by different research stations and agricultural universities of India. These varieties were obtained from IGFR, Jhansi. The varieties used were JO-3-93, UPO-94, JHO-2004, HFO-114, JO-1, JHO-851, JHO-99-2, UPO-212, Kent, JHO-2010-1, JO-03-91, NDO 1, JHO-99-1, JHO-2001-3, SKO-10, OS-6, HJ-8, RO-19, NDO-2, JHO-822, OS-346, OS-7, Sabazar (SKO-7) and OL-125.

Table 1: Description of environments

Environments	Locations	Date of sowing	Sowing season	pH of the soil	EC of soil (dsm ⁻¹)
Environment I (E1)	Student Research Farm, CSAUA&T, Kanpur	16 Oct, 2021	Early sown	7.5	0.31
Environment II (E2)	Student Research Farm, CSAUA&T, Kanpur	10 Nov, 2021	Normal sown	7.5	0.31
Environment III (E3)	Student Research Farm, CSAUA&T, Kanpur	24 Dec, 2021	Late sown	7.5	0.31

The observations were recorded on individual plant basis on five competitive randomly selected plants from each replication for fifteen characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), numbers of reproductive tillers per plant, leaf length (cm), leaf width (mm), stem girth (mm), panicle length (cm), number of nodes per plant, number of leaves per plant, number of seeds per main spike, 1000 seeds weight (g), seed yield per plant (g).

Results and Discussion

Genetic variability

Any selection program mainly depends upon the extent and nature of genetic variability present add on also the genetic architecture off yield add the component characters with high heritability as it is likely to give high genetic advance provided the traits are direct components of yield. Ample variation among twenty-four genotypes for all the traits indicated its significance for the estimation of further parameters of variation in the material studied. Considering mean performance of genotypes, the timely sown were found better than the early sown and late sown conditions for fodder yield, seed yield and other component traits. Early flowering was observed in E1. Wide range of variation was observed in E2 followed by E1 and E3. High seed yielding genotypes were JO-3-93 followed by JHO-2004, JHO-851, HJ-8, OS-6, JHO-2010-1, OS-7, JO-03-91, OL-125, JHO-2001-3 and JHO-99-1. From the above, it can be suggested that the above genotypes can be selected and used as one of the parents in hybridization programme. High genotypic coefficient of variation was observed for dry matter yield followed by green fodder yield, seed yield per plant, L:S ratio, number of reproductive tillers per plant, number of leaves per plant, 1000 seeds weight, number of nodes per plant, number of seeds per main spike, days to maturity, days to 50% flowering, plant height, leaf width, leaf length and spike length. The studies of Prasad *et al.* (2003) [15], Krishna *et al.* (2013) [12] indicated presence of enough variability for various traits in Oat confirming to the results of the present study.

Heritability in broad sense

The high estimates of heritability in broad sense were observed for days to 50% flowering, days to maturity, plant height, number of nodes per plant, number of leaves per plant, number of seeds per main spike, 1000 seeds weight, L:S ratio, green fodder yield, dry matter yield and seed yield per plant. Medium heritability was observed for number of reproductive tillers per plant and low heritability was observed for leaf length, leaf width and spike length. The results were in

concordance with Krishna *et al.* (2013) [12] and Surje *et al.* (2014) [19] where the characters like grain yield per plant had significantly showed higher values for heritability.

Genetic advance (as percent of mean)

High genetic advance was observed for number of reproductive tillers per plant, number of nodes per plant, 1000 seeds weight, L:S ratio, green fodder yield, dry matter yield and seed yield per plant. Medium genetic advance was observed for days to 50% flowering, days to maturity, plant height and number of leaves per plant. Low genetic advance was observed for leaf length, leaf width and spike length. The genetic advancement as percent mean was found to be highest for grain weight followed by dry matter yield, green fodder yield, number of spikelet's/panicle, 1000 seed weight and panicle length in the experiment carried out by Surje *et al.* (2014) [19].

Heritability and genetic advance

Expressed that high heritability together with high genetic advance was an indicative of additive gene effects and high heritability associated with low genetic advance was indication of dominance and epistatic effects. In the present study, high heritability coupled with high genetic advance was observed for number of reproductive tillers per plant, number of nodes per plant, number of leaves per plant, 1000 seeds weight, L:S ratio, green fodder yield, dry matter yield and seed yield per plant on pooled basis. This indicated that in these traits improvement could be made by simple selection. These results are in conformity with those of Singh *et al.* (2019) [17], Kumari *et al.* (2019) [14].

Conclusion

High seed yielding genotypes were JO-3-93 followed by JHO-2004, JHO-851, HJ-8, OS-6, JHO-2010-1, OS-7, JO-03-91, OL-125, JHO-2001-3 and JHO-99-1. High genotypic coefficient of variation was observed for dry matter yield followed by green fodder yield, seed yield per plant, L:S ratio, number of reproductive tillers per plant, number of leaves per plant, 1000 seeds weight, number of nodes per plant, number of seeds per main spike, days to maturity, days to 50% flowering, plant height, leaf width, leaf length and spike length. High heritability coupled with high genetic advance was observed for number of reproductive tillers per plant, number of nodes per plant, number of leaves per plant, 1000 seeds weight, L:S ratio, green fodder yield, dry matter yield and seed yield per plant on pooled basis.

Table 2: Analysis of variance for seed yield and its components in Oat for first location

		Mean sum of squares															
Sources	D.F	Days to 50% flowering	Days to maturity	Plant Height (cm)	Number of reproductive tillers per plant	Leaf length (cm)	Leaf width (mm)	Spike length (cm)	Number of nodes per plant	Number of leaves per plant	Number of seeds per main spike	1000 seeds weight (gm)	L: S ratio	Green fodder yield (gm)	Dry matter yield (gm)	Seed yield per plant (gm)	
E1	Replications	2	26.055*	32.000	147.120**	24.000**	1.398	0.032	1.398	30.500**	1.680	24.000**	1.227	0.001	90.059**	1.398	0.294
	Genotypes	23	200.535**	392.289**	380.122**	22.153**	6.250**	0.065**	6.456**	37.746**	33.810**	187.072**	100.201**	0.012**	6530.560**	15553.6777**	6.230**
	Error	46	7.446	21.333	0.193	0.463	1.388	0.013	1.389	0.268	0.724	2.898	1.389	0.001	0.193	10.084	0.222
	CV (%)		2.629	3.309	0.254	4.630	3.335	4.711	3.551	2.309	3.929	2.080	3.119	0.208	4.161	5.985	10.361
	CD at 5%		4.485	7.591	0.722	1.119	1.936	0.193	1.936	0.851	1.398	2.798	1.936	0.722	5.219	0.774	0.058
E2	Replications	2	3.125	0.222	62.052**	7.097*	1.491	0.026	0.097	16.125**	6.013**	20.222**	1.527	0.001	165.573**	3.225	0.087
	Genotypes	23	157.211**	402.541**	359.606**	18.113**	7.168**	0.130**	5.999**	37.458**	34.564**	174.802**	102.366**	0.010**	6525.674**	1569.551**	6.360**
	Error	46	7.212	2.657	0.200	2.184	1.389	0.013	0.125	0.545	0.521	0.106	1.389	0.001	0.274	2.657	0.555
	CV (%)		3.435	0.408	3.186	10.893	0.251	2.206	3.364	2.966	1.310	0.265	10.412	4.831	1.105	3.300	3.379
	CD at 5%		1.186	0.536	1.937	0.054	0.861	2.679	0.387	4.414	2.679	0.736	2.439	0.194	0.581	1.214	1.937
E3	Replications	2	12.722**	1.389	107.745**	16.125**	1.410	0.026	0.877	24.222**	14.680**	3.555	1.385	0.010*	120.406**	13.629	0.294
	Genotypes	23	223.787**	441.737**	356.340**	23.739**	6.395**	0.130**	5.339**	35.492**	36.071**	189.903**	102.366**	0.013**	6445.127**	1633.902**	6.188**
	Error	46	1.389	7.504	0.193	0.603	1.389	0.013	0.889	0.106	0.289	2.772	1.389	0.002	0.487	6.702	0.367
	CV (%)		1.525	2.502	0.263	5.753	3.382	4.871	3.170	1.444	2.604	2.114	3.191	0.340	3.539	8.558	18.699
	CD at 5%		1.937	4.502	0.722	1.276	1.936	0.194	1.549	0.536	0.883	2.737	1.937	1.147	4.255	0.996	0.088
P	Replications	2	34.042**	5.352	105.054**	13.116**	4.283	0.082	1.962	9.671**	13.115**	7.629*	4.113*	0.003	43.120**	10.405	0.032
	Genotypes	23	568.717**	1217.062**	1079.812**	54.425**	12.585**	0.159**	9.071**	109.313**	103.579**	547.552**	302.796**	0.032**	19500.036**	4742.857**	18.345**
	Error	46	5.614	10.312	2.179	2.010	1.945	0.031	1.691	0.402	0.492	1.972	1.308	0.001	0.404	6.645	0.215
	CV (%)		2.617	2.586	0.869	10.031	3.983	7.201	4.110	2.826	3.323	1.752	3.071	0.305	3.462	6.340	13.517
	CD at 5%		2.203	2.987	1.373	1.319	1.297	0.164	1.209	0.590	0.652	1.306	1.064	0.592	2.397	0.431	0.039

P=Pooled analysis, * significant at 5%, ** significant at 1%.

Table 3: Mean, range, coefficient of variation, heritability and genetic advance for seed yield and its components in Oat

Characters		Mean	Range	GCV	PCV	Heritability (broad sense) (%)	Genetic advance (% of mean)
Days to 50% flowering	E1	103.76	89.66-126.66	7.73	8.16	89.63	15.08
	E2	90.54	78.00-107.33	7.80	8.35	87.39	15.03
	E3	72.27	64.00-99.33	11.14	11.24	98.16	22.74
	P	90.52	77.22-111	8.73	9.12	91.77	17.24
Days to maturity	E1	138.66	120-157.66	8.01	8.63	85.29	15.25
	E2	124.38	110.33-146.33	9.28	9.37	98.05	18.93
	E3	109.47	92.66-131.66	10.99	11.27	95.07	22.07
	P	124.17	108.55-144.22	9.32	9.67	92.86	18.51
Plant Height (cm)	E1	173.33	147.96-187.04	6.49	6.49	99.85	13.36
	E2	168.65	144.09-183.88	6.48	6.49	99.83	13.35
	E3	167.05	142.13-181.96	6.52	6.52	99.84	13.42
	P	169.68	144.72-184.27	6.44	6.50	98.2	13.16
Number of reproductive tillers per plant	E1	14.70	10.00-19.00	18.28	18.88	93.97	36.36
	E2	14.19	9.66-18.00	16.22	19.28	70.85	28.14
	E3	13.50	9.00-19.00	20.57	21.36	92.75	40.80
	P	14.13	9.55-18	17.07	19.80	74.34	30.25
Leaf length (cm)	E1	35.32	31.87-37.84	3.60	4.91	53.85	5.44
	E2	34.88	31.45-37.63	3.97	5.22	58.11	6.24
	E3	34.84	31.42-37.59	3.70	5.01	54.57	5.64
	P	35.01	32.54-37.61	3.10	5.05	37.80	3.93
Leaf width (mm)	E1	2.50	2.25-2.81	5.23	7.04	55.24	8.01
	E2	2.43	1.93-2.77	8.06	9.40	73.62	14.26
	E3	2.42	1.91-2.75	8.13	9.48	73.62	14.38
	P	2.43	2.10-2.62	4.86	8.68	31.30	5.60
Spike length (cm)	E1	33.18	29.33-35.30	3.91	5.28	54.88	5.97
	E2	31.98	29.63-34.69	4.37	4.51	94.00	8.73
	E3	29.73	26.94-31.68	4.09	5.18	62.53	6.67
	P	31.63	29.83-33.28	2.86	5.00	32.66	3.36
Number of nodes per plant	E1	22.42	14.00-29.00	15.76	15.93	97.90	32.13
	E2	22.37	14.00-29.00	15.67	16.02	95.76	31.60
	E3	22.56	14.00-29.00	15.21	15.28	99.11	31.21
	P	22.45	14.00-29.00	15.49	15.74	96.78	31.39
Number of leaves per plant	E1	21.65	13.33-28.33	15.33	15.83	93.84	30.60
	E2	21.07	12.66-27.66	16.03	16.39	95.61	32.28
	E3	20.65	12.33-26.67	16.72	16.92	97.63	34.04
	P	21.10	12.77-27.55	16.03	16.37	95.88	32.34
Number of seeds per main spike	E1	81.83	67-96	9.57	9.79	95.49	19.27
	E2	79.94	65-94	9.54	9.55	99.82	19.64
	E3	78.78	63.67-92.67	10.02	10.24	95.74	20.20
	P	80.18	65.22-94.22	9.70	9.86	96.85	19.68
1000 seeds weight (gm)	E1	37.77	24.94-43.55	15.12	15.50	95.95	30.65
	E2	36.98	23.40-43.44	15.68	16.00	96.04	31.66
	E3	36.93	23.35-43.39	15.07	16.02	96.04	31.70
	P	37.23	23.90-43.38	15.54	15.54	96.24	31.41
L: S ratio	E1	0.33	0.25-0.48	17.79	20.58	90.01	35.11
	E2	0.30	0.21-0.44	18.15	21.17	97.42	42.067
	E3	0.28	0.19-0.45	20.83	27.99	84.09	37.16
	P	0.30	0.21-0.45	18.82	23.17	65.99	31.50
Green fodder yield (gm)	E1	211.26	143.63-308.96	22.08	22.08	74.67	31.66
	E2	208.51	140.28-306.16	22.36	22.36	73.43	32.06
	E3	205.07	137.32-301.61	22.60	22.60	55.40	31.95
	P	208.28	140.41-305.58	22.34	22.35	99.98	46.03
Dry matter yield (gm)	E1	76.31	44.66-130.72	29.72	30.01	99.99	45.49
	E2	73.89	42.14-128.01	30.92	31.00	99.96	46.07
	E3	73.15	37.33-127.406	31.83	32.03	99.98	46.55
	P	74.45	42.77-128.71	30.81	31.00	98.75	63.00
Seed yield per plant (gm)	E1	7.78	5.47-10.32	17.96	18.93	98.08	60.64
	E2	7.00	4.73-9.44	20.68	20.96	94.49	63.55
	E3	7.08	4.72-9.43	19.67	21.45	98.78	65.18
	P	7.32	4.97-9.72	19.38	20.93	90.34	37.95

P = Pooled analysis, GCV & PCV are Genotypic and Phenotypic coefficients of variation respectively

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