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Research Abstract

Epigenetic Analysis of The Pathogenicity of *Macrophomina phaseolina* (Tassi) Goid.

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Abstract: Epigenetic mechanisms like DNA methylation and histone modifications regulate gene expression and control the cell specialization. It is known that fungal pathogenesis involves cell differentiation. *Macrophomina phaseolina* (Tassi) Goid. is a cosmopolitan and aggressive plant pathogenic fungus with a broad host range (more than 500 species) including common bean (*Phaseolus vulgaris* L.). We analyzed the pathogenicity of *Macrophomina phaseolina* on *P. vulgaris* L. from an epigenetic perspective using the histone acetyltransferase inhibitors, garcinol and CPTH2. We identified the potential molecular targets of these inhibitors on *M. phaseolina*. Garcinol and CPTH2 affected significantly fungal growth rate, macroscopic morphology of colonies and microsclerotia diameter on solid minimum medium. In spite of this, we did not find evidence of changes in the ability of the fungus to produce disease in the plants of *P. vulgaris* under the inhibition conditions tested. Moreover, it was assessed the expression of some pathogenicity genes in plant-fungus interactions using RT-PCR assays. The increased expression level of *PMK1* under the effect of garcinol with respect to the controls suggests that this inhibitor could deregulate the MAPK pathway, which has been related to fungal pathogenesis.

Keywords: Epigenetics, histone acetyltransferase inhibitors, pathogenicity, Macrophomina phaseolina.

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