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Research Project in Bioinformatics

Reconstruction of *Corynebacterium striatum* KC-Na-01

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1 Background and Motivation

The Corynebacterium species are catalase-positive, Gram-positive rods. *Corynebacterium striatum* is one of the more commonly isolated coryneform bacteria [18]. It is increasingly being recognized as a source of opportunistic diseases in immunocompromised patients.

Figure 1 | Coryneform morphology of *C. striatum* with Gram stain [21].

C. striatum has frequently been cultured from various surfaces and medical equipment in hospital settings [16]. Although early reports are stating that *C. striatum* might be susceptible to a wide range of antibiotics, multidrug-resistant phenotypes have been recently reported in most *C. striatum* strains leading to increased mortality [19, 20]. Furthermore, Ramsey et al. found that microbe-microbe interactions between nasal *Staphylococcus aureus* and human nasal commensal *C. striatum* may diminish *S. aureus* virulence and shift it towards commensalism in response to Corynebacterium spp. [15]. *S. aureus* reacts to the presence of Corynebacterium spp., including *C. striatum*, with altered expression of genes involved in colonization and virulence [15]. Its expression is similar to the transcriptomes of agrQS loss-of-function mutants of *S. aureus* [3, 4, 14], leading to a decrease in the production of secreted virulence factors, e.g., hemolysin, and to an increase in cell-surface activities associated with colonization, e.g., epithelial cell adhesion and SpA activity [15].

In the last years, the standardized construction of genome-scale metabolic models (GEMs) has been a goal. As described in a paper by Lieven et al., MEMOTE allows standardized testing of GEMs. Reliable quality and generality have to be assured to improve the usage of GEMs as resources in research questions.

2 Aim

This research project aims to finalize the *Corynebacterium striatum* model by annotating evidence scores to the model developed in an earlier lab rotation project. The model is, for example, still missing reactions and pathways from the databases such as KEGG [8] or BiGG [13] and growth behavior in the Synthetic Nasal Medium [10].

3 Approach

1. Familiarization with the given model: growth simulation.
2. Work on the repository structure to enable automated tests.
3. Extensive literature research for coverage of given bacterium
4. Annotation of scores based on literature
5. Planning of additional experiments to annotate more reactions

4 Requirements

(1) Fundamental understanding of biochemistry (2) interest in systems biology modeling (3) enthusiasm and a sense for detail (4) python programming.

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