

**TITLE:** BIOPROSPECTION FOR ANTIBIOTIC RESISTANCE IN STRAINS OF *Vibrio* AND *Shewanella* ISOLATED FROM MARINE SPONGES

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**ABSTRACT:**

Antibiotic resistance is a global public health problem. The *qnr* and *bla*<sub>OXA-48</sub> genes encode resistance mediators to quinolones and carbapenems, respectively, and were been detected in the chromosome of *Shewanella* strains. Genes encoding similar Qnr proteins were detected in strains of *Vibrio*. Both genera are Gram-negative bacilli, found in marine environments and are often isolated from marine sponges. Because they are filter feeders, marine sponges can accumulate environmental contaminants such as antibiotics, which might induce the selection of associated bacteria expressing determinants of resistance to these substances. Thereby, strains carrying genes conferring resistance to antibiotics specially in mobile genetic elements, might transfer these genes to pathogenic bacteria, thus underlining the importance of resistance encountered in bacteria associated with marine sponges. The aims of the present study were to determine the susceptibility profile to antibiotics (SPA) and to verify the presence of antibiotic resistance genes in strains of *Vibrio* and *Shewanella* isolated from marine sponges collected in Cabo Frio, Brazil and Marseille, France. Previously, a total of 108 strains, 69 *Vibrio* sp. and 39 *Shewanella* sp., were isolated and identified by *rrs* gene sequencing. SPA determination was done using the Kirby-Bauer antimicrobial disk diffusion procedure on Mueller Hinton Agar plates. Preliminary results were obtained for 41 strains (23 *Vibrio* sp. and 18 *Shewanella* sp.). These strains were tested for 21 different antibiotics. Twenty-one strains (51.2%, 11 *Vibrio* sp. and 10 *Shewanella* sp.), showed concomitant resistance to cefepime, aztreonam and ceftazidime. Interestingly, one *Shewanella* sp. was multiresistant (to  $\beta$ -lactams, aminoglycosides and quinolones). Overall, 25 (60.9%) strains were resistant to aztreonam; 24 (58.5%) to ceftazidime; 21 (51.2%) to cefepime; 9 (21.9%) to nalidixic acid; 7 (17.0%) to erythromycin; 7 (17.0%) to cefoxitin; one (2.4%) to cephalixin; one (2.4%) to tobramycin, amikacin and gentamycin; and one (2.4%) to ciprofloxacin and ofloxacin. Only 5 (12.2%) strains were sensitive to all antibiotics tested. In the future, we will use PCR to detect antibiotic resistance genes and perform plasmid profile analysis of *Vibrio* and *Shewanella* strains. We expect to contribute to the understanding of the roles of so-called native resistance genes in natural microbial communities.

**Keywords:** antibiotic resistance, *Vibrio*, *Shewanella*, marine sponges

**Financial support:** FAPERJ, CNPq and Capes.