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BOOK OF ABSTRACTS

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P-070 - DISTRIBUTION OF ARSENIC TOLERANCE GENES (ARSA) AMONG ENTEROCOCCUS SPP. FROM DIFFERENT SOURCES, CONTINENTS AND TIMEFRAMES (<1906-2015)

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Abstract

Successful bacteria accumulate different genetic features shaping their evolution and fitness to diverse environments/hosts. Arsenic-compounds are widespread in nature and possibly contribute to selection of particular strains. The aim of this study was to evaluate the dispersion of *arsA* genes among *Enterococcus* from different sources, continents and timeframes.

The *arsA* genes (coding for arsenical-pump-driving-ATPases) were searched in GenBank *Enterococcus* genomes and used to construct a maximum-likelihood phylogenetic-tree. A PCR scheme+sequencing was developed to detect *arsA* alleles from all phylogenetic subgroups identified among 333 isolates (Portugal; human/animal/environment/food; 1996-2012)[1]. Na_2HAsO_4 susceptibility was evaluated by agar dilution (0,25 to 128mM; n=143 isolates).

Results & Conclusions

Two major phylogenetic groups (A; B) and 5 subgroups (55-70% nucleotide identity; AI-GenBank-EFU15692.1, AII-EEU88411.1, BI-EOT39237.1, BII-SET88118.1, BIII-EOH82892.1; n=42 isolates) were detected. In all phylogenetic-subgroups *arsA* was distributed in different sources and/or species: *arsA*_AI - n=13 (human/animal/environment/food; *E. faecalis*-10/ *E. faecium*-3; Europe/North-America/Asia; <1906-2015); *arsA*_AI + *arsA*_AII - n=13 (human/animal/feed; *E. faecalis*-13; Europe/North-America/Australia/Africa/Asia; 1951-2012); *asrA*_BI - n=5 (human/food; *E. dispar*-1/*E. malodoratus*-1/*E. avium*-1/*Enterococcus sp*-2; North-America; <1991-unknown); *arsA*_BII - n=6 (human; *E. faecium*-1/*E. raffinosus*-1/*Enterococcus sp*-4; Europe; unknown date); *arsA*_BIII - n=2 (animal; *E. villorum*-1/*E. hermanniensis*-1; Europe/North-America; 1981-unknown). PCR+sequencing identified *arsA*-AI/AII/BII in 7% (n=24/333) of Portuguese *Enterococcus* also from diverse sources and species. Variable Na_2HAsO_4 phenotypes were observed: *arsA*_AI+*arsA*_AII (MIC=32-64mM/n=7); *arsA*_AI (MIC=4-8mM/n=3; 32-128mM/n=5); *arsA*_AII (MIC=0,5-4mM/n=7); *arsA*_BII (MIC=4mM/n=1); no-genes (MIC=0,5-2mM/n=108, MIC=4-128mM/n=11 suggesting the occurrence of new genotypes).

The *arsA* genes have been spread in the last 100-years among *Enterococcus* from diverse origins. The A/B phylogenetic groups seem to reflect diverse evolutionary pathways, with A-group including *E. faecalis/E. faecium* and B-group mainly other species. These data potentially reflect diverse genetic exchanges in bacterial communities including *Enterococcus* and other *Firmicutes* also carrying these *arsA* variants.

References & Acknowledgments

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