(AM-151C) with an MIC of 500 μg/mL (92.9 ± 1.0%). The sample from the leaves (AM-151F) was not considered active against *S. aureus*.

Conclusion: The results show a strong antimicrobial potential of *Vismia brasiliensis* as an alternative to be employed in the development of topical formulations for the treatment of skin infections caused by *Staphylococcus aureus*.

Keywords: *Staphylococcus aureus*, *Vismia brasiliensis*, Antimicrobial.

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BAYWATCH – SURVEILLANCE OF MDR *ESCHERICHIA COLI* PRODUCING ESBL IN BEACHES OF NITERÓI/RJ

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Introduction/Objective: The Tricycle Protocol was created by the World Health Organization in response to the increase in bacterial resistance to antimicrobials and the spread of their genetic determinants. The initiative aims at multisectoral monitoring and surveillance of *Escherichia coli* producing extended-spectrum beta-lactamases (ESBL-Ec) under the One Health approach, which, along with other species of *Enterobacterales*, is one of the critical priority pathogens for the production and development of new antimicrobials. Thus, the objective of this study was to evaluate the occurrence and profile of ESBL-Ec strains isolated from the waters of beaches in Niterói/RJ.

Methods: Water samples collected from Icaraí, Piratininga, and Jurujuba, presumptive for *E. coli*, were identified by mass spectrometry. The confirmed strains were subjected to selective pressure in CHROMagar ESBL and MacConkey agar with ceftriaxone at 4.0 μg/mL. The phenotypic susceptibility analysis was performed by disk diffusion against 22 antimicrobials. Genes for resistance to beta-lactams, quinolones, integrases, and virulence genes were investigated by polymerase chain reaction. Hemolysin production was analyzed phenotypically.

Results: A total of 299 *E. coli* strains were isolated, of which 33 were potential ESBL producers. A high frequency of resistance to ampicillin and third-generation cephalosporins (> 80%) was observed. In 30 strains, ESBL genes (blaCTX-M-1,2, blaCTX-M-8, blaCTX-M-14, blaTEM, and blaSHV) were detected, with blaCTX-M-1,2 being the most prevalent, both in Icaraí and Jurujuba. Additionally, the qnrS, intl1, and intl2 genes were also detected. Furthermore, 18 ESBL-Ec strains were classified as multidrug-resistant (MDR). Among the ESBL-Ec strains, six carried the papC gene, which encodes fimbriae associated with adhesion and colonization in extra-intestinal infections, as well as the hlyA gene for hemolysins; of these, five were MDR and two showed an alpha-hemolytic phenotype.

Conclusion: This is the first study describing MDR ESBL-Ec strains in beach waters of Niterói. This result highlights the importance of surveillance in natural ecosystems; however, the findings of this study, where MDR ESBL-Ec strains with resistance to quinolones, presence of integrase genes, and indication of extraintestinal virulence were detected, suggest the role of this ecosystem as a platform for persistence and dissemination of these anthropogenic-origin pathogens.

Keywords: *Escherichia coli*, ESBL, MDR, Antimicrobial resistance, Beaches.

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CALCULATOR FOR ANTIMICROBIAL DOSE ADJUSTMENT IN OBESE PATIENTS

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Introduction: Obesity presents itself as a growing challenge for healthcare, especially in the treatment of infections due to pharmacokinetic changes that compromise the effectiveness of antimicrobials at conventional doses. Furthermore, its association with comorbidities such as type 2 diabetes mellitus impairs the immune response, increasing the risk of severe infections and the need for intensive care unit admissions.

Objective: To develop a digital calculator for dose adjustment of antimicrobials in obese patients, promoting rational and safe use of these drugs.

Methods: A literature review from the last 10 years was carried out in the UptoDate, Sanford Guide, and PubMed databases, aiming to identify studies addressing dose adjustment of antibiotics, antivirals, antifungals, and antituberculosis agents in obese adults. Fourteen articles were selected for detailed analysis. Discrepancies in antimicrobial adjustment data were resolved by technical consensus between clinical pharmacists and infectious disease specialists from the Hospital Infection Control Service. The extracted data were then incorporated into a digital platform supported by artificial intelligence for the creation of the calculator to be used in a quaternary private hospital in São Paulo.