

Title: GENETIC SIMILARITY OF STRAINS ISOLATED IN THE RESPIRATORY CARE OF CRITICALLY ILL PATIENTS WITH AND WITHOUT PNEUMONIA

Authors: Hermann, P.R.S.¹, Campioni, F.², Souza, R.A.², HAAS, V.J.², Watanabe, E.², Falcão, J.P.², Andrade, D.²

Institution: ¹ UnB – Universidade de Brasília (Área especial 1, Centro Metropolitano, Ceilândia – Brasília/DF), ² Universidade de São Paulo (Avenida dos Bandeirantes, 3900. Campus Universitário - Bairro Monte Alegre. Ribeirão Preto/SP)

Abstract

Ventilator-Associated Pneumonia (VAP) is the nosocomial infection with a high incidence rate in the Intensive Care Unit (ICU), causing an increase in the period of hospitalization, the rates of mortality, and considerably increased costs. Patients undergoing mechanical ventilation have 6-21 times the risk higher of developing pneumonia. The analysis of microorganisms involved in infections with regard to their genetic structure is essential to support the monitoring process and strategies for prevention and control. In this regard, the role of microbial molecular typing is to determine whether there is an epidemiological link between isolates. Objective: to evaluate patients with endotracheal tube undergoing mechanical ventilation in the clinical and microbiological perspective in order to determine the dispersion of *Staphylococcus aureus*, coagulase-negative *Staphylococcus* and *Pseudomonas aeruginosa*. This is a prospective observational study conducted in the intensive care unit of a Brazilian hospital. The samples were from saliva, tracheal secretion, tracheal tubes, and from the gloves used in the suction of the tubes. Classical phenotypical methods were used for bacterial isolation and identification, and Enterobacterial Repetitive Intergenic Consensus Sequence (ERIC-PCR) and Pulsed-field Gel Electrophoresis (PFGE) were used for molecular typing. From 44 patients, 34 (77.3%) were male, with a mean age of 39.9 years. Ventilator-associated pneumonia (VAP) rate was 15 (34.1%). The intubation period of the endotracheal tube ≥ 8 days was a risk factor for VAP ($p < 0.001$). Twelve strains of *Staphylococcus aureus*, nine of coagulase-negative *Staphylococcus* resistant to oxacillin and 26 *Pseudomonas aeruginosa* were analyzed by ERIC-PCR and PFGE. It is revealed that strains from saliva and tracheal secretion were also indistinguishable. There was no dispersion of strains among different patients, however it was revealed in different places on the same patient. There is a possibility of displacement of the oral microorganisms to elsewhere in the respiratory system.

Keywords: Ventilator-Associated Pneumonia; *Staphylococcus* spp.; *Pseudomonas aeruginosa*; Molecular Typing

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