IDENTIFICATION AND PRESERVATION OF MULTIRESISTANT BACTERIA ISOLATED FROM BLOODSTREAM INFECTIONS OF PATIENTS AT A HOSPITAL IN BRAZIL

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The university hospital Cassiano Antônio de Moraes (HUCAM), Federal University of Espírito Santo, Brazil, is a hospital of high complexity that offers treatments in several clinical and surgical specialties. Bloodstream infections with Gram-positive bacteria of hospitalised patients, some of them caused by methicilin-resistant (MRSA) *Staphylococcus aureus,* are a significant cause of morbidity and mortality. Multiresistant bacteria have emerged as a serious public health problem worldwide and require consistent and intensified surveillance efforts. The accurate identification and availability of this biological material for additional tests and studies were the core motivators for the establishment of the Bacterial Strain Reference Culture Collection (CCBR) of HUCAM. The CCBR-HUCAM was established in 2011 and preserves bacterial isolates, from internal and external analysis, with high interest for clinical studies. The main aim of this current work is to present the identification and preservation methodology used in CCBR-HUCAM for multiresistant bacterial strains isolated from blood cultures from January to December 2011 at HUCAM.

Blood cultures were received at the Laboratory of Microbiology, HUCAM and incubated in the Bactec 9240 system at 35°C. Positive blood cultures were subcultured to identify microorganisms by a) conventional phenotypic techniques, b) Vitek 2 assays and c) antimicrobial susceptibility. A total of 471 positive blood culture was analysed. Of these, 283 (60%) were *E. coli, K. pneumoniae, A. baumanii, P. aeruginosa, S. aureus, S. epidermidis* and *Enterococcus* spp.; from which 107 (38%) were Gram-negative and 175 (62%) were Gram-positive. Also, 127 (45%) presented resistance to various classes of antibiotics used in conventional treatments. All the bacteria were cryopreserved at -20 °C. The MALDI-TOF MS technique is being applied for identifications and for proteomic comparisions between similar species with different profiles of resistance. Furthermore, molecular biology will be used to confirm the classical and phenotypical approaches.