GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria

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Abstract

Background

Development of drug resistance in bacteria causes antibiotic therapies to be less effective and more costly. Moreover, our understanding of the process remains incomplete. One promising approach to improve our understanding of how resistance is being acquired is to use whole-genome comparative approaches for detection of drug resistance-associated mutations.

Results

We present *GWAMAR*, a tool we have developed for detecting of drug resistance-associated mutations in bacteria through comparative analysis of whole-genome sequences. The pipeline of GWAMAR comprises several steps. First, for a set of closely related bacterial genomes, it employs eCAMBer to identify homologous gene families. Second, based on multiple alignments of the gene families, it identifies mutations among the strains of interest. Third, it calculates several statistics to identify which mutations are the most associated with drug resistance.

Conclusions

Based on our analysis of two large datasets retrieved from publicly available data for *M. tuberculosis*, we identified a set of novel putative drug resistance-associated mutations. As a part of this work, we present also an application of our tool to detect putative compensatory mutations.