ASSESSMENT OF ALLELIC VARIATION IN THE *blaZ* LOCUS OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* CLONES

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Background: *Staphylococcus aureus* is among the most important human pathogens causing both hospital and community-acquired infections worldwide. This species causes also great concern due to its high capacity to rapidly acquire antibiotic resistance traits. Resistance to β-lactam antibiotics in *S. aureus* can be mediated by the production of β-lactamases encoded by the *blaZ* gene, which encodes for resistance to penicillins only, and by the acquisition of an extra penicillin-binding protein - PBP2A, the gene product of *mecA*, which encodes for cross-resistance to all β-lactams. Interestingly, in spite of the cross-resistance provided by the *mecA* gene, the great majority of contemporary clinical MRSA strains are still positive for the β-lactamase genes.

Objectives: To evaluate the allelic variability of *blaZ* gene among methicillin-resistant *S. aureus* (MRSA) strains belonging to different genetic lineages.

Methods: The allelic variability of the *blaZ* locus was addressed by DNA sequencing of a DNA internal fragment of 533bp within the *blaZ* gene in a representative collection of previously fully characterized MRSA clones. Nucleotide sequences were aligned and the phylogenetic trees were constructed.

Results and conclusions: The results obtained identified the presence of 13 allotypes among the 53 *blaZ*-positive MRSA strains tested. No correlation could be established between the *blaZ* allotype and MRSA lineages, suggesting that the *blaZ* evolution did not parallel the evolution of the MRSA clones.