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Letters to the Editor

The Colistin-Only-Sensitive Brazilian *Pseudomonas aeruginosa* Clone SP (Sequence Type 277) Is Spread Worldwide[▽]

We read with great interest the recent publication by Salabi et al. (8), which reported the first case of a bla_{SPM-1} metallo-β-lactamase gene outside Brazil. The authors stated that an SPM-1-positive *Pseudomonas aeruginosa* strain, BH121, recovered from a Swiss inpatient coming from Recife, Brazil, was genetically related to the Brazilian *P. aeruginosa* clone SP, which is endemic in Brazil (1, 2, 6). In fact, such study showed that, even though the bacterium isolation had occurred in Switzerland, this patient had probably been infected in Brazil. Here, we applied the *P. aeruginosa* multilocus sequence typing (MLST) scheme (3) for determining the epidemiology of colistin-only-sensitive (COS) Brazilian *P. aeruginosa* clone SP harboring bla_{SPM-1}, and it was demonstrated that this clone had already been circulating outside Brazil before the BH121 identification in Europe (8).

Thirty-seven SPM-1 ($n = 27$) and non-SPM-1 ($n = 10$) isolates presenting the COS phenotype were recovered from different inpatients between 2001 and 2006 from Rio de Janeiro and São Luís, two Brazilian cities 3,000 km apart. These strains were analyzed by MLST and pulsed-field gel electrophoresis (PFGE) in order to characterize and compare both approaches. The *P. aeruginosa* MLST scheme was applied as proposed (3). PFGE was performed as described previously (5), and the macrorestriction profile was analyzed according to the criteria of Tenover et al. (9).

PFGE and MLST analysis showed that the COS *P. aeruginosa* strains harboring bla_{SPM-1} clustered together in clone SP and belonged to sequence type (ST) 277, while COS SPM-1-negative strains grouped in another clone, and they were assigned to ST 244. Therefore, in our study, PFGE and MLST demonstrated the same resolution power as reported previously (4). Since the Brazilian clone was previously named clone SP (6), we decided to use the same nomenclature to define all strains from ST 277.

Interestingly, according to the *P. aeruginosa* MLST database, ST 277 had already been assigned to a strain isolated in Austria in 2006, showing the presence of clone SP in Europe before the description by Salabi et al. (8). Moreover, ST 277 was also assigned to isolates from China and Australia, showing its potential to be widespread, its high fitness, and its being established as an international clone. Nevertheless, there are no data concerning the presence of bla_{SPM-1} in those isolates from clone SP/ST 277 identified outside Brazil. However, considering that the bla_{SPM-1} gene is a marker of clone SP in Brazil, it would be of interest to investigate its presence also in ST 277 isolates from other countries.

ST 244 was assigned to isolates from outbreaks in Poland (2003 to 2007) (4) and from surveillance studies in China (2006) and the United States (2001 to 2004) (7), as well as with an environmental isolate from the United Kingdom (1998), showing that this clone is also widespread.

The majority of the 932 STs available in December 2009 in the MLST database belonged to unique isolates. Few STs were assigned to more than one strain; however, they were restricted to one country. The exceptions, so far, have been STs 17, 27, 111, 155, 175, 179, 235, 244, 253, 277, 649, and 712, which have been reported in different countries over several years. None of these widespread STs formed clonal complexes with clone SP ST 277.

The present study associated ST 277 with Brazilian clone SP, which has been revealed as a public health problem since it presents a COS resistance profile, beyond its persistence and dissemination in hospitals from a country with continental dimensions such as Brazil. Our analysis showed that this clone has an epidemic/pandemic potential. Human beings can be vectors promoting its spread, as clearly demonstrated in the study by Salabi et al. (8).

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