

## Characterization of *Staphylococcus* strains collected throughout the production chain of a Ewe's milk cheese dairy plant

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The *Staphylococcus* genus is ubiquitously distributed in nature, and several species inhabit specific ecological niches. Those microorganisms are part of the adventitious microflora on the skin and mucous membranes of warm-blooded animals (including humans), but have also been isolated from a wide range of foodstuffs (meat, cheese and milk), and from environmental sources (soil, sand, air and water). Under specific circumstances, some staphylococci may pose a risk to public health worldwide, since they may be agents of infectious disease. Hence, owing to their widespread nature and pathogenicity of specific strains, it has become imperative for diagnosis to accurately identify them at the genus and species level. This study has been designed to encompass the staphylococcal microbial community from an ewe's raw milk cheese manufacturing plant. It comprised enumeration, molecular typing, detection of staphylococcal enterotoxin and toxic shock syndrome toxin-1 genes, as well as presence of virulence factors. A total of 107 isolates were thus obtained, which were subject to such molecular techniques as Multiplex-PCR and ARDRA for typing on the genus and species level.

The viable counts of staphylococci in cheese ranged from 4.0 log cfu ml<sup>-1</sup> in raw milk to 5.8 (cheese surface) or 6.0 (cheese core) log cfu g<sup>-1</sup> by 30 d of ripening. Nevertheless, during cheese manufacture said viable counts ranged from 2.6 to 4.2 log cfu g<sup>-1</sup> in environment samples, thus suggesting that microbial populations are characterized by different numbers depending on the location within the dairy plant.

Ten species were identified in the whole cheese production chain: *S. saprophyticus*, *S. aureus*, *S. epidermidis*, *S. chromogenes*, *S. simulans*, *S. lentus*, *S. sciuri*, *S. equorum*, *S. haemolyticus* and *S. caprae*. The predominant strains isolated belong to *S. equorum* (32.7%) and *S. saprophyticus* (25.2%) species. A low incidence of enterotoxigenic strains was observed: 12 strains (11%) tested positive for one or more toxin genes. The most frequently detected genes were *seo* and *tst*. With regard to antibiotic resistance, the fraction of resistant strains was 57%; resistance to penicillin, ampicillin and erythromycin appeared to dominate. Additionally, 29% of the wild strains showed to be multiresistant — up to six antibiotics acting simultaneously. Our study permitted a comprehensive insight into *Staphylococcus* incidence in a traditional cheesemaking plant. Additionally, the cleaning procedure used therein appeared to be efficient in removing the staphylococcal microflora from the equipment surfaces, so the major focus of contamination was apparently the raw milk itself.