Clams as animal sentinels in a One Health approach to antimicrobial resistance in coastal environments

Alisson Godino Sanchez*†[1,2,3], Michèle Gourmelon*‡[2], Sabine Delannoy[4], Patrick Fach[4], Mélody Lebrun[1], Alexandre Mrozinski[2], Joelle Serghine[2], Matthieu Waeles[1], Stephanie Madec*[1], Cyril Noel*§[5], and Gwenaelle Le Blay*[1]

[1]Laboratoire des Sciences de l'Environnement Marin (LEMAR) – Institut de Recherche pour le Développement, Institut français de Recherche pour l'Exploitation de la Mer, Université de Brest, Institut Universitaire Europeen de la Mer, Centre National de la Recherche Scientifique – France

[2]Unité Dynamiques des Écosystèmes Côtiers – Institut français de Recherche pour l'Exploitation de la Mer – France

[3]Institut Français de Recherche pour l'Exploitation de la Mer – PDG-ISR-SEBIMER – France

[4]Laboratoire de sécurité des aliments, sites de Maisons-Alfort et de Boulogne-sur-Mer – Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail – France

[5]Ifremer – Institut Français de Recherche pour l'Exploitation de la Mer (IFREMER), Institut Français de Recherche pour l'Exploitation de la MER - IFREMER – France

Résumé

The spread of antimicrobial resistance between animals and humans is well-known; however, the role of Manilla clams remains less explored. Sediments and estuarine waters can be polluted by faecal bacteria carrying antibiotic-resistance genes (ARGs), and/or by chemicals (heavy metals, biocides). Due to their high filtration capacity, clams can accumulate bacteria, ARGs, and pollutants. This 18-month study investigated the microbiome, resistome, and environmental factors driving the spread of ARGs in coastal areas to better understand their prevalence and dynamics in clams from the Bay of Brest. The presence of ARGs and bacterial community composition were investigated using high-throughput microfluidic qPCR and 16S rDNA sequencing. Environmental parameters (rainfall, temperature, salinity...) and pollutants were also studied. Finally, correlations between ARGs, bacterial diversity and environmental factors and faecal contamination were analysed. Fifteen ARGs, conferring resistance to aminoglycosides, β-lactams, tetracyclines, sulfonamides, polymixin, macrolides and integron were sporadically detected in clams. These ARGs were found more frequently in waters and sediments with significant correlations to environmental and chemical factors. Bacterial community analysis revealed that 24.1% of genera were shared between clams, waters, and sediments, accounting for 75% of total bacterial abundance. Notably, Arcobacter, a ubiquitous pathogen-associated taxon, showed significant correlations (Pearson's $r > 0.8$) with several ARGs. It was detected in clams, river, and estuarine waters and its abundance increased after rainfall and correlated significantly with the agricultural pollutant metolachlor ($p < 0.01$). These findings highlight clams as key bioindicators and potential vectors of antibiotic resistance in estuarine ecosystems, emphasising the environmental dimension of the One Health challenge.

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[*] Intervenant

[†] Auteur correspondant: alisson.godinosanchez@univ-brest.fr

[‡] Auteur correspondant: Michele.Gourmelon@ifremer.fr

[§] Auteur correspondant: cyril.noel@ifremer.fr

Mots-Clés: clams, sentinel, pollution, antibiotic resistance, one health