Immune response of female *Aedes aegypti* to infection by the entomopathogenic fungus *Metarhizium anisopliae*

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In mosquitoes the innate immune response is largely regulated by three pathways: Toll, IMD and JAK-STAT, transducers and activators of the transcription signaling pathways. Among the receptors, Toll5A (homologous to the factor NF-κB dorsal from *Drosophila*) is considered to be the principal pathway of the immune response to fungal infection in *A. aegypti*. This pathway is activated by cytokine (SPZ 1C). This study investigated the immune response of female mosquitoes when infected with isolate ESALQ 818 of the fungus *Metarhizium anisopliae* (1x10^7 conidia / ml), by monitoring the gene expression of the proteins Toll5A and SPZ 1C. Seven females were collected at five time periods following infection (0, 24, 48, 72 and 96h). Trizol was used for total RNA extraction and reverse transcribed using a cDNA synthesis kit with random primers. The cDNA was used for real-time PCR (LightCycler 1.5, Roche®) with specific primers for the genes in question. A significant increase in the expression of Toll5A 24 hours after infection was observed. There was a gradual decrease in expression at 48 and 72h post-infection. The same pattern was observed for Spz1C, consistent with results for survival analysis showing mortality at 72 h post-infection. Despite the early immune response of *A. aegypti*, high levels of infection and mortality were seen. ESALQ 818 is currently being tested for control of this mosquito.

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