

ARTHROPOD GENOMICS SEMINAR



Title: MICROARRAY ANALYSIS OF *RHIPICEPHALUS (BOOPHILUS) MICROPLUS* GENE EXPRESSION ASSOCIATED WITH *BABESIA BOVIS* INFECTION

Speaker: Dr. Felix D. Guerrero, Research Physiologist
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Date: Friday, May 1, 2009

Time: 1:30 p.m.

Place: West Waters Hall Room #129

Abstract: We utilized a *Rhipicephalus (Boophilus) microplus* gene index, containing 13,643 unique sequences, to design a *R. microplus* microarray and investigated the molecular interactions between *Babesia bovis* and the host tick, *R. microplus*, following ingestion of *B. bovis*-infected blood. We obtained tick ovary and gut tissue by placing tick larvae on an infected calf or a control uninfected calf, collecting engorged adult females after dropping from the calf, and dissecting ovary and gut from both the infected and uninfected females. DNA-free RNA from both uninfected and *B. bovis*-infected ovary and gut was isolated, labeled, and hybridized to array slides in duplicate for each experimental condition. There were 33 and 15 genes with statistically significant up-regulation associated with *B. bovis*-infection in the gut and ovary samples, respectively. Conversely, there were 43 and 0 genes with statistically significant down-regulation associated with *B. bovis*-infection in the gut and ovary samples, respectively. Five of the gut up-regulated, 19 of the gut down-regulated, and 3 of the ovary up-regulated had matches to GenBank entries with putative functional annotation ($e < 10^{-25}$). Further investigations into the roles of these genes in facilitating *B. bovis* interactions with *R. microplus* are underway.

Co-sponsored by the Department of Entomology

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