

Poster (Painel)**MH-052 Determination of *ccr* gene allotypes and characterization of antimicrobial resistance of methicillin-resistant *Staphylococcus aureus***

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Resumo

Methicillin-resistant *Staphylococcus aureus* (MRSA) are important agents of nosocomial infection. MRSA carry a mobile genetic element staphylococcal cassette chromosome mec (SCCmec) constituted of the *mecA* gene that codified an altered penicillin-binding protein (PBP2a), which determines methicillin resistance; the *ccr* gene complex that encodes recombinases; and J region that carry resistance determinants to non beta-lactamics drugs. Eight types of SCCmec have been described, being types I, II, and III most common in nosocomial infections. The aim of this study was: (1) determine the resistance profile of the MRSA isolates to 14 antimicrobial drugs; (2) determine the minimal inhibitory concentration to vancomycin; (3) detect the *mecA* gene and determine the allotypes of the *ccr* gene complex by multiplex PCR and (4) detect *lukS* gene. These analyses were performed using 50 nosocomial MRSA isolates, being 20 surveillance isolates and 30 clinical isolates obtained from the Department of Microbiology of Laboratory of Clinical Pathology of São Lucas Hospital – PUCRS during the period from January to October 2009. Determination of antimicrobial susceptibility and MIC were performed according the guidelines recommended by CLSI (2009). DNA extraction was carried out using guanidine thiocyanate. The multiplex PCR 1 was used to detect *mecA*, *ccrAB1* and *ccrAB2*, amplifying fragments of 533 bp, 700 bp and 1 kbp, respectively. The multiplex PCR 2 was carried out to detect the *ccrAB3* and *ccrC*, amplifying fragments of 1.6 kbp and 520 bp, respectively. A conventional PCR was performed to detect of *lukS* gene. All strains were resistant to azithromycin, cefoxitin, clindamycin, gentamicin and oxacillin and susceptible to linezolid, quinupristin/dalfopristin, tigecycline and vancomycin. The *mecA* was found in all isolates. The allotypes *ccrAB1*, *ccrAB3* and *ccrC* were detected in 9 (30%), 21 (70%) and 21 (70%) of clinical isolates and 13 (65%), 7 (35%) and 7 (35%) of surveillance isolates, respectively. All isolates that showed *ccrAB3* allotype presented also *ccrC* gene. The *ccrAB2* and *luk* gene were not found in any isolate. The results showed the prevalence of *ccrAB1* and *ccrAB3* associated with *ccrC* in surveillance isolates and clinical isolates, respectively. Also, the isolates belonged to SCCmec III were more associated with resistance to non beta-lactam drugs. Apoio: CNPq – FAPERGS.

Palavras-chave: *Staphylococcus aureus*, MRSA, *ccr* gene allotypes