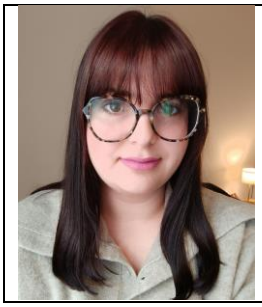	**Ioanna Gkoni (2024-2027)**
	Incidence of pharmaceuticals and microbial coalescence on sediment microbial communities and the occurrence of antimicrobial resistances and bacterial pathogens
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	Doctoral School E2M2: Evolution Ecosystems Microbiology Modeling

INTRODUCTION

The environmental prevalence of antimicrobial resistance (AMR) and pathogens is recognized as one of the foremost public health concerns of the 21st century. Evidence is emerging that chemical pollutants, and especially antibiotic pharmaceuticals, drive AMR development in environmental microbial communities, with risks for the subsequent transfer of resistance factors to animal and human pathogens [1]. Indeed, a growing body of research demonstrates that antibiotic concentrations able to select for AMR include concentrations frequently detected in various ecosystems [2].

River sediments are known to be environmental reservoirs of AMR and pathogens [3]. Effluents from domestic and hospital origins are identified as main sources of these biological contaminants, contributing to their dissemination and implementation in the benthic microbial communities of the receiving river ecosystems [4]. However, it has also been shown that small rivers, especially headwater streams, are strongly influenced by their interactions with their surrounding terrestrial environment. Such interactions include biological transfers from soil to aquatic compartments due to erosion and runoff events [5]. The entry of microorganisms of terrestrial origin into stream ecosystems thus results in community coalescence processes, which correspond to the mixing of initially distinct microbial communities and their respective initial environments [6]. Studies dealing with microbial coalescence along the soil-sediment continuum in freshwater environments are still rare [17], and, to the best of our knowledge, none of them has addressed the question of its influence on the establishment and development of AMR and pathogens in river sediment.

MAIN OBJECTIVES AND HYPOTHESES

In the context described above, the ***main objectives*** of the PhD project are to assess:

1. the resistance and resilience of riverbed native microbial communities exposed to mixed anthropogenic pressures leading to contamination by PhACs and exogenous soil bacteria;

2. the ability of exogenous soil bacteria including pathogens and antimicrobial-resistant bacteria to get established among native sediment bacterial communities exposed to PhACs.

Various ***hypotheses*** could be tested throughout this project, including the ones below:

1. Increasing levels of exposure to antibiotics enhance the implementation of antibiotic resistant pathogens from soil in the exposed sediment (due to an increase in their fitness);

2. Decreasing microbial diversity in the sediment enhance the implementation of antibiotic resistant pathogens from soil (due to decrease in microbial competition);

3. Increasing abundance of antibiotic resistant pathogens in the soil enhance their implementation in the sediment;

4. The implementation of antibiotic resistant microorganisms from soil contributes to the increase of sediment community tolerance to antibiotics.

EXPERIMENTAL STRATEGIES AND METHODS

To reach the objectives, laboratory experimentations will be carried out using microcosms that will allow testing various exposure scenarios of sediment microbial communities to a panel of pharmaceuticals and exogenous soil microbial communities.

Microbial responses of sediment communities will be assessed in terms of bacterial diversity (16S rRNA gene sequencing), functional traits (microbial activities measurement), resistance (screening of AMR genes through qPCR and shotgun metagenomics) and tolerance (pollution induced community tolerance - PICT- measurement) to selected pharmaceuticals (including sulfonamide and quinolone antibiotics). A special attention will be given to pathogens using microbial source tracking (MST) and quantification of pathogen-related genes through digital droplet PCR (ddPCR) or qPCR. Advanced chemical analyses will be performed to establish links between the observed microbial responses and the exposure scenarios. These, hand in hand with bioinformatics and biostatistics analyses, will make possible assessing correlations and the inference of associated causal relations.

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PHARM - ERA

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