**Antibiotic resistance assessment of coagulase-negative staphylococci as potential starter cultures**

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The antimicrobial resistance of beneficial microorganisms associated with food, like coagulase-negative staphylococci (CNS), is problematic since these microorganisms can serve as reservoirs and lead to a potential spreading resistance throughout the food chain. EFSA created an approach, "Qualified Presumption of Safety" (QPS), which considers the antibiotic resistance and horizontal transfer of resistance genes (HGT) essential safety issues. According to QPS, microorganisms cannot harbor transferable resistant genes to be used as starter cultures. This study aimed to characterize CNS for their antimicrobial resistance by studying the phenotypic expression of resistance and the presence of resistance genes. For this purpose, antibiotic resistance was assessed on 104 CNS recovered from different sources of the pork meat chain using the disc diffusion method. These CNS belonged to different species and had different genetic profiles, obtained through PCR fingerprinting. Overall, high resistant rates were observed, with 91% of isolates resistant to at least one antibiotic. Susceptible CNS belonged to the species *Staphylococcus carnosus* and *Staphylococcus equorum*. One *S. equorum* S2M7 from this group of CNS was of particular interest since it had previously demonstrated to be a potential good starter culture. However, it was observed that this strain expressed phenotypic resistance to penicillin and erythromycin but was susceptible to clindamycin and fosfomycin. Thus, it was further analyzed through whole-genome sequencing (WGS) utilizing pair-end Illumina sequencing. WGS together with the web tool ResFinder (version 4.1) permitted the identification of genes responsible for the phenotypic resistance to penicillin, the *blaZ* gene, and erythromycin, the *msr(A)*. The *blaZ* gene, which is associated with the β-lactamase-mediated mechanism of resistance in CNS and encodes for penicillinase that inactivates penicillin by catalyzing the hydrolysis of the β-lactam ring, while the *msr(A)* gene encodes for efflux pumps that can export macrolide and streptogramin B antibiotics (MSB phenotype). Interestingly, the gene *fosB* was also identified, although no phenotypic expression was detected since the strain was susceptible to fosfomycin.In addition, a possible presence of plasmids was identified in the *S. equorum* S2M7 strain genome, by the utilization of several bioinformatic tools including plasmidspades (SPades version 3.15.3) and PlasmidFinder (version 2.1). However, it was not possible to characterize the plasmids. As such, further investigation must be performed. In conclusion, it was possible to detect one *S. equorum* with desired characteristics for starter cultures. However, the phenotypic expression of resistance and the potential presence of plasmids need to be checked to discard the risk of horizontal transfer of resistance genes and use this strain as a starter culture to produce fermented food.

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Palabras Clave: Whole-genome sequencing, *Staphylococcus equorum*, food safety, pork meat chain