Title: Finding novel bacterial non-coding RNAs by analyzing genomic sequences

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(Feel free to drop this talk if there are many other potential talks.)

The discovery of new classes of non-coding RNAs can reveal information about RNA biochemistry and the biological processes that involve these RNAs. We recently performed two projects that demonstrated the discovery of novel non-coding RNAs in bacteria.

The first project targeted self-cleaving ribozymes, which are catalytic RNAs whose role in bacteria remains mysterious. Previous work demonstrated that two classes of self-cleaving ribozymes, called the twister and hammerhead ribozymes, are often located nearby to specific classes of protein-coding genes. Although the reason for this association between genes and ribozymes is unknown, we were able to exploit the association by analyzing non-coding regions nearby to these protein-coding genes in order to find novel ribozymes. We found 3 novel structural classes of self-cleaving ribozyme, adding to the only 6 structural classes that were previously known.

The second project investigated riboswitches, which are RNAs that directly sense a metabolite and regulate genes accordingly. Although proteins are routinely observed to evolve new ligand specificity, only 4 validated cases are known in which riboswitches have altered their ligand specificity. We designed a pipeline to exploit atomic resolution structures, genome annotations and RNA multiple-sequence alignments in order to identify homologs of known riboswitches that are specific to a new ligand. We found two new examples of riboswitch ligand evolution, and several more candidates.