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Genome Sequencing Analysis of Laboratory Isolate of *Francisella noatunensis* subs. *orientalis*

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As a member of the Kathryn Ramsey Laboratory in the Department of Cell and Molecular Biology at the University of Rhode Island, I aimed to determine the genetics differences between a laboratory isolate of *Francisella noatunensis* and the wild-type. *F. noatunensis* is a known fish pathogen. It was most notably isolated from tilapia off the coast of Costa Rica, which represents the wild-type genome used for this study. Both genomes were sequenced using Next-Generation Sequencing. For my Honors Project, it was my goal to computationally analyze the genomes of two isolates and identify any discrepancies between them as it pertains to virulence and/or growth requirements.

I worked closely with Jamie Wandzilak, a graduate student researcher in the KRamsey Lab. Together we used the University of Rhode Island clusters program, Bluewaves, to align the sequences and highlight any differences between them. Next, we uploaded the genomes to the Integrative Genomics Viewer from the Broad Institute to visualize the aligned sequences. Overall, we found several mutations in the laboratory isolate which differentiated it from the wild-type. Although several of these mutations occurred in genes which encode proteins, we are unsure at this time if they contribute to a difference in virulence or pathogenesis. We will explore these possibilities in future studies.