28th ECCMID EUROPEAN CONGRESS OF CLINICAL MICROBIOLOGY AND INFECTIOUS DISEASES
Madrid, Spain
21 – 24 April 2018

P1741 Molecular characterization of clonal complex 398 (CC398) methicillin-resistant Staphylococcus aureus (MRSA) isolates in humans in Hungary: emergence of a PVL-positive MRSA ST1232

Erika Ungvári[1], Brigitta Berta[1], Noémi Derzsy[1], Andrea Torma[1], Gyula Kispál[2], Miklós Kovács[3], Hilda Osztie[5], Ildikó Wolf[4], Akos Toth*[1]

[1]National Public Health Institute, Budapest, Hungary, *[2]Géza Hetényi County Hospital, Szolnok, Hungary*, *[3]Bethesda Children's Hospital, Budapest, Hungary*, *[4]Kálmán Pándy County Hospital, Gyula, Hungary*, *[5]Synlab Hungary Ltd, Synlab Budapest Diagnostic Center, Microbiology Laboratory, Budapest, Hungary*

Background: In the past decade, livestock-associated (LA)-MRSA strains, particularly those of CC398 have emerged European-wide especially in areas with high density of pig farming. LA-MRSA is not only successful in colonising humans, but also capable of causing infections and further spreading without any livestock exposure. In Hungary LA-MRSA CC398 was first detected in 2009. The aim of this study was to perform molecular characterization of LA-MRSA isolated since then.

Materials/methods: MRSA isolates obtained from human clinical or screening samples were submitted to the National Staphylococcal Reference Laboratory for molecular typing between January 2009 and June 2017. From these we selected NT-MRSA (nontypable by *Sma*I restriction in PFGE) isolates (n=79) for further characterization by antimicrobial susceptibility testing, *spa*-, SCC*mec* typing and investigated for presence of Panton-Valentine leukocidin (PVL) genes. Whole genome sequencing of seven isolates representing prevalent genotypes was performed using Illumina 250-bp paired-end sequencing. Sequence data were used for core genome (cg)MLST by SeqSphere+ (Ridom) and identification of resistome and virulome by ResFinder and VirulenceFinder tools.

Results: 100% of the NT-MRSA isolates were resistant to tetracycline, 54.4% to erythromycin, 65.8% to clindamycin, 19% to ciprofloxacin and 15.2% to gentamicin. Nine *spa* types were identified: t011 (32/79), t034 (30/79), t108, t567, t571, t899, t1197, t1250, t4208. SCC*mec* type IV and V were present in 21.5% and 72.1% of the isolates, respectively. The most prevalent genotypes were t034-V (36.7%), t011-V (22.8%) and t011-IV (15.2%). One isolate with t034-V genotype proved PVL-positive. From the seven selected t034-V isolates six belonged to ST398 and the PVL-positive isolate to ST1232. The ST398 isolates could be further divided into two complexes by cgMLST. Three of seven isolates, including the PVL-positive showed the genetic features of the human-adapted subclone of CC398 carrying the human immune evasion cluster (IEC) genes.

Conclusions: This is the first description of a PVL+ LA-MRSA strain in Hungary. Our results showed presence of the human-adapted subclone of LA-MRSA in Hungary. IEC re-acquisition by LA-MRSA-CC398 strains could constitute an emerging public health problem. It would represent an evolutionary step towards LA-MRSA-CC398's adaptation to humans, and might enhance its invasiveness and ability to human-to-human transmission.