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Bachelor Thesis

Unraveling metabolic insights of *Staphylococcus warneri* using systems biology

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1 Background

Staphylococcus warneri is a Gram-positive bacterium belonging to the *Staphylococcus* genus. These bacteria are typically clustered and have spherical cells [2]. *S. warneri* is named after Arthur Warner, from whom this organism was initially isolated [3] in 1975. It is classified as a coagulase-negative *Staphylococcus* species, which means it lacks the enzyme coagulase, rendering it unable to clot plasma [4]. Unlike highly pathogenic coagulase-positive *Staphylococcus* species like *S. aureus*, coagulase-negative *Staphylococci* are typically commensal organisms within the human body.

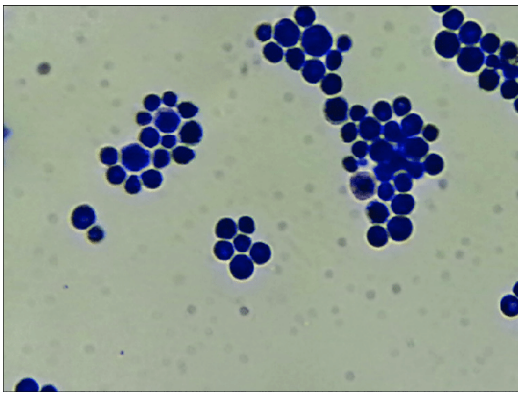

Figure 1 | *S. warneri* cells under light microscope (Gram stain $\times 1000$) [1]

S. warneri is commonly found as a part of the natural microbial flora on human skin and mucous membranes[5]. It typically constitutes less than 1 % of the *Staphylococcal* skin flora [6]. While generally considered less pathogenic than other *Staphylococcus* species, there have been reported infections in immuno-compromised individuals [6] and newborns [7]. Notably, *S. warneri* is responsible for 8 % to 16 % of all cases of coagulase-negative *Staphylococcus*-induced sepsis in newborns [8, 9].

In adults, *S. warneri* is associated with urinary tract infections [10], orthopedic infections [5], and endocarditis [11]. Recent research has identified *S. warneri* as a natural member of the human gut microbiome, with the ability to invade intestinal cells, raising questions about its potential to trigger local inflammation through the natural immune response[12]. Furthermore, *S. warneri* was isolated from the cervix of an adult woman with unexplained infertility. This bacterium contains multiple proteins responsible for complete sperm agglutination, prompting inquiries into its suitability as a contraceptive agent [13].

2 Aim

This thesis aims to create a high-quality systems biology model of *S. warneri* AW 25 and compare it to the existing automated metabolic reconstruction of the SG1 strain. The model will be reconstructed using automated tools such as CarveMe and findings from literature research. The quality of the model will be validated by testing the biomass yield.

3 Requirements

(a) Basic understanding of biochemistry, (b) interest in systems biology, particularly in constraint-based modeling, (c) Python programming using packages (e.g., COBRApy [14], libSBML [15]), and (d) interest in learning the usage of tools to improve the model gradually (e.g., CarveMe [16], REMOTE [17]).

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