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Antimicrobials: Resistance surveillance

Resistance to quinolones in *Ureaplasma parvum* isolates in Greece: new polymorphisms

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Objectives: The aim of this study is to investigate molecular mechanisms of resistance to quinolones in *Ureaplasma parvum* strains in Greece.

Methods: The study included twelve clinically isolated strains of *U. parvum*, well characterized at serovar (SV) level, with moderate or complete resistance to two quinolones. Three isolates were resistant to ciprofloxacin and ofloxacin, three showed resistance to ciprofloxacin and moderate susceptibility to ofloxacin, three were moderately susceptible to both quinolones and three were moderately susceptible to ciprofloxacin and susceptible to ofloxacin. The DNA encoding bacterial subunits of topoisomerase ?? was amplified by PCR and then sequenced. Sequences were compared to the corresponding reference strains.

Results: Most of the nucleotide/aminoacid changes to quinolones were found at the protein subunits of topoisomerase IV, in particular subunit ParC. The isolates resistant to both quinolones presented the typical mutations Glu87Lys and Ser83Leu. Furthermore, 21 polymorphisms were detected outside the quinolone resistance region of ParC and ParE subunits. Eleven of them in the ParC (Phe149Leu, Asp150Asn, Glu210Lys, Val315Ile, Asn345Ser, Thr445Ser, Glu455Lys, Val593Ile, Ser789Asn, Cys804Tyr, Ile831Thr) and one in the ParE (Glu467Lys) have never been reported internationally before. However strains with the same phenotypic sensitivity contained different mutations, while no aminoacid changes were detected in two moderately susceptible strains.

Conclusion: Strains possessing different specific mutations present similar phenotypical sensitivity, an observation which suggests that all mutations are not strongly associated with resistance. The new polymorphisms could act supplementary upon resistance phenotype, since moderately susceptible strains possessed them while fully resistant strains possessed them together with a typical mutation each. Coexistence of other resistance mechanisms seems possible. Further studies are necessary to investigate whether the existence of the new polymorphisms can cause changes to the phenotype of *U. parvum* and how their presence is correlated with the risk of resistance to quinolones.