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## Performance of Maize Genotypes on the Basis of Stability Analysis in Pakistan

H.I. Javed, M.A. Masood, S.R. Chughtai,  
H.N. Malik, M. Hussain and A. Saleem

Maize, Sorghum and Millet Programme, National Agriculture Research Centre, Islamabad, Pakistan

**Abstract:** Six maize genotypes were evaluated in National Uniform Maize Yield Trials across six contrasting locations having different agro-climatic conditions. Pooled analysis of variance for grain yield indicated significant differences for genotypes across the environments, environment across genotypes and their interactions. These significant interactions indicated uneven performance of the genotypes across the environments and years. In stability analysis, all the parameters applied proved two genotypes as the most stable across the environments. These genotypes gave the highest grain yield and were also earlier in maturity. One genotype showed fitness for favourable environments and two for poor yielding environments.

**Key words:** Maize, *Zea mays*, genotypes, performance, stability, environments

### INTRODUCTION

Maize (*Zea mays* L.) is the leading world cereal both in terms of production and productivity (FAO, 2004). It has great significance for countries like Pakistan, where rapidly increasing population has already outstripped the available food supplies. It is annually grown on an area of about 0.896 million hectares with annual grain production of about 2.8 million tonnes (FAO, 2004). The current maize yield in Pakistan (2097 kg ha<sup>-1</sup>) is much lower than the world's average (FAO, 2004). Furthermore, within Pakistan there is a large gap between potential and actual maize yields (UN, 2000). Maize is consumed as food, feed and fodder and also has many industrial uses. It has high potential for more nutritive food and it is a good source of high quality edible oil (UN, 2000; Serna-Saldivar *et al.*, 1994).

With shrinking land resources and increasing population, the best option is to strive for progressive yield growth in all major food crops. Maize being the most productive cereal in the world and being a traditional crop in Pakistan offers the best opportunity to narrow the gap between population growth and food production (FAO, 2000a). An important reason for low production of maize is less coverage under high yielding hybrids which is only 25% of total maize area in Pakistan (Chughtai *et al.*, 2003). The national average yields of maize could be raised if significant improvements are made in the genetic content of the crop in the lower productivity regions (CIMMYT, 1989; Rajaram *et al.*, 1998). Farmers should be encouraged to adopt the best hybrids to increase maize productivity in Pakistan

(Tran *et al.*, 2001). Chand and Longmire (1990) observed 62% increase in yield by the use of improved variety only.

Maize crop possesses great genetic diversity and can be grown across varied agro-ecological zones (Ferdus *et al.*, 2002). According to CIMMYT (1991), improved varieties gave high and stable yields across the environments where they were adapted. The improved genotypes should have the characteristics of adaptability across a range of diverse environments. Unstable varieties are a major source of risk. Stability in performance of a genotype over a range of environments is a desirable attribute and depends on the magnitude of genotype x environment interactions (Ahmad *et al.*, 1996). The stability parameters have been studied in different crops for measuring phenotypic stability (Anonymous, 1995; Bakhsh *et al.*, 1995; Sharif *et al.*, 1998; Qureshi, 2001), but very little information is available on stability of maize varieties. Some genotypes show highly specific response to a particular environment, others are uniform in performance over a range of environments. The objectives of present study were to evaluate and identify the genotypes with wider adaptation over a range of environments and yield performance.

### MATERIALS AND METHODS

Six maize genotypes were evaluated in National Uniform Maize Yield Trials conducted during 2001 and 2002 across six contrasting locations. The genotypes were Hycorn-11, Hycorn-798, R-2302, R-2210, EV-5098 and EV-6098 and the locations were D.I. Khan, Bahawalpur, Faisalabad, Jaglot, Chiniot and Yousafwala having

different agro-climatic conditions. At each location, the experiment was planted under Randomised Complete Block Design (RCBD) with three replications. Each genotype was sown on four row plot (5.0 meter long and 0.75 m apart). The central two rows were used for observations.

All the inputs and cultural practices were same at all locations. Data regarding agronomic traits were recorded. In this paper, data of mid silking (days) as indicator of maturity and grain yield (kg ha<sup>-1</sup>) were discussed. Data were analysed across all locations and years using pooled data. Analysis of Variance and Duncan's Multiple range Test (Gomez and Gomez, 1987) were used for significance of the results. The mean yield data across locations and years were subjected to stability analysis by using different stability parameters like genotype mean, variance (S<sub>i</sub><sup>2</sup>), ecovalence (W<sub>i</sub><sup>2</sup>), interaction variance (σ<sub>i</sub><sup>2</sup>), regression slope (b<sub>i</sub>), deviation mean square (δ<sub>i</sub><sup>2</sup>) and coefficient of determination (R<sup>2</sup>). Several of these have been summarized and compared by Lin (1986). The models used for these parameters are:

Genotype Means  $(y_{i.}) = \sum_j y_{ij}/q$   
 Genotype Variance  $(s_i^2) = \sum_j (y_{ij} - \bar{y}_{i.})^2 / (q-1)$   
 Ecovalence  $(W_i^2) = \sum_j (y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y})^2 / [p(p-1)(q-1)]$   
 Interaction Variance  $(\sigma_i^2) = [SSGE / (p-1)(q-2)] - (q-1)$   
 Regression Slope  $(b_i) = [\sum_j (y_{ij} - \bar{y}_{i.})(\bar{y}_{.j} - \bar{y})] / \sum_j (\bar{y}_{.j} - \bar{y})^2$   
 Deviation Mean Square  $(\delta_i^2) = [1 / (q-2)] [(y_{ij} - \bar{y}_{i.})^2 - b_i^2 \sum_j (\bar{y}_{.j} - \bar{y})^2]$   
 Coefficient of Determination (R<sup>2</sup>)  $= [b_i^2 \sum_j (\bar{y}_{.j} - \bar{y})^2] / \sum_j (y_{ij} - \bar{y}_{i.})^2]$

**RESULTS AND DISCUSSION**

On the average across the locations and years, R-2302 showed excellent performance (Table 1) with highest yield of 7650 kg ha<sup>-1</sup> followed by R-2210 (7071 kg ha<sup>-1</sup>) and EV-5098 (7026 kg ha<sup>-1</sup>). R-2302 was the earliest genotype (Table 2) with 54.89 days to mid silking followed by EV-5098 (55 days). Because, Jaglot is cooler place, the mid silking was late (58.50 to 62.67 days). The

mean mid silking period over genotypes was the lowest at D.I. Khan (54.17) and Chiniot (54.22). Pooled analysis of variance (Table 3) for grain yield indicates statistically significant difference for genotypes across locations and years and for all interactions. These significant interactions indicated uneven performance of the genotype across the locations and years. High yield should not be the only criterion for a genotype unless its superior performance is confirmed over the varying environmental conditions (Qari *et al.*, 1990; Kinyua, 1992; Golmirzaie *et al.*, 1990; Liu *et al.*, 1992).

The variation in grain yields was detected in all the environments in which maize genotypes were evaluated. Bahawalpur gave the highest mean grain yield of 8324 kg ha<sup>-1</sup> and Yousafwala gave the lowest mean grain yield of 5092 kg ha<sup>-1</sup> (Table 1). This variation shows the influence of the environments on expression of yield potential. Environmental factors contributing to these differences in mean grain yields across all the six environments and two years may include the soil type, sowing dates, sunshine hours and rainfall during the whole crop cycle. Across the locations and years, analysis of variance (Table 3) of grain yield showed statistically significant genotype × environment interaction. For the six environments and two years, the genotypes showed wide variation in their reactions. The lower and upper bounds for reliable intervals for linear regression coefficients were determined to be 0.91 to 1.18 and those for grain yields were 6872 to 7650 kg ha<sup>-1</sup> (Table 4). The genotypes within this range of regression coefficient were considered stable. Maize genotypes with stable yield performance across this set of environments are R-2302, R-2210 and Hycorn-11. Further, these genotypes contributed the least to the genotypes × environment interaction as measured by ecovalence (W<sub>i</sub><sup>2</sup>) and the interaction variance (σ<sub>i</sub><sup>2</sup>). In addition, these three genotypes have the smallest deviation from regression on site index as measured by the deviation mean square (δ<sub>i</sub><sup>2</sup>) of all genotypes. Of these genotypes, R-2302 (b = 1) is the most stable genotype followed by R-2210 (b = 0.91). They produced the highest grain yields of 7650 and 7071 kg ha<sup>-1</sup>, respectively across location. They appear to be broadly adapted across the six test environments (Petersen, 1988; Shukla, 1972 and

Table 1: Evaluation of maize genotypes across the locations during 2002-2003 (Grain yield, kg ha<sup>-1</sup>)

Genotype	DI Khan	Bahawalpur	Faisalabad	Jaglot	Chiniot	Yousaf-Wala	Mean
Hycorn-11	7847	8855	6584	5493	7672	4782	6872
Hycorn-798	7521	9007	7611	5156	7047	3113	6576
R-2302	8960	8880	7825	5822	8878	5539	7650
R-2210	8053	7849	7026	5609	8286	5608	7071
EV-5098	6742	8012	7681	5636	7915	6170	7026
EV-6098	6247	7344	5739	5620	6426	5339	6119
Mean	7561	8324	7078	5556	7704	5092	

Table 2: Evaluation of maize genotypes across the locations during 2002-2003 (50% silking, days)

Genotype	DI Khan	Bahawalpur	Faisalabad	Jaglot	Chiniot	Yousaf-Wala	Mean
Hycron-11	53.33	55.33	54.83	61.17	53.33	55.67	55.61
Hycorn-798	56.50	59.50	56.67	62.67	58.33	60.33	59.00
R-2302	51.17	55.50	54.50	59.33	53.67	55.17	54.89
R-2210	54.83	56.50	54.83	60.50	54.00	58.50	56.53
EV-5098	54.67	53.50	55.83	58.50	53.00	54.50	55.00
EV-6098	54.50	54.67	53.00	60.67	53.00	55.50	55.22
Mean	54.17	55.83	54.94	60.47	54.22	56.61	

Table 3: Pooled analysis of variance for grain yield (kg ha<sup>-1</sup>) of maize genotypes during 2002-2003

Source of variation	D.f	Sum of squares	Mean square	F. value	Prob.
Year (Y)	1	3849072	3849072	6.31*	0.0134
Locations (L)	5	295917911	59183582	96.97**	0.0000
Year×Location (Y×L)	5	534928872	106985774	175.29**	0.0000
Re. (Location×Year)	24	23259176	969132	1.59*	0.0548
Genotype (G)	5	47644881	9528976	15.61**	0.0000
Year×Genotype (Y×G)	5	13077189	2615438	4.29**	0.0013
Location×Genotype (L×G)	25	72622246	2904890	4.76*	0.0000
Year×Location×Genotype (Y×L×G)	25	26707615	1068305	1.75*	0.0245
Error	120	73241995	610350		
Total	215	1091248957			

\* = p < 0.05, \*\* = p < 0.01

Table 4: Stability parameters for six genotypes across location and years

Genotype	Mean yield (T/HA)	S <sup>2</sup>	CV (%)	Wt <sup>2</sup>	σ <sup>2</sup>	b <sub>i</sub>	δ <sup>2</sup>	R <sup>2</sup>
Hycron-11	6872	1540.890	22.42	705812	90740	1.18	110484	0.96
Hycorn-798	6575	2102.500	31.98	4680941	1283279	1.56	526509	0.90
R-2302	7650	1585.390	20.72	963170	167947	1.00	153732	0.95
R-2210	7071	1210.380	17.12	871419	140422	0.91	194127	0.89
EV-5098	7026	994.193	14.15	2228829	547645	0.67	326627	0.74
EV-6098	6119	722.934	11.82	2650206	674058	0.50	144147	0.78

S<sup>2</sup> = Genotype variance, Wt<sup>2</sup> = Ecovalence, σ<sup>2</sup> = Interaction variance, b<sub>i</sub> = Regression slope, δ<sup>2</sup> = Deviation mean square, R<sup>2</sup> = Coefficient of determination and CV = Coefficient of Variance

Eberhardt and Russell, 1966). Hycorn-798 has the regression coefficient significantly above unit (b = 1.56) and considered to be adoptable to favourable environments. On the other hand, EV-5098 (b = 0.67) and EV-6098 (b = 0.5), with the regression coefficient significantly below the unit and are considered to be adaptable to poor environments. Petersen (1988) and Finlay and Wilkinson (1963) described that the genotypes with regression slope (b) significantly greater than unity were specifically adapted to high yield environments and the genotypes with regression slope significantly lower than unity were better adapted to low yielding environments. According to CIMMYT (1991), improved varieties gave high and stable yield across the environments where they are adopted.

The identified stable genotypes should be recommended for a wide range of environments while the genotype which proved to be suitable for high yielding or low yielding environments, should be recommended for the respective areas.

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