
LETTER TO THE EDITOR

ROLE OF RARE CARBAPENEMASES IN THE DIFFUSION OF CARBAPENEM RESISTANCE IN *PSEUDOMONAS AERUGINOSA*

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The recent article by Monica Străuț *et al.* published in the latest issue of the *Romanian Archives of Microbiology and Immunology* provided an overview of the β -lactamase genes and the diversity of the surrounding genetic structures associated with resistance to ceftazidime in Romania [1]. In total, the authors have evaluated 93 non-duplicate isolates, most of which (n = 74) were obtained from the respiratory tract.

Even though not the primary interest of this study, the authors highlight the need for the detection of carbapenem resistance in *P. aeruginosa*.

The main carbapenem-resistance mechanisms in *P. aeruginosa* are:

- Overproduction of chromosomally-encoded cephalosporinase (AMPC) associated to overexpression of efflux pumps and/or porin deficiency

- Quantitative or qualitative alteration of porin D2

- Production of carbapenemases, mostly Ambler's class B metallo- β -lactamases (MBL).

This, however, does not take into account the diversity of carbapenemases encountered in that species. First, a large diversity of MBL has been identified including more than fifteen variants of bla_{VIM} -type or bla_{IMP} -type carbapenemases but also more rarely described MBLs such as bla_{GIM-1} , bla_{SPM-1} , bla_{AIM-1}

[2]. Noticeably, class A carbapenemase were also identified in *P. aeruginosa* including bla_{GES} -type and bla_{KPC} -type carbapenemase [3, 4].

In addition to this wide diversity, we have recently characterised four *P. aeruginosa* isolates producing OXA-198, an Ambler class D carbapenemase from Belgian Hospitals from 2010 to 2013 [5,6].

These isolates, including the original index strain, belonged to the Sequence Type 446 (by multilocus sequence typing, MLST) and serotype O11. OXA-198 was carried by an IncP11-type plasmid transferable but not conjugative.

In a previous survey conducted in the Cluj County in Romania, Dortet *et al.* reported a large variety of β -lactamases identified in *Enterobacteriaceae* and *P. aeruginosa* [7]. Among the *P. aeruginosa* isolates, the bla_{VIM-2} and bla_{IMP-13} genes were identified. Overall, epidemiological data concerning Romania remain scarce. In order to limit the spread of these highly drug resistant Enterobacteriaceae and non-fermenters continuous monitoring of the drug resistance levels, but also of the underlying resistance mechanisms is mandatory.

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