Genome-scale metabolic model of Staphylococcus epidermidis ATCC 12228 matches in vitro conditions

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Authors

Nantia Leonidou Alina Renz Benjamin Winnerling

Anastasiia Grekova Fabian Grein Andreas Dräger

Abstract

Staphylococcus epidermidis, a commensal bacterium inhabiting collagen-rich areas like human skin, has gained significance due to its probiotic potential in the nasal microbiome and as a leading cause of nosocomial infections. While infrequently leading to severe illnesses, S. epidermidis exerts a significant influence, particularly in its close association with implant-related infections and its role as a classic opportunistic biofilm former. Understanding its opportunistic nature is crucial for developing novel therapeutic strategies, addressing both its beneficial and pathogenic aspects, and alleviating the burdens it imposes on patients and healthcare systems. Here, we employ genome-scale metabolic modeling as a powerful tool to elucidate the metabolic capabilities of S. epidermidis. We created a comprehensive computational resource for understanding the organism's growth conditions within diverse habitats by reconstructing and analyzing a manually curated and experimentally validated metabolic model. The final network, iSep23, incorporates 1,415 reactions, 1,051 metabolites, and 705 genes, adhering to established community standards and modeling guidelines. Benchmarking with the Metabolic Model Testing suite yields a high score, indicating the model's remarkable semantic quality. Following the findable, accessible, interoperable, and reusable (FAIR) data principles, iSep23 becomes a valuable and publicly accessible asset for subsequent studies. Growth simulations and carbon source utilization predictions align with experimental results, showcasing the model's predictive power. Ultimately, this work provides a robust foundation for future research aimed at both exploiting the probiotic potential and mitigating the pathogenic risks posed by S. epidermidis.