FUNCTIONAL GENOMICS STUDIES OF RHIPICEPHALUS (BOOPHILUS) ANNULATUS TICKS IN RESPONSE TO INFECTION WITH THE CATTLE PROTOZOAN PARASITE, BABESIA BIGEMINA

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Abstract: Ticks are obligate haematophagous ectoparasites of wild and domestic animals as well as humans, considered to be second worldwide to mosquitoes as vectors of human diseases, but the most important vectors of disease-causing pathogens in domestic and wild animals. Babesia spp. are tick-borne pathogens that cause a disease called babesiosis in a wide range of animals and in humans. In particular, Babesia bovis and Babesia bigemina are transmitted by cattle ticks, Rhipicephalus (Boophilus) annulatus and Rhipicephalus microplus, which are considered the most important cattle ectoparasites with major economic impacts on cattle production. The objectives of this study were to identify R. annulatus genes differentially expressed in response to infection with B. bigemina. Functional analyses were conducted on selected genes by RNA interference in both R. annulatus and R. microplus ticks. Eight hundred randomly selected suppression-subtractive hybridisation library clones were sequenced and analysed. Molecular function Gene Ontology assignments showed that the obtained tick sequences encoded for proteins with different cellular functions. Differentially expressed genes with putative functions in tick-pathogen interactions were selected for validation of SSH results by real-time reverse transcription-PCR. Genes encoding for TROSPA, calreticulin, ricinusin and serum amyloid A were over-expressed in B. bigemina-infected ticks while Kunitz-type protease inhibitor 5 mRNA levels were down-regulated in infected ticks. Functional analysis of differentially expressed genes by double stranded RNA-mediated RNAi showed that under the conditions of the present study knockdown of TROSPA and serum amyloid A significantly reduced B. bigemina infection levels in R. annulatus while in R. microplus, knockdown of TROSPA, serum amyloid A and calreticulin also reduced pathogen infection levels when compared with controls. Several studies have characterised the tick-pathogen interface at the molecular level. However, to our knowledge this is the first report of functional genomics studies in R. annulatus infected with B. bigemina. The results reported here increase our understanding of the role of tick genes in Babesia infection/multiplication. (C) 2012 Australian Society for Parasitology Inc. Published by Elsevier Ltd. All rights reserved.

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