

TITLE: STAPHYLOCOCCUS AUREUS IN NURSING STUDENTS: A POSSIBLE RESERVOIR OF HEMOLYSIN-CODING GENES

MARINHO DE SOUZA, J.^{1,2}, GONÇALVES, G. B.¹, TAVARES, E. R.^{1,2}, YAMAUCHI, L. M.^{1,2}, Rodrigues, M. V. P.², YAMADA-OGATTA, S. F.¹

¹ Universidade Estadual de Londrina, Londrina, PR (Rodovia Celso Garcia Cid, PR-445, Km 380, CEP: 86057-970, Londrina – PR, Brazil).

²Universidade do Oeste Paulista, Presidente Prudente, SP (Rua José Bongiovani, 700 - Cidade Universitária, CEP 19050-920, Presidente Prudente – SP, Brazil).

ABSTRACT

Staphylococcus aureus is commonly isolated in the nose cavity of healthy individuals, forming the normal microbiota of this site. Hence, it can act as a reservoir of essential virulence genes. We evaluated the presence of *hla* and *hlb* genes, which encode alpha (Hla) and beta (Hlb) hemolysins, respectively, in *S. aureus* isolated from the anterior nostrils of nursing students. We collected nasal swab samples from 19 students who had not had previous contact with the health care environment in a work way. Then, swabs were transported in Tryptic Soy Broth (TSB) medium and seeded on Sal Mannitol agar to isolate *Staphylococcus* sp. Among the isolates obtained (n=67), 47 were identified as *S. aureus* using a Polymerase Chain Reaction (PCR) targeting the *coa* and *nuc* genes. Complementary sequences to the *hla* and *hlb* genes were identified by PCR. A total of 40 isolates had both *hla* and *hlb* genes; 6 isolates showed only *hlb*, and one did not show *hla* or *hlb*. Hla and Hlb hemolysins, also called toxins, can lead to cytotoxicity and cell death. *Hla* promotes pores in the host cell membrane, leading to an electrolyte imbalance with consequent necrosis. In contrast, *Hlb* promotes hydrolysis of sphingomyelin, a lipid from the plasma membrane of erythrocytes. Hemolysin-producing *S. aureus* in the nostrils of healthy individuals is not directly related to the hospital environment. However, future health professionals may carry these strains and disseminate them in a health care environment, compromising or worsening the condition of debilitated patients. Thus, awareness of good hospital hygiene practices can make it difficult to transfer these potential pathogens to immunocompromised individuals.

Keywords: cross-contamination, virulence, nosocomial infection.

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