Microbial diversity and antibiotic resistance among enterococci isolated from food and food-processing surfaces

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Enterococci are often found as commensals in the gastrointestinal tract of humans and other warm-blooded animals but are also present in soil, water, food of animal origin and vegetables. Nowadays these bacteria are known to be leading causes of nosocomial infections and the increase of multiresistant isolates turns enterococci a public health challenge worldwide. The present investigation evaluated the presence and microbial diversity of Enterococcus spp. isolated from distinct foods and food-processing surfaces. Using both phenotypic and molecular methodologies, a total of 149 enterococcal isolates were obtained from a cheese factory, a slaughterhouse and a supermarket. Subsequently, in order to assess for microbial diversity of the enterococci included in our collection, and eliminate duplicate/clones from further analysis we performed PCR-fingerprinting with primers (GTG)₅ and OPC19 in independent amplification reactions. Analysis of the patterns using the BioNumerics software allowed the construction of a dendrogram and led to the selection of 71 enterococci as representative of all groups present. Then, we assessed for enterococcal susceptibility to 19 agents representing distinct antibiotic classes and found the following resistance patterns: sulphamethoxazole/trimethoprim (100%), streptomycin (6%), erythromycin (31%), chloramphenicol (3%), dalfopristin-quinupristin (25%), tetracycline (55%), penicillinG (4%), bacitracin 10 (55%), rifampicin (39%), 0% for gentamicin-120, linezolid, ampicillin, amoxicillin/clavulanic acid, vancomycin, teicoplanin, nitrofurantoin, norfloxacin, levofloxacin and ciprofloxacin. Considering multi-drug-resistant (MDR) the enterococci non-susceptible to more than 3 antibiotics from distinct classes and bacterial targets, 67% of the isolates under analysis are MDR, a clear risk for consumers, especially those with impaired immune system.