EDAR8
Environmental Dimensions of Antimicrobial Resistance
Brisbane, 2-7 August 2026

WORKSHOP OVERVIEW

Workshop Title	Novel, quantitative methods in AMR research and surveillance
Facilitators and contributors Details of the individuals leading and contributing to the workshop, including: • Workshop facilitators • Guest speakers or contributors • Their roles in the session	David Kneis 1 Magali de la Cruz Barron 1 Thomas Berendonk 1 Sefi Vernick 2 Antti Karkman 3 1 TU Dresden, Institute of Hydrobiology, Germany 2 Agricultural Research Organization, Israel 3 University of Helsinki, Department of Microbiology, Finland
Background An overview of the context and rationale for the workshop, outlining the key issue, challenge, or opportunity it addresses, and why this topic is timely and relevant.	Studying AMR in environmental samples in a comprehensive manner necessarily relies on the analysis of metagenomic DNA. Traditionally, analysis was restricted to the quantification of few genetic markers but opportunities for multiplexing have improved substantially and the focus is shifting towards gene context analysis. Besides that, technological innovations allow for new application scenarios. Selecting the appropriate approach to AMR quantification in a given context remains challenging as it requires unbiased information about a methods' specific pros and cons.
Workshop Aims A description of the purpose of the workshop and its intended focus. This section highlights what participants can expect to explore, learn, or develop during the session.	The workshop aims to inform participants about novel trends and experiences in marker quantification and gene context analysis. Specifically, the participants will: • Learn about electrochemical sensors for the specific quantification of marker sequences • Understand the pros and cons of ddPCR and qPCR in environmental applications • Become familiar with contrasting approaches to gene context identification: multiplex ddPCR and long-read sequencing
Participant Takeaways A summary of what participants will gain from attending the workshop. This may include new knowledge, practical skills, tools, frameworks, or shared resources, as well as any tangible outputs (e.g. ideas, draft materials, or collaborative outcomes).	Participants will: • understand the fundamental concepts behind the contrasting technologies for analyzing metagenomic DNA • be able to select the most appropriate method for a specific use case in view of theoretical and practical strength and weaknesses • learn about anticipated future use cases Besides that, participants are invited to contribute to methodological advancement through: • proposing benchmarks • suggesting applications in their specific fields • initiating collaborative development and grant writing
Expected Impact An outline of the broader value of the workshop, including how it may: • Influence research, policy, or practice • Support collaboration and knowledge exchange • Contribute to future work or ongoing initiatives	The workshop will enable users to choose and apply the most appropriate technology in their particular context with realistic expectations regarding sensitivity and specificity. Participants will spread the gained knowledge further into the community. The novel approaches to metagenomic DNA analysis are expected to benefit both AMR surveillance and research and allow for new insights into AMR dynamics in the environment. In particular, the application of electrochemical

	sensors can facilitate AMR surveillance in low resource settings where other technology is unavailable or unaffordable. The discussed approaches to gene context analysis will help direct the focus of AMR surveillance to the actual primary hazards, namely multiple resistance and resistance mobility.
Who should attend? Information on the intended audience for the workshop, including: • Relevant backgrounds, sectors, or expertise • The level of participation expected (e.g. discussion, group work, problem-solving)	Participants should have an interest and/or background in the culture-independent quantification of AMR in environmental samples. Ideally, the group of participants comprises technology users but also developers to reflect their respective views in the discussion.
Workshop Schedule and Duration A summary of the structure and flow of the workshop, including: • Key session components • Interactive or breakout activities	The 90 minute workshop is split into two thematic sessions. The first session addresses marker quantification, the second one focuses on gene context identification. Each session is opened with two presentations about contrasting methods followed by a topical discussion.