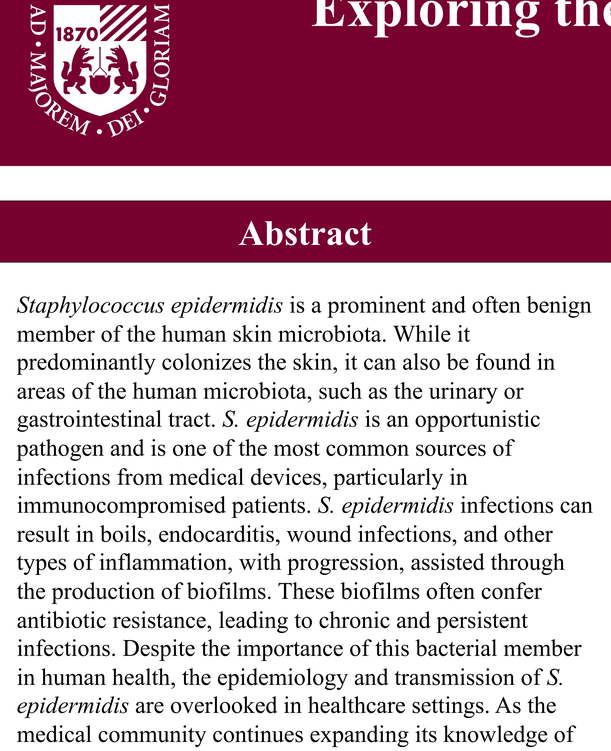
Exploring the genomic diversity of *Staphylococcus epidermidis* from different isolation sources

Sandra Jablonska[1] Adriana Ene[1,2], Swarnali Banerjee[3], Catherine Putonti[1,2]
[1]Bioinformatics Program [2] Department of Biology [3]Deparment of Mathematics and Statistics

Abstract

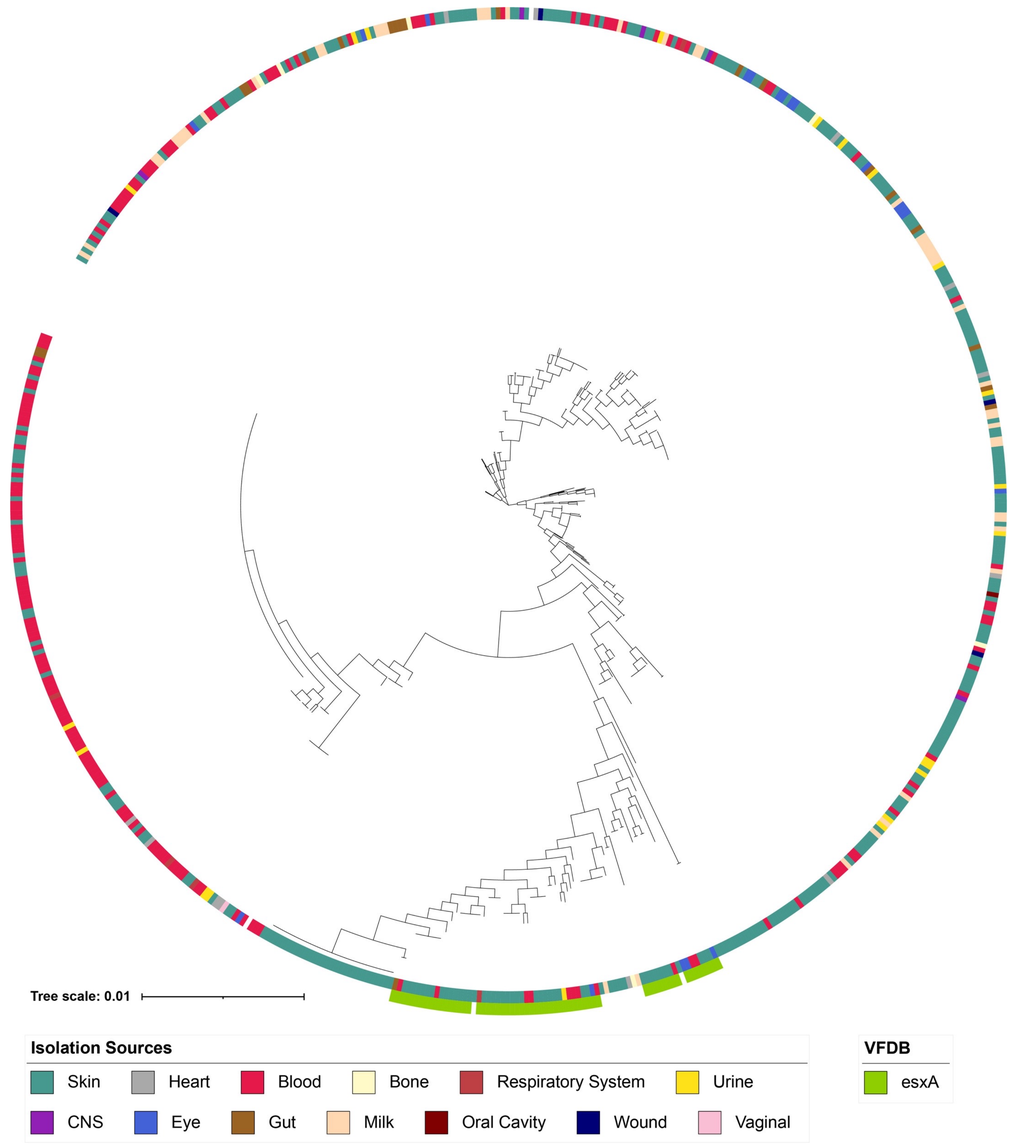
Staphylococcus epidermidis is a prominent and often benign member of the human skin microbiota. While it predominantly colonizes the skin, it can also be found in areas of the human microbiota, such as the urinary or gastrointestinal tract. *S. epidermidis* is an opportunistic pathogen and is one of the most common sources of infections from medical devices, particularly in immunocompromised patients. *S. epidermidis* infections can result in boils, endocarditis, wound infections, and other types of inflammation, with progression, assisted through the production of biofilms. These biofilms often confer antibiotic resistance, leading to chronic and persistent infections. Despite the importance of this bacterial member in human health, the epidemiology and transmission of *S. epidermidis* are overlooked in healthcare settings. As the medical community continues expanding its knowledge of human microbiomes, understanding the critical role of *S. epidermidis* is needed.

Methods



References:
1. Parks et al. 2015. Genome Res. 25:1043-1055.
2. Jolley et al. 2018. Wellcome Open Res. 3:124.
3. Letunic & Bork. 2021. Nucleic Acids Res. 49:W293-W296.
4. Seemann. https://github.com/tseemann/abricate

Results



Of the 1,135 genome assemblies retrieved, 693 were of high quality and isolated from human. 638 of these were classified via MLST, and they were used to derive a phylogenetic tree.

For each strain, the isolation source was identified either from the GenBank record or the literature. The isolation source was mapped on the tree following the colors indicated by the legend.

All 693 human-associated strains were screened for virulence factors. 73 different genes were identified. The most frequently identified gene was *esxA*. Strains encoding for *esxA* are indicated in the tree.

Gene:	# of genomes with gene present:
esxA	68

Next, the 693 human-associated strains were screened for antibiotic resistance genes. The most frequently detected genes are shown here:

Gene:	# of genomes with gene present:	% of genomes with the gene present:
mgrA	681	98.27 %
norA	678	97.84 %
dfrC	668	96.39 %
PC1_beta-lactamase_(*blaZ*)	553	79.80 %

Discussion

- The phylogenetic tree displays genetic diversity among *S. epidermidis* strains taken from different ecological niches of the human body. It does not suggest niche specialization.
- The *esxA* gene is of concern it is an evolving virulence factor and the target site of vaccine development. It was predominantly found in the strains from the skin. Furthermore, the phylogenetic tree indicates that it is associated with strains of similar MLSTs.
- The most frequent predictions for antibiotic resistance genes within the *S. epidermidis* strains were *mgrA*, *norA*, *dfrC*, and *blaZ*.
- Most of the strains examined encoded for *mgrA*, which has been associated with resistance to the following antibiotics families: cephalosporin, fluoroquinolone, and tetracycline.

Future Directions

I hypothesize that there are genotypic differences between strains inhabiting different ecological niches, i.e., body sites. While the publicly available data does not support this, it is important to note that these isolates are from different individuals. *Is strain diversity between individuals greater than within the same individual?* I aim to characterize and assess genetic and phenotypic differences between strains isolated from different niches from the same individual. These areas differ with respect to temperature, aerobic conditions, and pH. I also hope to explore the effects and evolution of antibiotic resistance in those niches.

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