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# EVALUATION OF INBRED MAIZE LINES FOR RESISTANCE TO MAJOR DISEASES

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The objective of the research was to monitor maize collection material for resistance to major diseases under field conditions of experimental plots of the Institute of Genetics, Physiology and Plant Protection. This made it possible to identify and expand the genetic diversity of maize in terms of tolerance and adaptability. It contributed to the expansion of specialized collections with resistance donors. The field trials utilized 8 inbred maize lines from the maize collection of the Plant Genetic Resources Laboratory at the Institute of Genetic Resources for Food Crops. The collection samples were evaluated under natural infection conditions. When setting up the field trials, the traditional planting scheme and agricultural practices for this crop were used. The morphological and biological parameters of the plants were characterized according to the classification system for this crop.

For morphological assessment of diseases, two indicators were determined in field: the spread or number of infected plants in the plot, and the progression or degree of organ infection. A point-based assessment of disease severity was conducted using the following scale: 0-healthy plants; 1-mild infection of an organ or plant; 2-moderate infection, with no severely infected organs; 3-severe infection of plant parts and plant death. Symptom assessment was coupled with molecular analysis via PCR tests with primers to certain fungal diseases.

The effectiveness of assessing the disease resistance of collection samples depends on the presence of an infectious background and the conditions that shape it. Excessive precipitation at the beginning of 2023 contributed to the spread of a number of diseases. Symptoms of smut and powdery smut were observed before and after the flowering phase of male and female inflorescences. The prevalence of Ustilago maydis in mid-early lines was recorded at 2.2% (mean value), with disease severity ranging from 0 to 2 points. The Chișinău 245 (CP386) line, as well as the MAN 2450B line (R = 9%), exhibited the highest susceptibility (R = 12%). The

inbred line MAN 2457 (R = 5%) was classified as slightly susceptible. No characteristic symptoms of this phytopathogen were detected in plants of the following lines: MAN2084, MAN2457, MAN2010, MAN2460, and A634, which allowed them to be classified as resistant.

During harvesting, the severity of damage was assessed while culling cobs infected with Fusarium wilt. Analysis of the data revealed genotypic differences in the prevalence and progression of the disease. The average percentage of damaged cobs across the selected samples in the collection was low (2.1%). The Chișinău 245 line was identified as the most susceptible to Fusarium wilt (R=24%). This index was significantly lower (5%) for the MAN2084 line. No symptoms of Fusarium wilt were detected in six inbred lines. Molecular analysis revealed sources of infection such as F. verticillioides and F. oxysporum.

Therefore, field evaluations identified four self-pollinated maize lines that exhibited resistance to major diseases under natural infection conditions

**Keywords:** maize, fungi, PCR.

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