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EVALUATION OF RESISTANCE TO TOXIGENIC FUNGI IN SEVERAL MAIZE INBRED LINES

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Maize is attacked by a wide range of pathogenic fungi that cause devastating diseases and lead to significant yield losses. Precise identification of fungi in agricultural products is the key aspect of any pest prevention and management program, providing essential information for crop health and food safety. The aim of this paper was to evaluate new maize genotypes based on resistance to fungal phytopathogens. It allows creating the specialized collection within the active corn collection of the Laboratory of Plant Genetic Resources of IGFPP.

Twelve new inbred lines obtained from synthetic populations were used in the study. The collection samples were evaluated in the field under climatic conditions of 2021. During harvesting, the number of cobs with symptoms of Fusarium spp. infection was determined. The analysis of the obtained data revealed a genotypic difference in the degree of attack and the intensity of disease development. The rate of plants infected with Fusarium ear rot ranged from 0 to 100% depending on the genotype. The mean value of the infection rate was 26.3%. The maximum level of plant damage (70% and 100%) was recorded in MAN2425 and MAN2448 respectively, which allowed them to be classified as highly susceptible. Four lines with an infection rate of 30 to 50% (MAN2424, MAN2461, MAN2281 and MAN2451) were considered as the moderately susceptible group. Genotypes with a disease prevalence of less than 30% were classified as poorly susceptible (MAN2308, MAN2459, MAN2526, MAN2413, MAN2452 and MAN2414). Molecular identification of fungi was performed using nested-PCR with a set of primers developed in the Molecular Genetics Laboratory based on genomic sequences, associated with the synthesis of trichothecenes, aflatoxins and fumonisins from the GenBank database. Positive amplification was marked by a band of 152 bp for *A. flavus*, 120 bp for *A. parasiticus*, 147 bp - *F. graminearum*, 179 bp - *F. verticillioides*, 123 - F. paroliferatum. Thus, all five species of toxigenic fungi were identified in MAN2459 and MAN2461 kernels. *F. proliferatum* was absent, and only *A. flavus, F. gramiearum* and *F. verticillioides* were identified in MAN2451 kernels. The toxigenic race of *F. graminearum* was absent in MAN2308 and MAN2526 kernels. In two lines (MAN2425 and MAN2452) only toxigenic *A. flavus, F. verticillioides* and *F. proliferatum* were identified. Only *F. graminearum* was absent in the MAN2414 line, and in the case of the MAN2413 genotype two Fusarium species were absent. *F. graminearum* and *F. proliferatum* were absent in MAN2424 kernels, as well as four species of toxigenic fungi were identified in MAN2448 inbred line.

The most infected corn lines were MAN2459 and MAN2461, in whose kernels 5 species of toxigenic fungi were detected. And the least infected was the MAN2452 line - only *F. verticillioides* was identified in grain samples.

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