Antibiotic resistance in *Staphylococcus equorum:* phenotypic and genomic analyses

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Abstract:

Fermented dairy products may play a key role in the dissemination of antibiotic resistance genes (ARGs) within the food chain. Cheeses contain complex mixtures of bacterial populations, among which that of *Staphylococcus equorum* has been detected as a majority in traditional blue-veined cheeses made of raw milk. Antibiotic resistance in *S. equorum* has been scarcely studied, even though strains of this species could have a technological role in cheese ripening. In the present work, the antibiotic resistance-susceptibility profile of 30 *S. equorum* strains to 16 antibiotics was tested by broth microdilution. To link phenotypic resistance with a genetic basis, 13 strains were then subjected to genome sequencing and analysis. In general, the minimum inhibitory concentration (MIC) for all antibiotics was low, although some strains displayed MICs compatible with acquired resistances. MICs of this study (and others from the literature) were used to propose *S. equorum* species-specific cut-offs. Genome analysis revealed the presence of several ARGs, but these were not always associated with phenotypic resistance. As such, a plasmid-located *cat* gene (mobilizable to *Staphylococcus aureus* by electroporation) was identified in a chloramphenicol-resistant strain, and variants of *msr*(A) and *fosB/fosD* genes were detected in erythromycin and fosfomycin resistant strains. In contrast, *lnu*(A) and *nor*(A) genes, and the *blaR1-blaZI* operon were detected, respectively, in strains susceptible to clindamycin, quinolone, and ampicillin/penicillin. Either silent or expressed, the presence of acquired ARGs in food bacteria is considered a hazard. Therefore, the antibiotic resistance status of starter and adjunct culture candidates should be thoroughly examined.

Keywords: *Staphylococcus equorum;* cheese; antibiotic resistance genes (ARG); adjunct cultures