

multi-Risk sciEnce for resilienT commUnities undeR a changiNgclimate

Codice progetto MUR: **PE00000005** – F83C22001660002



Deliverable title: Report on antimicrobial resistance

Deliverable ID: DV 4.3.9 (preliminary report)

Due date: 29th February 2024

Submission date: 29th February 2024

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1. Technical references

Project Acronym	RETURN
Project Title	multi-Risk sciEnce for resilienT commUnities undeR a changiNg climate
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Project Duration	December 2022 – November 2025 (36 months)

Deliverable No.	DV 4.3.9 (preliminary report)
Dissemination level*	CO
Work Package	WP3 – Enhancing capability to observe, model, and assess environmental hazards
Task	T3.5 – Pathogens and biological invasion
Lead beneficiary	OGS
Contributing beneficiary/ies	OGS, PoliMI

* PU = Public

PP = Restricted to other programme participants (including the Commission Services)

RE = Restricted to a group specified by the consortium (including the Commission Services)

CO = Confidential, only for members of the consortium (including the Commission Services)

Document history

Version	Date	Lead contributor	Description
0.1	26.02.2024	OGS: Viviana Fonti; Gianpaolo Zampicinini; Federica Relitti; Celia Laurant; Ginevra Rosati; Donata Canu PoliMI: Manuela Antonelli; Beatrice; Cantoni; Luca Penserini	First draft
0.2	28.02.2024	Viviana Fonti (OGS, task leader), Manuela Antonelli (PoliMi, WP leader), Beatrice Cantoni (PoliMi)	Critical review and proofreading
0.3	29.02.2024	Viviana Fonti (OGS, task leader), Manuela Antonelli (PoliMi, WP leader)	Edits for approval
1.0	29.02.2024	Viviana Fonti (OGS, task leader)	Final version

2. ABSTRACT

Antimicrobial resistance (AMR) has emerged as a global problem, making the treatment of infectious diseases increasingly difficult and costly. Water-borne microbial taxa (including wastewater-borne ones) are linked to diseases in humans and to infections and mass mortalities of ecologically and economically important species. Natural aquatic environments, acting as both a receptor and then a source of transmission, are now widely recognized as playing a pivotal role in the propagation and dissemination of AMR and opportunistic pathogenic bacteria. Similarly, antibiotic resistance genes (ARGs) can persist in the effluents of Wastewater Treatment Plants (WWTPs) and being then carried in the environment by discharge into receiving water bodies or by reuse for agricultural purposes.

Despite an increasing research effort, there are still several knowledge gaps, including a need for a more comprehensive understanding of environmental dissemination pathways and of the role played by natural microbial communities in either promoting or hindering the establishment of ARGs and pathogenic elements in natural settings.

Molecular techniques, especially next-generation sequencing (NGS) of bulk DNA in environmental samples (metagenomics) can provide a comprehensive view of natural microbial communities and of the genetic material exchanges with and within the environment. This study aims to assess the presence, prevalence, and distribution of microbial pollutants using metagenomic approaches.

The Gulf of Trieste is currently under investigation for the assessment of the presence, prevalence and distribution of microbial pollutants in marine coastal ecosystems. The results of this study will be also investigated considering the environmental variables (such as the fluxes of organic materials and their terrigenous origins) and the Gulf circulation, with the final scope of improving our understanding of the ecological processes involved in the spread and distribution of microbial pollution in coastal marine environments.

The effluent of a WWTP located in the North of Italy and its receiving water body are focusing on microbial pollutants fate and behavior in a reclaimed water reuse system.

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