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Comparison of Different Methods of Evaluating Genotypes in National Uniformity Wheat Yield Trials in Pakistan

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Abstract: Twenty genotypes of wheat were evaluated at thirty locations for stability parameters of grain yield. Genotype x Environment interaction was significant indicating the influence of environment on grain yield. Mean square due to genotype x environment was highly significant indicating genetic differences among genotypes for linear response to various environments. Stability using parametric approach only three genotypes namely V-97024, V-97112 and IBW-96405 satisfied criterion given by Eberhart and Russell (1966), but only one genotype (V-97024) was declared as a stable cultivator for grain yield considering high mean yield, regression coefficient (b) close to unity and low value of deviation from regression. Cluster analysis was also used to classify similar cultivars but the classification did not classify according to stability parameters. Therefore it is concluded that the conventional stability approach used by Eberhart and Russell and other parameters like ecovalence, deviation from regression and interaction variance should be used for categorizing cultivars.

Key words: Genotypes, genotype x environment interaction, stability parameters, cluster analysis, dendogram, Pakistan

Introduction

The goal of a plant breeding program is to produce genotypes which are, in some sense, optimum for the conditions under which they will be grown. Many models have been developed to measure the stability parameters and partitioning of variation due to GxE interactions (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966). The model proposed by Eberhart and Russel (1966) is considered more appropriate to interpret the stability statistics and is more commonly used for stability studies in crops. Lin ***et al.*** (1986) has established three concepts of stability. Type 1 stability measures (genotype mean square=S^2_i and genotypic coefficient of variation=CV_i) are those which measure the variation within a genotype across environment. These statistics do not depend upon the other genotypes which might be included in the trials. Thus they provide very broad based inference and are commonly avoided for making the final decision. Type 2 stability measures (ecovalence=W^2_i and Shukla's stability variance (σ^2_i) which basically measure the deviation of the individual genotype from the location means of all genotypes in test. Type 3 (regression slope = b_i) stability is calculated by the residual mean square from the regression of individual cultivar yields on an environmental index (Eberhart and Russell, 1966). In this

method, the slope of regression provides an indication of regions of adaptability as well as stability. It also indicates the cultivar response to the predictable component of the environment. Naazar ***et al.*** (2002) indicated that GxE interaction was highly significant. A top yielding genotype SLM-046 was found a stable cultivar for grain yield. Genotypes Regent, Cobra and A.W. were found suitable for favorable environments, Whereas PF-7045/91 and Eureka could be recommended for poor environments. The objective of the present study was to evaluate and identify the promising genotypes which could be considered adaptable under broad environmental conditions and can be grouped together.

Materials and Methods

The data comes from normal duration replicated NUWYT trials for 2000-2001. Two seeding dates (Normal and Late) were used for trials at 30 locations in Pakistan. Twenty candidate genotypes submitted by various wheat breeders of the country were sown with a local check at each location. It was recommended that each plot consists of 6 rows, 5 m long and 30 cm apart and each genotype is grown in four replicates. A randomization plan was given by wheat program NARC to lay out experiments at different locations. Data was collected at maturity and sent to wheat program, NARC for further evaluation.

The methods of analysis used for this data set were done in the following sequence. The combined analysis of variance of yield data over all environments, using Genotype-Environment interaction data for stability analysis with conventional and unconventional approaches. This was supplemented by graphical representation of the data using GEBI software which uses cluster analysis to form groups of genotypes which are similar to one another based on response pattern towards grain yield.

Results and Discussion

The combined analysis of variance revealed significant GxE indicating the influence of environments on the yield performance of genotypes (Gomes and Gomes, 1984) (Table 1).

Since in the combined analysis GxE interaction was highly significant therefore a stability analysis based on location index was in order. However rather than depending only on the Eberhart and Russell (1966) approach a more comprehensive set of stability analysis as summarized by Lin ***et al.*** (1986) was employed. The results of stability analysis are summarized in Table 2.

The more frequently used method of stability analysis involves comparing the competing genotypes with respect to other genotypes by regressing yields attained by each genotype at different locations over an environmental index which is based on average yield of all genotypes at each location. The resulting slope for each genotype can then be considered as a measure of stability using a unit slope to be stable standard. The deviations from the regression line are also considered as they provide a good measure of fit. However Finlay and Wilkinson (1963) pointed out that the slope provides an indication of regions of adaptability as well as stability. Genotypes that have a slope significantly greater than one are specifically adapted to high

Table 1: Pooled analysis of variance of the gain yield data of wheat genotypes

Source of variation	d.f	Sum of squares '000'	Mean squares '000'	F-ratio
Total (corrected)	4796	6180189		
Location (L)	29	3042649	104918	495.4**
Replication (L))	90	89154	990	4.7**
Genotype (G)	19	80121	4216	19.9**
G x L	551	438815	796	3.76**
Date (D)	1	1103923	1103923142	5213.0**
LxD	29	393660	13574	64.2**
G x D	19	15115	795	3.86**
LxGxD	551	274107	497	2.4**
Pooled Error	3507	742642	211	

** Statistically significant at 1% level

Table 2: Stability Statistics for twenty genotype of wheat grown at thirty locations in Pakistan, 2000-2001

	Stability Measure								
Genotype	Institute	Mean	VAR	C.V.	Ecova-Lence	INTVAR	B_i	DEVMSQ	RSQR
V-7005	WRI,Sakrand	3488	529805	20.87	1971954	70025	0.85	55571	0.90
SD1200/14	NIA,Tandojam	3396	596696	22.74	3151269	115210	0.87	101435	0.84
V-8964	Univ. Agri. Fsd	3502	599274	22.11	3080770	112509	0.88	99571	0.84
91BT010-5	Biotech-AARI,Fsd	3372	605368	23.07	2944982	107306	0.88	96060	0.85
V-97052	ARRI,Faisalabad	3641	679069	22.63	3219834	117837	0.93	111955	0.84
SI-91195	NIA,Tandojam	3565	721117	23.82	4383450	162420	0.93	153644	0.79
PR-70	CCRI, Pirsabak	3598	675143	22.83	3021027	110220	0.94	105054	0.85
V-7004	WRI,Sakrand	3139	675814	26.19	1535370	53298	0.97	54407	0.92
V-97024	ARRI,Faisalabad	3676	672134	22.30	981821	32089	0.99	34944	0.95
92T009	AZRI, Bhakhar	3365	815201	26.83	4558064	169110	1.00	162786	0.81
97B2236	RARI,Bahawalpur	3509	747320	24.64	2405963	86654	1.01	85898	0.89
Inqalab	AARI, Faisalabad	3527	828104	25.80	3654520	134491	1.04	129672	0.85
V-97112	AARI, Faisalabad	3668	784585	24.15	2153807	76993	1.04	75747	0.91
IBW-96405	NIFA, Peshawar	3489	798101	25.60	2493458	90006	1.04	87799	0.89
DN-16	ARI, D.I.Khan	3546	792829	25.11	1723308	60499	1.06	59168	0.93
V-97046	AARI, Faisalabad	3614	838211	25.33	1788295	62989	1.09	58109	0.93
PR-73	CCRI, Pirsabak	3649	875020	25.64	2638426	95561	1.10	87734	0.90
D-97603	AARI, Faisalabad	3646	934503	26.52	3912543	144377	1.11	131568	0.86
Local Check	-	3586	888356	26.29	2394299	86207	1.11	76625	0.92
97B2210	RARI,Bahawalpur	3631	949675	26.84	2818412	102457	1.15	85379	0.91

yielding environments. On the other hand, genotypes with a slope less than one are insensitive to change in environment and are, therefore better adapted to poor environments. The competing genotypes in the seeding trials on the basis of regression model can be divided into three distinct groups.

The first group which is categorized as stable group has b values ranging from 0.97 to 1.04 include 7 genotypes V-7004, V-97024, 92T009, 97B2236, Inqalab, V-97112 and IBW-96405. However some of these genotypes are weak on other measures of stability which makes it dangerous to recommend these on the basis of b value only. The genotypes that can be safely termed as stable are V-7004 and V-97024. The other genotypes in the stable group have high values of ecovalence

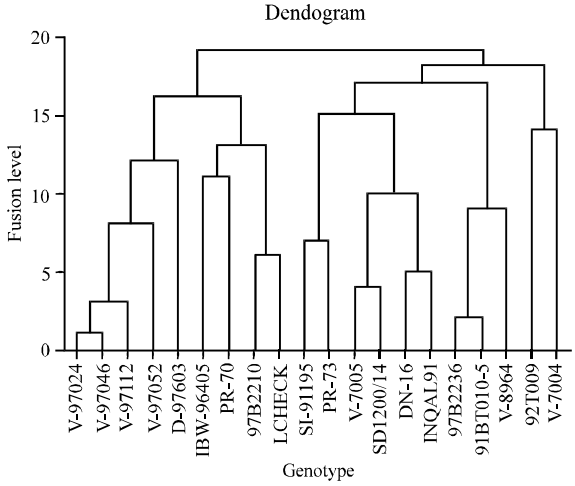

Fig. 1: Dendogram showing clustering of genotypes

Locations

1	Quetta	11	Bhakhar	22	NARC
2	Hydabad	12	Layyah	23	D.I. Khan
3	Sag.(LF)	13	Vehari	24	Lakki Marwat
4	Sag. (LF)	14	K.Wal	25	Tarnab
5	N. Shah	15	T.T. Sing	26	Nowshera
6	Larkana	15	FSD/AARI	27	Mardan
7	Khairpur	16	FSD/UAF	28	Swat
8	R.Y.K	17	Sahiwal	30	Gilgit
9	BWP/PARI	20	Hafizabd		
10	BW/CRI	21	Gujranwala		

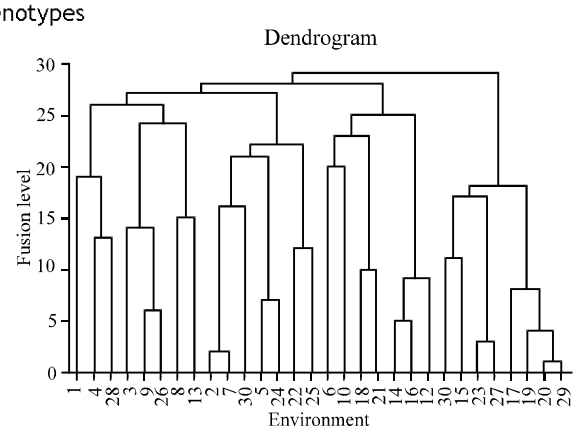

Fig. 2: Dendogram showing clustering of different locations of experiment

so we should use these with some caution. The other group consists of 6 genotypes which have values significantly greater than one are DN-16, V-97046, PR-17, D-97603, 97B2210 and local check. The last group of seven genotypes comprises of those genotypes which by and large are insensitive to environmental change. These genotypes are V-7005, SD1200/14, V-8964, 91BT010-5, V-97052, SI-91195 and PR-73 (Table 2).

The last technique that is used to process this data set is multivariate method of cluster analysis (Sneath and Sokal, 1973). The data of genotype x environment (G X E) tables of yields, clustering is used to simplify the data set by grouping the genotypes, over all environments, with similar response patterns of all yields. In a similar fashion growing of the environments, over all genotypes, with similar response pattern for all yields (Byth ***et al.***, 1976). The method used for hierarchical classification requires a measure of association (proximity measure) among the individuals and a fusion strategy. The proximity measure provides a measure of the distance or closeness in multidimensional space.

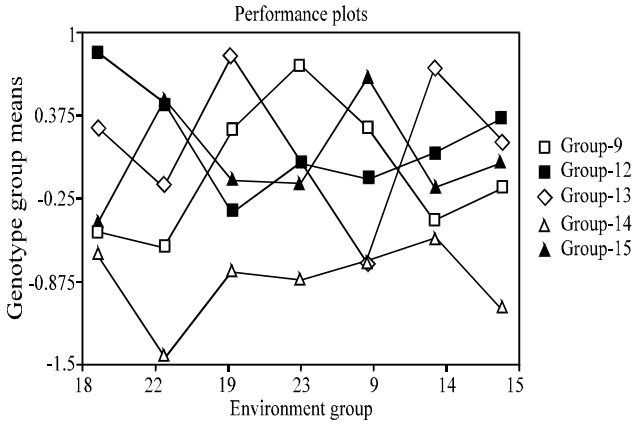

Fig. 3: Performance plots showing performance of different groups of genotypes

The pictorials include dendograms and performance plots. Two major contributors accounted for the overall variability in the genotype × environment data. Genotypes accounted for about 15.98% and G×E interaction contribution was 84.02%. The dendogram of genotypes is given in Fig. 1. Clearly five groups at fusion level of 15 are formed. Similarly environments are be grouped into seven clusters (Fig. 2).

Fig. 3. shows that consistently no group performed well over all environment groups. However performance of some groups was much better than the others. It is therefore necessary that performance plots are given due consideration while deciding on better genotypes. The genotypes in group-14 performed consistently poor on all seven environmental group positions, but group-15 and group-9 genotypes performed poorly on only four out of seven. In this respect the genotypes in groups 12 and 13 performed much better as at only two environment group locations they performed at below par and at five environment group locations they performed better than average. This makes eight genotypes and local check as the better genotypes than the others in the group for these trials and can be recommended for wider adaptation. The names of these genotypes are V-97024, V-97046, V-97112, V-97052, D-97603, IBW-96405, PR-70, 97B2210 and LCHECK. When compared with the recommendations made for stability using parametric approach only three genotypes namely V-97024, V-97112 and IBW-96405 satisfied criterion given by Eberhart and Russell (1966), but only V-97024 was declared as stable considering other parameters of stability.

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