



Differential expression of genes involved in entomopathogenicity of the fungi *Metarhizium anisopliae* var. *anisopliae* and *M. anisopliae* var. *acridum* (Clavicipitaceae)

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ABSTRACT. Expression analysis of the genes involved in germination, conidiogenesis and pathogenesis of *Metarhizium anisopliae* during its saprophytic and pathogenic life stages can help plan strategies to increase its efficacy as a biological control agent. We quantified relative expression levels of the nitrogen response regulator gene (*nrr1*) and a G-protein regulator of genes involved in conidiogenesis (*cag8*), using an RT-qPCR assay. Comparisons were made between *M. anisopliae* var. *anisopliae* and *M. anisopliae* var. *acridum* during germination and conidiogenesis and at different stages of pathogenesis. The *cag8* gene was repressed during germination and induced during conidial development and the pathogenic phase, and the *nrr1* gene was induced during germination, conidiogenesis and the pathogenic phase. Both genes were more expressed in *M. anisopliae* var. *anisopliae*, demonstrating

that different varieties of *M. anisopliae* differ in activation of genes linked to virulence for certain environments and hosts. This suggests that differences among these varieties in the ability to adapt could be attributed not only to specific genomic regions and genes, but also to differential gene expression in this fungus, modulating its ability to respond to environmental stimuli.

Key words: Biocontrol; Entomopathogenic fungi; Quantitative RT-PCR; Pathogenicity gene