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DETECTION OF GENOTYPES WITH MULTIPLE DISEASE RESISTANCE IN ARGENTINEAN MAIZE GERMPLASM

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Maize (*Zea mays* L.) is usually affected by multiple co-occurring pathogens. Therefore, selection of multiple disease resistance (MDR) is becoming a necessary area of research. In this study, we aimed to reveal genotypes with MDR in the Argentine public inbred maize collection and to determine the best selection strategy for their identification. We evaluated 87 Argentinean inbred lines for their response to four foliar diseases: common rust (CR), northern corn leaf blight (NCLB), southern corn leaf blight (SCLB) and bacterial leaf streak (BLS) in up to five environments of Argentina. All diseases were evaluated using a 1-5 scale, where 1=highly resistant and 5=highly susceptible. Phenotypic data was analyzed using mixed models to obtain the BLUP (best linear unbiased predictors) of genotypes. We assayed four strategies for multi-trait selection: MDR variable, Elston index, principal component analysis (PCA), and Factor analysis and ideotype-design. Then, we compared them based on their efficiency and genetic gain. Our results showed that the panel of genotypes was plenty of genotypes resistant to CR and BLS, while resistant genotypes to NCLB and SCLB were scarce. We obtained significant genotypic variation and high heritability ($H^2 > 0.82$) for all disease resistances, indicating that selection can be performed with a high efficiency for all of them. We found twelve genotypes resistant to all diseases in the panel of genotypes. The PCA showed the highest efficiency for selecting those genotypes (92%) and presented an average genetic gain of 19%. Our findings will benefit breeders for strengthening broad-spectrum resistance in temperate breeding programs, as well for the study of MDR.

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