Staphylococci phenotypes and genotypes are associated with different sources on a dairy farm.

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Abstract:
This project examined the potential associations between Staphylocci bacterial phenotype, genotype, and their epidemiological sources on a single dairy farm in Vermont that produces artisan cheese. Isolates were found from 25 different sources on the farm and speciated using the tuf, rpoB, and 16S genes. *Staphylococcus aureus*, *S. auricularis*, *S. chromogenes*, *S. cohnii*, *S. epidermidis*, *S. equorum*, *S. haemolyticus*, *S. simulans* were the most frequently isolated species on this farm. Isolates most often associated with intramammary infection were *S. aureus*, *S. auricularis*, *S. chromogenes*, and *S. simulans*. Phenotypic and genotypic testing for antibiotic resistance and staphyloxanthin expression were also examined. These factors were selected because they may contribute to survival in the host and pathogenesis of mastitis infections. Overall, *S. simulans* isolates showed the most resistance to the greatest number of antibiotics. Other species with notable resistance included *S. chromogenes*, *S. cohnii*, *S. epidermidis*, *S. equorum*, and *S. haemolyticus*. The genes that encode for penicillin and methicillin resistance were also screened for in this study. *S. auricularis* isolates were commonly found to carry the *blaZ* gene, which codes for penicillin resistance, while *S. sciuri* isolates were found to commonly carry the *mecA* gene, which codes for methicillin resistance. Overall, the species associated with cow/milk associated sources more frequently carried antibiotic resistance markers than species associated with other sources. Staphyloxanthin expression was also examined on this farm but the primers used ended up only being suitable for *S. aureus*, not coagulase negative species of Staphylococci, therefore very few isolates were found to carry the gene.