Reconstruction of *Moraxella catarrhalis* RH4

Research Project

Background and Motivation

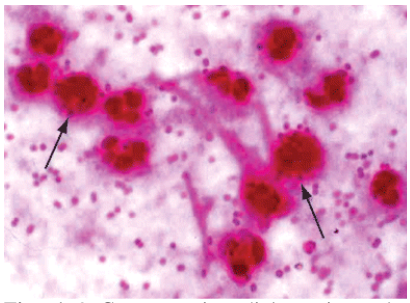

Fig. 1 | Gram-negative diplococci as the exclusive bacterial form and intracellular bacteria [1].

The aerobe Gram-negative bacterium *M. catarrhalis* (**Fig. 1**) belongs to the group of γ-proteobacteria and was first discovered in 1896. This exclusive human pathogen [1] causes wide range of infectious diseases of the respiratory tract [2]–[4]. Until now, attempts to develop a vaccine did not yield fruitful results [5], [6]. It has been observed that *M. catarrhalis* is often β-lactamase positive and therefore resistant against treatment with ampicillin. In addition, several studies highlight its interaction with other multi-resistant germs of the nasal microbiome, such as *Staphylococcus aureus* or *Haemophilus influenzae* [7]–[10]. In many applications, genome-scale metabolic models have demonstrated their usefulness to predict biological features and their potential applicability for treatment discovery. Until now, no curated computational model is available for this important organism. An automatically generated draft model of the strain RH4 resulted from the so-called "path2models" project [11] based on the information of the databases KEGG [12] and MetaCyc [13] in July 2011. This model is freely available from BioModels database [14]. The BiGG Models knowledgebase [15] does currently not provide any reconstruction for this organism.

Aim

The aim of this project is to create a first version of a curated genome-scale reconstruction (GEM) of the organism's metabolic capabilities in SBML Level 3 Version 1 format [16] by following the standard reconstruction protocol [17].

Approach

The following steps will be executed:

1) Obtain the path2models draft model from BioModels database[1].
2) Download the genome of the organism from NCBI[2].
3) Apply automatic reconstruction tools, such as CarveMe [18], ModelSEED [19], KBase [20], Raven 2.0 [21], etc.
4) Compare all models, possibly by using libSBML [22], e.g., for Python and model annotation, e.g., using ModelPolisher [23]
5) Simulate model growth in relevant media using COBRApy [24], including the synthetic nasal medium SNM3 [25].
6) Draw parts of the model in form of a metabolism chart using software such as Escher [26] or Krayon[3].

Literature

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