Multiresistant epidemic clones of Pseudomonas aeruginosa in the Czech Republic

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Objective: To determine whether the high prevalence of antimicrobial resistance among bloodstream isolates of Pseudomonas aeruginosa in the Czech Republic is associated with the clonal spread of multidrug resistant (MDR) strains.

Methods: The study set included 108 bloodstream isolates, which were selected from 437 isolates of P. aeruginosa collected in the Czech Republic within the European Antimicrobial Resistance Surveillance System (EARSS) project in 2007. The 108 isolates originated from 49 hospitals in 36 cities. They were tested for susceptibility to piperacillin, cefazidime, cefepime, meropenem, imipenem, ciprofloxacin, gentamicin, trimethoprim and amikacin by E-test. The genotypes of the isolates were assessed by multilocus sequence typing (MLST), macrorestriction analysis of genomic DNA and class 1 integron typing.

Results: Forty-six isolates were susceptible to all antimicrobial agents while 16 and 46 isolates were resistant or intermediate to 1–3 and 4–9 agents, respectively. A total of 41 multilocus sequence types (ST) were identified, which, except for four unique STs, differed from each other in at least three alleles. ST235 and ST175 included 19 and 16 isolates, respectively. The isolates with either ST235 or ST175 originated from 25 hospitals in 19 cities. Each of other eight STs included 3–7 isolates, seven STs were found in 2 isolates and the remaining 24 isolates yielded each a unique ST. Isolates of the same ST had highly similar macrorestriction profiles. ST235 and ST175 encompassed 34 (74%) of 46 isolates resistant to more than 3 agents. Class 1 integrons were found in 47 MDR isolates, with at least 18 different integron variable regions. Twelve isolates with ST235 harboured an integron with a 1.9 kb variable region while 15 isolates with ST175 shared an integron with a 1.6 kb variable region.

Conclusion: The high prevalence of antimicrobial resistance in P. aeruginosa isolates in the Czech Republic is predominantly associated with two MDR epidemic clones, one of which (ST235) belongs to international clonal complex CC11. Supported by grant NR/9428–3 of the Ministry of Health of the Czech Republic.

Emergence and persistence of multidrug-resistant Pseudomonas aeruginosa serogroups O11 and O12


Objectives: In 1989 Pitt et al. (Epidemiol. Infect. Dec;103(3):565–76) reported the emergence of a European multidrug resistant (MDR) serotype O12 clone, and in 1998 Tassios et al. (J Clin Microbiol. Apr;36(4):897–901) reported the emergence of MDR in the ubiquitous and dominant serogroup O11. The objective of the present study was to investigate the emergence, spread and actual status of these MDR serogroups in the light of the global P. aeruginosa population structure.

Methods: 328 unrelated P. aeruginosa clinical CF (43) and non-CF (142), environmental (63) and animal (55) strains, including 61 serotype O11 and 24 O12 strains, collected between 1882 and 2008 in 69 localities (30 countries, 5 continents) were characterised by fingerprinting (FAFLP), MLST (oprI, oprLand oprD genes), pyoverdine fingerprinting, prevalence of exoS and exoU genes and serotyping.

Results: The prevalence of 23 ‘Antibiotic Resistance Genes’ (ARGs) (15 coding for β-lactamases and 8 for aminoglycoside-modifying enzymes) was determined by PCR. The MIC values for 21 antibiotics were determined using the VITEK 2 Advanced Expert System (AES).

Isolation and characterisation of an imported pan-resistant Pseudomonas aeruginosa clinical isolate producing three different ESBL enzymes, hyperproducing multidrug-efflux pumps

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Objectives: Pseudomonas aeruginosa is one of the most frequently isolated nosocomial pathogens, causing life-threatening infections, such as pneumonia, bacteremia, and wound infections. It exhibits intrinsic resistance to several β-lactams and acquire easily additional resistance mechanisms, including the production of extended spectrum β-lactamases (ESBLs), down-regulation of porins, hyperproducing multidrug efflux-pumps, confer resistance to almost all antimicrobials.

Methods: During the period of 2004 to 2008 we isolated 27 cefazidine resistant, non-mucoid P. aeruginosa isolates from different non-cystic fibrosis patients, hospitalised in nine different hospital wards of South-Hungary. Identification by VITEK 2 system and susceptibility test by disk-diffusion method was performed, using CLSI breakpoints. The genes of the extended spectrum β-lactamases (PER-1, PER-2, TEM, SHV, GES, VEB-1, OXA groups) were looked for by PCR methods. The iso-electric focusing of the β-lactamases was performed, the enzymes were visualised with nitrocefin. To investigate the location of the β-lactamase gene plasmid purification, PCR detection of the Tn1213 specific IS element were performed. The transcription of the chromosomal genes encoding the OprD, ampC, and the efflux pumps MexAB-OprM, MexXY-OprM, MecC-D-OprF was studied with real-time PCR assays. The genetic relatedness of the strains was investigated by PFGE and MLST analyses.

Results: PCR experiments revealed the presence of blaPER, blaOXA-1, II group in one isolate. Sequencing of the coding region and the RFLP analyses identified the PER-1, OXA-2 and OXA-74 genes. The real-time PCR assays revealed, that this strain hyperproduces two different multidrug-efflux-pumps, namely the MexAB-OprM and the MexXY-OprM. According to the MLST typing analyses, this strain belongs to a clonal complex, previously identified in VIM metallo-β-lactamase producers in Hungary, namely CC11. Interestingly, the pan-resistant strain was isolated from a polytraumatised Romanian citizen on admission to the hospital of Szeged. This suggests the possibility, that this strain was imported to Hungary from abroad.