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Usefulness of *Acinetobacter baumannii* MLST-Pasteur scheme for *Acinetobacter ursingii* isolates typing

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Background. *Acinetobacter baumannii* is considered to be the most clinically relevant *Acinetobacter genomic*-species, however increasing reports of community and nosocomial infections caused by non-*baumannii Acinetobacter* were observed. Moreover, *A. ursingii* has been recently recognized as an unsuspected reservoir of resistance genes including carbapenemases. Previously, we described the emergence and dissemination of IMP-1-producing *A. ursingii* isolates. Herein, we evaluated the ability of *A. baumannii* MLST-Pasteur (Aba-MLST) scheme to subtype *A. ursingii* isolates.

Methods. Four *Acinetobacter* spp. isolates from the NRL-Collection, identified as *A. ursingii* by MALDI-TOF (Bruker), were analyzed. Genetic relationship was evaluated by *Sma*I-PFGE. MLST scheme was performed according http://pubmlst.org/abaumannii/. Additional primers for amplification/sequencing of rpoB gene were designed, rpoBAur-F 5´- GGTGAAATGACAGAGAACCA-3´, and rpoBAur-R 5´-GAGTCTTCGTAGTTATAACC-3´. DNA alignment was performed using ClustalX software, and a bootstrap of 1,000 replicates.

Results. The four *A. ursingii* isolates were unrelated by PFGE analysis (>6 bands of difference). Using Aba-MLST primers 6/7 genes were amplified by PCR. However, rpoB gene was not amplified under different PCR conditions. Therefore, a new set of rpoB primers, yielding a 1076bp fragment, was designed. The sequence identity for the 7 genes against available alleles at the Aba-MLST database, ranged between 83.4-93.8%. Individual DNA alignment of each 7 genes against the database grouped the four *A. ursingii* isolates in a cluster. Phylogenetic analysis of concatenated sequences showed a compact cluster separated from others *Acinetobacter* species. Comparison of the phylogenies obtained using each gene individually showed strong congruence among the concatenated sequences.

Conclusions: We propose the use of Aba-MLST scheme for *A. ursingii* typing. A new set of primers for rpoB gene amplification is require to include *A. ursingii* isolates in the Aba-MLST database. This tool will allow the molecular surveillance of “non-classic” pathogens other than *A. baumannii* using the MLST approach.