Reconstruction of *Corynebacterium striatum*

Research Project

Background and Motivation

The Corynebacterium species are catalase-positive, Gram-positive rods. *Corynebacterium striatum* is one of the more commonly isolated coryneform bacteria (Suh *et al*., 2019). It is increasingly being recognized as a source of opportunistic diseases in immunocompromised patients. *C. striatum* has frequently been cultured from various surfaces and medical equipment in hospital settings (Renom *et al*., 2014). 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 (Wang *et al*., 2016, Verroken *et al*., 2014).

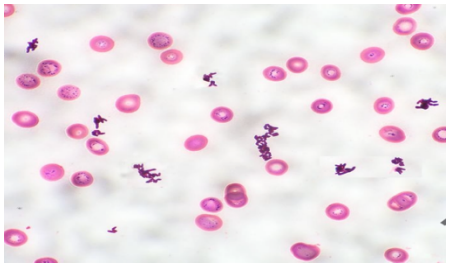

Figure 1: C. striatum Gram stain in blood culture; Source: http://microbe-canvas.com/Bacteria.php?p=1208

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. (Ramsey *et al*., 2016).

S. aureus reacts to the presence of *Corynebacterium* spp., including *C. striatum*, with altered expression of genes involved in colonization and virulence (Ramsey *et al*., 2016). Its expression is similar to the transcriptomes of *S. aureus* agrQS loss-of-function mutants (Dunman et al., 2001, Cassat et al., 2006, Queck et al., 2008), leading to a decrease in production of secreted virulence factors, e.g., hemolysin, and to an increase in cell-surface activities associated with colonization, e.g., epithelia-cell adhesion and SpA activity (Ramsey *et al*., 2016).

Aim

This project aims to create the first version of a curated genome-scale reconstruction (GEM) of the organism's metabolic capabilities in the SBML Level 3 Version 1 format (Hucka *et al*., 2019) by following the standard reconstruction protocol (Thiele & Palsson, 2010).

Approach

The following steps will be executed:

1. Download the genome of the organism from NCBI[1].
2. Apply automatic reconstruction tools, such as CarveMe (Machado *et al*., 2018), ModelSEED (Henry *et al*., 2010) and KBase (Arkin *et al*., 2018).
3. Compare all models, possibly by using libSBML (Bornstein *et al*., 2008), e.g., for Python and model annotation, e.g., using ModelPolisher (Römer *et al*., 2016).
4. Simulate model growth in relevant media using COBRApy (Ebrahim *et al*., 2013), including the synthetic nasal medium SNM3 (Krismer *et al*., 2014).
5. Draw parts of the model in the form of a metabolism chart using software such as Escher (King *et al*., 2015).

[1] https://www.ncbi.nlm.nih.gov/assembly/GCF_000245815.1

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