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### Stability analysis for morphological characters in oats (*Avena sativa* L.)

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#### Abstract

An experiment was carried out with twenty five genotypes of oats under three random environmental conditions in central zone of Uttar Pradesh. Significant variation among genotypes was observed for all the traits, indicating presence of high level of variability. Significant GXE interaction was observed for all the traits. Partitioning of GXE interaction revealed that both the components were highly significant in all the characters with predominance of the linear component, thereby, suggesting that the performance of genotypes across environments could be predicted with greater precision. The twenty three genotypes namely; CSAOFSC12-2, JHO2007-2, CSAOFSC14-6, SKO101, JHO03-93; SKO105, JHO2007-2, JHO851, JHO99-2, OS1, CSAOFSC12-1, CSAOFSC11-4, CSAOFSC11-1, NDO25, JHO03-91, ANDO2, OS403, CSAOFSC14-4, ANDO1, Kent, OS1, CSAOFSC11-5 and OS344 were well adopted and rest of the genotypes were stable for poor and favorable environments. Genotypes namely; CSAOFSC12-2, CSAOFSC11-5, ANDO1, OS344, OS1, SKO105, CSAOFSC14-6, JHO0391 and JHO851 were found to be stable and well adopted to all environments for most of the yield and yield related traits. These genotypes would be exploited as elite gene pool in future breeding programme for the genetic improvement of oats.

**Keywords:** Oats, genotypes, environment, morphology and stability

#### Introduction

Oat (*Avena sativa* L.  $2n=6x=42$ ) a constituent of family *poaceae*, ranks sixth in the world cereal production and is cultivated for use as food, feed and fodder. The crop has been adopted well by the farmers because of its multicut nature and high yield of nutritious palatable fodder. Oat has been used as food and fodder since ancient times but gradually it is used from dates back to till date for consumption in different ways by human. Oats are one of the highly nutritious cereals for human use, but suffer due to the advantage of large proportion of hulls (20-30%) which need to be removed from the grains. In human health point of view, the use of oat meal/whole grain in breakfast lower the cholesterol levels prevent heart failure enhance immune response to infection and stabilize blood sugar. On the other hand, it is also used as medicinal ingredient to protect against cancers and heart diseases, enhance immune response to infection, stabilize blood sugar, smooth skin conditions and other ailments, as well as use as an antispasmodic, a diuretic, an emollient, a nerve tonic, a supplement, an aphrodisiac, and a stimulant. Oat mostly recognized as an animal feed but oats may also be consumed by human in different ways, such as oat grain is an ingredient in a wide range of food products including breakfast cereals, porridge, cookies, breads and muffins, crackers, snacks, beverages, meat extenders and baby foods. In order to genetic diversity the genotypic profile of oats in U.P. it is necessary to identify and evolve more number of genotypes having high potential of grain and fodder yield and quality through application of well and systematic breeding programme. The GXE interactions are of major significance to breeders in the process of evolution of new genotypes. The breeders objective is to evolving strains which may be give the maximum mean economic yield over environments and exhibit consistent performance. A cultivar is considered to be well stable one if it has a high mean yield but low degree of fluctuations in yielding ability when grown over diverse environments (Arshad *et al.*, 2003) [4].

Desirable advances have made in the measurement of contribution of the cultivar over environments by using by using the regression techniques. Stability model proposed by Eberhart and Russell (1966) [9] is a powerful tool which enables to measure the phenotypic stability related to performance of genotypes.

Mean value, regression slope of the genotype and deviation from the regression is considered while assessing the performance of a genotype in a given environment. Taking in view the above considerations, the present study was carried out over a set of 3 diverse environments to characterize the nature of GXE interaction and to calculate the stability parameters for identification of stable genotypes across environments.

### Materials and Methods

Material for the present study comprised of twenty five genotypes originate from different institutes viz., CSOFSC12-2, CSOFSC11-5, Kent, CSOFSC11-4, CSOFSC11-1, CSOFSC12-1, UPO212, ANDO1, JHO03-91, CSAOSC12-1, ANDO2, OS403, OS344, OS1, SKO105, NDO25, JHO2007-2, CSAOSC14-6, SKO101, JHO2007-2, JHO03-93, NDO612, OS6, JHO851 and JHO99-2. The genotypes were tested at Students Instructional Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur in randomized block design with three replications on three different dates of sowing as early (15 November), normal (30 November) and late (15 December) respectively. The sowing was done by hand in lines 25 (cm) apart. The plot size was 3.6 m<sup>2</sup> comprising of four rows each 3.0 m long. The plant to plant distance was maintained at 10 cm by proper thinning and border rows were also planted to neutralize the border effect apart in *rabi* 2016-17 and 2017-18. Observations were recorded on five randomly selected and tagged competitive plants from each experimental plot in each replication for fifteen traits namely; days to 50% flowering, days to maturity, numbers of reproductive tillers per plant, leaf length (cm), leaf width (cm), plant height (cm), number of nodes per plant, number of leaves per plant, biological yield per plant (g), spike length (cm), number of seeds per main spike, dry weight per plant (g), test weight (g), harvest index (%), spike length, and seed yield per plant (g).

The data was subjected to analysis of variance for single as well as pooled over environments and stability analysis (Eberhart and Russell's 1966) [9]. The stability analysis technique partitions the genotypes x environment interaction components of variance of each genotype into two parts. Therefore, each genotype is characterized by three parameters viz.; (A) mean yield ( $\bar{x}$ ) over all environments, (B) a linear regression coefficient ( $b_i$ ) in relation to environment index and (c) the deviation from linear regression ( $S^2_{di}$ ). Since, the average slope for the environmental index is 1.0, regression coefficient for each genotype may be 1.0 or greater or lesser than 1.0. The genotype with regression value of 1.0 is considered to have an average adaptability, where as the value less than 1.0 or higher than 1.0 would mean below average and above average adaptability respectively. The test of significance of difference among genotypes with respect to mean was done using t-test and Deviation from regression for each genotype was tested using F-test. Another stability parameters ( $S^2_{di}=0$ ) is considered to be stable as suggested by Singh and Chaudhary (1985) [15].

### Results and Discussion

For genotype to be economically successful, it must perform well across a range of environments in which the genotype has to be cultivated. Because the GXE has masking effect on the phenotype several breeders attempt to calculate the magnitude of interaction variance attributable to GxE interactions so that the precise estimate of genotypic variance could be obtained. Analysis of variance (Table-1, 1a, 1b, 1c,

1d and 1e) showed that all the genotypes had significant genetic variability for all traits in separately six ( $E_1, E_2, E_3, E_4, E_5$  and  $E_6$ ) environments, indicating that performance of genotypes varied from environment to environment therefore, selection for stable genotypes may be effective. Combined analysis of variance (Table -2 and 2a) revealed that all the genotypes had significant genetic variability for all traits in three environments, it is imperative to select the suitable genotype as per environmental conditions. Analysis of pooled data (Table-3) revealed that all the genotypes had significant genetic variability for all traits in three environments as interaction between genotype x environment was found significant for all the characters. It reflected significant variability among the genotypes under study. General analysis of pooled data (Table-4) over environments indicated significant differences among the test genotypes for the all traits, indicating available spectrum of variation in used genotypes. Analysis of variance based on pooled estimates (Table-5) showed that all the genotypes had significant genetic variability for all traits, exhibiting scope for selection of stable genotype under diverse environment. Mean square due to environments was significant for all the characters indicating influence of environment on their expression. The mean square due to Environment + Genotypes x Environment was significant for all the traits exhibiting variable response of the genotypes for all traits in the changing environment. The E x G interaction component was also showed significant differences for all the characters among the test genotypes exhibiting that these characters were not stable over the environments. Singh and Chaudhary (1985) [15] suggested that if genotype with unit regression coefficient ( $b_i=1$ ) and the deviation not significant by different from zero ( $S^2_{di}=0$ ) are considered as stable. Pham and Kang (1988) indicated that genotype x environment interactions minimize the usefulness of genotypes by confounding their yield performance. Backer and Leon (1988) [5] also indicated that assessment of stability across many locations and years could increase both repeatability and heritability of important traits.

Further component analysis of environment + genotype environment mean square revealed that differences between the environments existed and they had considerable influence on all the traits. The major portion of these variations could be attributed to linear regression. Significance of linear component implied that the behavior of the genotypes for all the traits was predictable over environments and this had resulted from the linear function of the environmental component. Significance of nonlinear component for all the traits revealed that the behavior of deviation from regression existed among genotypes for all the traits. When genotype x environment is due to variation in predictable environment factors, Oat breeders have the alternatives of either developing specific varieties for different environments (location, soil type, winter type, spring type etc.) or broadly adapted cultivars that can perform well under variable conditions. However, when genotype x environment interaction results from variation in unpredictable environmental factors, such as year to year variation in rainfall distribution, the breeders needs to develop stable genotypes that can performs reasonably well under a range of environmental conditions. Similar results have been reported by Wani *et al.*, 2002 [16]; Akcura *et al.*, 2005 [3]; Nehvi, *et al.*, 2007 [13]; Mushtaq, *et al.*, 2016 [1], Mehraj *et al.*, 2017 [12]; Zeki *et al.*, 2018 [17], Emilian, *et al.*, 2019 [10].

Identification of stable genotypes having adoptability over a wide range of agro-climatic conditions is of major

significance in crop Improvement. Comstock and Moll (1963) suggested that selection would not be effective due to presence of significant GXE interaction; therefore breeders should give emphasis on stable performance of a line over a wide range environments. According to Ebarhart and Russel (1966) a stable genotype was defined as one which showed high mean yield, regression coefficient  $b_i$  around unity and deviation from regression  $S^2_{di}$  nearer to zero. The non significant linear  $b_i$  and non Linear  $S^2_{di}$  components indicated average stability with high precision across environmental changes. Whereas, significant  $b_i$  and non-significant  $S^2_{di}$  components suggest above average stability for favorable environments. The significant/non-significant and  $S^2_{di}$  component indicates that behavior of genotypes is highly unpredictable and they are not suitable for changed environments. Estimates of stability parameters for 25 different genotypes for fifteen traits revealed significant mean square deviations from regression  $S^2_{di}$  with respect to days to 50% flowering (5) genotypes; for days to maturity (4) genotypes; for number of reproductive tillers per plant (2) genotypes; for leaf length (2) genotypes; for leaf width (2) genotypes; for plant height (1) genotype; for number of nodes per plant (4) genotypes; for number of leaves per plant (1) genotype; for biological yield of plants (4) genotypes; for number of seeds per main spike (1) genotype; for dry weight per plant (5) genotypes; for test weight (5) genotypes; for harvest Index (3) genotypes; for spike length (2) genotypes; and for seed yield per plant (10) genotypes. The genotypes showing non-significant mean square deviation from regression (pooled deviation) indicated that non-linear component (heterogeneity from regression) was equal to zero, hence the performance of these genotypes for a given environment could be predictable. Accordingly a genotype whose performance could be predictable (i.e.,  $S^2_{di} = 0$ ) was classified as stable.

The Linear regression ( $b_i$ ) deviated from unity for days to 50% flowering (20) genotypes; for days to maturity (21) genotypes, days to 50% flowering (5) genotypes; for days to maturity (21) genotypes; for number of reproductive tillers per plant (23) genotypes; for leaf length (23) genotypes; for leaf width (23) genotypes; for plant height (24) genotypes; for number of nodes per plant (21) genotypes; for number of leaves per plant (24) genotypes; for biological yield of plants (21) genotypes; for number of seeds per main spike (24) genotypes; for dry weight per plant (21) genotypes; for test weight (20) genotypes; for harvest index (22) genotypes; for spike length (23) genotypes and for seed yield per plant (15) genotypes. Hence, they could be considered as more responsive. However, considering their mean value, deviation from regression ( $S^2_{di}$ ) and desirability of the traits, the genotypes showing above average stability for favorable environment were identified in Oats-19, CSAOFSC12-2, days to 50% days to maturity flowering, leaf length, number of leaves per plant, number of leaves per plant, test weight, spike length and for seed yield per plant; JHO2007-2, for, days to 50% flowering and days to maturity; CSAOFSC14-6 for days to 50% flowering, days to maturity, plant height, harvest index, spike length and seed yield per plant, SKO101 for days to 50% flowering and harvest index and seed yield per plant JHO03-93; for days to 50% flowering, days to maturity and harvest index; SKO105 for plant height, spike length and seed

yield per plant, JHO851 for leaf length, leaf width, spike length and seed yield per plant, JHO99-2 for number of reproductive tillers per plant OS1 for leaf width, spike length and seed yield per plant, CSAOFSC12-1 for number of nodes per plant and dry weight per plant, CSAOFSC11-5 for number of leaves per plant and seed yield per plant, CSAOFSC11-4 for number of leaves per plant; CSAOFSC11-1 for number of leaves per plant, NDO25 for biological yield of plants, JHO03-91 for number of seeds per main spike, test weight and seed yield per plant, ANDO2 for dry weight per plant, and seed yield per plant, OS403 for number of seeds per main spike and test weight, CSAOFSC14-4 for test weight, ANDO1 for test weight and seed yield per plant, Kent, for harvest index OS1 for spike length and seed yield per plant, CSAOFSC11-5 for seed yield per plant and OS344 for seed yield per plant and no genotype was identified to exhibit above average stability for favorable environments.

The genotypes not deviating significantly from unit regression for a particular trait revealed that they were average in stability with high prediction across environments and as such were either poorly or well adapted to all the environments depending upon the mean performance. However, the non-significant Linear regression coefficient ( $b_i$ ) was valid only for genotypes with non-significant deviation from regression ( $S^2_{di}$ ). Genotypes that showed average stability and were well adopted to all the environments included Genotypes viz, CSAOFSC12-2, JHO2007-2, CSAOFSC14-6, SKO101 and JHO03-93 were found stable for early flowering ; SKO105, JHO2007-2 JHO851 and JHO99-2 for early maturity; CSAOFSC12-2 and JHO851 for number of reproductive tillers per plant; OS1 and JHO851 for leaf length; CSAOFSC14-6 and SKO105 for leaf width; CSAOFSC12-1 for plant height; CSAOFSC12-2, CSAOFSC11-5, CSAOFSC11-4 and CSAOFSC11-1 for number of nodes per plant; NDO25 for number of leaves per plant; ANDO1, JHO03-91, ANDO2, and OS403 for biological yield per plant; CSAOFSC12-1 for number of seeds per main spike. Genotypes namely, CSAOFSC12-2, CSAOFSC14-4, ANDO1, JHO03-91 and OS403 were found stable for dry weight per plant. Genotype viz; CSAOFSC12-2, Kent, CSAOFSC14-6 SKO101 and JHO03-93 were found stable for test weight. Genotype viz, OS1, CSAOFSC14-6 and JHO851 for harvest index; SKO105 and SKO101 for spike length; CSAOFSC12-2, CSAOFSC11-5, ANDO1, JHO03-91, ANDO2, OS344, OS1, SKO105, CSAOFSC14-6, and JHO851 were found stable for seed yield per plant. None of the genotype was well adopted for all the traits to all the environments (Table-6). However, nine genotypes namely, CSAOFSC12-2, CSAOFSC11-5, ANDO1, OS344, OS1, SKO105, CSAOFSC14-6, JHO03-91 and JHO851 were found stable for all types of sowing conditions and along with the various characters including seed yield per plant exhibited stability and were well adopted to all the environments for most of the yield and yield related traits. Akcura *et al.* (2005) also reported wide adoptability of oat genotypes across the locations. Gupta and Singh (1997) also reported stable performance of several genotypes in respect of various yield and quality traits. Dubey *et al.* (1995) also identified genotypes that were best suited to poor environments, normal and high input conditions.

**Table 1:** Analysis of variance for seed yield and its component in oat Over Environment -1 during 2016-2017(E<sub>1</sub>)

Source of Variation	D.F.	DF	DM	NRTPP	LL(cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW(g)	HI (%)	SL(cm)	SYPP(g)
Replication	2	2.52	4.82	0.09	32.21	0.07	13.43	0.12	0.61	6.96	83.68	2.86	0.07	22.63	28.37	0.01
Treatment	24	22.71**	14.28**	17.90**	54.16**	0.18**	63.52**	1.30**	1.08**	2.41**	455.49**	1.52**	0.84**	21.29**	15.23**	0.29**
Error	48	0.78	0.29	1.72	25.37	0.04	14.29	0.12	0.24	0.23	59.83	0.32	0.04	3.59	3.21	0.02

**Table 1(a):** Analysis of variance for seed yield and its component in oat Over Environment -2 during 2016-2017(E<sub>2</sub>)

Source of Variation	D.F.	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW	HI (%)	SL(cm)	SYPP(g)
Replication	2	2.82	0.08	1.77	94.08	0.11	21.97	0.12	0.00	2.20	70.68	0.48	0.04	17.81	34.77	0.06
Treatment	24	12.06**	17.22**	13.85**	84.30**	0.18**	72.63**	0.26**	0.36**	1.83**	491.85**	0.97**	0.78**	40.96**	34.51**	0.23**
Error	48	1.54	0.68	1.84	2.04	0.01	5.99	0.18	0.25	0.33	1.15	0.33	0.04	4.18	0.94	0.02

**Table 1(b):** Analysis of variance for seed yield and its component in oat over Environment -3 during 2016-2017(E<sub>3</sub>)

Source of Variation	D.F.	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW(g)	HI (%)	SL(cm)	SYPP(g)
Replication	2	1.01	4.42	1.12	13.81	0.01	11.21	0.06	0.00	0.44	135.64	0.11	0.03	5.36	0.52	0.13
Treatment	24	3.81**	15.25**	11.22**	138.91**	0.09**	28.53**	0.34**	0.67**	1.84**	621.51**	0.73**	0.68**	37.43**	35.39**	0.39**
Error	48	0.40	0.79	0.90	4.72	0.01	8.31	0.06	0.08	0.09	77.10	0.03	0.04	6.83	4.23	0.09

**Table 1(c):** Analysis of variance for seed yield and its component in oat Over Environment -1 during 2017-2018 (E<sub>1</sub>)

Source of Variation	D.F.	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW(g)	HI (%)	SL(cm)	SYPP(g)
Replication	2	3.62	6.45	5.37	34.29	0.06	1.97	0.54	0.82	7.43	194.94	3.82	0.07	14.90	45.23	0.05
Treatment	24	31.31**	15.02**	13.28**	53.35**	0.20**	197.52**	1.29**	1.14**	2.77**	295.10**	2.48**	1.20**	33.05**	14.63**	0.51**
Error	48	0.40	0.15	1.53	21.17	0.03	8.21	0.27	0.26	0.04	42.84	0.06	0.08	0.53	5.43	0.01

**Table 1(d):** Analysis of variance for seed yield and its component in oat over Environment -3 during 2016-2017(E<sub>3</sub>)

Source of Variation	D.F.	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	SW(g)	HI (%)	SL(cm)	SYPP(g)
Replication	2	0.38	0.70	0.04	119.26	0.11	6.26	0.04	0.17	2.98	1.96	1.56	0.18	4.89	2.57	0.09
Treatment	24	10.61**	14.22**	14.60**	68.86**	0.13**	119.89**	0.61**	0.67**	1.79**	433.07**	1.06**	0.89**	37.33**	35.02**	0.31**
Error	48	0.36	0.48	0.72	4.03	0.01	9.56	0.18	0.22	0.04	6.82	0.24	0.10	0.94	1.09	0.02

**Table 1(e):** Analysis of variance for seed yield and its component in oat Over Environment -1 during 2017-2018 (E<sub>3</sub>)

Source of Variation	D.F.	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW	HI (%)	SL(cm)	SYPP(g)
Replication	2	1.62	1.36	0.09	62.57	0.00	55.69	0.04	0.01	2.08	209.65	1.01	0.03	11.62	7.64	0.06
Treatment	24	4.31**	13.16**	11.70**	19.93**	0.05**	57.09**	0.28**	0.77**	1.50**	414.14**	1.39**	0.68**	41.81**	14.79**	0.25**
Error	48	0.50	0.79	0.62	9.78	0.01	16.35	0.05	0.22	0.04	47.49	0.03	0.04	1.75	0.28	0.01

**Table 2:** Analysis of variance mean sum square of oat genotypes for twenty traits based on pooled E<sub>1</sub> and E<sub>1</sub>

Source of Variation	DF	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW	HI (%)	SL(cm)	SYPP(g)
Replication	2	1.51	5.47	1.10	33.24	0.06	2.17	0.26	0.68	7.13	130.88	3.36	0.07	18.48	35.35	0.02
Treatment	24	26.01**	14.58**	14.93**	46.54**	0.19**	225.30**	1.03**	1.01**	2.42**	351.79**	1.44**	1.00**	23.68**	14.53**	0.38**
Error	48	0.39	0.16	1.18	19.82	0.03	7.47	0.12	0.19	0.08	36.70	0.09	0.05	1.10	3.43	0.01

**Table 2a:** Analysis of variance mean sum square of oat genotypes for twenty traits based on pooled E<sub>2</sub> and E<sub>2</sub>

Source of Variation	DF	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW (g)	HI (%)	SL(cm)	SYPP(g)
Replication	2	0.34	0.27	0.39	106.29	0.11	12.24	0.01	0.04	2.52	22.84	0.25	0.09	10.10	13.92	0.08
Treatment	24	10.92**	15.54**	12.75**	71.38**	0.15**	109.61**	0.31**	0.45**	1.69**	457.40**	0.88**	0.81**	34.46**	34.08**	0.24**
Error	48	0.44	0.44	0.80	1.77	0.00	6.32	0.14	0.19	0.10	2.25	0.24	0.05	1.40	0.65	0.01

**Table 2(b):** Analysis of variance mean sum square of oat genotypes for twenty traits based on pooled E<sub>3</sub> and E<sub>3</sub>

Source of Variation	DF	DF	DM	NRTPP	LL (cm)	LW(cm)	PH(cm)	NNPP	NLPP	BYPP(g)	NSPMS	DWPP(g)	TW	HI (%)	SL(cm)	SYPP(g)
Replication	2	1.24	2.61	0.16	33.66	0.00	28.81	0.04	0.00	1.11	39.77	0.47	0.03	0.34	2.92	0.08
Treatment	24	3.91**	13.82**	11.30**	62.66**	0.06**	33.55**	0.29**	0.38**	0.86**	521.419**	0.56**	0.68**	14.87**	13.48**	0.13**
Error	48	0.33	0.63	0.53	4.84	0.01	8.66	0.05	0.09	0.04	29.56	0.01	0.04	2.14	1.13	0.02

**Table 3:** General ANOVA for 15 Characters for environments in 25 genotypes of Oat on based pooled

S.V.	D.F.	DF			DM			NRTPP			LL (cm)			LW(cm)			PH(cm)		
		E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>
Rep.	2	1.51	0.34	1.24	5.47	0.27	2.61	1.10	0.39	0.16	33.24	106.29	33.66	0.06	0.11	0.00	2.17	12.24	28.81
Tret.	24	26.01**	10.92**	3.91**	14.58**	15.54**	13.82**	14.93**	12.75**	11.30**	46.54**	71.38**	62.66**	0.19**	0.15**	0.06**	225.30**	109.61**	33.55**
Er	48	0.39	0.44	0.33	0.16	0.44	0.63	1.18	0.80	0.53	19.82	1.77	4.84	0.03	0.00	0.01	7.47	6.32	8.66

  

S.V.	D.F.	NNPP			NLPP			BYPP(g)			NSPMS			DWPP(g)			TW(g)		
		E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>
Rep.	2	0.26	0.01	0.04	0.68	0.04	0.00	7.13	2.52	1.11	130.88	22.84	39.77	3.36	0.25	0.47	0.07	0.09	0.03
Tret.	24	1.03**	0.31**	0.29**	1.01**	0.45**	0.38**	2.42**	1.69**	0.86**	351.79**	457.40**	521.419**	1.44**	0.88**	0.56**	1.00**	0.81**	0.68**
Er	48	0.12	0.14	0.05	0.19	0.19	0.09	0.08	0.10	0.04	36.70	2.25	29.56	0.09	0.24	0.01	0.05	0.05	0.04



NDO25	131.67	1.28*	-2.79	5.50	1.79*	0.02	5.94	0.79	0.00	11.21	0.86*	0.04	71.71	0.62*	5.49*
JHO2007-2	124.83	1.20*	21.67**	4.86	1.80*	0.22	4.72	0.23	0.00	12.25	1.45*	0.47	75.53	0.45*	7.18*
CSAOSC14-6	119.72	1.12*	4.67	5.06	0.27	-0.03	5.43	0.41	0.12	10.46	0.78*	0.05	75.33	1.81*	3.18*
SKO101	127.28	1.10*	-0.78	5.06	1.04*	0.05	5.19	0.42	0.06	10.81	0.55*	0.80	85.89	1.16*	6.06*
JHO2007-1	122.72	0.96*	19.06**	5.21	0.96*	0.03	5.30	1.30*	0.16	10.99	1.14*	0.15	70.07	1.01*	4.90*
JHO03-93	127.00	1.22*	3.46	5.11	0.26	-0.02	5.19	1.13*	-0.05	11.06	1.14*	0.10	77.88	2.04*	4.51*
NDO612	121.17	1.09*	8.43**	5.34	1.21*	-0.03	5.47	0.79*	0.07	11.43	1.02*	-0.03	69.47	0.76*	2.38
OS6	133.94	1.42*	-2.47	5.02	-0.38	0.00	5.19	0.22	0.24	11.12	0.89*	0.05	88.76	0.37*	4.18*
JHO851	129.39	0.97*	4.88**	5.48	1.73*	0.00	5.71	1.37*	0.07	10.98	0.97*	0.06	72.02	0.35*	7.63*
JHO99-2	133.11	1.40*	0.95	5.20	0.30	0.14	5.44	1.15*	0.11	11.31	0.95*	0.15	83.38	1.19*	6.63*
Popmean	125.76			5.29			5.50			11.45			74.28		
Se (mean)	1.15			0.14			0.18			0.21			4.56		
SE (b)		0.07			0.43			0.64			0.10				0.32

Genotypes	DWPP(g)			TW			HI (%)			SL(cm)			SYPP(g)		
	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
CSAOFSC12-2	8.80	0.92*	0.21	4.64	0.97*	-0.02	29.07	1.07*	1.93	28.40	0.91*	-0.20	3.831	0.93*	0.021
CSAOFSC11-5	8.83	1.06*	0.13	3.30	0.7*9	-0.02	30.23	1.44*	2.81*	28.75	0.84*	5.26*	3.458	0.77*	0.023
Kent	7.99	0.80*	0.06	4.15	0.60*	-0.02	31.13	1.40*	10.09**	26.29	0.31*	5.03*	3.315	0.65*	0.100
CSAOFSC11-4	9.11	0.91*	0.07	3.82	1.76*	-0.01	27.44	1.83*	0.32	26.00	0.54*	0.90	3.256	1.17*	0.010
CSAOFSC11-1	8.98	1.04*	0.19	3.78	0.92*	-0.02	28.69	1.57*	1.32	32.35	1.32*	24.10**	3.229	0.93*	0.012
CSAOFSC12-1	9.34	1.02*	0.07	4.39	1.20*	-0.02	27.16	1.01*	-0.27	31.57	1.00*	2.05	3.268	0.98*	0.003
UPO212	9.17	1.07*	0.22	3.55	1.13*	-0.01	26.98	0.52*	1.29	29.49	0.97*	8.35**	3.391	1.06*	0.001
ANDO1	8.71	0.94*	-0.02	4.19	1.03*	0.06	29.84	0.95*	1.18	27.71	0.92*	3.62*	3.442	0.84*	0.014
JHO03-91	9.02	0.83*	0.29	4.73	1.43*	0.00	28.34	-0.06	1.94	28.68	0.90*	2.16	3.497	0.84*	0.008
CSAOSC12-1	9.41	1.39*	0.33	3.75	1.05*	-0.02	29.78	0.31	1.59	30.97	1.13*	0.68	3.662	1.10*	-0.008
ANDO2	8.39	0.96*	0.21	3.83	-0.09	-0.02	30.87	0.92*	6.08*	29.27	0.96*	7.80*	3.656	0.57*	0.134
OS403	8.62	0.87*	0.05	3.37	0.49*	-0.01	30.75	0.65*	3.16*	29.53	1.01*	-0.49	3.620	1.01*	0.000
OS344	8.25	0.97*	0.11	3.85	0.73*	-0.02	31.37	0.86*	3.45*	27.66	0.90*	11.54**	3.506	0.91*	-0.002
OS1	8.51	1.10*	0.05	3.22	0.23*	-0.02	31.16	0.62*	1.41	28.20	1.00*	-0.18	3.573	0.98*	-0.004
SKO105	8.27	0.84*	0.23	3.49	0.71*	0.00	31.38	1.10*	0.81	29.08	0.97*	2.42	3.389	0.99*	-0.006
NDO25	8.21	0.81*	0.23	3.76	1.24*	-0.01	33.05	1.84*	2.39	29.80	1.12*	3.11*	3.722	1.21*	0.014
JHO2007-2	9.44	1.33*	0.45	3.84	0.78*	-0.02	30.02	-0.05	4.90*	29.76	1.20*	1.26	3.634	1.03*	0.000
CSAOSC14-6	8.03	1.17*	0.57	4.60	0.45*	-0.01	31.78	0.80*	0.01	27.98	1.01*	38.95**	3.816	0.89*	-0.004
SKO101	8.20	0.81*	0.25	4.46	0.77*	-0.01	33.00	1.68*	12.46**	30.14	0.90*	1.51	3.563	1.06*	0.002
JHO2007-1	8.08	0.91*	0.27	5.08	1.09*	0.00	35.61	2.93*	43.05**	30.97	1.04*	4.58*	4.073	1.76*	0.322
JHO03-93	8.93	1.28*	0.08	4.15	0.51*	-0.02	27.61	1.02*	0.76	30.81	1.09*	-0.65	3.051	1.02*	-0.004
NDO612	7.92	0.92*	0.26	4.30	3.15*	0.02	36.68	2.25*	3.20*	27.44	0.86*	7.29*	4.190	1.41*	0.058
OS6	8.13	1.05*	0.39	4.65	1.07*	-0.01	32.67	1.02*	0.02	30.26	1.38*	5.04*	3.647	1.05*	-0.001
JHO851	8.14	1.05*	0.01	4.59	1.73*	-0.02	31.50	0.78*	-0.57	27.64	1.28*	4.83*	3.463	0.95*	0.003
JHO99-2	8.93	1.08*	0.21	3.46	1.27*	-0.01	29.10	0.37*	-0.29	27.97	1.45*	1.60	3.272	0.79*	0.024
Popmean				4.04			30.61			29.07			3.35		
Se (mean)				0.05			1.02			1.14			0.09		
SE (b)		0.16			0.22			0.50			0.22				0.13

DF= Days to flowering DM= Days to maturity BYPP= Biomass yield per plant (g) NRTPP= Number of Reproductive Tillers per plant LL= Leaf length (cm) LW= Leaf width (cm) PH= Plant height (cm), NNPP= Number of Nodes per plant NLPP= Number of Leaves per plant BYPP= Biological yield per plant (g) NSPMS= Number of seeds per main spike DWPP= Dry weight per plant TW= Test Weight HI= Harvest Index (%) SL= Spike Length SYPP= Seed Yield per Plant (g)

**Table 6:** Summary of stable Oat genotypes based on Eberhart & Russells model

Sl. No.	Genotypes	Characters based on Eberhart & Russell's Models
1	CSAOFSC12-2	Dry weight per plant and Test
2	CSAOFSC11-5	Days to flowering, Number of Nodes per plant and Seed Yield per Plant (g)
3	Kent	-
4	CSAOFSC11-4	Days to flowering and Number of Nodes per plant
5	CSAOFSC11-1	Number of Nodes per plant
6	CSAOFSC12-1	Days to flowering, Number of Reproductive Tillers per plant and Number of seeds per main spike
7	UPO212	Spike length
8	ANDO1	Biological yield per plant (g) Dry weight per plant and Seed Yield per Plant (g)
9	JHO03-91	Biological yield per plant (g) and Dry weight per plant
10	CSAOSC12-1	-
11	ANDO2	Biological yield per plant (g) and Spike Length (cm)
12	OS403	Biological yield per plant (g)
13	OS344	Seed yield per plant (g)
14	OS1	Leaf length and seed yield per plant (g)
15	SKO105	Days to maturity, Leaf width (cm), Spike Length (cm) and Seed Yield per Plant (g)
16	NDO25	Number of leaves per plant
17	JHO2007-2	Days to flowering and Days to maturity
18	CSAOSC14-6	Days to flowering, Leaf width (cm) and Seed Yield per Plant (g)

19	SKO101	Days to flowering, Number of Reproductive Tillers per plant, Test Weight and Spike Length (cm)
20	JHO2007-1	-
21	JHO03-93	Days to flowering and Seed Yield per Plant (g)
22	NDO612	-
23	OS6	-
24	JHO851	Days to maturity Plant height (cm), Harvest Index (%) and Seed Yield per Plant (g)
25	JHO99-2	Days to maturity and number of reproductive tillers per plant

### Conclusions

Based on the as per for going study, it can be concluded that the cultivars namely; CSOFSC12-2, CSOFSC11-5, ANDO1, OS344, OS1, SKO105, CSAOFSC14-6, JHO0391 and JHO851 were found to be stable and well adopted to all environments along with various traits including seed yield per plant. Hence, these cultivars may be recommended for cultivation under diverse environmental conditions.

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