Background

Successful bacteria accumulated different genetic features shaping their evolution and fitness to diverse environments/hosts. Mercury (Hg) is widespread in Nature and possibly contributed for selection of particular strains.

Objectives

To evaluate the dispersion of diverse merA alleles among enterococci from several origins and clonal backgrounds.

Methods

merA alleles was searched in Enterococcus available genomes, used to construct a maximum-likelihood phylogenetic tree. A PCR scheme+RFLP+sequencing was developed to detect the six merA alleles identified, namely I-(GenBank-AECE01000068), IIA-(AIUL01000023.1), IIB-(ASDU01000008.1), III-(NZ_KB947199.1), IV-(AECE01000068.1) and VI-(NZ_KB030055.1), among 918 Enterococcus (Portugal; human/animal/environment/food; 1996-2012). Clonality was evaluated by PFGE/MLST, merA-transfer by conjugation and Hg-phenotype in m_Enterococcus+128mg/L HgCl₂.

Conclusions

merA were found in 4% (n=37/918) of Enterococcus studied. PCR+RFLP+sequencing distinguished the six alleles previously found at Genbank and a new one (type V). They were distributed among diverse sources and clones, in our and GenBank isolates: types I and IV-human E. faecalis (Efls; n=5; USA; 1987-88; ST9/ST206); IIA-human/pig/trout/feed/hospital-sewage E. faecium-
*Efml/E. hirae/Enterococcus* sp (n=17/1/1; Portugal/France/Denmark/Germany; 1989-2012; 12ST-*Efml* including from ST78-ST17-ST18-lineages-CC17); IIB-human *Efls/E. dispar* (n=2/1; Portugal/USA; 1926-2001; ST206/ST105/ST107); III-human/animal/hospital-sewage *Efls/E. casseliflavus* (n=15/1; Portugal/France/USA/Canada/Japan; 1961-2012; ST64/ST9/ST30/ST159/ST245); V-human/trout/pig-manure *Efml* (n=4; Portugal; 2001-2006; ST94/ST890); VI-human/hospital-sewage/piggery-soil/piggery-manure/trout *Efml* (n=23; Portugal, Italy France, Germany, Denmark, Hungary, Switzerland, Ireland, Norway, Brazil, USA; 1961-2012; 14ST including ST78-ST17-ST18-lineages-CC17). The presence of *merA* among major *Efml/ST9-Efls* lineages associated with human infections, suggests that mercurial-compounds potentially contributed for their selection/maintenance. *merA*-*Enterococcus* grown in >128mg/L-HgCl₂. Transfer occurred for IIA and VI alleles. All but VI-*merA* alleles, were also identified in genomes of different species of Firmicutes (data not shown), suggesting genetic exchange of enterococci with bacteria sharing the same communities/environmental challenges.