

Name

Michaela Smith

Email

mjsmith1@bu.edu

Institutional Affiliation

Boston University

Campus

Charles River Campus

School

College of Arts & Sciences

Department

Molecular, Cell Biology, & Biochemistry

Position Held at Institution

Graduate

Poster Submissions**Poster Title**

An integrative analysis of Wolbachia-host microbiota interactions.

Authors and their Affiliation

Michaela Smith, Boston University
Natalie Vaisman, Boston University
Rama Simhadri, Boston University
Joanna Bybee, New England Biolabs
Brian Anton, New England Biolabs
Alexey Fomenkov, New England Biolabs
Rick Morgan, New England Biolabs
Barton Slatko, New England Biolabs
Horacio Frydman, Boston University

Please describe the extent of your work in this research

I isolated the mosquito gut bacteria (7 of the 11 isolated species) and prepared DNA extracts for sequencing. For all 11 symbiotic gut bacteria, I prepared sequencing libraries and sequenced the full genome. After an initial hierarchical de novo genome assembly, I trimmed genomes, closed and edited them. I annotated these genomes and assembled metabolic models for all 11 genomes using established software (RAST and SEED). Lastly, I constructed alignments and comparisons to determine novel species and genome rearrangements relative to previously published closely related species.

Abstract Submission

- [Genome-Science-Institute-symposium-2015-Abstract.docx](#)

Would you like your abstract to be considered for an oral presentation (students and post docs only)?

Yes

An integrative analysis of *Wolbachia*-host microbiota interactions.

Authors: Michaela Smith, Natalie Vaisman, Rama Simhadri, Joanna Bybee, Brian Anton, Alexey Fomenkov, Rick Morgan, Barton Slatko, Horacio Frydman

Wolbachia pipientis are intracellular endosymbionts which cause severe reproductive phenotypes in their insect hosts. Estimated to infect 40% of all insects¹, *Wolbachia* are the largest pandemic in the world. *Wolbachia* are emerging as a novel approach to control vector transmitted diseases. Mosquitos infected with the wMel strain of *Wolbachia* are unable to transmit deadly human pathogens including dengue virus and *Plasmodium sp.* (Malaria)^{2,3}. In addition to *Wolbachia*, other bacteria have been shown to affect the competence of mosquitos to transmit disease⁴. Furthermore, a gut bacterium has been shown to block *Wolbachia* transmission⁵. However, the interactions of *Wolbachia* and commensal bacteria, are largely unexplored. Recent work in our lab has shown that *Wolbachia* alters the gut microbiota of its host. To build metabolic models to predict microbial interactions and their role in pathogen control in insect hosts, we isolated and sequenced the full genomes of 11 bacterial species from two of our model organisms, *Culex pipiens* mosquitos and *Drosophila melanogaster*. Our results indicate at least two novel bacterial species and many large inversions in the genomes. Genomic alteration is an important part of co-evolution between symbiotic organisms and host. This often indicates a shift in metabolism supporting an intertwined relationship between host and symbiont⁶. The knowledge derived from this work is relevant for improving *Wolbachia*-based disease control approaches and elucidating the mechanisms of bacteria-driven phenotypes in insects.

1. Zug, R. & Hammerstein, P. Still a Host of Hosts for Wolbachia: Analysis of Recent Data Suggests That 40% of Terrestrial Arthropod Species Are Infected. *PLoS ONE* **7**, e38544 (2012).
2. Walker, T. et al. The wMel Wolbachia strain blocks dengue and invades caged *Aedes aegypti* populations. *Nature* **476**, 450-453 (2011).
3. Moreira, L.A. et al. A Wolbachia symbiont in *Aedes aegypti* limits infection with dengue, Chikungunya, and Plasmodium. *Cell* **139**, 1268-78 (2009).
4. Weiss, B. & Aksoy, S. Microbiome influences on insect host vector competence. *Trends Parasitol* **27**, 514-22 (2011).
5. Hughes, G.L. et al. Native microbiome impedes vertical transmission of Wolbachia in *Anopheles* mosquitoes. *Proceedings of the National Academy of Sciences* **111**, 12498-12503 (2014).
6. Toft, C., Williams, T.A. & Fares, M.A. Genome-wide functional divergence after the symbiosis of proteobacteria with insects unraveled through a novel computational approach. *PLoS Comput Biol* **5**, e1000344 (2009).