

Abstract

Proteomics as a Potential Tool for Identifying Biomarkers for Host Resistance to Cattle Tick [†]

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Abstract: The cattle tick, *Rhiphicephalus microplus*, and the diseases it transmits lead to massive economic losses to cattle industries in tropical and subtropical countries. The emergence of widespread resistance to acaricide drugs and the absence of an effective vaccine for tick control had led to genetic selection of host resistance as a method of choice for non-chemical control of cattle tick. Research to identify host genetic markers associated with tick susceptibility or resistance has been limited to the comparison of local breeds in specific geographic regions. Previous studies have also focused on gene expression profiles, localizing cellular and humoral immune responses, and genome-wide association studies (GWAS) to identify functional genetic variants associated with tick resistance/susceptibility. Given the fact that gene expression results and actual dynamics occurring at the protein level often do not correlate due to post-transcriptional, post-translational and degradation regulation, host proteomics may provide reliable biomarkers to assist in selection to support traditional breeding programs. The present study aims to investigate the variation in protein profiles among tick resistant and susceptible cattle following tick infestation. Preliminary findings suggest that different serum proteins exist between tick resistant and susceptible Santa Gertrudis cattle. This research is supported by Meat & Livestock Australia.

Keywords: cattle ticks; *Rhiphicephalus microplus*; host resistance; proteomics; biomarker discovery

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