Research Note

Genotype x environmental interaction and stability analysis for grain quality and yield in oats (*Avena sativa* L.)

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Abstract
Ten genotypes of oats were planted at three diverse environments to assess genotype environment interaction and determine stable oat (*Avena sativa* L.) cultivar in Kashmir division for grain quality and grain yield using randomized block design during 2011 to 2012. Stability analysis for grain quality and yield was carried out to check the response to Genotype x Environment interactions. The mean squares due to G x E (linear) were significant reveals genetic differences among genotypes for linear response to varying environments, while mean squares due to pooled deviations were highly significant, reflecting considerable differences among the genotypes for non-linear response. Out of ten genotypes, only three oats lines i.e., SABZAAR, SKO-208 and SKO-209 had non-significant deviation from regression and their regression coefficient values were close to unity classified as stable varieties for grain quality and grain yield.. The cultivar, "SKO-208" with regression coefficient value of 1.009, the smallest deviations from regressions (S^2di) value and the highest grain yield could be considered the most widely adapted cultivar. The other test cultivars were sensitive to production-limiting factors, their wider adaptability, stability and general performance to the fluctuating growing conditions within and across environments.

Oat (*Avena sativa* L.) is a cereal crop of global importance used for food, feed, and forage. Differing from other cereal grains such as wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.), oat is rich in the antioxidants α -tocotrienol, α -tocopherol, and avenanthramides, as well as total dietary fiber including the soluble fiber β -glucan. The amount of oats used for human consumption has increased progressively, owing its dietary benefits and nutritional value. In fact, the health effects of oat rely mainly on the total dietary fibre and *β*-glucan content (Kerckhoffs *et al.,* 2003). The popularity of oatmeal and other oat products again increased after a January 1998 decision by the Food and Drug Administration (FDA), when it issued a final rule that allows food companies to make health claims on food labels of foods that contain soluble fibre from whole oats (oat bran, oat flour and rolled oats), noting that 3.0 g of soluble fibre daily from these foods may reduce the risk of heart disease. Oats are a rich source of soluble fiber, well-balanced proteins and several vitamins and minerals essential for the human health (Esposito *et al.,* 2005). Oats are viewed by consumers as one of the wholesome, healthiest; natural food with the result there is rising global food demand for oats and increasing production, milling and trade. The protein of rolled (flakes) oats is generally greater than that found in other cereal grains. Oats is the only cereal containing globulin or legume-like protein, avenalin, as the major (80%) storage protein. Many of the vitamins and minerals found in oats are combined in the bran and germ. Most oat food products use the entire groat, making it a nutritious cereal grain. Health issues related to diet have become a major problem facing developing countries over the past few decades. In many countries this problem is more emphasized in teens where levels of obesity and cases of type-2 diabetes have been on the rise. Consumption of oats as a whole grain has consistently been shown to have a positive impact on cholesterol, diabetes, and obesity. The positive health benefits of consuming oats as a whole grain food are attributed in part to beta glucan, a soluble fiber found in the cell walls. Oat is considered to be a nutritious source of protein, carbohydrate, fibre, vitamins, and minerals as well as of compounds with beneficial effects on health. As food oats are mostly preferred in breakfast items, oats are viewed by consumers as one of the wholesome, healthiest; natural food with the result there is rising global food demand for oats and increasing production, milling and trade. Out of cereals, the highest amounts of β-glucans are found in barley and oat grains (Ahmad and Zaffar, 2014). Therefore, there is an urgent need of exploiting new research technologies to boost grain yield with desirable quality parameters and increasing the nutritional value of the crop for human consumption and develop stable cultivar under different environmental conditions of Kashmir valley in India.

The phenotypic performance of a genotype may not be the same under diverse agro climatic conditions. This variation is due to G x E interactions, which reduces the stability of a genotype under different environments. Many models have been developed to measure the stability of various parameters and partitioning of

variation due to G x E interactions. The most widely used model (Eberhart & Russell, 1966) was followed to interpret the stability statistics in different crops. The yielding ability of a variety is the result of its interaction with the prevailing environment. Environmental factors such as soil characteristics and types, moisture, sowing time, fertility, temperature and day length vary over the years and locations (Ahmad *et al.,* 2014a). There is strong influence of environmental factors during various stages of crop growth (Bull, *et al.,* 1992), thus genotypes differ widely in their response to environments. Many research workers are of the view that average high yield should not be the only criteria for genotype superiority unless its superiority in performance is confirmed over different types of environmental conditions. Therefore, in the present investigation an attempt has been made to evaluate oat genotypes for grain quality and yield under different environments to identify genotypes with suitable performance in variable environments.

The basic material for the present study consisted of ten diverse genotypes of Oats (*Avena sativa* L.) *viz.,* SKO-204, SKO-205, SABZAAR, SKO-207, SKO-208, SKO-209, SKO-210, SKO-211, SKO-212, and SKO-213 (Table 1) selected from the germplasm collection maintained at Division of Plant Breeding and Genetics, SKUAST-K, Shalimar were evaluated at three locations viz., Experimental Farm of the Division of Plant Breeding and Genetics, SKUAST-K, Shalimar, Mountain Research Centre for Field Crops, Khudwani Anantnag and FOA, Wadura. During *rabi* 2011-2012 in a randomized block design with three replications at each location and each treatment was sown in 2 rows each of 4 meter length. Row to row and plant to plant spacing was maintained at 30 and 10 cm. The observations were recorded on quality parameters *viz.,* grain protein content (Jackson, 1973) and beta-glucan was determined by the MEGAZYME (Mc-Cleary Methods, 2006) method. Briefly, samples (0.5 g) were suspended and hydrated in ethanol (1 ml, 50% v/v) and sodium phosphate buffer solution (5 ml, 20 mM, pH 6.5) and then incubated at 40oC for 1 h with purified lichenase enzyme (0.2 ml, 10 U) and filtered. An aliquot of the filtrate was then hydrolysed to completion with purified Beta-glucosidase (0.1 ml, 0.2 U in 50 mM acetate buffer pH 4.0). The D-glucose produced was assayed using a glucose oxidase/peroxidase reagent (GOPOD) (3 ml). The absorbance was measured at 510 nm. Beta-glucan content is expressed as a percentage of d.m. Grain yield kg ha^{-1}, was recorded after weighing the total seeds obtained by threshing 20 tagged plants separately and averaged to a per pant basis. Data was subjected to analysis of variance to find significant differences among genotypes for the recorded data. After obtaining the significant differences, data were subjected to

stability analysis according to Eberhart and Russell (1966).

The combined analysis of variance (Table 2) revealed that there were significant differences among environments and genotypes for quality and yielding trait indicating the presence of variability in genotypes as well as diversity of growing conditions at different locations. The G x E interaction was highly significant reflecting the differential response of genotypes in various environments (Ahmad *et al*, 2014). By partitioning G x E interaction into linear and nonlinear (pooled deviation) components, it is noted that differences between environments (environment linear) were highly significant, which indicated the genetic control of genotypic response to environments (Nehvi *et al*, 2007). The G x E interactions, were however of non-linear type, because G x E (linear) significant, reflecting there is a genetic differences among genotypes for their response to varying environments. While pooled deviations were highly significant against pooled error (Table III) showing that the differences in stability were due to deviation from linear regression only. Thus, both linear (predictable) and non-linear (un-predictable) components significantly contributed to genotype x environment interactions observed for all the characters. This suggested that predictable as well as un-predictable components were involved in differential response of stability. Similar results were reported by (Ackura and Ceri, 2011 and Ahmad *et al*., 2013). Baker, (1988) regarded deviation from regression (S^2d) to be the most appropriate criteria for measuring phenotypic stability in an agronomic sense, because this parameters measure the predictability of genotypic reaction to environment, with these parameters, high and desirable per se performance of a variety over environment is also a positive point to rate the variety as a better and highly stable genotype.

The stability parameters for all cultivars are given in (Table 3). Eberhart and Russell (1966) emphasized the need of considering both linear (b_i) and non-linear (S^2d) components of genotype-environment interactions in judging the stability of a genotype. A wide adaptability genotype was defined as one with b_i =1 and with S^2d=0. In this study values for the regression coefficient (b_i) ranges from 1.002 (SKO-208) to 3.056 (SKO-210) for grain protein, 1.010 (SKO-208) to 4.442 (SKO-212) for beta glucan, 0.591 (SKO-210) to 2.033 (SKO-205) for grain yield plant $^{-1}$ (g). The regression coefficient (b_i) of genotypes *viz.,* SABZAAR, SKO-208 and SKO-209 for grain quality and grain yield plant $^{-1}$ (g) were non-significant and almost approaching unity (b_i =1) and it had the lowest and non-significant deviation from regression and was most suitable for grain quality and grain yield plant $^{-1}$ (g) over all the locations. The regression coefficient of genotypes

SKO-208 is almost one and deviation from regression line approaching to zero for grain protein (%), beta glucan (%) and grain yield plant^{-1} (g) and highest grain yield above the average which reveals it is stable for cultivation across all diverse environments for human consumption and also this genotype can be used in breeding programmes for increasing the β-glucan content of adapted local germplasm (Welch *et al.*, 2002).

In this study the regression co-efficient for the genotype SKO-208 and SKO-209 for grain quality and grain yield plant^{-1} (g) was non-significant and almost approaching unity (bi =1) and it had the lowest and non-significant deviation from regression and found most suitable for grain quality and grain yield/ plant (g) over all environments and also these two lines can be used in the hybridization programme to increase the beta glucan and grain protein content in the adopted local germplasm and meet the scarcity of quality oat for human consumption as well as increase the nutritional and economic value of this crop.

Acknowledgement

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Table 1. Oats genotypes used in the study with their accession number

S. No.	Genotype	EC number/ Place of collection
1.	SKO-204	EC-529089
2.	SKO-205	EC-529090
2.	SKO-205	EC-529090
3.	SKO-207	EC-529092
4.	SKO-208	EC-529093
5.	SKO-209	EC-529094
6.	SKO-210	EC-529095
7.	SKO-211	EC-529096
8.	SKO-212	EC-529097
9.	SKO-213	EC-529098
10.	Sabzaar	Released variety (SKUAST-Kashmir)

Table 2. Analysis of variance for stability for grin quality and seed yield traits in oats

Source of variation	df	Mean square		
		Grain protein (%)	β- glucan (%)	Grain yield plant^{-1} (g)
Genotype (G)	9	0.877**	0.080**	4.324**
Environment (E)	2	0.983**	0.764**	3.422**
G x E	18	0.231**	0.114**	6.163**
Pooled error	54	0.010	0.002	0.006
Environment + (G x E)	20	0.545**	0.104**	9.289**
E (Linear)	1	0.002**	0.006**	14.845**
G X E (Linear)	9	0.135**	0.030**	5.308**
Pooled Deviation	10	0.010**	0.007**	0.016*

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

Table 3. Stability parameters for grain quality and grain traits in oats

Genotype	Grain protein (%)			β- glucan (%)			Grain yield plant^{-1} (g)		
	Mean	bi	S^{2}d	Mean	bi	S^{2}d	Mean	bi	S^{2}d
SKO-204	8.09	2.098	1.076**	4.77	1.860	1.336**	8.18	0.954	5.229**
SKO-205	8.37	1.980	1.004*	6.03	2.097	1.557*	10.70	2.033	8.9366**
SABZAAR	7.23	1.080	0.007	3.77	1.012	0.234	7.31	1.074	0.039
SKO-207	8.72	2.345	1.562**	7.23	1.907	2.089*	10.67	0.747	0.976**
SKO-208	10.75	1.002	0.004	8.56	1.010	0.005	10.70	1.009	0.001
SKO-209	9.17	1.043	0.067	8.29	1.078	0.055	10.69	1.072	0.397
SKO-210	8.55	3.056	-2.543**	6.34	3.002	1.803**	10.66	0.591	1.720**
SKO-211	8.40	1.984	0.508**	6.23	3.331	1.221**	10.68	1.031	2.019**
SKO-212	8.29	1.885	-3.001**	5.53	4.442	2.498**	8.57	1.069	2.006*
SKO-213	8.43	1.450	1.023*	6.25	1.249	1.023**	9.92	1.030	2.048*
Population mean	**8.6**			**6.3**			**9.92**		
SE ±	**0.274**			**0.439**			**0.279**		

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