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Title. A Putative RNA Structure from Actinobacteria Allows Regulation in Response to S15

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In combination with the ribosomal RNA, ribosomal proteins are necessary for protein translation. The Meyer Lab is interested in studying how bacteria can control expression of ribosomal proteins through autogenous regulation. In this paradigm, excess ribosomal proteins not needed for ribosome biosynthesis bind a structured portion of their mRNA operons to prevent further expression of the operon. Ribosomal protein S15 interacts with several distinct regulatory structures that are narrowly distributed to different bacterial phyla. These structures are diverse from each other, but have the same biological function. Using comparative genomics, the Meyer lab discovered a putative RNA structure we hypothesize allows autoregulation of S15 in Actinobacteria. This predicted structure is different from the others previously discovered, but the structure of the biologically active RNA is still unknown. Two plasmid Miller assays are being employed to investigate the ability for this putative mRNA regulator from *M. smegmatis* to regulate gene expression in response to the S15 homolog from *Mycobacterium smegmatis* (Ms S15). We have found that mutations to a specific stem region of the RNA structure affect its ability to regulate, which suggests that the highly conserved regions of the RNA are important for gene regulation. Our results demonstrate the biological function for an additional example of the varied and diverse RNA structures that serve the same biological function.