

Master Thesis

Reconstruction of strain-specific metabolic models of *Staphylococcus haemolyticus*

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1 Background and Motivation

In 1975 Schleifer and Kloos [1, 2] published a comprehensive description of the bacterium *Staphylococcus haemolyticus* (*SH*) containing detailed specifications for the type strain DSM 20263. Nowadays also referred to as ATCC 29970. *SH* belongs to the coagulase-negative staphylococci (short: CoNS) [3–6], and it can be found on and in humans [5, 6], plants, as well as on copper coins [6]. This bacterium is closely related to *Staphylococcus epidermidis* [3, 4]. These bacteria are the most significant CoNS concerning nosocomial infections [4]. Like *S. epidermidis* *SH* can form a biofilm [7, 8]. So far, *SH* has been found in conjunction with catheter-related bacteremia [8], septicemia, peritonitis, otitis media and diabetic foot ulcer infections [5]. Additionally, it is known for the highest level of antimicrobial resistance among the CoNS [7]. According to Argemi et al. [8], the presence of virulence genes has yet to be discovered for *SH*. The study by Eltwisy et al. [5] started to fill this gap and categorised *SH* as a critical opportunistic pathogen.

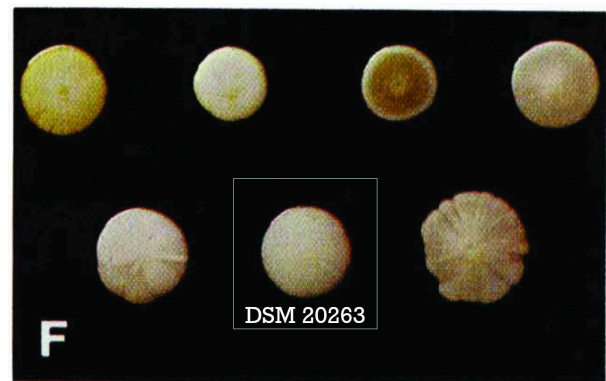


Figure 1 | *Staphylococcus haemolyticus* strain colonies [1, 2]. Type strain DSM 20263 colony highlighted with white rectangle. Modified from [2].

2 Aim and Approach

To computationally predict and analyse the pathogenicity along with possible drug targets of *SH*, a high-quality metabolic reconstruction of the type strain ATCC 29970 mentioned above will be developed. Furthermore, the new reconstruction will be compared to the existing model of *SH* for the strain JCSC1435 from the Virtual Metabolic Human database ¹.

¹https://www.vmh.life/#microbe/Staphylococcus_haemolyticus_JCSC1435

The reconstruction process will closely follow the protocol of Carey et al. [9]. Thereby, essential steps are: (a) analysing the draft model, (b) literature research to find testable growth conditions as well as to improve the model, (c) model assessment to check the model for compatibility with the existing experimental data, and (d) finally, compare the resulting model to the reconstruction for the strain JCSC1435.

3 Requirements

(a) Understanding of biochemistry and molecular mechanisms, (b) interest in systems biology, basic knowledge of Python programming, (c) attentiveness for details, and (d) interest in learning Biology Markup Language [10], MIRIAM annotations [11], and the Systems Biology Ontology [12].

References

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