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Dissemination of metallo-beta-lactamase-producing *Pseudomonas aeruginosa* in the Czech Republic, 2012

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Objectives

Carbapenem-resistant *Pseudomonas aeruginosa* is a serious challenge for antimicrobial therapy of nosocomial infections. Several mechanisms are involved in resistance to carbapenems, such as beta-lactamase production, efflux pumps and decrease in membrane permeability. The most serious mechanism of resistance to carbapenem antibiotics in *P. aeruginosa* is an expression of metallo-beta-lactamases (MBL), which efficiently hydrolyse almost all clinically available beta-lactams and are not susceptible to beta-lactamase inhibitors. The prevalence of carbapenem resistance mediated by acquired MBL including the most important imipenem (IMP), Verona integron-encoded (VIM) and New Delhi metallo-beta-lactamases (NDM) are increasing in several countries worldwide. The objectives of this epidemiological study were to phenotypically detect MBL in carbapenem-resistant *P. aeruginosa*, to monitor main genes encoding MBL, to compare the resistance profile of MBL-producing and non-MBL-producing strains and to realize spreading of MBL-producers in the Czech Republic during the period 2012.

Methods

Three hundred seventy-two *P. aeruginosa* isolates with reduced carbapenem susceptibility were collected consecutively over the period 2012 from 52 local microbiology laboratories in the Czech national reference laboratory. Minimum inhibitory concentrations (MICs) to 11 antibiotics were determined according to the EUCAST recommendations. All carbapenem-resistant *P. aeruginosa* (n=165) were tested for MBL production by MALDI-TOF meropenem hydrolysis assay. Phenotypic identification of carbapenemases was performed by the EDTA-inhibitor-based method and the detection of *bla* genes, encoding important carbapenemase types, was assessed by PCR using specific primers for *bla*(IMP), *bla*(VIM), and *bla*(NDM).

Results

All (n=53) MBL-producing *P. aeruginosa* exhibited multidrug-resistant phenotypes and remained susceptible to colistin. Non-MBL-producing isolates were susceptible to a number of antimicrobial agents. Among 53 MBL-producing isolates, 11 (20,8 %) carried the *bla*(VIM) gene and 42 (79,2 %) carried the *bla*(IMP) gene. No *bla*(NDM) gene was detected. MBL-producers were found in 19 (36,5 %) cooperating microbiology laboratories.

Conclusions

Our data demonstrated, that MBL-producers were observed in more than one of third collaborating laboratories and the most prevalent MBL gene is *bla*(IMP). The spread of these dangerous phenomenon are still increasing over the Czech republic in comparison previously data and it is necessary to control their spreading.

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