

Functional genomics of the *Rhipicephalus microplus* tick infection process by *Metarhizium anisopliae*: unraveling the mechanisms of host-pathogen infection

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Abstract

Metarhizium anisopliae is an entomopathogenic fungus that causes infections in several arthropod species. The biological control of parasitic arthropods such as the tick *Rhipicephalus microplus* has great economic and sanitary interest, since they bring losses in Brazilian livestock. Several acaricides are available in the market, but they leave residues in meat, milk and derivatives. Sustainable alternatives have been studied and one of the best-known models is *Metarhizium anisopliae*. However, the development of an efficient control method is hard because it is yet not possible to completely understand their infection mechanisms. This project aims to help in the understanding of the evolutionary history of these organisms and pathogenicity related genes. The research was performed considering the pathogenicity, size, assembly status, GC content of the *Metarhizium* genomes deposited in public databases. We identified ortholog gene groups in the 12 species found using OrthoFinder. These sequences were aligned with PRANK software and, subsequently, a supermatrix was constructed from multiple alignments with SCAfos software. Finally, distance and probabilistic methods of phylogenetic reconstruction were applied with the MEGA software, and these processes were documented and used in the building of a pipeline. We selected 5,509 groups of orthologous genes, from which we obtained a phylogenomic tree with high statistical support. A selected tree depicts an evolutionary relationship between the twelve genomes of the genus *Metarhizium*, corroborating some of the data available in the literature. We were able to identify genes shared among different species and those specific to each organism. This has allowed the establishment of the relationships among *Metarhizium* species and the identification of genes related to pathogenicity.

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