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Abstract (publication only)

Phenotypic and molecular characterisation of resistance and virulence features of environmental Enterococci isolated from surface waters

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Enterococci are commensals of the gastrointestinal tract of vertebrates, but also a frequent cause of urinary tract infections, endocarditis and hospital-acquired infections. Objective: enterococcal isolates obtained from surface waters were analyzed for the distribution of species, antibiotic resistance, and virulence determinants, in order to establish whether certain species harboring different virulence and resistance profiles were associated with different types of polluted waters. Methods. 85 *Enterococcus* spp. strains were isolated from water samples (ISO SR EN ISO 7899-2/2002) collected from 14 sampling points, representing urban, hospital and poultry wastewaters (71) and receiving rivers (14), in accordance with. Susceptibility to ampicillin, tetracycline, ciprofloxacin, erythromycin, gentamicin high, streptomycin high, vancomycin and, linezolid was determined by disk diffusion and E-TEST. The genetic support of the resistance to macrolides (*ermA*), high level resistance to aminoglycosides (*aac(6')-Ie-aph(2')Ia*), vancomycin (*vanA*, *vanB* and *vanC*), linezolid (point mutations in the genes encoding the V domain of the 23S rRNA) and virulence (*esp*, *gelE*, *asaI*, *cylA*, and *hyl*) was investigated by PCR and PCR-RFLP. Results. The most predominant species was *E. faecium*, followed by *E. durans*. The highest resistance and multiresistance rates were noticed in hospital, followed by urban and poultry wastewaters. The highest resistance was registered for linezolid in hospital (100%), urban (81.25%) and poultry (72.5%), and for quinolones (86.6%), tetracyclines and macrolides (60%) in hospital wastewaters. Lower resistance rates were registered for vancomycin and gentamicin high (26.6%) in hospital wastewaters. The molecular investigation did not detect any virulence gene in the isolates derived from receiving rivers, while in strains isolated from the hospital wastewaters the presence of *aac(6')-Ie-aph(2')Ia* and *vanB* genes was correlated with the genes encoding for gelatinase, enterococcal surface protein, aggregation substance and hyaluronidase. Conclusion. We have found that *Enterococcus* spp. derived from hospital, urban and poultry sewage and effluents could represent a potential risk of contamination of environmental water bodies. Environmental water quality studies may benefit from focusing on a certain profile of resistance and virulence features harbored by *Enterococcus* spp. consistently associated with sources of faecal pollution.