

THESIS: Mapping of Structural Changes to the ykkCD Antibiotic Sensor RNA Caused by Tetracycline Binding

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Abstract:

A riboswitch is a noncoding RNA that controls gene expression response to changes in the cellular environment. Most riboswitches regulate genes responsible for transporting, synthesizing or recycling small metabolites in bacteria.¹ These riboswitches, primarily found at the 5' region of messenger RNA, recognize the metabolic product of the gene being regulated. When a metabolite concentration threshold is reached, expression is turned off. In contrast, the ykkCD putative riboswitch increases production of an efflux pump that ejects toxins from the cell by binding to the antibiotic tetracycline. As tetracycline binds to ykkCD riboswitch, structural changes take place that trigger the production of the efflux pump.² We will present terbium fragmentation and other nucleic acid footprinting methods to map the tetracycline site and to visualize the allosteric changes that take place due to tetracycline binding.

References:

1. Barrick, J.E.: Edited by Alexander Serganov. Department of Structural Biology, New York, NY. In *Riboswitches Methods and Protocols: Predicting Riboswitch Regulation on a Genomic Scale* pp1-14
2. Howell, L. A. Mapping the structural change caused by tetracycline binding to the ykkCD antibiotic sensor RNA. Ball State University, Muncie, IN, 2013