Multiresistant epidemic clones of *Pseudomonas aeruginosa* in the Czech Republic

Alexandr Nemec,¹ Martina Maixnerová,¹ Lenka Křížová¹ & Martin Musílek²

¹Laboratory of Bacterial Genetics and ²National Reference Laboratory for Meningococcal Infections, National Institute of Public Health, Prague, Czech Republic

Objective

In 2005 and 2006, the Czech Republic reported one of the highest proportions of antimicrobial resistance in invasive isolates of *Pseudomonas aeruginosa* among European countries [www.rivm.nl/earss]. The aim of this study was to determine whether this high level of resistance was associated with the spread of particular multidrug resistant (MDR) clones.

Conclusions

The multidrug resistance of invasive *P. aeruginosa* isolates in the Czech Republic in 2007 was predominantly associated with two MDR clones, one of which (ST235) belongs to international clonal complex CC11 [5].

Selection of isolates

- The set of 437 isolates from 49 hospitals of *P. aeruginosa* isolates in the Czech Republic in 2007 was predominantly associated with two MDR clones, one of which (ST235) belongs to international clonal complex CC11 [5].
- 1 – 3 isolates selected from each hospital
- A total of 110 isolates selected (Fig. 1)

Methods

- Susceptibility testing using E-test (imipenem, meropenem, piperacillin, ceftazidime, cefepime, gentamicin, tobramycin, amikacin, ciprofloxacin, colistin) [1]
- PFGE. Isolates of the same ST had similar SpeI macrorestriction profiles (Fig. 2).
- Multilocus sequence typing (MLST) [2]
- Macrogenome analysis of genomic DNA by using pulsed field gel electrophoresis (PFGE) [3]
- Integron typing [4]

Results

- Antibiotic susceptibility. 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.
- MLST. A total of 41 multilocus sequence types (ST) were identified, which, except for four unique STs, included 19 and 16 isolates, respectively. 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.
- PFGE. Isolates of the same ST had similar SpeI macrorestriction profiles (Fig. 2).
- Integron typing. 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.
- The isolates with either ST235 or ST175 originated from 39 hospitals in 23 cities (included in the EARSS study of 2007). ST215 encompassed 34 (74%) of 46 isolates resistant to more than 3 agents (Fig. 3).

References


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Correspondence. Alexandr Nemec, National Institute of Public Health, Šrobárova 21, 183 00 Praha, Czech Republic. anemec@szu.cz

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