

Session: P049 Living together in a world of resistance

**Category: 3d. Resistance mechanisms**

24 April 2017, 13:30 - 14:30  
P1083

### Prevalence of antibiotic resistance phenotypes and genes in the cultivable aquatic microbiota from some Romanian natural fishery lakes

Veronica Lazar<sup>1</sup>, Irina Gheorghe<sup>\*2</sup>, Lia-Mara Ditu<sup>3</sup>, Alina Holban<sup>4</sup>, Carmen Curutiu<sup>5</sup>, Ioana Savin<sup>6</sup>, Florina Marinescu<sup>7</sup>, Cristea Violeta Corina<sup>8</sup>, D Dobre<sup>9</sup>, Mariana Carmen Chifiriuc<sup>10</sup>

<sup>1</sup>*Research Institute of the University of Bucharest, Maximilian Association; Microbiology*

<sup>2</sup>*University of Bucharest; Faculty of Biology; Microbiology*

<sup>3</sup>*University of Bucharest, Faculty of Biology, Department of Microbiology-Immunology*

<sup>4</sup>*University of Bucharest, University of Bucharest, Research Institute of the University of Bucharest*

<sup>5</sup>*University of Bucharest, Faculty of Bucharest, Departament of Microbiology-Immunology*

<sup>6</sup>*National Institute for Research and Development in Environmental Protection*

<sup>7</sup>*National Institute for Research and Development in Environmental Protection Incdpm*

<sup>8</sup>*Synevo Romania; Microbiology*

<sup>9</sup>*Maximilian Association*

<sup>10</sup>*Research Institute of Bucharest University, Microbiology Immunology*

**Background:** Characterization of the antibiotic resistance phenotypes and encoding genes in bacterial strains isolated from some Romanian aquatic fishery lowland salted lakes.

**Material/methods:** This study was conducted on 44 bacterial strains isolated in 2016 from four natural fishery lakes; 20 strains were belonging to *Enterococcus* sp. [*E.faecalis* (n=7), *E.faecium* (n=8), *E.mundtii* (n=2), *E.casseliflavus* (n=3)] and 24 to Gram-negative rods (GNR) [*Escherichia coli* (n=9), *Enterobacter cloacae* (n=2) and one of each the following species: *Klebsiella pneumoniae*, *K.oxytoca*,

*Enterobacter kobei*, *E.ludwigii*, *E.cowanii*, *E.hermannii*, *Serratia marcescens*, *S.rubidaea*, *Hafnia alvei*, *Pantoea ananatis*, *Raoultella ornithinolytica*, *Acinetobacter calcaoceticus*]. All 44 isolates were identified using the MALDI Biotyper and tested for their antibiotic susceptibility by disk diffusion method, according to CLSI/2016. Simplex and multiplex PCR were performed on genomic DNA in order to identify the genes encoding for resistance to  $\beta$ -lactams (NMD, OXA-48, VIM, IMP, CTX-M, TEM), quinolones (QnrA, QnrB, QnrS), sulfonamides (Sul1, Sul2), tetracyclines (TetA, TetB, TetC, TetD, TetM), aminoglycosides (aac3Ia), vancomycin (VanA, VanB, VanC), macrolides (ermA, ermB, ermC) and integrons (Int1, drfA1-aadA1).

**Results:** From all 20 isolates of *Enterococcus* sp., 35% were resistant to vancomycin and 75% were resistant to erythromycin; the enterococcal strains harboured the VanA (*E.faecalis*-5%) and ermA - genes (*E.faecalis* - 10%, *E.faecium* - 5%). The GNR strains exhibited a high level of resistance to  $\beta$ -lactams in the following decreasing order: cefuroxime (54.16%), cefazolin (41.66%), ceftriaxone (8.33%), ceftazidime and aztreonam (4.16% each). The molecular study revealed the presence of bla<sub>CTX-M</sub>-like (33%), bla<sub>NDM</sub>-like and bla<sub>IMP</sub>-like (8.33%) genes encoding for  $\beta$ -lactamases production. The resistance to non- $\beta$ -lactam antibiotics was ascertained to the following genes: quinolones (QnrS-like - 4.16%); sulfonamides (Sul1 - 75%, Sul2 - 4.16%); aminoglycosides (aac3Ia - 4.16%); tetracyclines (tetA-like – 25%, tetC-like - 15%). The integrase gene was founded in more than 50% of the studied strains (58.33%).

**Conclusions:** The cultivable aquatic microbiota from fishery lakes is mainly represented by enterococci and *Enterobacteriaceae* strains. The GNR strains exhibited high levels of  $\beta$ -lactam resistance mediated by ESBL and metallo-  $\beta$ -lactamases, accompanied with a lower frequency resistance to the majority of all other important classes of non-  $\beta$ -lactam antibiotics. The majority of *Enterococcus* sp. isolates were resistant to macrolides and also to vancomycin. The high level and diversity of resistance markers, correlated with a high frequency of integrons is suggesting that this environment could act as an important reservoir of antibiotic resistance genes with a great probability to be horizontally transmitted to other associated species in sediments microbiota, rising also the potential zoonotic risk for fish consumers.