

TITLE: BETA-LACTAMASES RESISTANCE GENES IN GRAM-NEGATIVE BACTERIA OF ESKAPE GROUP ISOLATED IN SANTA CATARINA STATE.

AUTHORS: TARTARI, D.C.; ZAMPARETTE, C.P.; MARTINI, G.; CHRISTAKIS, S.; COSTA, L.H.; SILVEIRA, A.C.O.; SINCERO, T.C.M.

INSTITUTION: UNIVERSIDADE FEDERAL DE SANTA CATARINA, FLORIANÓPOLIS, SC (R. ENG. AGRÔNOMICO ANDREI CRISTIAN FERREIRA, S/N, 88040-900 - FLORIANÓPOLIS - SC, BRAZIL)

Health care-associated infections (IRAS) are recognized as a public health problem, accounting for 700,000 deaths per year and an estimated 10 million deaths by the year 2050. Most of these infections are caused by bacteria resistant to various classes of antimicrobial agents, such as the Gram-negative bacteria members of the ESKAPE group: *K. pneumoniae*, *A. baumannii*, *P. aeruginosa* and *Enterobacter spp.*, which were listed as a critical priority for research by the WHO document of 2017. These bacteria produce enzymes that confer clinical resistance to various classes of antimicrobials, such as carbapenemases that can hydrolyze carbapenems, one of the last alternatives for the treatment of Gram-negative infections. With the knowledge of the main circulating resistance mechanisms, prevention measures can be taken to reduce IRAS. Thus, the objective of this study is to evaluate multidrug-resistant bacteria in hospitals in the state of Santa Catarina and to characterize the main circulating resistance mechanisms genotypically. Detection of resistance genes associated with extended spectrum beta-lactamases (ESBL), carbapenemases, and metallo-beta-lactamases (MBL) was performed by the qPCR technique. In all, we selected 154 samples (Jan-2018 to Jan-2019) from 11 hospitals distributed among 5 regions of the state. To date, 13 resistance genes have been investigated for 105 of these samples. Most of the samples are non-fermenters, *A. baumannii* (43) and *P. aeruginosa* (35) followed by enterobacteria *K. pneumoniae* (22) and *Enterobacter spp.* (5). The most commonly found genes were ESBL-type, where *bla_{TEM}* was the most prevalent, followed by the KPC carbapenemase gene. The most frequent gene in *K. pneumoniae* was the *bla_{SHV}* gene (95%) in *Enterobacter spp.* was the *bla_{TEM}*, and *bla_{KPC}* gene, both with 80% positivity, *A. baumannii* had 74% of the *bla_{TEM}* and in *P. aeruginosa* the *bla_{CTX-M-2}* was the most found gene with 6%. Some samples of *K. pneumoniae* stand out because they have a coproduction of resistance genes, some with up to 5 genes, including two strains harboring both *bla_{NDM-1}* and *bla_{KPC}* genes. These samples will be analyzed by complete sequencing to understand how these genes are allocated in the genome of those bacteria, if they share the same plasmid, and the conjugative capacity of them.

Keywords: ESKAPE group, resistance genes, antimicrobial resistance.

Agency: FAPESC - Programa Pesquisa para o SUS (PPSUS).