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### **Stalk and root rot in maize hybrids: analysis of genotype × environment interaction using GGE biplots**

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#### INTRODUCTION

Stalk and root rot (SRR) is one of the most important maize (*Zea mays* L.) crop diseases in Argentina, as it is widely spread and has high incidence and severity (Buchaca, 2008). The most efficient, economical and environmentally sustainable control method involves the use of resistant genotypes. The disease presents diverse symptoms with different degrees of manifestations and incidence values among the analyzed populations. As a consequence, resistance indices have been proposed (Grau *et al.*, 1982); here we propose the multidimensional indicator of stalk and root rot (MISRR). The response of the different hybrid genotypes to the disease is influenced by environmental conditions; therefore, evaluating the materials in different environments is an interesting approach. The differential genotype response to a disease in diverse environments results in a genotype × environment interaction; quantifying the magnitude of the interaction is of interest when evaluating genotypes.

To describe genotype adaptability and stability, different statistical methods that explore the genotype × environment interaction and estimate it with improved accuracy have been proposed. Although the phenotypic character of interest is the result of the effects of genotype (G), environment (E) and their interaction (G×E), only the main effects of G and of G×E are relevant to genotype evaluation (Yan *et al.*, 2000; Yan and Tinker, 2006). Unlike the analysis of variance (ANOVA) and comparison of means, which only allow us to select those genotypes that are above a given yield level, sites regression models (SREG) (Cornelius *et al.*, 1996; Crossa and Cornelius, 1997; Crossa *et al.*, 2002) are recommended when environment effects are an important source of variation. These models have the additional advantage of providing a graphical analysis known as GGE biplot (Yan *et al.*, 2000; 2001). The aim of the present work was to study G×E interaction via a multidimensional indicator of SRR in maize using the GGE biplot analysis.

## MATERIALS AND METHODS

The multidimensional indicator of stalk and root rot (MISRR) was estimated in 12 maize hybrids from different seed companies (Table 1) based on field evaluations conducted in three localities from the semiarid region of Argentina during a crop season: Buchardo (34°45'19''S, 63°31'27''W) and Olaeta (Córdoba province; 32°58'52''S, 63°47'50''W) and Papagayo (San Luis province; 32°42'41''S, 65°11'47''W). The hybrids were selected because they are the most widely used by the Asociación Argentina de Consorcios Regionales de Experimentación Agrícola (AACREA: Argentine Association of Regional Consortiums for Agricultural Experimentation).

**Table 1.** Seed companies and name of the evaluated commercial hybrids

Seed companies	Hybrid	Seed companies	Hybrid
Illinois	I880MG	Pannar	PANPEX168MG
KWS ARG	KM4911TDMAX	Pionner	P1979Y
La Tijereta	LT622MGRR2	Pionner	P2053Y
La Tijereta	LT632MG	Pionner	P2069Y
Monsanto	DK190MGRR2	Syngenta	NK880TDMAX
Monsanto	DK747MGRR2	Syngenta	NK910TDMAX

The indicator (MISRR) is a measure of the response to the disease and is classified according to the simultaneous expression of the selected symptoms, weighted by the incidence of the different degrees along a scale in a set of plants of each hybrid. MISRR can range from 0 to 100, with 100 corresponding to severely affected genotypes.

$$\text{MISRR} = \sum_{i=0}^3 \left( \frac{\text{degree}_i \times \text{number of plants in the category}_i}{\text{total number of plants} \times 3} \right) \times 100$$

The following rating scale was defined: 0= no symptoms, 1= change in pith color (dark or pink) or presence of stripes on the basal internodes; 2= pith disintegration or changes in color and striping in the lower internodes, 3= pith disintegration, with change in color and presence of stripes.

The experimental design used in the three localities was a complete random block, with three replications. Each sample consisted of five plants; the number of plants with each one of the

symptoms of stalk and root rot (infected) and the number of healthy plants were counted to determine the incidence of each symptom.

The data obtained across environments was analyzed using ANOVA and SREG statistical model for multi-environments (Cornelius *et al.*, 1996; Crossa and Cornelius, 1997; Crossa *et al.*, 2002), which includes  $G + G \times E$  in the bi-linear term. This model provides an easy-to-understand graph known as GGE biplot (Yan *et al.*, 2000; 2001), which facilitates the analysis of genotype behavior as well as the effect of the interaction with the environment. This graph is built based on the first two principal components (PCs) of the SREG model. The use of the biplot allows us to identify the genotypes of highest production in each environment as well as those of highest stability. In addition, the model shows clustering of genotypes and environments with similar response pattern and identifies the environments that are most representative and that can best discriminate among genotypes. Experimental data were analyzed with Infogen statistical software (Balzarini *et al.*, 2013).

## RESULTS

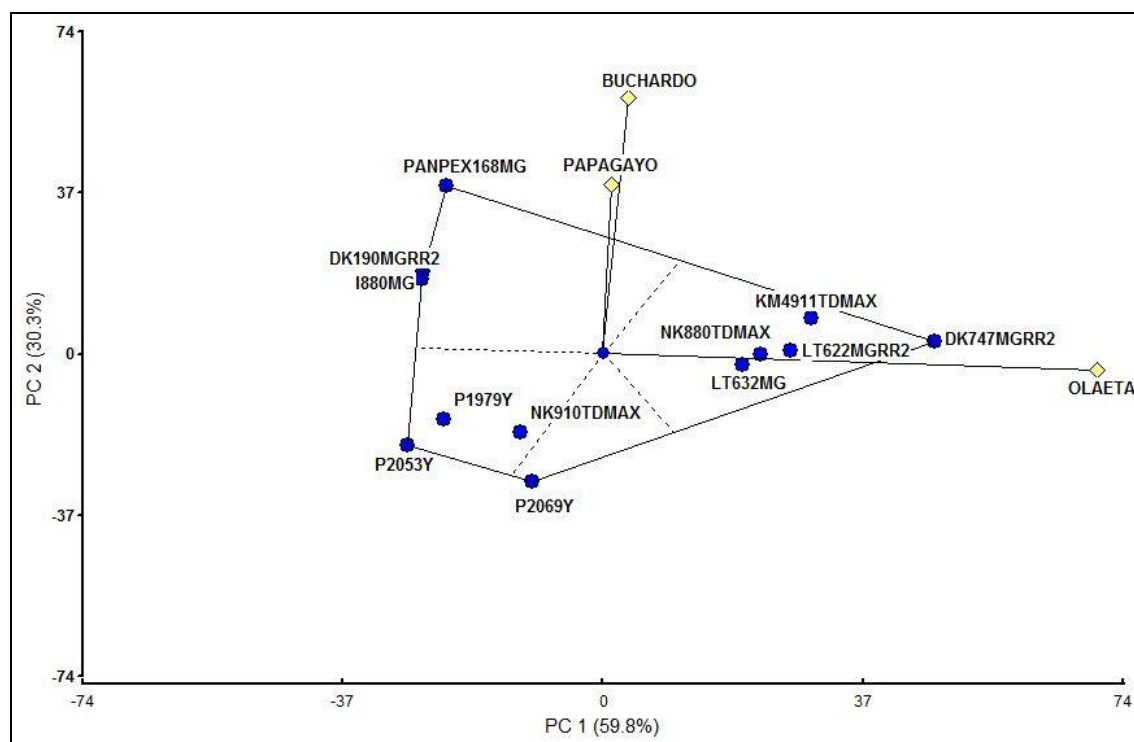
Results of the ANOVA of the MISRR for the 12 hybrids evaluated in the three localities are shown in Table 2. The results evidence a statistically significant  $G \times E$  interaction for the studied character ( $p < 0.001$ ); i.e., differences between means of hybrids varied depending on the environments where they were evaluated.

**Table 2.** Mean square and significance of the analysis of variance of the multidimensional indicator of stalk and root rot for 12 maize commercial hybrids evaluated in Buchardo, Olaeta and Papagayo.

SV	df	MS	p
Locality (E)	2	11224.84	0.0009
Hybrid (G)	11	1501.99	0.0002
Locality>Block	6	404.87	0.3941
Hybrid*Locality ( $G \times E$ )	22	1085.10	0.0006
Error	66	381.13	

SV: Source of variation; df: degrees of freedom; MS: Mean square

The response of the maize commercial hybrids was analyzed simultaneously for the three localities with the biplot obtained from the SREG model (Figure 1). The GGE biplot resulting from the analysis of the two first PCs accounted for 90% of MISRR variability.



**Figure 1.** GGE biplot for the multidimensional indicator of stalk and root rot (MISRR) of 12 maize commercial hybrids analyzed in the localities of Buchardo, Olaeta and Papagayo.

In the three evaluated localities, environmental conditions influenced disease manifestation in the different hybrids. The SREG model and graph analysis showed, on the one hand, a group composed of the localities of Buchardo and Papagayo, with hybrids exhibiting a similar response pattern, with intermediate MISRR values, low discriminating ability and representativeness of the hybrids. On the other hand, the locality with greatest discriminating capacity and the most representative one (the ideal environment) was Olaeta, where the genotypes exhibited the greatest differences in reaction to the disease, therefore allowing a better genotype characterization.

The values of the multidimensional indicator analyzed via the biplot allowed us to identify the response of the evaluated materials. The greatest interaction was detected in the hybrid PANPEX168MG, a genotype specifically adapted to Buchardo and Papagayo environments.

Genotype DK747MGRR2 exhibited the poorest behavior (i.e., the highest MISRR score) in all the environments. The hybrids P2053Y, I880MG and DK190MGRR2 exhibited the best behavior and were the most stable ones, with low MISRR values in all the evaluated environments (i.e., ideal genotype).

## DISCUSSION

The GGE biplot was an efficient visual tool to reveal the interrelations among G, E and G×E interaction. This tool was used in studies focused on selection by multiple characters, comparison of selection strategies and in the analysis of diallel data to estimate combinatory ability (Yan *et al.*, 2000; Yan and Tinker, 2006; Yan, 2013). The G×E interaction observed might be explained by elements that compose the indicator. Indeed, as it is well known, genotypes can be resistant to a given causal agent of stalk and root rot and be susceptible to others. Thus, the environments with intermediate disease levels, such as those of the group composed of Buchardo and Papagayo, might have exhibited not only a high pathogen pressure but also a great diversity of pathogens. Hence, all the materials analyzed were largely affected by the disease, hindering the possibility of being differentiated. By contrast, in Olaeta, the environment characterized by better hydric conditions, only a few causal agents might have generated high pathogen pressure. For this reason, certain genotypes susceptible to these microorganisms were distinguished by higher indicator values, although they exhibited the lowest values in the other two localities, therefore generating the G×E interaction. The greatest interaction was represented by the hybrid PANPEX168MG, with low MISRR levels in Buchardo and Papagayo, and very high ones in Olaeta. The genotype DK747MGRR2 is the least recommendable one because it exhibited high susceptibility in all the environments. Three hybrids, P2053Y, I880MG and DK190MGRR2, were found to be the most recommendable ones for their tolerance and stability in all the environments. These possible differences in the composition of microorganisms responsible for stalk and root rot in each locality were not represented by MISRR. Hence, although this indicator was a very useful tool to differentiate hybrids in Olaeta, in certain environments implementing MISRR may require complementary studies for pathogen identification. Another possibility is that the indicator may be used only when artificial inoculation is performed with a single isolated microorganism, ensuring the uniform presence of the pathogen in all genotypes, as proposed by Todd and Kommedahl (1994), Buchaca (2008) and Szóke *et al.* (2009).

The results indicate that GGE biplot accounts for a high proportion of the total variation of the data estimated for MISRR. Therefore, the graph describes the interrelations between genotypes and environments, and is used for the identification of hybrids and environments that show a good response to the disease.

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