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

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## 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 37 cities (included in the EARSS study of 2007)
- 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]
- Multilocus sequence typing (MLST) [2]
- Macrorestriction 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, differed from each other in at least three alleles. ST235 and ST175 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 macro-restriction 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 25 hospitals in 19 cities (Fig. 1).
- ST235 and ST175 encompassed 34 (74%) of 46 isolates resistant to more than 3 agents (Fig. 3).

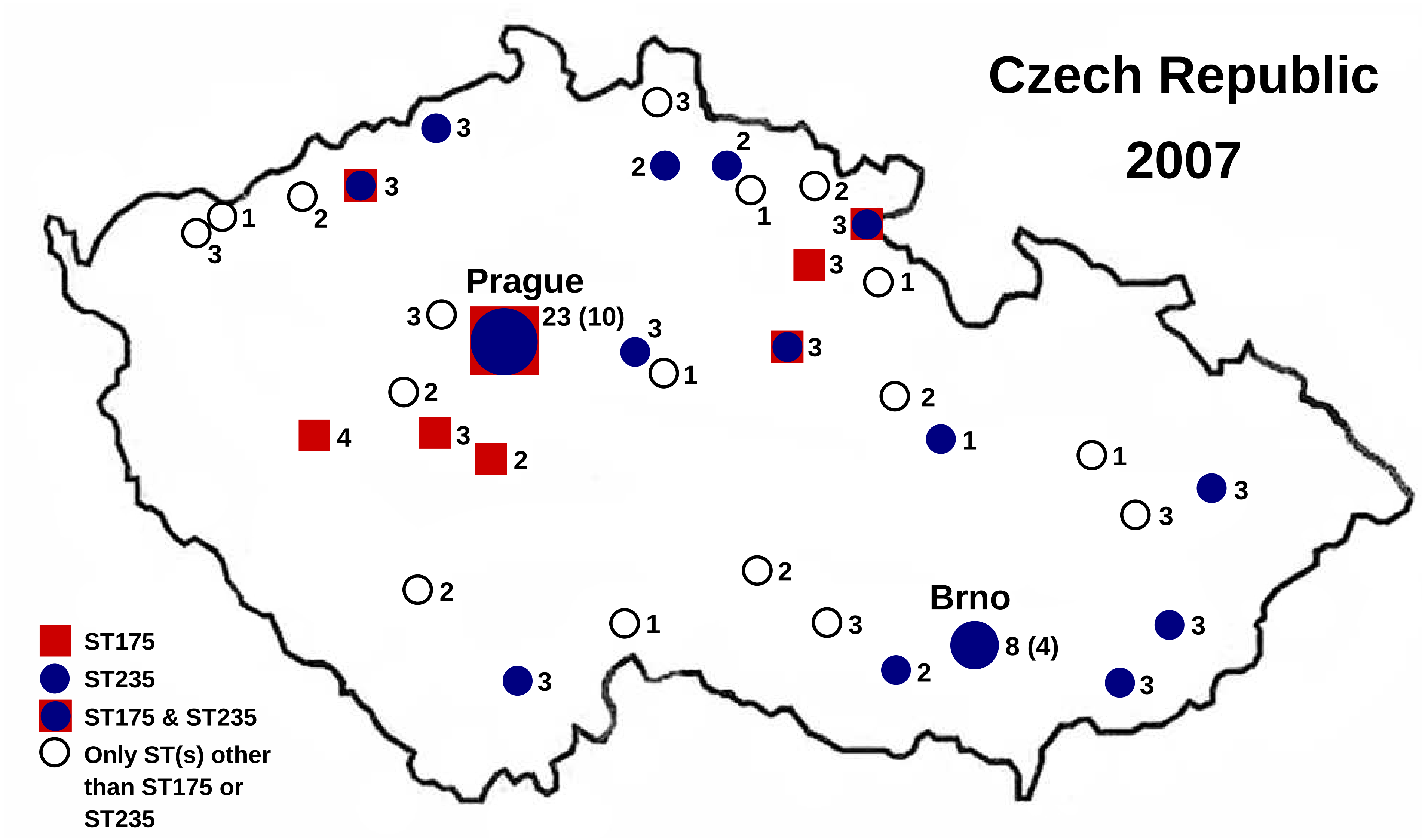

**Fig. 1. Geographic origin of the 110 isolates included in this study.** Indicated are numbers of isolates received from a city; the numbers of different hospitals in a city are shown in parentheses.

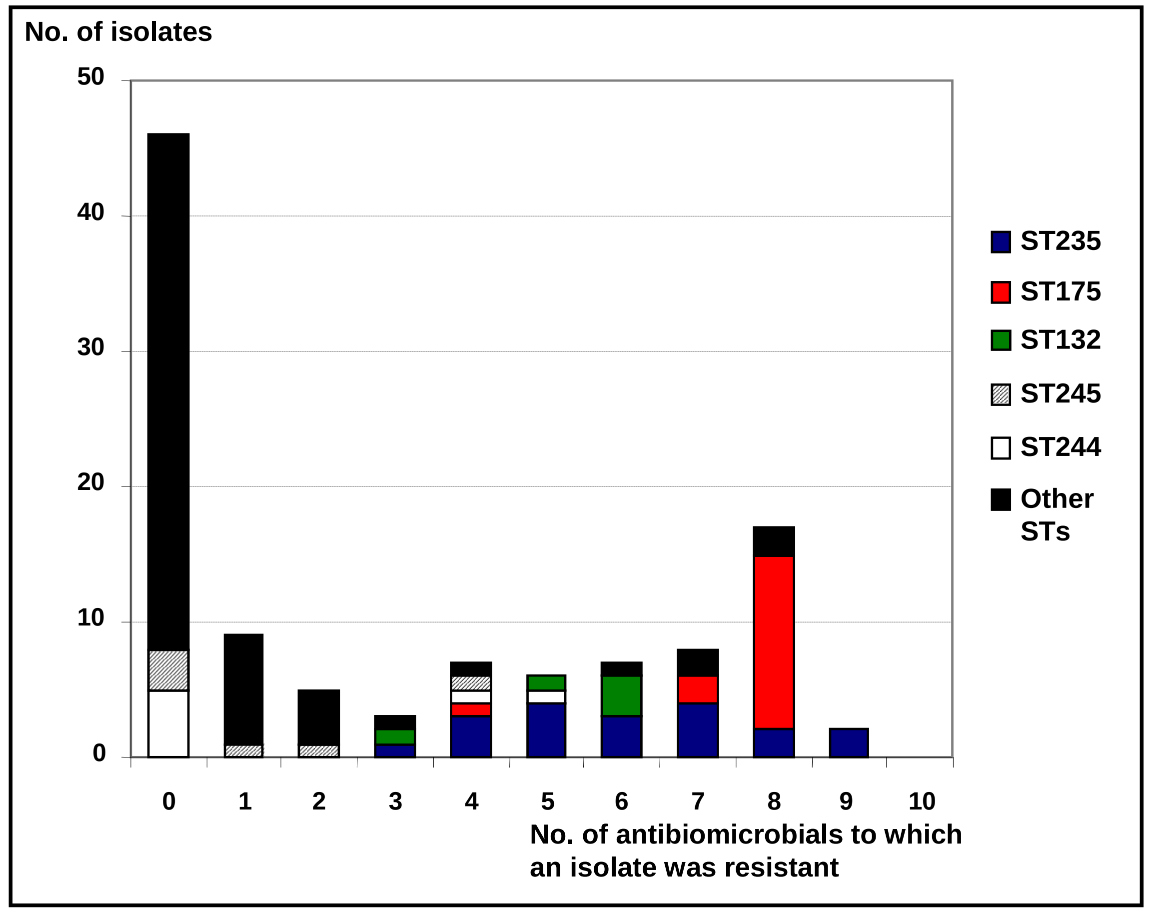

**Fig. 3. Distribution of the *P. aeruginosa* isolates according to the number of antimicro-bial agents to which individual isolates were resistant.**

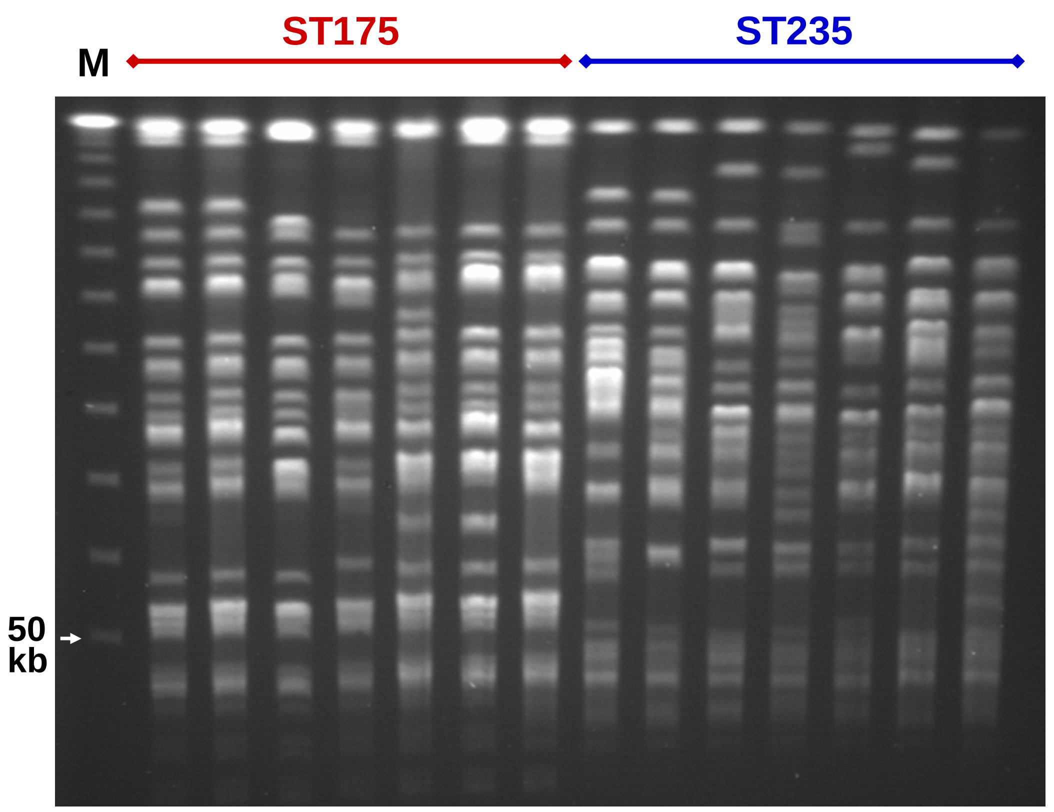

**Fig. 2. *Spe*I-macrorestriction patterns of the genomic DNAs of 14 isolates belonging to ST175 or ST235.**

**Rerefences**

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**Acknowledgements.** Supported by grant NR/9428-3 of the Internal Grant Agency of the Ministry of Health of the Czech Republic.

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*Presented at the 19th ECCMID, May 16 – 21, 2009, Helsinki, Finland.*