



ORIGIN, FATE, AND EFFECTS OF CHEMICAL AND MICROBIOLOGICAL CONTAMINATION IN AQUACULTURE PRACTICES: IMPLICATIONS FOR HUMAN AND ENVIRONMENTAL HEALTH

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The widespread environmental dispersion of pharmaceuticals and the rise of antibiotic-resistant microorganisms have been pressing concerns for human and environmental health. Despite extensive research, the full impact of various pollution sources remains unclear, particularly the role of aquaculture practices. While representing a fundamental food source for the world population with a constant production growth of 6% per year since 2001, aquaculture is a highly complex and dynamic productive system, variably influenced by environmental, biological, cultural, and socio-economic factors (Brunton et al., 2019). The current practices retain the use of antibiotics to treat or prevent fish diseases, but also promote the development of resistance strategies in many potentially harmful bacterial populations, including human and fish pathogens. Furthermore, continuous exposure to antibiotics have direct detrimental consequences on aquatic biodiversity and local ecosystem services. Finally, aquaculture systems may act as either sources or sinks of chemical and microbiological contaminants, which can circulate among humans, animals, and the environment (Watts et al., 2017).

My PhD project proposal aims to explore the fate and consequences of antibiotics retrieved at aquaculture settings, including mariculture, Recirculating Aquaculture Systems (RAS) and Integrated multi-trophic aquaculture (IMTA). Through the collaboration between the Water Research Institute (IRSA) and the Laboratory of Experimental Ecology and Aquaculture (LESA) of the University of Rome Tor Vergata, particular attention will be paid to the identification of antibiotics, the expression of resistance genes, the occurrence of potential pathogenic microorganisms, and changes in the structural and functional composition of the aquatic microbial community. The project plan will lead to the identification and characterization of contamination levels in the environmental matrices relevant in classic aquaculture (e.g. water, farmed fish, feed, sediments) and in RAS (e.g. water, farmed specimens, organisms of different trophic levels). Three lines of research will be carried out: (1) the identification and quantification of antibiotic residues, using both consolidated and innovative early warning techniques; (2) the analysis of microbial diversity and possible variations in the expression of antibiotic resistance genes; and (3) the analysis of the physiological responses of the microbial community following exposure to antibiotics. Overall, the project is expected to significantly contribute to our understanding of the complex issue of antibiotic pollution in aquaculture and to the development of sustainable aquaculture practices that protect the environment and human health.



References

Brunton, L. A., Desbois, A. P., Garza, M., Wieland, B., Mohan, C. V., Häslér, B. & Guitian, J. (2019). Identifying hotspots for antibiotic resistance emergence and selection, and elucidating pathways to human exposure: Application of a systems-thinking approach to aquaculture systems. *Science of the total environment*, 687, 1344-1356.

Watts, Joy E. M., Harold J. Schreier, Lauma Lanska, and Michelle S. Hale. 2017. "The Rising Tide of Antimicrobial Resistance in Aquaculture: Sources, Sinks and Solutions" *Marine Drugs* 15, no. 6: 158. <https://doi.org/10.3390/md15060158>

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