

Abstract

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major nosocomial pathogen that has spread into the community since the 90s. In general, the community-associated (CA-MRSA) strains are more virulent, but less resistant to antimicrobials than the hospital-acquired strains (HA-MRSA). Some lineages of MRSA such as sequence type 8 have been transmitted more successfully around the world than others and there are situations where a dominant lineage has been replaced by a new one. The factors that are crucial for the selection of dominant lineage are often not clear. As part of this thesis, a longitudinal study of MRSA epidemiology in the Motol University Hospital during the period of 2018-2020 was performed and the occurrence of MRSA clonal complexes was characterized. A multicenter study of the epidemiological situation of MRSA in Slovakia during the period of January – April 2020 was also performed concomitantly. Moreover, several isolates from dominant lineages were further characterized by their phenotype. In the Motol University Hospital study, it was found that the HA-MRSA of the clonal complex 5 dominates and is represented mainly by *spa*-type t586; a finding that concurs with recent studies from the Czech Republic. In Slovakia, similar to the Czech Republic, MRSA lineages from clonal complex 5 were predominant. Other lineages were also significantly present e.g. HA-MRSA lineages from clonal complex 22, also known as EMRSA-15 (20% of isolates) and more importantly, the epidemic USA300 clone was detected, which is an epidemic clone in the United States, but has so far been rarely reported in Europe.