The Pharma Innovation Journal 2022; 11(9): 578-583

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(9): 578-583

www.thepharmajournal.com
Received: 13-05-2022
Accepted: 21-07-2022

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

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Abstract
A trial was conducted at Research Station, Daleep Nagar, Kanpur Dehat (highly alkaline conditions) 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 and dry matter yield on pooled basis.

Keywords: oat, alkaline, 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. The genus *Avena* is known for its tolerance of high alkalinity and oats is tolerant of high pH conditions and quite tolerant of salt stress. Bhagmal *et al*. (2009) [19] reported that oats possessed high tolerance of salinity. High oat yields can be achieved in saline and alkaline soils if irrigation is provided. Therefore, there is a need for a better understanding of the genetic variations affecting saline/alkaline tolerance in a large population of oat genotypes, and a method of screening for these.

Material and Methods
A trial was conducted at Research Station, Daleep Nagar, Kanpur Dehat (highly alkaline conditions) 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 IGFRI, 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)	Research Station, Daleep Nagar, Kanpur Dehaat	17 Oct, 2021	Early sown	9.6	1.59
Environment II (E2)	Research Station, Daleep Nagar, Kanpur Dehaat	15 Nov, 2021	Normal sown	9.6	1.59
Environment III (E3)	Research Station, Daleep Nagar, Kanpur Dehaat	27 Dec, 2021	Late sown	9.6	1.59

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 environments 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 on pooled basis. High seed yielding genotypes were OS-6, JO-3-93, JO-03-91, JHO-851, JHO-2004, HJ-8, JHO-2010-1, OL-125, OS-7, JHO-99-1, JO-1, JHO-822 and JHO-2001-3. 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, number of reproductive tillers per plant, number of leaves per plant, number of nodes per plant, number of nodes per plant, L:S ratio, seed yield 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 reproductive tillers, leaf width, number of nodes per plant, number of leaves per plant, green fodder yield and dry matter yield. Medium heritability was observed for number of seeds per main spike, L:S ratio and seed yield per plant and low heritability was observed for leaf length, leaf width and spike length. The results were in concordance with Amar Deep *et al.* (2019) [20] where the characters like days to 50% flowering had significantly showed higher values for heritability and Shekhawat (2016) [21] where the characters like green fodder yield 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, number of leaves per plant, 1000 seeds weight, L:S ratio, green fodder yield and dry matter yield. Medium genetic advance was observed for days to 50% flowering, days to maturity, plant height, number of seeds per main spike and seed yield 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/panicles, 1000 seed weight and panicle length in the experiment carried out by Surje *et al.* (2014) [22] and moderate genetic advance for days to 50% flowering and the number of seeds per main spike in the experiment carried out by Amar Deep *et al.* (2019) [23].

Heritability and genetic advance: Panse (1957) [24] 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 and dry matter yield on pooled basis. This indicated that in these traits improvement could be made by simple selection. These results are in conformity with those of Shekhawat (2016) [21], Singh *et al.* (2019) [17], Kumari *et al.* (2019) [14].

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

	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	14.542	6.500	68.146**	27.555**	0.652	0.013	1.336	23.013**	18.500**	13.347*	0.094	0.001	118.844**	6.361	0.375
	Genotypes	23	179.342**	399.951**	377.137**	20.347**	4.684**	0.149**	4.522**	39.564**	35.920**	10.506**	100.782**	0.010**	6493.697**	1604.918**	2.962**
	Error	46	6.585	3.195	0.202	0.628	0.541	0.024	0.550	1.260	0.528	3.332	2.171	0.001	0.226	5.562	0.239
	CV (%)		2.389	1.277	0.262	6.899	2.357	7.875	2.606	5.218	4.430	6.021	4.126	0.231	3.336	3.406	10.885
	CD at 5%		4.217	2.938	0.739	1.302	1.208	0.259	1.219	1.840	1.195	3.000	2.422	0.782	3.876	0.803	0.053
E2	Replications	2	168.388**	58.722*	137.089*	28.222**	2.740	0.002	2.790	16.125**	15.389**	38.222*	2.696	0.001	109.269**	48.415	0.124
	Genotypes	23	151.961**	357.504**	381.871**	23.955**	8.146**	0.137**	5.928**	38.762**	36.345**	188.743**	99.192**	0.008**	6578.577**	1550.987**	7.024**
	Error	46	7.548	11.533	32.277	1.613	1.675	0.014	1.260	0.545	0.432	4.830	1.675	0.001	0.193	18.115	0.055
	CV (%)		3.032	2.725	3.413	10.017	4.027	5.044	3.684	3.811	3.581	3.076	3.644	0.213	5.965	4.378	9.403
	CD at 5%		4.514	5.581	9.337	2.087	2.127	0.193	1.840	1.213	1.080	3.621	2.127	0.722	6.995	0.387	0.040
E3	Replications	2	32.889*	27.125*	66.656**	24.125**	0.322	0.006	0.876	54.125**	16.889**	15.389	0.094	0.001	99.879**	16.095	0.220
	Genotypes	23	207.910**	377.342**	355.885**	23.717**	6.199**	0.130**	4.503**	36.125**	37.468**	193.128**	102.275**	0.009**	6501.067**	1479.410***	6.612**
	Error	46	6.657	6.646	0.193	0.125	0.500	0.014	0.545	0.429	0.425	10.084	2.374	0.001	0.174	5.419	0.182
	CV (%)		3.226	2.296	0.269	3.052	2.209	5.073	2.804	4.084	3.749	4.299	4.612	0.207	3.338	9.513	14.432
	CD at 5%		4.240	4.237	0.722	0.581	1.162	0.194	1.213	1.076	1.071	5.219	2.532	0.684	3.826	0.703	0.053
P	Replications	2	70.264**	39.893**	239.569**	20.042**	3.047	0.015	4.703*	18.115**	34.667**	62.375*	0.899	0.001	327.428**	60.676**	0.014
	Genotypes	23	521.307**	1118.721**	1080.439**	54.649**	10.828**	0.188**	7.998**	112.763**	108.927**	270.341**	298.610**	0.018**	19572.772**	4613.127**	8.971**
	Error	46	7.436	7.353	12.475	2.263	1.704	0.042	1.458	0.769	0.447	19.816	2.010	0.001	0.219	10.048	1.072
	CV (%)		2.943	2.158	2.127	12.623	4.107	9.919	4.249	4.624	3.847	7.604	4.065	0.229	4.490	12.821	16.134
	CD at 5%		2.536	2.522	3.285	1.399	1.214	0.190	1.123	0.816	0.622	4.140	1.319	0.435	2.948	0.963	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	103.27	95.33-139.00	7.06	7.46	89.74	13.79
	E2	90.61	81.33-110.66	7.65	8.23	86.44	14.66
	E3	79.97	70.00-120.00	10.24	10.74	90.97	20.12
	P	92.65	82.44-114.22	8.15	8.67	88.48	15.80
Days to maturity	E1	139.95	125.66-162.00	8.22	8.31	97.64	16.72
	E2	124.63	111.00-147.00	8.61	9.03	90.91	16.92
	E3	112.29	98.33-134.33	9.89	10.16	94.90	19.86
	P	125.62	111.71-147.77	8.84	9.10	94.38	17.70
Plant Height (cm)	E1	168.34	143.10-181.85	6.65	6.66	99.84	13.71
	E2	166.44	139.69-180.86	6.48	7.32	78.31	11.82
	E3	163.26	138.67-178.10	6.66	6.67	99.84	13.72
	P	166.01	140.94-180.27	6.56	6.89	90.49	12.85
Number of reproductive tillers per plant	E1	11.48	7.00-15.00	22.32	23.36	91.28	43.90
	E2	12.68	8.00-18.00	21.52	23.73	82.19	40.19
	E3	11.58	7.00-17.00	24.20	24.40	98.44	49.48
	P	11.91	7.33-15.22	20.24	23.85	72.01	35.39
Leaf length (cm)	E1	31.20	29.0-33.68	3.76	4.44	71.85	6.57
	E2	32.14	28.79-34.96	4.56	6.09	56.28	7.06
	E3	32.00	28.52-34.69	4.30	4.84	79.17	7.89
	P	31.78	29.30-34.15	3.16	5.18	37.29	3.98
Leaf width (mm)	E1	2.01	1.59-2.59	10.16	12.86	62.50	16.55
	E2	2.33	1.75-2.66	8.67	10.03	74.73	15.44
	E3	2.32	1.82-2.65	8.47	9.87	76.32	14.98
	P	2.22	1.93-2.52	5.74	10.84	28.10	6.27
Spike length (cm)	E1	28.46	26.00-30.58	4.04	4.81	70.65	7.00
	E2	30.47	28.31-33.37	4.09	5.50	55.25	6.26
	E3	26.33	24.18-28.30	4.36	5.18	70.76	7.55
	P	28.42	26.36-30.14	2.99	5.20	33.25	3.56
Number of nodes per plant	E1	21.51	13.33-28.33	16.60	17.40	91.02	32.64
	E2	19.37	11.00-26.00	18.42	18.81	95.90	37.16
	E3	16.04	7.66-22.66	21.50	21.88	96.52	43.51
	P	18.97	10.66-25.66	18.58	19.15	94.17	37.16
Number of leaves per plant	E1	16.42	8.00-23.00	20.92	21.38	95.71	6.92
	E2	18.36	10.00-25.00	10.95	11.38	92.70	21.73
	E3	17.38	9.00-24.00	20.20	20.55	96.67	40.92
	P	17.38	9.00-24.00	19.96	20.33	96.42	40.38
Number of seeds per main spike	E1	30.32	23.33-32.00	5.10	7.89	41.78	6.79
	E2	71.44	57.00-86.00	10.95	11.38	92.70	21.73
	E3	73.86	59.00-88.33	10.57	11.41	85.82	20.18
	P	58.54	48.66-68.00	9.01	11.79	58.41	14.18
1000 seeds weight (gm)	E1	35.71	22.76-41.37	16.05	16.57	93.80	32.03
	E2	35.52	22.00-41.00	16.05	16.45	95.10	32.24
	E3	33.41	19.16-39.70	17.27	17.87	93.34	34.37
	P	34.88	31.48-40.36	16.45	16.95	94.25	32.91
L: S ratio	E1	0.29	0.18-0.45	18.56	21.51	24.41	32.98
	E2	0.25	0.18-0.38	19.29	21.46	80.81	35.73
	E3	0.22	0.12-0.37	23.35	27.45	72.36	40.92
	P	0.26	0.18-0.34	16.13	16.73	51.84	24.82
Green fodder yield (gm)	E1	205.61	138.16-302.83	22.62	22.62	99.99	46.60
	E2	205.57	137.76-302.98	22.77	22.77	99.99	46.98
	E3	201.52	133.97-298.93	23.09	23.10	99.99	47.58
	P	204.23	136.63-301.58	22.83	22.83	99.99	47.03
Dry matter yield (gm)	E1	70.69	35.88-128.60	32.65	32.82	98.97	66.92
	E2	71.35	40.15-126.02	28.31	28.65	97.66	57.64
	E3	69.74	38.20-120.74	31.78	31.95	98.91	65.10
	P	70.59	38.07-125.12	32.03	32.34	98.07	65.35
Seed yield per plant (gm)	E1	14.35	13.16-16.11	6.63	7.45	79.15	12.16
	E2	5.38	3.05-8.12	31.68	32.23	96.58	64.13
	E3	4.49	2.15-6.89	32.55	33.91	92.13	2.89
	P	8.07	6.30-9.72	11.59	17.28	44.99	16.02

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

Conclusion

High seed yielding genotypes under highly alkaline conditions were OS-6, JO-3-93, JO-03-91, JHO-851, JHO-2004, HJ-8, JHO-2010-1, OL-125, OS-7, JHO-99-1, JO-1, JHO-822 and JHO-2001-3. High genotypic coefficient of variation was observed for dry matter yield followed by green fodder yield, number of reproductive tillers per plant, number of leaves per plant, number of nodes per plant, number of nodes per plant, L:S ratio, seed yield 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 and dry matter yield on pooled basis.

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