

Identification and antibiotic resistance profiling of marine bacteria with relevance to wastewater contamination from deep-sea samples

Vanessa Silva¹⁻⁴, Bruno Tavares⁵, José Eduardo Pereira^{6,7}, Luís Maltez^{6,7}, Carmen Torres⁸,
Carmen Gonzalez⁸, Gilberto Igrejas¹⁻³, Patricia Poeta^{1,4,6,7}

¹LAQV-REQUIMTE, Department of Chemistry, NOVA School of Science and Technology, Universidade Nova de Lisboa, Caparica, Portugal

²Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal.

³Functional Genomics and Proteomics Unit, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal

⁴Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal.

⁵Clínica Veterinária da Boa Nova, Leça da Palmeira, Porto, Portugal.

⁶Associate Laboratory for Animal and Veterinary Sciences (AL4Animals), Portugal

⁷CECAV – Veterinary and Animal Research Centre, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal

⁸Area of Biochemistry and Molecular Biology, OneHealth-UR Research Group, University of La Rioja, Logroño, Spain

Marine environments, particularly in areas impacted by human activity, act as reservoirs for diverse microbial communities, including bacteria that may harbor antibiotic resistance genes. The potential contamination of marine ecosystems by wastewater effluents raises concerns about the dissemination of antibiotic-resistant bacteria. This study investigates the isolation, identification, and antibiotic resistance profiling of bacteria from deep-sea samples collected near Sesimbra, Portugal, emphasizing the implications for wastewater contamination and public health risks.

Fifteen samples were collected from two deep-sea dives off the coast of Sesimbra, including samples from algae, water, sediment, sea cucumber aspirate, sea cucumber feces, sea cucumber tentacles, and sea urchin swabs. The bacteria were isolated using general, selective, and differential media, identified through MALDI-TOF mass spectrometry, and tested for antibiotic resistance, focusing on potentially pathogenic strains, particularly those listed as priority pathogens by the WHO.

A total of 28 bacterial strains were isolated, including *Bacillus* spp., *Enterobacter cloacae*, *Enterococcus faecalis*, *Vibrio alginolyticus*, *Escherichia coli*, *Vibrio mytili*, *Rothia mucilaginosa*, and *Proteus mirabilis*. Antibiotic susceptibility testing revealed the presence of resistant strains, including *Enterococcus faecalis* showing resistance to quinupristin-dalfopristin and *Enterobacter cloacae* resistant to ceftazidime and amoxicillin-clavulanic acid. Three *Escherichia coli* strains from sea cucumber samples exhibited multidrug resistance, including resistance to ampicillin, ciprofloxacin, tetracycline, and chloramphenicol.

The presence of antibiotic-resistant bacteria in deep-sea environments, potentially influenced by wastewater contamination, highlights the critical need for surveillance of microbial diversity and resistance patterns in marine ecosystems. These findings emphasize the importance of monitoring marine environments for the spread of clinically significant antibiotic resistance, particularly in areas affected by wastewater discharge.

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