

Search for New Laboratory Verified Operon Pairs in *Mycobacterium tuberculosis*

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Abstract

Today, tuberculosis is one of the greatest world health concerns because of its infectious nature and ability to build resistance to preventive and treatment drug regimens. Operon pairs within a genome are genes that are cotranscribed and usually found to have a very similar function; therefore, they are an effective way to gain a broader view of the genomes transcriptional organization and increase our ability to interrupt its life cycle. Our research to find new laboratory verified operon pairs via searching through published literature and performing RT-PCR enables us to gain a better training set in which to build a predictive model for operon pairs. We found an additional 30 operon pairs which were then used to improve our model, reaching a higher specificity as well as sensitivity. In hopes, our model will be able to formulate an operon map for the MTB genome and be used to better understand this pathogen and lead to new drug regimens to enhance our ability to fight this infectious disease.