Title
Antisense RNA genes in bacterial genomes

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Introduction: Several small RNAs affect mRNA translation through base pairing interactions near the RBS of genes. These interactions can alter mRNA structure and/or stability resulting either to inhibition or promotion of ribosome binding.

The sRNA are small RNA molecules that have a small region which is complementary to the target mRNA and is responsible for the specificity of the interaction. The rest of the molecule can interact with proteins, such as Hfq in *E.coli*, resulting to the mRNA-sRNA complex degradation. The detection of these molecules is difficult and several approaches have been used.

Method: We developed a method that allowed us to search for regulatory sRNA in XX of the currently available bacterial genomes. The method relies on the detection of regions in the intergenic space, similar to each other, which align well to the 5’ region of homologous genes, in genomes of phylogenetically close organisms.

Results: Preliminary experimental data support the presence of predicted sRNAs in *Escherichia coli*.

Results, based on computational analysis, suggest that a large number of these sRNA molecules can be predicted in bacterial genomes. However, their presence appears to be related to the presence of Hfq and the lifestyle of the organism. Genomes, which do not have Hfq homologs, exhibit small numbers of this type of RNA genes. Among them intracellular pathoges exhibit a small number of transcriptional regulators as well, suggesting a substantial loss of complex gene regulation systems.

Conclusion: An attempt to predict antisense regulatory RNAs in bacterial genomes reveals the presence of a large number of these genes in organisms that have Hfq homologs.