Mid Atlantic Microbial Pathogenesis Meeting Abstract
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Oral Presentation
Gram-Negatives

Title: How does a Wzx-Wzy-type polysaccharide biosynthetic pathway play a role in *Brucella* virulence?

Authors: Jodi M. Ogle[1], Dariel A. Hopersberger[1], Gail G. Hardy[2], Ian S. Barton[1], Connor B. Cribb[1], Graham J. Bitzer[1], Clay Fuqua[2], Daniel W. Martin[1], and R. Martin Roop II[1]

[1]East Carolina University, Greenville, NC
[2]Indiana University, Bloomington, IN

Abstract:

Brucella spp. are the causative agents of brucellosis, one of the world's most prevalent zoonoses. In the natural animal host, brucellosis is marked by spontaneous abortion and infertility. However, in humans, brucellosis causes a chronic flu-like illness characterized by an undulant fever. Belonging to the *Rhizobiales* order of the alphaproteobacteria, *Brucella* spp. are closely related to the plant pathogen *Agrobacterium tumefaciens*. Despite differences in host preference and pathogenicity, members of the alphaproteobacteria often share genes and pathways that contribute to successful interactions with their eukaryotic hosts.

A. tumefaciens employs a Wzx-Wzy-type polysaccharide biosynthetic pathway to produces a unipolar polysaccharide (UPP) on one pole of the cell. This structure is crucial for surface attachment and biofilm formation by *A. tumefaciens* as mutants in this pathway are attenuated and unable to form biofilms. *Brucella* spp. encode homologs of many of the *A. tumefaciens upp* genes, suggesting that *Brucella* has the genetic potential for UPP or exopolysaccharide production. Strikingly, a *B. abortus* mutant lacking the genes encoding the outer membrane polysaccharide transporter and the initiating glycosyltransferase components of the UPP biosynthetic pathway, *uppC* and *uppE* respectively, display an attenuation in cultured mammalian cells and C57Bl/6 mice. These results implicate *Brucella* UPP involvement in virulence. However, the precise function of the *Brucella* putative UPP biosynthetic pathway and the mechanism leading to virulence remains unclear.

Here, we implement a heterologous complementation approach to identify individual *upp* genes in *B. abortus* that can restore wild-type levels of biofilm production in the respective *A. tumefaciens upp* mutants. This approach aims to determine the roles of *upp* genes in *Brucella* polysaccharide biosynthesis, and ongoing research will delve into the impacts of individual *upp* genes on *Brucella* virulence.