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Poster #84: Systematic characterization of prophage integration sites in Staphylococci

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Staphylococci - among them the important human pathogen *S. aureus* - represent key constituents of the nasal and skin microbiome (1). Temperate bacteriophages are major drivers of staphylococcal evolution, leading to the spread of virulence factors and resistance genes (2,3). The effects of lysogeny on the fitness of Staphylococcal species have not been explored in a systematic manner, especially for commensal non-*S. aureus*-staphylococci. In this work, a bioinformatic pipeline called StaPhI was developed to systematically assess prophage insertion sites across several staphylococcal species. The first species to be explored was the major skin commensal *Staphylococcus epidermidis* by analyzing over 150 high-quality genomes from various sources. We identified 8 new *attB* sites and corresponding integrases, of which a sizable number are shared across staphylococci, highlighting potential avenues of cross-species horizontal gene transfer (HGT). Our results showed that *S. epidermidis* prophages integrases are highly selective for their *attB* sequence, even when they have an alternative insertion site that also contains the same *attB*. Here, temperate prophages showed diverse integration strategies ranging from targeting intergenic regions (10%), redundant genes (50%), or essential genes (40%). In the latest case, as an example of host-virus mutualisms, prophages avoid disrupting the open reading frames of essential genes by introducing a stop codon in the same position as the wild-type protein. Our results provide the first steps to a systematic understanding of mechanisms of cross-species HGT in staphylococcal communities.

Reference #1

Lindsay, J. A. (2014). Staphylococcus aureus genomics and the impact of horizontal gene transfer. Internat

Reference #2

Gerlach, D., Guo, Y., De Castro, C. et al. Methicillin-resistant Staphylococcus aureus alters cell wall gl

Reference #3

Chen et al., Genome hypermobility by lateral transduction. Science 62,207-212(2018). https://doi.org/10.1

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