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P2714 Great clonal diversity and replacement of Brazilian epidemical clone of *Staphylococcus aureus* in a university hospital of southern Brazil

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Background: *Staphylococcus aureus* are microorganisms of extreme medical importance, being among the most prevalent agents causing infection. Its wide distribution, variety of infectious processes and great profile of antimicrobial resistance make it a pathogen of great clinical importance.

Materials/methods: A total of 239 *S. aureus* from pneumonia and bacteremia were analyzed from patients hospitalized at a University Hospital in southern Brazil from 2010 to 2016. Data analysis was divided into three stages. First period from January to June 2010 (55/239), second period from July 2010 to December 2013 (123/239) and third period from January 2015 to December 2016 (61/239). The *mec*A gene, as well as the types of SCC*mec*, were identified using multiplex PCR. The clonal complexes and sequence typing for 53 isolates from the third period were determined using RTq-PCR.

Results: All 239 samples were positive for the *mec*A gene. SCC*mec* type III, classified as Brazilian Epidemic Clone (BEC) in the literature, presented a decrease in the frequency of 7.27% (4/55) in the first period, to 1.63% (2/123) in the second period and 1.64% (1/61) in the third period. This was replaced by SCC*mec* type II, which presented percentages of 43.64% (24/55), 53.66% (66/123) and 60.66% (37/61), respectively. There was also a consecutive increase in the frequency of isolates belonging to SCC*mec* type IV, related to community infections, emerging in the hospital environment, with percentages of 3.64% (2/55) in the first, 8.13% (10/123) in the second and 22.95% (14/61) in the third period. It is possible to observe a great clonal variability, since the 53 analyzed isolates are inserted in 18 clonal complexes and 20 different sequence typings, with CC5 and ST63 being the most prevalent.

Conclusions: Therefore, with this study, a substitution of the type of SCC*mec* related to BEC for SCC*mec* type II was found. This fact can be explained by the great clonal variability and significant increase presence of isolates belonging to SCC*mec* type II, CC5, related to the New York / Japan clone.