RESISTANCE AND CLONALITY ATTRIBUTES OF *Staphylococcus aureus* AND COAGULASE-NEGATIVE *Staphylococcus* ISOLATES FROM ANTERIOR NARES AND FECES OF ATOPIC DERMATITIS PEDIATRIC PATIENTS

AUTHORS: AUGUSTO, M.F[1], AGNE, D.B[1], FERREIRA, D.C[2], OLIVEIRA, T.L.R[1], GUIMARÃES. L.C.[1], CAVALCANTE, F.S[3], SAINTIVE, S.[4], ABAD, E.D.[4], SANTOS, K.R.N[1].

INSTITUTIONS: [1]Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, RJ; [2]Faculdade de Enfermagem, Universidade do Estado do Rio de Janeiro, RJ;[3]Universidade Federal do Rio de Janeiro, Campus Macaé, RJ; [4]Instituto de Puericultura e Pediatria Martagão Gesteira, Universidade Federal do Rio de Janeiro, RJ.

ABSTRACT:
Atopic Dermatitis (AD) is a chronic, relapsing skin disease. AD patients may have high rates of nasal colonization by *Staphylococcus aureus*, which may be associated with worsening of the disease. Coagulase-negative *Staphylococcus* (CoNS), highlighting the species *Staphylococcus epidermidis*, are commensal microorganisms recently related to modulation of *S. aureus* colonization. This study aimed to evaluate the presence and characterize *Staphylococcus* species isolated from anterior nares and feces of 55 AD pediatrics patients attended in a public pediatric hospital in Rio de Janeiro. Bacterial identification was performed by phenotypical tests and MALDI-TOF/MS (Biotyper). The antimicrobial susceptibility was determined by disk-diffusion test and the minimal inhibitory concentration (MIC) to mupirocin was done by E-Test. Methicillin-resistant *S. aureus* (MRSA) and methicillin-resistant *S.epidermidis* (MRSE) isolates were detected by cefoxitin disk and confirmed for *mecA* gene by PCR. The presence of PVL genes was evaluated by PCR and clonal lineage was determined by Pulsed-Field Gel-Electrophoreses. One hundred fifty-seven *Staphylococcus* spp. isolates were identified from nasal and fecal samples, being 91 *S. aureus*, 39 *S. epidermidis*, 13 *S. haemolyticus*, 4 *S. saprophyticus*, 3 *S. hominis*, 2 *S. sciuri*, 2 *S. warneri*, 1 *S. cohnii*, 1 *S. pasteuri* and 1 *S. simulans*. Among 91 *S. aureus* isolates, 38 (41.6%) were MRSA, 21 nasal and 17 fecal, isolated from 24 (49%) patients. Among 39 *S. epidermidis*, 23 (58.9%) were MRSE, ten nasal and 13 fecal, isolated from 19 (65.5%) patients. Among MRSA isolates, two nasal isolates were mupirocin-resistant and all of them were SXT-susceptible. SCC*mec* IV was identified in 86.8% of MRSA and SCC*mec* V was prevalent in MRSE (40.9%) isolates. PVL genes were detected in 16 (17.6%) *S. aureus* isolates (11 MRSA and five MSSA) from 11 (20%) patients. The clonal lineages USA800/ST5 and USA1100/ST30 were prevalent among *S. aureus* from 26 (47.3%) patients. The same clones were observed in nares and gastrointestinal tract of 21 (38.2%) patients, and in 12 of them MRSA isolates were detected. The present study showed high rates of MRSA colonization in nares and feces of AD pediatric patients and many children colonized by the same genotype in both niches, highlighting the importance of monitoring colonization by virulent and resistant pathogens in this group of patients.

Keywords: *Staphylococcus aureus*, *S. epidermidis*, atopic dermatitis, antimicrobial susceptibility, clonal lineages.

Development Agency: CAPES, CNPq, FAPERJ