POSTER PRESENTATION

Jyl Matson, Major Advisor

R 87 * UDGXDWH UHVHDUFK Robert Blumenthal, Ph.D. (co-advisor) IRUXP 0DUFK Alexei Federov, Ph.D.

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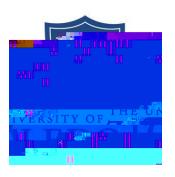
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R , , 7 5 H V H D U F K) R U X P 2 F W Rendage U. Williams, Ph.D., Graduate School

The University of Toledo College of Medicine and Life Sciences

Infection, Immunity & Transplantation (IIT) Track

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DISSERTATION PRESENTATION

Yvette Unoarumhi

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Evolution of Bacterial Global regulator– Lrp

MSBS in Bioinformatics, Proteomics and Genomics

Abstract

Global regulators each control hundreds of genes in bacteria, and it is still unclear how these regulators evolve, especially considering that gene regulation changes more rapidly than the regulated genes themselves. Leucine-responsive regulatory protein (Lrp) is a global regulator in enteric bacteria, controlling both metabolic and virulenc e-associated genes. Lrp orthologs are found among both Bacteria and Archaea. Surprisingly, even within the phylum -Proteobacteria, Lrp is a global regulator in some orders and a local regulator in others. This raises important questions about the evolution of Lrp functions. The way global regulators function is cruciall y important to bacterial physiology. This thesis presents studies on the evolution and regulation pattern of Lrp, carried out with the goal of providing insights into global regulators more gener-

Two independent studies of Lrp were carried out. The first compared Lrp sequences from four bacterial orders within the -Proteobacteria: Enterobacteriales, Vibrionales, Pasteurelalles, and Alteromonadales. AsnC was also analyzed in parallel for comparison, as it is a paralog of Lrp that in all known cases is a local regulator controlling a small number of genes. As expected, Lrp and AsnC sequences form ed two distinct clusters diverging from a common ancestor. These each divided into subclusters representi ng the Enterobacteriales, Vibrionales, and Pasteurella les. However, the Alteromonadales did not yield unitary clusters for either Lrp or AsnC, in contrast to the expected order-specific clustering we observed with the control housekeeping genes for 16S rRNA and RNA polymerase subunit RpoB.

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