P1500
Paper Poster Session
Quinolone resistance

Investigation of qnrD-harbouring plasmid in Morganella morganii

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Background: The presence of *qnrD* plasmid-mediated quinolone resistance determinant was investigated in Enterobacteriaceae strains that were identified in urinary tract infections.

Material/methods: 214 non-replicate Enterobacteriaceae strains were inlcuded in this study namely, 99 *Escherichia coli,* 36 *Proteus spp.,* 32 *Klebsiella spp.,* 20 *Enterobacter spp.,* 15 *Serratia spp.,* 6 *Citrobacter spp.,* 5 *Morganella sp.,* and a *Providencia stuartii.* All strains were isolated from urine samples during 2014 at the Semmelweis University, Budapest, Hungary. Minimal inhibitory concentraions (MICs) were determined by Müller-Hinton broth microdilution method for ampicillin, cefotaxime, ceftazidime, ceftriaxone, imipenem, meropenem, amikacin, tobramycin, ciprofloxacin and interpreted based on EUCAST. Screening by PCR was conducted for *qnrD*. PCR positive reactions were sequenced and were analyzed based on NCBI database. Inverse PCR and primer walking was done to detect *qnrD*-harbouring plasmid. Quinolone resistance-determining regions of DNA gyrase and topoisomerase enzmyes were detected by PCR and sequencing.

Results: Ciprofloxacin MIC values of tested strains ranged between 0.06-128 µg/ml. Among them two *M. morganii* yielded *qnrD1* and they exhibited resistant phenotype (ciprofloxacin MIC:2 µg/ml), and were susceptible to ampicillin, cefotaxime, ceftazidime, ceftriaxone, meropenem, and exhibited low-level resistance to imipenem, and one of them was resistant to amikacin and tobramycin. Primer walking and nucleotid sequencing resulted in 2662 bp plasmid that included *qnrD1* coding sequence, flanked by mobile insertion cassettes, whereas appart from *qnrD1* no other coding sequence was detected. An aminoacid substitution S80I in *parC* was detected.

Conclusions: Our study detected low-prevalence of *qnrD* as two out of 214 Enterobacteriaceae strains carried this resistance determinant. The investigeted *qnrD*-harbouring plasmid showed 95-98% similiarity to earlier detected *qnrD* plasmids. Our plasmid nulceotide sequence appart from *qnrD1* is novel. Mobile insertion cassettes may play a role in mobilization of *qnrD* to other plasmids. The fully sequenced plasmid is submitted to GenBank on the following accession number KU160530.