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Molecular characterization of hospital- and community-acquired methicillin-susceptible and resistant *Staphylococcus aureus* isolates in Bucharest, South Romania

Othman Almahdawy^{*1}, Irina Gheorghe², Otilia Banu³, Cristea Violeta Corina⁴, Veronica Lazar⁵, Grigore Mihaescu⁶, Mariana Carmen Chifiriuc⁷

¹*Faculty of Biology; Microbiology*

²*University of Bucharest; Faculty of Biology; Microbiology*

³*Institute for Cardiovascular Diseases "c.C. Iliescu"*

⁴*Synevo Romania; Microbiology*

⁵*Research Institute of the University of Bucharest, Maximilian Association; Microbiology*

⁶*Faculty of Biology*

⁷*Research Institute of Bucharest University, Microbiology Immunology*

Background: Hospital- (HA), but also community-acquired (CA) methicillin resistant *S. aureus* clones are known for their emergent multi-drug resistance phenotypes and implications in both ambulatory and nosocomial infections, as well as outbreaks worldwide. The architecture of staphylococcal cassette chromosome *mec* (SCC*mec*) type, as well as the presence of panton valentine leukocidin (PVL) toxin are two of the most important genotypic markers that differentiate among CA-MRSA and HA-MRSA. Our aim was to comparatively analyze the resistance phenotypes and to perform a molecular characterization of MSSA and MRSA strains isolated from hospitalized patients *versus* out-patients attending a private clinical laboratory in Bucharest, Romania.

Material/methods: This study was conducted on a total of 45 *S. aureus* clinical strains isolated in November 2015 from Prof. C.C. Iliescu hospital, out of which a significant percentage were recovered from wound secretions, followed by tracheal secretions and urine taken from patients hospitalized for cardiovascular surgery, harboring infections with different localizations and respectively, 30 *S. aureus*

strains isolated during the same period from the ambulatory sector of the Central Reference Laboratory Synevo in Bucharest, from pus collections followed by urine, nasal secretions, femoral wound secretions, sputum, tracheal aspirates and chronic leg ulcers. Simplex and multiplex PCR were performed on genomic DNA from MSSA and MRSA isolates in order to identify the SCCmec central elements, as well as other resistance (*aaca-aphD*, *blaZ*, *tetK*, *tetM*, *ermA*, *ermC*) and virulence genes (*luk-PV*, *nuc* and *spa*).

Results: The CA strains exhibited a slightly higher percentage of methicillin resistance (43.3%), as compared to the HA strains (37.9%). The antibiotic resistance phenotypes of the HA and CA *S. aureus* isolates were: penicillin (75%/80%), tetracycline (44.8%/36.7%); gentamicin (20.7%/67%), rifamycin (20.7%/6.7%), ciprofloxacin (24.1%/10%), clindamycin (48.3%/50%), erythromycin (48.3%/50%), moxifloxacin (24.1%/10.5%). It is to be noticed the higher resistance rates to penicillin, gentamicin and macrolides in the CA strains. The comparative frequency of the investigated virulence and resistance genes in the HA versus CA *S. aureus* strains was the following: *mec A* (15.55% /3.33%); *aaca-aphD* resistance to gentamicin (82.22% /50%), *blaZ* (64.44%/20%), *tetM* (37.77%/50%), *tetK* (33.33%/6.66%) *ermA* resistance to erythromycin (13.33%/3.33%), *ermC* (8.88% /3.33%), *nuc* (48.88%/3.33), *luck-PV* (1.33%/0%) and *spa* (84.4% /40%).The HA-MRSA strains belonged to the SCCmec types I, II, III, V, VIII, while the CA-MRSA strains to the SCCmec types II and IVa.

Conclusions: The significant levels of resistance of some CA-*S. aureus* strains highlights the need for continuous surveillance and molecular characterization studies, of not only HA-, but also of CA isolates. The variate genetic context of methicillin resistance in MRSA strains proves the capability of MRSA strains to evolve and thus implies for further studies regarding the correlation between different types of cassettes and the clinical outcome of the infection.