

**Research Article****Genotype x environment interaction for forage yield and its components in oats (*Avena sativa* L.)****Uzma Mehraj, Ishfaq Abidi, Mushtaq Ahmad\*, B.A. Wani, S.D. Mir, Gul-Zaffar, Z.A. Dar, Ansarulhaq, Aijaz A. Lone, M.A. Rather and M.A. Mir**

Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir Shalimar campus, Srinagar -191 121

**E-mail:** drmushtaqdarskuastk@rediffmail.com

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**Abstract**

The present investigation was carried out to study stability performance over six environments for forage yield and its components in 12 genetically diverse genotypes of oats using a randomized complete block design. The partitioning of (environment + genotype x environment) mean squares showed that environments (linear) differed significantly and were quite diverse with regards to their effects on the performance of genotypes for forage yield and its yield components. Stable genotypes were identified for wider environments and specific environments with high per se performance (over general mean) for forage yield ha<sup>-1</sup>. The investigation revealed that the genotype SKO-90, SKO-96 and Sabzaar were desirable and stable across the environments. Other genotypes SKO-148, SKO-160, SKO-166 and SKO-167 were found to be suitable for favourable situations, while genotype SKO-20 was responsible to poor environments for forage yield.

**Key words**

G x E interaction, stability analysis, forage yield, oats

**Introduction**

Oats (*Avena sativa* L.) is important forage cereals in temperate areas and economically is ranked as one of the sixth important crop in the world with global production of 22.59 million metric tons on an area of about 9.50 million hectares (Anonymous, 2015) following wheat, maize, rice, barley and sorghum. Compared to other cereal crops, oat is reputed to be better suited for production under marginal environments, including cool- wet climates and soils with low fertility (Lorenzetti *et al.*, 2006) and can be sensitive to hot, dry weather from head emergence through to maturity. For these reasons, world oat production is generally concentrated between latitudes 35– 65°N, including Finland and Norway, and 20 to 46°S, including Argentina, Brazil, and Chile. The EU (European Union) is the world's largest oat producing region followed by Russia, Canada, US and Australia. Russia remains the largest producer of oats worldwide, at 20% of total global production.

Oat grain has always been an important form of livestock feed. In many parts of the world, oats (*Avena sativa* L.) is grown for use as nutritious grain as well as for forage and fodder, straw for bedding, hay, haylage, silage and chaff. Livestock grain feed is still the primary use of oat crops, accounting for an average of around 74 per cent of the world's total usage in 1991 to 1992 (Welch, 1995). Oats account for less than 2 per cent of total grain production, with the bulk used on farms for feed. However, oats are also used in production of many human food products and in some industrial applications. Food uses for oats include oatmeal, oat flour, oat bran, and oat flakes, which are used for breakfast cereals and as ingredients in other

food products. A wide range of other applications for oats includes food manufacture, cosmetics, pharmaceuticals, and nutraceuticals.

In India fodder oat is grown in an area of 1.0 million ha with 35-50t/ha green fodder productivity (IGFRI, 2011). As per national estimate, by 2015 and 2025 A.D., sixty crores animals will need 1097 and 1170 million tons of green fodder, respectively. Deficiency of green fodder will be about 64.9 per cent and for dry fodders it may go up to 24.9 per cent in 2025 A.D. (Anonymous, 2001) At present, the country faces a net deficit of 63(%) green fodder, 24 per cent dry crop residues and 64 per cent feeds (Kumar *et al.*, 2012). The state of Jammu and Kashmir in general and Kashmir valley in particular is ideally suited for fodder oats cultivation because of its temperate climate. In valley, the oats is grown as a *rabi* crop in paddy fields, orchard areas and on Karewa lands. In Jammu and Kashmir during year 2012 the state had an area of about 0.143 million ha under fodder oats with a production of 0.322 million tonnes while in Kashmir region it occupies an area of 0.015 million ha with an annual production of 1.02 metric tonnes (Anonymous, 2012). State livestock population as per the estimate is 7.8 million so the fodder production is not sufficient enough to meet the requirements of a burgeoning livestock population (Anonymous, 2009). A specific genotype does not always exhibit the same phenotypic characteristics under all environments and different genotypes respond differently to a specific environment. Gene expression is subject to modification by the environment; therefore, genotypic expression of the phenotype is environmentally dependent (Kang, 1998). The development of new cultivars involves breeding of

cultivars with desired characteristics such as high forage yield, tolerance or resistance to biotic and abiotic stresses, traits that add value to the product, and the stability of these traits in target environments. Inconsistent genotypic responses to environmental factors such as temperature, soil moisture, soil type or fertility level from location to location and year to year are a function of genotype x environment (GE) interactions. Genotype x environment interactions has been defined as the failure of genotypes to achieve the same relative performance in different environments (Baker, 1988). Identification of yield contributing traits and knowledge of GE interactions and yield stability are important for breeding new cultivars with improved adaptation to the environmental constraints prevailing in the target environments. Currently, there is a need to develop and identify oat varieties having higher forage yield potential. To avoid genetic vulnerability associated with the narrowing of the genetic base of any crop, the GE interactions of the germplasm are important (Kang, 1998). Therefore, in the present investigation an attempt has been made to evaluate oat genotypes for yield and its component characters under different environments to identify genotypes with suitable performance in variable environments.

#### Materials and methods

The experiment was conducted with 12 genotypes of oats viz. SKO-20 (Shalimar fodder oats – 1), SKO-90 (Shalimar fodder oats – 2), SKO-96 (Shalimar fodder oats – 3), SKO-98 (Shalimar fodder oats – 4), SKO-117, SKO-148, SKO-160, SKO-166, and SKO-167, SKO-176, Sabzaar and Kent, during *rabi* 2013-14 in Districts of Ganderbal, Shopian, Srinager, Bandipora and Pulwama of Kashmir valley for laying out of trails at farmers field as well as research stations and KVK's including Experimental Farm of Division of Genetics and Plant Breeding, SKUAST-Kashmir, Shalimar district Srinagar; Krishi Vigyan Kendra, Malangpora, Pulwama district Pulwama; Mountain Livestock Research Institute (MLRI), Manasbal district Bandipora. These six location were selected because there is a acute deficiency of fodder during lean period (from November to March). Therefore, in the present investigation an attempt has been made to evaluate oat genotypes for higher green forage yield over the environments, so that farmers preserve this green forage in the form silage and hay during these winter months. Each genotype was planted in a randomized complete block design with three replications and trials were represented by five rows of five meter length with row to row and plant to plant spacing of 25 and 15 cm respectively. Observations were recorded on ten randomly selected plants from each genotype in all the three replications for days to 50% flowering, number of leaves plant<sup>-1</sup>, number of tillers metre

row<sup>-1</sup>, culm diameter (mm), plant height (cm), leaf to stem ratio, flag leaf length (cm), green fodder yield meter row<sup>-1</sup> (kg), dry matter yield meter row<sup>-1</sup> (kg), fodder yield ha<sup>-1</sup>, moisture (%), leaf area index (LAI) of randomly selected leaves from each plot was measured by canopy analyzer (Acuapar LP-80) at the beginning of anthesis. The chlorophyll content was measured in field on fully expanded flag leaves at anthesis with the help of chlorophyll meter (SPAD-502, Konica Minolta Sensing). The data were statistically analyzed and the genotypes were assessed for their stability of performance across environments following the method described by Eberhart and Russell (1966).

#### Results and discussion

The stability analysis (Table 1) indicated the presence of significant G x E interactions for all the characters studied. Higher magnitude of mean squares due to environments indicates considerable differences between environments for all the characters and these characters were greatly influenced by environments; thereby suggesting the large differences between environments along with greater part of genotypic response was a linear function of environments. These results are in agreement with the earlier findings of Dillion *et al.*, (2009) and Jai Dev *et al.*, (2009). The partitioning of mean squares (environments + genotype x environments) (Table-1) showed that environments (linear) differed significantly and were quite diverse with respect to their effects on the performance of genotypes for forage yield and majority of yield components. Further, the higher magnitude of mean squares due to environments (linear) as compared to genotype x environment (linear) exhibited that linear response of environments accounted for the major part of total variation for majority of the characters studied. The significance of mean squares due to genotype x environment (linear) component against pooled deviation for all the traits suggested that the genotypes were diverse for their regression response to change with the environmental fluctuations. Similarly, the significant mean squares due to pooled deviation observed for all the characters studied suggested that the deviation from linear regression also contributed substantially towards the differences in stability of genotypes. Thus, both linear (predictable) and non-linear (un-predictable) components significantly contributed to genotype x environment interactions observed for forage yield and yield component characters. This suggested that predictable as well as un-predictable components were involved in the differential response of stability. Similar results were reported by (Ackura and Ceri, 2011, Ahmad *et al.*, 2014).

The mean values for forage yield and its components, regression coefficient (bi), and deviation from regression (S<sup>2</sup>di) for 12 genotypes

over six environments are presented in Table 2. The stable genotypes identified for wider environments and specific (either favourable or poor) environments with high per se performance (over general mean) for forage yield per meter row<sup>-1</sup> are presented in Table 2. It is evident from the table that genotypes viz., SKO-90, SKO-96 and Sabzaar, were found stable and widely adapted with high mean performance, average responsiveness ( $b_i \sim 1$ ), and non significant deviation from regression line ( $S^2 d_i \sim 0$ ). These varieties for forage yield per meter row<sup>-1</sup> were also stable for other yield contributing traits including plant height (cm), number of tillers per meter<sup>-1</sup>, number of leaves per plant, leaf stem ratio, flag leaf length (cm), leaf area index (LAI), moisture(%) and chlorophyll content and could be utilized for all the environments to achieve higher and stable forage yield increment.

On the other hand, four genotypes, SKO-148, SKO-160, SKO-166 and SKO-167 were found suitable for favourable situations with predictable performance as they passed high forage yield per plant along with below average responsiveness ( $b_i > 1$ ) and non-significant deviation from regression line. Genotypes, SKO-20 found suitable for poor environments with predictable performance as they exhibited high per se performance for forage yield along with above average responsiveness ( $b_i < 1$ ) and non-significant deviation from regression line. Other high yielding genotypes, SKO-160 and SKO-166, were found suitable under poor environments with un-predictable performance due to significant deviation from regression line. The stability of genotypes for forage yield and its components in oats has also been reported by different researchers in various studies and higher green fodder yield, dry fodder yield and other related traits under wide range of environments were noted by Nehvi *et al.*, (2007), Sharma *et al.*, (2012) and Ahmad *et al.*, (2013).

### Conclusion

In conclusion, this study showed the presence of GE interactions among the 12 oat genotypes and their yield components. High-yielding genotypes with broad adaptation and some genotypes with specific adaptation were identified. Among the cultivars used in this study, SKO-90 and Sabzaar showed high mean forage yield and were found to be stable over the environments and therefore; could be used in the breeding programme for the development of high yielding stable genotypes over environments for future use.

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**Table 1. Analysis of variance for different morphological, yield and yield component traits in fodder oat (*Avena sativa* L.) genotypes across six locations (environments)**

Source	df	Mean squares												
		DFE	PH	NT	LSR	NLP	FLL	CD	CC	M	LAI	GFY	DFY	FY
Genotypes	11	97.024**	375.378**	396.044**	0.005**	0.809*	8.349**	3.859**	49.637**	6.909**	0.821**	0.149**	0.023**	13233.520**
Environment + (Genotypes × Environment)	60	4.084*	11.163**	105.100**	0.050**	0.063**	3.546**	0.761*	0.661**	1.684**	0.035**	0.542**	0.009**	363.492**
Environment	5	23.199**	31.186*	628.948**	0.003**	0.098**	31.011**	7.969**	7.769**	10.787**	0.111**	0.147**	0.064**	1588.824**
Genotypes × Environment	55	7.346**	11.343**	47.478**	0.008**	0.093**	1.049**	0.105*	0.105**	0.856**	0.028**	0.922**	0.004**	252.099*
Environment (linear)	1	115.998**	155.930**	3144.73**	0.015**	0.348**	155.05**	39.846**	39.846**	53.936**	0.556**	0.738**	0.321**	7944.121**
Genotype × Environment (linear)	11	4.146*	18.952**	28.968**	0.023**	0.156**	3.536*	0.0303**	0.030**	1.309**	0.007*	0.179**	0.011**	218.716**
Pooled deviation (non linear)	48	1.738**	18.791*	8.997**	0.070**	0.088**	0.392*	0.051**	0.051*	0.981**	0.030**	0.021**	0.003**	224.991**
Pooled error	132	0.356	5.604	28.287	0.001	0.026	0.262	0.034	0.034	1.088	0.001	0.026	0.262	3.647

\*, \*\* significant at 5 and 1 per cent level, respectively

DFE - Days to 50% flowering

PH - Plant height(cm)

NT - No. of tillers meter row<sup>-1</sup>

LSR - Leaf stem ratio (%)

NLP - No. of leaves plant<sup>-1</sup>

FLL - Flag leaf length (cm)

CD - Culm diameter (mm)

CC - Chlorophyll content

M - Moisture (%)

LAI - Leaf area index

GFY - Green fodder yield meter<sup>-1</sup> row

DFY - Dry fodder yield meter<sup>-1</sup> row

FY - Fodder yield ha<sup>-1</sup> (q)



**Table 2. The mean values for forage yield and its components, regression coefficient (bi), and deviation from regression (S<sup>2</sup>di) for 12 genotypes of fodder oats (*Avena sativa* L.) evaluated across six random environments in the Kashmir valley**

Genotypes	Days to 50% flowering			Plant height (cm)			Number of tillers meter row <sup>-1</sup>			Number of leaves plant <sup>-1</sup>			Leaf stem ratio		
	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>
SKO-20	164.1	1.03	1.00*	125.7	2.38	4.40**	127.0	0.43	1.00*	5.32	4.96	0.46	0.46	0.33	0.00**
SKO-90	164.9	1.01	0.00	122.4	1.01	0.06	142.3	1.01	0.00	5.00	1.20	0.53	0.53	1.00	0.00
SKO-96	169.4	1.01	0.01	122.5	1.00	0.00	129.5	1.09	0.01	4.46	1.09	0.50	0.50	1.09	0.07
SKO-98	166.8	1.55	2.10**	119.8	1.71	1.80	130.5	0.54*	2.10**	4.26	0.42	0.47	0.47	1.21	-0.00
SKO-117	167.2	1.64	5.20**	117.7	1.35	5.10	131.1	0.41*	5.20**	4.44	-1.04*	0.45	0.45	1.41	-0.00
SKO-148	165.9	0.56*	-0.30	125.1	1.34	-0.20	140.2	1.12	-0.30	4.29	-1.12*	0.47	0.47	0.71	0.00
SKO-160	167.0	1.82*	0.00	107.6	-0.07	-2.90	139.4	2.43	0.00	4.76	2.25	0.45	0.45	-0.26*	-0.00
SKO-166	166.2	1.67	0.40	116.2	0.53	3.50	144.4	1.07	0.40	4.75	0.79	0.47	0.47	1.16	0.00
SKO-167	166.2	1.45	0.40	118.7	-0.26	6.40	135.5	0.75*	0.40	4.32	-1.19*	0.49	0.49	1.40	0.00
SKO-176	167.3	0.78	1.10*	119.9	0.32	-4.80	132.4	0.36*	1.10*	5.10	-1.99*	0.46	0.46	1.75	-0.00
Sabzaar	158.2	1.01	0.01	137.7	1.02	0.01	153.0	1.00	0.01	4.58	1.02	0.43	0.43	1.03	0.00
Kent	155.5	-0.03*	0.50	133.9	1.61	-2.60	147.9	1.55	0.50	4.18	-0.12*	0.41	0.41	-0.43	-0.00
<b>Population mean</b>		164.9			122.3			137.8			4.62			0.47	
<b>SE (m)</b>		0.6			1.3			2.8			0.08			0.01	
<b>SE (bi)</b>		0.4			0.8			0.4			1.11			0.65	

  

Genotypes	Leaf area index			Culm diameter (mm)			Chlorophyll content (SPAD reading)			Flag leaf length (cm)			Moisture %		
	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>	( $\bar{X}$ )	b <sub>i</sub>	S <sup>2</sup> d <sub>i</sub>
SKO-20	4.50	0.97	-0.06	5.59	1.14	0.01	54.12	1.60*	1.80	344.6	344.6	344.6	74.89	1.49	-0.61
SKO-90	4.79	1.04	0.03	6.39	1.01	0.00	56.03	1.05	0.00	401.3	401.3	401.3	75.93	1.09	0.09
SKO-96	4.95	1.02	0.03	6.40	1.05	0.02	55.55	1.00	0.01	351.5	351.5	351.5	75.81	1.80*	-1.26
SKO-98	4.43	1.47	0.01	6.25	1.32*	-0.03	55.65	0.81	2.67	342.9	342.9	342.9	75.77	0.18	-0.95
SKO-117	4.28	0.86	0.04**	7.18	1.41	0.08*	55.68	0.86	-0.27	335.5	335.5	335.5	74.84	1.42	-0.88
SKO-148	4.59	0.29	0.01	6.21	0.56*	-0.03	54.80	0.90	-1.31	332.7	332.7	332.7	75.37	1.05	0.02
SKO-160	4.06	0.94	-0.09	6.86	1.12	-0.03	55.50	0.89	-0.85	337.8	337.8	337.8	75.39	0.63	0.14
SKO-166	4.59	0.61	0.03	6.10	0.76*	-0.03	54.24	0.66*	-1.25	334.4	334.4	334.4	75.80	0.64	-0.90
SKO-167	3.85	1.09	-0.00	6.30	0.79	-0.01	56.02	0.95	0.73	310.6	310.6	310.6	76.23	0.84	-0.97
SKO-176	4.63	0.60	-0.01	6.34	0.82*	-0.03	56.00	1.16	-0.78	307.9	307.9	307.9	75.44	1.07	-1.13
Sabzaar	4.18	1.08	0.01	4.68	1.08	0.01	51.02	1.00	0.02	345.8	345.8	345.8	75.27	1.11	-1.03
Kent	3.74	0.88	0.04**	4.43	0.68	0.01	46.61	0.49	5.49**	333.6	333.6	333.6	72.09	1.33	-0.31
<b>Population mean</b>		4.38			6.06			54.39			26.60			75.24	
<b>SE (m)</b>		0.07			0.11			0.67			0.28	-		0.36	
<b>SE (bi)</b>		0.81			0.12			0.15			0.17	-		0.11	

\*, \*\* significant at 5 and 1 per cent level, respectively



**Table 2. Contd.,**

Genotypes	Green fodder yield (kg meter row <sup>-1</sup> )			Dry fodder yield (kg meter row <sup>-1</sup> )			Green fodder yield ha <sup>-1</sup> (q)		
	( $\bar{X}$ )	$b_i$	$S^2 d_i$	( $\bar{X}$ )	$b_i$	$S^2 d_i$	( $\bar{X}$ )	$b_i$	$S^2 d_i$
SKO-20	1.52	0.99	0.40	0.93	0.06	0.03	344.6	0.59	0.03
SKO-90	1.72	1.17	0.52	1.02	0.03	0.03	401.3	1.17	0.03
SKO-96	1.53	1.07	0.46	1.13	0.08	0.02	351.5	1.37	0.02
SKO-98	1.38	0.46	0.40	1.14	0.06	0.01	342.9	0.46	0.00
SKO-117	1.42	1.42	0.42	1.57	0.01*	0.02	335.5	1.42	0.00
SKO-148	1.50	1.16	0.45	1.82	0.08	0.03	332.7	1.16	0.00
SKO-160	1.53	1.40	0.45	1.33	0.12	0.01**	337.8	1.40	0.01**
SKO-166	1.50	1.45	0.44	2.2	0.70**	0.06**	334.4	1.45	0.06**
SKO-167	1.40	1.16	0.36	0.95	-0.02	0.06	310.6	1.16	0.00
SKO-176	1.45	1.03	0.41	1.5	0.02	0.56	307.9	1.03	0.05
Sabzaar	1.39	1.15	0.38	1.01	0.04	0.01	345.8	1.15	0.03
Kent	1.30	0.32**	0.33	0.69	0.03	-0.02	333.6	0.32**	-0.06
<b>Population mean</b>		1.48			0.43			339.9	
<b>SE (m)</b>		0.05			0.02			13.8	
<b>SE (bi)</b>		0.36			0.38			0.31	

\*, \*\* significant at 5 and 1 per cent level, respectively