Enterotoxigenic potential and genetic variability of *Staphylococcus* spp. strains isolated from raw milk and soft fresh cheese (abstract #734334)

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The genus Staphylococcus comprises several pathogenic species, including S. aureus, which is often related to food poisoning cases and outbreaks, especially in dairy products. Its pathogenic activity is due to the ability of some strains to produce thermostable enterotoxins (SE). S. aureus detection in foods usually involves time-consuming protocols that require additional tests to estimate the enterotoxigenic potential of the strains. The aim of this study was to evaluate the enterotoxigenic potential of *Staphylococcus* spp. isolates and determine their genetic variability. From a previously Staphylococcus spp. collection obtained from raw milk and soft cheese, 89 isolates were selected and submitted to phenotypical (coagulase and thermonuclease production, biochemical profile and SE production) and molecular analysis (Smal macrorestriction, SE gene detection by PCR and DNA sequencing). PFGE analysis obtained by Smal macrorestriction patterns revealed a highly heterogeneous population. Of the 89 isolates, 15.7% were capable of producing classical enterotoxins (SEA-SEE). 21.4% of isolates showed matching results between production of enterotoxins and detection of classical SE genes. 62.9% of isolates showed at least one of the classical SE genes, in association with other non-classical SE genes. SE genes were observed in all isolates and in different combinations, which revealed 59 distinct genotypes. sek was the least frequent observed SE gene, while sei was present in 98.9% of isolates. Partial sequencing of agr locus in 41 isolates showed the ocurrence of agr groups I (68.3%) and II (31.7%). No significant associations were found between agr groups, enterotoxin genes profiles, occurrence of egc cluster, PFGE profiles and/or SE production. Our findings suggest the absence of phenotypic or genotypic markers that significant correlate to enterotoxin production in staphylococci of food origin. Further studies could help elucidating the occurrence of these associations in staphylococci strains.