

## CHARACTERIZATION OF MULTI-RESISTANT PSEUDOMONAS AERUGINOSA IN CLINICAL AND MUNICIPAL WASTEWATER SYSTEMS OF TWO DIFFERENT CITIES

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**Background:** As antibiotic resistance is commonly found in wastewater systems, its persistence seems to be obvious. The factors determining the persistence of antibiotic resistance are largely unknown. Antibiotics or substances with a likewise mode of action may provide selection advantages for resistant bacteria.

**Objective:** *Pseudomonas aeruginosa* is a clinically important, opportunistic pathogen which exhibits high intrinsic resistance to numerous antimicrobial agents. The persistence of multi-resistant *Pseudomonas aeruginosa* carrying up to seven acquired therapeutically relevant antibiotic resistance mechanisms was studied in clinical and downstream municipal wastewater systems of two German cities.

**Method:** Such multi-resistant *P. aeruginosa* may be enriched by clinical as well as municipal wastewaters. Agar diffusion testing and molecular biology confirmed their multi-resistant phenotypes. Pulsed Field Gel Electrophoresis (PFGE) genotyping resulted in different groups of *P. aeruginosa* isolates depending on sampling points and numbers of resistances. It was shown previously that the overexpression of efflux systems in clinical isolates from patients can contribute to multi-resistance against various antibiotics. Thus, the expression of four important efflux pump systems (MexA-MexB-OprM, MexC-MexD-OprJ, MexE-MexF-OprN, and MexX-MexY-OprM) was analysed in multi-resistant *P. aeruginosa* as well as in antibiotic-susceptible isolates from different wastewater systems.

**Conclusions:** The highest expression rates were detected in antibiotic-susceptible *P. aeruginosa* strains. No overexpression of the efflux pump operons was observed, indicating that multi-resistances of the isolated *P. aeruginosa* strains were based on antibiotic-specific mechanisms.