ERASMUS Internship

Reconstruction of a metabolic model of *Staphylococcus lugdunensis*

Austėja Sungailaitė

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Mentor: Andreas Dräger

1 Background and Motivation

Staphylococcus lugdunensis is a coagulase-negative staphylococcus (CoNS) [1]. Even though *S. lugdunensis* is a commensal pathogen, it can cause clinically significant infections, such as endocarditis or prosthetic joint infections [2]. Endocarditis is an infection of the heart that leads to endothelial damage. It is usually caused by *Staphylococcus* species [3]. *S. lugdunensis* is part of the normal skin flora; however, it can also be found in the nasal cavity [4]. *S. lugdunensis* can produce a biofilm, making infections more difficult to treat even with a high susceptibility to most antibiotic treatments [5].

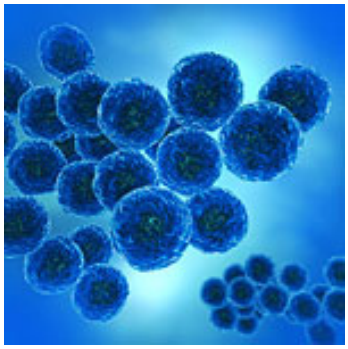

Figure 1 | *Staphylococcus lugdunensis* is a Gram-positive, spherical bacterium. Picture source: *bode-science-center.com*

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It is known that nasal *S. lugdunensis* can produce a peptide antibiotic called lugdunin. Lugdunin is a bactericide that inhibits the growth of the multi-resistant pathogen *Staphylococcus aureus* [6]. It was noticed that nasal colonization by *S. lugdunensis* interferes with *S. aureus* colonization. This observation suggests that lugdunin might help prevent staphylococcal infections [7].

2 Aim and Approach

This assessment focuses on the molecular mechanisms of *Staphylococcus lugdunensis* growth and the conditions to synthesize the antibacterial compound lugdunin within the nasal environment. During this internship, a detailed systems biology model of high quality will be created. This will follow the standard operating procedure developed within thikin research group and based on published protocols while using recent bioinformatics software solutions. The assessment includes: (a) analyzing the created model, (b) conducting literature research to identify the bacterium's growth conditions, (c) identifying potential gaps in the metabolic network, (d) defining test cases to check the correctness of the model, (e) running simulations, and (f) aligning the model with available data from experimental investigations.

3 Requirements

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

References

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