CHARACTERIZING THE ROLES OF PUTATIVE LIPOPROTEINS IN TICK-BORNE RELAPSING FEVER VECTOR COMPETENCE

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Background: Tick-borne relapsing fever (TBRF) is a neglected disease despite being a significant cause of morbidity and mortality in the developing world. Spirochetes from the Borrelia genus are the etiological agents of TBRF and cause recurring episodes of acute fever, pregnancy termination, and/or potential death if the infection is not treated. Soft ticks transmit the majority of the TBRF Borrelia species. To be maintained in nature, TBRF Borrelia need to adapt to both tick and mammalian environments. The mechanisms of mammalian infection are well understood and driven by antigenic variation. However, the molecular mechanisms enabling vector competence are poorly understood. We hypothesize that TBRF Borrelia adapt to these diverse environments by differentially regulating their gene expression as they complete their tick-mammalian transmission cycle. We hypothesize that TBRF Borrelia adapt to these diverse environments by differentially regulating their gene expression as they complete their tick-mammalian transmission cycle.

Materials/Methods: To test this, our lab developed the Ornithodoros turicata-Borrelia turicatae (vector-pathogen) model to investigate genes involved in TBRF Borrelia vector competence. Through transcriptional analysis, 18 B. turicatae genes, encoding putative surface lipoproteins, were found to be expressed at significantly higher levels during vector colonization compared to mammalian infection. To begin characterizing and the role(s) of nine of these putative lipoproteins in vector competence, we generated four multi-gene deletion mutants and performed murine needle inoculations and tick transmission studies.

Results: All mutants were able to infect mice at levels that allowed us to feed uninfected ticks and assess vector colonization. Preliminary studies suggest that a triple (Δbta134-bta136) and a double mutant (Δbta132-bta133) have attenuated murine infection following tick transmission. Furthermore, studies have shown that both mutants have a growth defect during cultivation at 22°C.

Conclusions: Together these results suggest that these five inactivated genes may have important roles in vector adaptation. These results may aid in identifying targets for a vaccine to prevent the establishment of early mammalian infection after tick transmission.

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