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Commensalism vs pathogenicity in Staphylococcus epidermidis - uncovered by an integrated omics approach

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SE is part of skin microbiota and contributes to its homeostasis and protection against pathogens. However, it is the most frequent cause of medical device-associated infections. Skin isolates belonging to clonal complex 2 (CC2) lineage are the major colonizers sharing their ecological niche with other minor genetic backgrounds (non-CC2). From genomic and proteomic data it was possible to identify relevant differences between the metabolic and biological processes of both lineages. Additionally, the intracellular metabolome and proteome associated with both lineages under pH environmental changes, mimicking the transition from the skin (pH 5.5) to blood (pH 7.4) were evaluated and showed specific responses [1]. The CC2 strain seems more prepared to survive in blood and to promote adhesion to medical-devices. The obtained results were complemented with time-course exometabolomic data during bacterial growth, which were also integrated in genome-scale metabolic models. Following a proteogenomic approach, obtained proteomics data are being used to refine the annotation of both strains genomes.

[1] L G Gonçalves, S Santos, L P Gomes, J Armengaud, M Miragaia, A V Coelho "Skin-to-blood pH shift triggers metabolome and proteome global remodelling in Staphylococcus epidermidis" Front Microbiol., 2022, 13:1000737. doi: 10.3389/fmicb.2022.1000737

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