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Lower respiratory tract infection by *Staphylococcus aureus* in an intensive care unit: genotypical characterisation

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Objectives. 1.To study the epidemiology of lower respiratory tract infection by *Staphylococcus aureus* in an intensive care unit (ICU) from a tertiary hospital. 2.To report the persistent isolation of the microorganism. 3.To describe molecular features of the isolated strains.

Material and methods. All strains isolated during year 2012 from tracheal aspirates (TA) of patients in ICU were selected. Patients were classified by expert clinicians into ventilator-associated pneumonia (VAP), tracheobronchitis or bronchial colonization. In order to study carriage, nasal swabs were obtained at the time of ICU admission. Clinical strains were phenotypically characterized and susceptibility testing was performed. A group of strains were genotypically characterized with a commercial array that includes the identification of clonal complex (CC) and accessory gene regulator (agr) as well as the presence of genes encoding virulence factors such as Chemotaxis Inhibitory Protein of *S.aureus* (CHIPS), Toxic shock syndrome toxin-1 (TSST-1) and Panton-Valentine leukocidin (PVL).

Results. *S.aureus* (16.4% MRSA) was isolated in 79 patients, being the more frequent (13.6%) after *Enterobacteriaceae* and *Pseudomonas*. In 25.3% of the cases, persistent isolation was reported. A subgroup of 31 patients were classified: 3 were diagnosed of VAP (100%MSSA), 8 of tracheobronchitis (50%MRSA), and 20 were considered bronchial colonization (10%MRSA). Strains from 10 nasal carriers (100%MSSA) were also included. As a result, 41 strains were genotypically analyzed. The percentage of MRSA in TA was 19.3%. Considering only VAP and tracheobronchitis, the percentage was 36.3%. Ten different clonal complexes were detected, being the more frequent CC5 (32.5%), CC8, CC30 and CC45 (15% each). CHIPS was detected in 80.4% of the strains (all 3 VAP, 4 tracheobronchitis, 16 colonization and 8 carriage) and TSST-1 in 19.5% (1 tracheobronchitis, 2 colonization and 5 carriage). All strains were PVL negative. *Agr* allele classification was as follows: 24.39% (10/41) displayed agrI, 39.02% (16/41) agrII, 21.95% (9/41) agr III and 14.6% (6/41) showed ambiguous result. In 5 cases (1 VAP and 4 tracheobronchitis), there was persistent *S.aureus* isolation (4 MRSA) despite adjusted antibiotic treatment [15.1 days (SD 17.7)]. Two of these strains were CC8-MRSA IV-[sea+]- Lyon Clone; two were CC45 and the last one CC22.

Conclusions. 1. *S.aureus* is the gram-positive more frequently isolated in TA in the ICU, with 16.4% of MRSA. 2. Persistent isolation is often reported, in some cases despite treatment adjusted to susceptibility pattern. 3. There is an important diversity of clonal complexes, including MRSA strains. The presence of the virulence factors genes analysed and *agr* alleles were not related to the patients'

study group. 4. Further studies combining specific host factors and differential virulence factors gene expression are required in order to understand the clinical outcome.