

TITLE: STAPHYLOCOCCUS AUREUS ISOLATED FROM NASOPHARYNX OF CHILDREN ATTENDING DAY CARE CENTERS IN THE CITY OF GOIÂNIA-GO: PREVALENCE, ANTIMICROBIAL SUSCEPTIBILITY AND VIRULENCE FACTORS

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ABSTRACT

Staphylococcus aureus is considered one of the most important human pathogens, accounting for infectious diseases that can range from simple infections to serious complications such as meningitis and sepsis, reaching to death. *S. aureus* naturally colonizes the human anterior nostrils and has a high spreading capacity, which may be potentiated according to some external factors, such as children crowded in day care centers. The aim of this study was to determine the prevalence of *S. aureus* colonization in children between 36 and 59 months, the antimicrobial susceptibility profile and to detect virulence factors in the isolated bacteria. From October to December 2010, swabs of nasal secretion from children in 59 Municipal Centers of Early Childhood Education were collected in the city of Goiânia, Goiás. The samples were sent to the Laboratory of Applied Bacteriology of Tropical Pathology and Public Health Institute at the Federal University of Goiás for processing. The isolation was performed by standardized methodology. The conventional PCR was used for detection of *femA* (identification of the species) and *mecA* and *lukS-F* genes (virulence factors). The susceptibility profile was determined by disk diffusion and Etest[®] method. In total, 1,135 swabs were collected. A prevalence of 30.7% (348 isolates) was achieved for *S. aureus*. Through the antimicrobial susceptibility test, isolates showed resistance to the following antimicrobials: penicillin (94.5%), quinupristin/dalfopristin (35.6%), erythromycin (34.1%), clindamycin (28.6%), sulfamethoxazole/trimethoprim (9.9%), tetracycline (6.1%), ciprofloxacin (4.7%), ceftiofur (3.5%) and rifampicin (0.9%). The inducible MLS_B phenotype was detected in 93 isolates (27.1%). Among the 12 isolates resistant to ceftiofur, five (0.44%) presented the *mecA* gene, characterized as MRSA. The multidrug resistance profile was identified in 107 isolates (31.2%). Gene *lukS-F* was found in 26 isolates (7.5%). The results showed that the prevalence of *S. aureus* and MRSA colonization in children at this age remain constant compared to previous studies. However, the multidrug resistance that was found in 1/3 of the isolates and the detection of the gene that encodes the PVL are cause for concern because represent difficulty of treatment, increased virulence and risk of dissemination in the community that the day care environment provides.

Keywords: colonization, *mecA*, *femA*, *lukS-F*, conventional PCR

Development Agencies: None