IDENTIFICATION OF A PUTATIVE GENE RESPONSIVE TO THE FUNGUS *Bipolaris maydis* IN GUINEA GRASS

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Guinea grass (*Panicum maximum* Jacq.) has been used in more intensive cattle production systems in tropical countries. The leaf spot caused by the fungus *Bipolaris maydis* represents one of the main diseases in *P. maximum* cultivars, which inhibits the development of the plant and promotes alteration in the quality of the forage. The use of resistant cultivars, as control methods, is the leading solution for diseases, due its low cost, simplicity of use and ease for farmers adoption. In this study, we aimed to identify the transcript fragments that are differentially expressed in response to the *B. maydis* in *P. maximum*. The experiments were conducted at Embrapa Beef Cattle, in Campo Grande (MS). Two genotypes (resistant and sensible) were analyzed under biotic stress and control conditions, infected and not infected by the fungus respectively. Samples of leaves were collected in 24h, 48h and 72h from triplicates of both genotypes in these two conditions. Total RNA was extracted from these samples and analyzed using the GeneSnare™ technique which allowed fast identification of ten differentially expressed sequences in *P. maximum*. After the sequencing in Applied Biosystems® 3130 Genetic Analyzer, a putative gene responsive to *B. maydis* was identified in infected samples after 24h which encoded a protein ethylene insensitive 3.like (EIN3). EIM3 is a transcription factor involved in the ethylene signal transduction pathway. Ethylene production early after inoculation is believed to be associated with disease resistance in plants. Our results still require validation, but they open up the possibility for new studies to understand the response mechanisms of guinea grass to the fungus *B. maydis*.

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