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GENETIC PARAMETER ESTIMATES FOR MAIZE SEEDLING RESISTANCE TO *Fusarium graminearum* Schwabe ROOT ROT USING DIFFERENT GENETIC AND STATISTICAL MODELS

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ABSTRACT

Root lodging is an important problem in corn fields, which may be caused by root rotting in many instances. The root rots are among the least studied and least understood diseases of corn. Fungi recovered from roots include seedling blight and stalk rot pathogens as well as a number of other pathogens and secondary invaders. *Fusarium* spp. are commonly isolated from corn roots. The objectives of this study were (1) to identify the main pathogens affecting maize lodging at harvest, and (2) to study the inheritance of maize seedling resistance to pathogens causing maize lodging. The *Fusarium graminearum* strain, 241 Fr1, was isolated from maize lodged plants and selected as the most pathogenic isolate for root rotting. Nine inbred lines of maize and all their diallel F₁ crosses plus eight control genotypes (four inbreds and four hybrids) were grown in a complete randomized design with three replicates. Twelve seedlings per replication and entry were inoculated at the stage of four-leaves, except for the control entries, which were not inoculated. Disease severity was measured as percentage of the root rotted area.

The square root transformation of raw data was made for adjusting to normality. There was a high significant difference between the means of the inoculated and non-inoculated sets. Three groups of genotypes were formed for the analysis of the inoculated genotypes. Group 1 included the inbreds and the F₁ hybrids; group 2 included only the hybrids; and group 3 included only the inbreds. Different genetic models were used for describing each group of genotypes. Group 1 was described according to the Gardner and Eberhart (GE) (1966) model and the method 2 of Griffing (1956). Group 2 was described by the method 4 of Griffing. The inbreds of group 3 were described according to a simple additive model. Two statistical approaches, the best linear unbiased prediction (BLUP) (i.e., the mixed linear model) (Henderson, 1985) and the general linear model (GLM) were applied to the analysis of the genetic models.

The most important effect detected was the heterosis of the hybrids over the inbreds. The hybrids were significantly more resistance to root rotting than the inbreds. The general combining ability (GCA) effects were also significant for all genetic models and statistical methods studied. In general, there was a fair agreement among the GCA estimated by the different models and methods. The GCA of inbred EC23D was highly significant and susceptible to *F. graminearum roseum*. This susceptibility was also transmitted to the hybrids involving EC23D as a parent. In opposite, inbred EC151 was the most resistant inbred per se, but its resistance was not fully transmitted to the hybrids. In reverse, inbred EC136 was susceptible per se, but conferred a fair resistance to their hybrids. Thus the type of gene action, either additive or dominance, showed a large variation among the parental inbreds.

Selection of additive effects based exclusively on inbred lines is not sufficient to confer resistance to the hybrids, additional selection should be practiced on the hybrid to look for important dominance effects. SCA effects of hybrids were not found significant for any of the genetic or statistical models studied, however partition of the SCA sum of squares resulted in highly significant effects for the average heterosis. The BLUP performed slightly better predictions than the GLM. Also the GE model after removing the SCA heterosis effects was better predictor than both Griffing's methods 2 and 4. It seems that the orthogonality of a model as

it occurs in Griffing's method 2 does not always guarantee the best description of the genetic situations. In the data of our experiment, where the average heterosis effect was important and the SCA effects were not significant, the GE model performed better than the Griffing's models.

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