

P1179 Genomic analysis of *E. coli* bearing 16S rRNA methyltransferases conferring resistance to plazomicin in waste water and rivers

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Background: The environment plays a critical role in the dissemination of antimicrobial resistance genes. This phenomenon can be natural or influenced by anthropogenic forces. Therefore, the aim of this work was to determine the genomic structure of 16S rRNA methyltransferase-carrying *E. coli*, which exhibit high level resistance to aminoglycosides, including plazomicin, from natural and human water sources using WGS.

Materials/methods: A total of 47 *E. coli* isolates resistant to aminoglycosides (25 from two waste water treatment plants, 18 from two rivers and 4 from two pig farms in Barcelona) were fully sequenced by Illumina technology (MiSeq). The strains were characterized according to sequence type (ST), serotype, antibiotic resistance genes and plasmid incompatibility groups by the Center for Genomic Epidemiology (CGE) services. The plasmid composition, resistome distribution and bacterial relationship was obtained using PLACNET data and it was analyzed by Geneious v8.1.0 among other software.

Results: In the waste water treatment plants two *E. coli* sequence types were extensively identified, ST632 and ST479. *rmtB* was the predominant 16S rRNA methyltransferase gene detected in this ecosystem. An IncFII plasmid harboured this gene, but the genetic context of the plasmid and the *rmtB* environment were highly variable depending on the sequence type. Notably, the colistin resistance gene *mcr-1* was highly present in ST632 *E. coli*.

In contrast, in river isolates the variety of sequence types observed was much higher. The 16S rRNA methyltransferase gene present in all of which was *armA*. This gene was mostly associated with an IncHI2 plasmid with a similar genetic structure and *armA* environment in different sequence types. Interestingly, the isolates obtained from pig farms also carried *armA* in a similar plasmid to the one identified in river isolates.

Conclusions: High level plazomicin resistant *E. coli* are present in rivers and waste water. The human influence favours the selection and maintenance of specific resistance genes associated to certain plasmids and sequence types. The resistome and plasmidome structure is more similar among different sequence types in *E. coli* isolates from rivers. Therefore, the anthropogenic activity drives the dynamic flux of genes and plasmids and its subsequent maintenance in specific clones.