

PROTEOMICS APPLICATIONS TO TICK RESEARCH

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Ticks are vectors of pathogens that affect human and animal health worldwide. Ticks and the pathogens that they transmit have co-evolved molecular interactions involving genetic traits of both the tick and the pathogen that mediate their development and survival. Proteomics and genomics studies of infected ticks are required to understand tick-pathogen interactions and identify potential vaccine antigens to control pathogen transmission. In the work reported here, two quantitative proteomics approaches were used to characterize differential protein expression in ticks and cultured tick cells in response to pathogen infection. Analyses were conducted using (a) two-dimensional differential in gel electrophoresis (DIGE) saturation labeling and (b) peptide iTRAQ labeling and isoelectric focusing fractionation, in combination with mass spectrometry. The results of these studies showed that proteomic analysis conducted from a limited amount of proteins using DIGE saturation labeling allowed the identification of host, pathogen and tick proteins differentially expressed as a consequence of infection. These results demonstrated pathogen- and tick species-specific differences in protein expression in ticks and cultured tick cells in response to pathogen infection and suggested the existence of post-transcriptional mechanisms induced by pathogens to control tick response to infection. These results also demonstrated that the stress response was activated in ticks and cultured tick cells after *Anaplasma* spp. infection and heat shock. However, in the natural vector-pathogen relationship, heat shock proteins and other stress response proteins were not strongly activated, which was most likely a result of tick-pathogen co-evolution.