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Bachelor Thesis

The first genome-scale reconstruction of *Corynebacterium simulans*

1 Background

Corynebacterium simulans is a Gram-positive and aerobic member of the phylum Actinobacteria. It was first described in 2000 as a non-lipophilic, fermentative species of the Genus Corynebacterium [11]. *C. simulans* is one of the less well-described Corynebacteria. Since the first report in 2000, there are not more than 30 reports in Pubmed journals on clinical microbiology and veterinary medicine journal combined. *C. simulans* and other Genus members are known as commensals of normal human flora, but they can occasionally act as pathogens. It was reported to inflict pyogenic spondylitis, a life-threatening condition [9]. Of note, *C. simulans* could be misclassified as *C. striatum* [7, 8]. Therefore, reconstructing the model can give more information about the qualitative attitude of this organism. It can also help in identifying the mechanisms which cause diseases or develop a therapy against them.

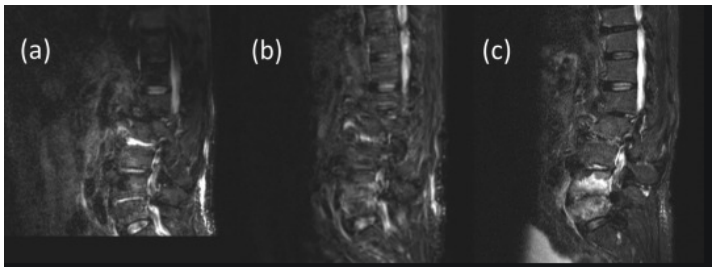

Figure 1 | Pyogenic spondylitis with acute course caused by *Corynebacterium simulans* [9].

2 Aim

This thesis aims to reconstruct and extend the model of *C. simulans* using automated tools such as CarveMe [6]. To build a precise and significant model and gain more information about the bacterium's role in the human body, manual curation by incorporating further information from relevant databases, such as KEGG [3], BioCyc [4], is required [10]. Also, the mass and charge need to be balanced. Further mandatory additions to the model include annotations of metabolites, reactions, and genes, as well as Systems Biology Ontology (SBO) terms. QC/QA (quality control/quality assurance) techniques will be applied to validate the model. Since *C. simulans* occupies a habitat of the nasal bacterial community, the growth ability of the organism on the synthetic nasal medium (SNM3) [5], which mimics the human nose environment, will be examined. In the end, the interactions with other bacteria, most prominently with *Staphylococcus aureus*, will be simulated and analyzed theoretically.

3 Requirements

Experience in Python programming and familiarity with COBRApy [2] and libSBML [1] for the reconstruction process. High motivation to improve the model and gain more knowledge is also of vital importance.

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