Altered Expression of Metabolism and Immune Response Genes in Tick Cells During Rickettsial Infections

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Introduction. Tick-borne diseases represent a concern for both veterinary and human medicine. The capacity of ticks for acquisition and transmission of specific pathogens is intimately dependent of the continuous interplay they have evolved during evolution. In order to characterize the molecular mechanisms driving the rickettsial vectorial capacity of Rhipicephalus (Boophilus) microplus ticks, we analyzed the transcriptomic response of the tick cell line BME26 infected with either a R. (B.) microplus-transmitted rickettsia (Anaplasma marginale) or a rickettsia not transmitted by this tick species (Rickettsia rickettsii). Material and Methods. BME26 cells were experimentally infected with A. marginale (941 rickettsiae/cell) or R. rickettsii (0.03 rickettsia/cell). The progression of infection and the viability of the BME26-infected cells were monitored at 6, 24, 48 and 72 h by absolute quantification and light microscopy, respectively. The expression levels of 130 genes from different functional categories were analyzed by high-throughput microfluidic qPCR. Results and Discussion. Whereas the number of A. marginale was relatively constant, we observed an increment in the number of R. rickettsii during the infective process. At 72 h post-infection, BME26 mortality reached 55% and 19% for R. rickettsii and A. marginale infection, respectively. Results from our high-throughput qPCR analyses revealed striking differences in gene expression in BME26 harboring A. marginale compared to BME26 cells succumbing to R. rickettsii infection. While the transcript abundance of genes related to cell metabolism (glycolysis, Krebs cycle, lipid and amino acid metabolism) was induced by A. marginale infection, in R. rickettsii-infected cells those genes were down-regulated. In addition, only the R. rickettsii infection up-regulated genes involved in tick immunity. Conclusions. Our transcriptome data highlighted the main candidate gene categories implicated in tick response to two contrasting rickettsial infections. In order to go further on the molecular mechanisms involved in tick-rickettsia interactions, functional characterization of modulated genes studies are underway.

Keywords: tick, rickettsia, host-pathogen interaction, high-throughput qPCR.
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