



EDAR8

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

DRAFT Presentations Program

EDAR8 Monday 3 August

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Time	Title	Speaker	Country
10:30am - 11:30am	S1.1 OPENING CEREMONY > EDAR8 Co-Chairs Official Opening > Welcome to Country > Opening Address > One Health, or Many Relationships? > From Science to Action: Strengthening Environmental Dimensions in the One Health Response to Antimicrobial Resistance > Progressing One Health AMR in Australia > Looking Past the Patient: Critical Role for One Health integration in Infectious Disease Surveillance & Outbreaks	Erica Donner & Ed Topp Tribal Experiences The Hon. Karlene Maywald Veronica Matthews Inger Anderson	Australia, France Australia Australia Australia Multinational
11:30am - 1:00pm	S1.2 PLENARY SESSION: The need for action and the nature of the challenge > Global AMR in 2026 - an infectious diseases perspective > Control of antimicrobial resistance in agrifood systems: The gen(i)e is out of the bottle > A European perspective on antimicrobial resistance in the food chain: Integrating monitoring and risk assessment for regulatory science > SmartChip biosecurity platform for One Health surveillance of AMR > The hidden resistome at the plant-soil interface: How mobile genes and co-selection challenge AMR surveillance	Norelle Sherry Jeffrey Lejeune Ernesto Liebana Windi Muziasari Sasha Tetu	Australia Italy Italy Finland Australia
1:00pm - 2:00pm	LUNCH		
2:00pm - 4:00pm	S1.3 PLENARY SESSION: Environmental AMR frontiers > A One Health framework for global and local stewardship across the antimicrobial lifecycle > Antimicrobial resistance across the hydrologic cycle: Research needed to reduce AMR evolution, transmission and spread in the environment > Turning the tide: Reducing antibiotic resistance in aquatic food systems > Operationalizing One Health for AMR control: A tiered framework to strengthen environmental sector engagement in the Philippines > A One Health perspective on controlling fungal diseases and AMR	Sabiha Essack David Graham Andrew Barnes Geminn Louis Apostol Bart Fraaije	South Africa United Kingdom Australia Philippines The Netherlands

Time	Title	Speaker	Country
9:00am - 10:30am	S2.1 PLENARY SESSION: From One Health impetus to action (Translating OH AMR policy into action) > Antimicrobial resistance: Ecology, evolution and environmental risk assessment > EU-JAMRAI 2: Creating a Community of Practice to address the environmental dimension of antimicrobial resistance across the EU > EU JAMRAI 2: Determining priority core elements for environmental AMR surveillance in Europe > 10 years of experience with wastewater surveillance of antibiotic resistance in The Netherlands	Aimee Murray Ane Laburu-Dañobeitia Roosmarijn Luiken Heike Schmitt	United Kingdom Spain The Netherlands The Netherlands
11:00am - 1:00pm	S2.2A CONCURRENT SESSION: Wastewater (One Health) surveillance and AMR > City-scale shotgun metagenomic surveillance of antimicrobial resistance across a sewage network including urban, hospital, and airport wastewater in Larnaca, Cyprus > Is surface water a good proxy for phenotypic antimicrobial resistance in healthcare facilities and informal settlement residents in developing countries? > Effect of urbanization on antimicrobial resistance genes carried by human populations - metagenomic analysis of an international transect of wastewaters > Retrospective wastewater surveillance reveals COVID-19 pandemic-driven shifts in community-level AMR profiles in Japan > Disentangling signal contributions from hospital biofilms to wastewater-based surveillance of antimicrobial resistance > Comprehensive evaluation in Africa and Europe supports wastewater monitoring for assessing antibiotic resistance prevalence in clinical isolates > Wastewater analysis to identify associations between chemical, demographic and socioeconomic drivers of antimicrobial resistance > Longitudinal wastewater-based surveillance reveals increased antimicrobial resistance in shelters for unhoused individuals relative to general populations > From burden to dynamics: allele-resolved wastewater surveillance reveals hidden AMR structure > Wastewater surveillance reveals insights into antibiotic resistance across the United States	Andrea Naziri Luther King Abia Akebe Peter Vikesland Miaomiao Liu Amanda Darling Carl-Fredrik Flach Jake O'Brien Shaelyn Xu Tristan Nolan Sooyeol Kim	Cyprus South Africa USA Japan USA Sweden Australia Canada Australia USA
11:00am - 1:00pm	S2.2B CONCURRENT SESSION: Environmental drivers, transmission and impacts of AMR in food production systems > The global surface water resistome in transition: sources, risks and drivers > The SeaBOS Keystone project on AMR: A quantitative resistance gene monitoring program for aquaculture systems > Mussels as natural biofilters: Experimental and shotgun metagenomic analysis of extracellular DNA-mediated accumulation of antimicrobial resistance from the marine environment > Quantitative modelling and qualitative traits of the allochthonous enteric microbiome, resistome and mobilome during manure fertilization of agricultural soils > Plasmid-mediated antibiotic resistance in flooded and non-flooded agricultural soils > Influence of agricultural intensification on microbial communities, resistomes, and mobilomes across 5000 years of Finnish agricultural history > Quantitative assessment of selective pressure driving antimicrobial resistance in dairy farm environments > A novel risk assessment framework to address antimicrobial resistance in the Australian vegetable supply chain > Phenotypic and genomic analysis of antibiotic resistance in pathogenic <i>Enterobacteriaceae</i> isolates from leafy vegetables > Honeybees as xenosurveillance agents for antimicrobial resistance sampling in agricultural environments	Xun Qian Oskar Nyberg Stefano Dalle Palle Marios I. Valmas Eva Kilcoyne Minna Maunula Arianna Peruzzo Barbara Drigo Min Qiao Anel Toledo Nauto	China Sweden Italy Greece Ireland Finland Italy Australia China USA

Time	Title	Speaker	Country
11:00am - 1:00pm	S2.2C CONCURRENT SESSION: From environmental AMR data to decisions > An introduction to regulatory science for effective environmental risk assessment > Advancing regulatory-ready microbial endpoints for AMR risk assessment of chemicals under Australian and New Zealand water quality guideline frameworks > Bayesian modelling to support water utilities in managing antimicrobial resistance risks > Infrastructures to monitor future AMR threats > When methods disagree: Evaluating concordance among environmental AMR monitoring approaches > A unified framework for antimicrobial resistance evidence integration > Extending the scope of environmental risk assessment to antimicrobial resistance in the general pharmaceutical legislation in the European Union > Panel discussion: Regulatory science for environmental risk assessment	Nicholas Ashbolt Monique Binet & Tony Bigwood Claire Hayward Johan Bengtsson-Palme Marcus Wenne Cai Chen Andreas Häner Ludovic Bernadaut, Rick van Dam, Andreas Häner, Joakim Larsson	Australia Australia Australia Sweden Sweden China Switzerland Multinational

Time	Title	Speaker	Country
9:00am - 10:30am	S3.1 PLENARY SESSION: Environmental AMR hotspots, reservoirs, transmission and exposure pathways > Antimicrobial resistance in soil-plant systems > Microbial resilience vs. AMR persistence: Elucidating the outcomes of wastewater-soil coalescence > Environmental dissemination and mitigation of antibiotic resistance genes in Brazilian aquatic systems: Insights from the Pantanal wetland and arsenic-impacted tropical streams > The great plastisphere reef: Microplastics as a novel niche for antimicrobial resistant pathogens > Tracking plasmid-mediated antibiotic resistance from hospitals to wastewater via plasmid systems	Yong-Guan Zhu Eddie Cytryn Juliana Calabria de Araújo Emily Stevenson Meghana Srinivas	China Israel Brazil United Kingdom Ireland
11:00am - 1:00pm	S3.2A CONCURRENT SESSION: Ecology and biology of Environmental AMR > When anthropogenic and river microbiomes collide: Who wins, who loses, what drives the spread of antimicrobial resistance? > Predicting the environmental persistence of invading antibiotic-resistant bacteria in freshwater biofilms > Antiviral defense systems drive persistence but limit the transfer of antimicrobial resistance genes in anaerobic digestion > Identification of metabolic niches and their association with the persistence of antibiotic-resistant bacteria in wastewater > Conjugation dynamics of wastewater-derived multidrug-resistant <i>Escherichia coli</i> reveal an overlooked dimension of AMR risk > H₂S drives the dissemination of plasmid-borne antibiotic resistance genes via the hijacking of intracellular glutamine > How metals and microplastics contribute to AMR in refugee camps and conflict settings: From molecular mechanisms to policy implications > Redox oscillation frequency regulates the evolutionary mode of antibiotic resistance via transcription-coupled repair > Characterisation of bacterial vesicle-mediated extended spectrum β-lactamase plasmid transfer and implications for AMR dissemination in reclaimed water > Ecological differentiation and transfer potential of IncP/P-1 plasmid subgroups	Christophe Merlin Uli Klümper Junya Zhang Orestis Kanaris Kseniia Erokhina Haining Huang Muhammad Zaman Naresh Singhal Stavri Karasiali Maho Tokuda	France Germany China Germany Israel China USA New Zealand Cyprus Japan
11:00am - 1:00pm	S3.2B CONCURRENT SESSION: Environmental AMR, wildlife and animal health > One Health and AMR - Why wildlife matter > Antimicrobial-Resistant Bacteria in Wild Raptors Across Europe > Global health risks lurking in livestock resistomes > Assessing the effectiveness of regulative interventions on AMR reduction in dairies > Genetic differences and plasmid-mediated antibiotic resistance in persistent Staphylococcal intramammary infections of dairy cows over the dry period > Strengthening environmental AMR surveillance in food animal production systems: Development of operational guidelines for national programs > Deciphering the formation dynamics and transmission driving mechanisms of antibiotic resistance in animal farming environments > Discontinuity between AMR in clinical populations and local wildlife: Insights from the <i>Enterobacteriaceae</i> > Anthropogenic land use exerts selection pressures on the resistome of a wild rodent	Michelle Power Monika Dolejska Xun Qian Sunny Jiang Jennifer Ronholm Roosmarijn Luiken Bing Li Bethany Hoye V́ctor Hugo Jarquín-Díaz	Australia Czech Republic China USA Canada The Netherlands China Australia Germany

Time	Title	Speaker	Country
11:00am - 1:00pm	S3.2C CONCURRENT SESSION: Understanding AMR in the water cycle		
	> Fate of clinically relevant antibiotic resistant gram negative bacteria from sewershed to watershed and comparison with regional clinical isolates	Thomas Byrne	USA
	> Gene-level insights into antimicrobial resistance distribution and machine-learning modeling in tropical Coastal waters	Zhixin Xiang	Singapore
	> Antimicrobial resistance and coliform bloom dynamics in a drinking water reservoir	Gabriel Mesole	USA
	> The U.S. wastewater resistome: Seasonal, regional, and treatment dynamics	Tala Navab-Daneshmand	USA
	> Spatial and temporal dynamics of antimicrobial resistant bacteria in a tertiary wastewater treatment plant using composite and passive sampling methods	Sarah Payne	Canada
	> Surveillance of antibiotic resistance genes in the phage fraction and phage-mediated transduction in wastewater and river ecosystems	Silvia Monteiro	Portugal
	> Sewer biofilms as persistent environmental reservoirs of antimicrobial resistance	Ishi Keenum	USA
	> Deciphering antimicrobial resistance mobilised in the aquatic plastisphere	Shu-le Li	China
	> Chlorine disinfection drives evolutionary dynamics of antibiotic resistance in waterborne pathogens	Zhigang Yu	Australia
	> Recycled water as an environmental interface for antimicrobial resistance: Genomic hazard profiling of <i>Escherichia coli</i>	Mika Dewi	Australia
	> The impact of climate change on antimicrobial resistance	Cara Patel	UK
	> Long-term plasmid–host coevolution modulates the persistence and conjugative spread of multidrug resistance plasmids	Yuanyuan Kang	Australia

Time	Title	Speaker	Country
9:00am - 10:30am	S4.1A CONCURRENT SESSION: AMR omics, informatics, and advanced analytics > Can we predict the transfer routes of mobile antibiotic resistance genes? > New sequence barcode system allows tracking horizontal gene transfer from multiple origins simultaneously > Quantitative metagenomic sequencing using whole-cell spikes for environmental resistome analysis > MobiGLM: An augmented genomic language model enabling mobility-tiered risk stratification for antibiotic resistance genes in environmental surveillance > Antibiotic resistance gene carriers in complex wastewater communities revealed by a novel methylation-based approach > Multimodal machine learning prediction of chemical synergy and antagonism for environmental antimicrobial resistance risk assessment > ARGContextProfiler: Extracting and scoring the genomic contexts of antibiotic resistance genes using assembly graphs	Erik Kristiansson Marko Virta Madeline Deck Changzhi Wang Antti Karkman Ji Lu Liqing Zhang	Sweden Finland Switzerland Saudi Arabia Finland Australia USA
9:00am - 10:30am	S4.1B CONCURRENT SESSION: One Water, One Health and AMR > Wastewater biological treatment levers to control antibiotic resistance at full scale > Does recreational inland water exposure increase the risk of faecal carriage of antimicrobial resistant bacteria? > Flux balance identifies post-denitrification units as reservoir and secondary source of beta-lactam resistance genes in wastewater treatment plants > Eukaryotic predation drives the dissipation of microbial and antibiotic resistance loads during effluent storage > Revealing keystone bacteria in the One Health network: a data-driven insight into antibiotic resistance spread > Antimicrobial resistance awareness and One Health understanding among dental students in Quebec	Celia Manaia William Gaze Zhiguo Su Liguan Li Marina Andreu Pazos Belinda Nicolau	Portugal UK Denmark China France Canada
11:00am - 1:00pm	S4.2A CONCURRENT SESSION: Environmental engineering, diagnostics and devices > Antimicrobial resistome dynamics during wastewater treatment > Evaluating advanced WWTP techniques for antibiotic resistance removal: A full-scale study > From lab to farm: Plasma-activated water as a chemical-free egg washing technology for AMR mitigation > Rapid quantification of multiple resistance and resistance mobility in environmental samples > Evaluation of UV-C and UV/H₂O₂ tertiary treatments for controlling bacterial vesicle-mediated horizontal gene transfer > A field-deployable recombinase polymerase amplification (RPA) - CRISPR lateral flow diagnostic platform for on-site AMR monitoring > Evaluation of a low-cost active air sampler for capturing airborne antibiotic resistance genes: A wastewater treatment plant case study > Removal of intracellular and extracellular ARGs in waste stabilization ponds: Evidence from full-scale monitoring and bench-scale tests > Elevated antimicrobial resistance in <i>Escherichia coli</i> in CAFO-impacted waters in California, Michigan, and Wisconsin: Modified kits correlate with standard methods	Ryo Honda Bas Van Der Zaan Tania Veltman David Kneis Andrea Naziri Nijoy John Naixiang Zhai Iftita Rahmatika Jennifer Jay	Japan The Netherlands Australia Germany Cyprus Australia Australia Indonesia USA

Time	Title	Speaker	Country
11:00am - 1:00pm	S4.2B CONCURRENT SESSION: Advances in AMR risk assessment (incl. S4.3A prep talks)		
	> Assessing AMR risks linking next generation Quantitative Microbial Risk Assessment (QMRA) and spatial modeling in water and wastewater applications	Kerry Hamilton	USA
	> Integrating experimental conjugation, growth, and plasmid loss rates into dynamic models and risk assessment of wastewater-derived multidrug-resistant <i>E. coli</i>	Hunter Quon	USA
	> A multi-criteria framework for assessing antimicrobial resistance risks across tropical aquatic environments	Qiyi Yuan	Singapore
	> Simulating environment to community AMR transfer using a stochastic SIRS model	David Roser	Australia
	> From Determinants to Dissemination: Environmental AMR Hotspots and Transmission Vectors for integration into QMRA	Nicholas Ashbolt	Australia
	> Moderated panel discussion	Amy Pruden (moderator)	Multinational
11:00am - 1:00pm	S4.2C CONCURRENT SESSION (Emerging Topic): A One Health perspective on antifungal resistance		
	> New tools for AMR surveillance: From agriculture to One Health	Fran Lopez Ruiz	Australia
	> The link between the use of azoles in non-medical applications and the spread of azole fungicide resistance in <i>Aspergillus</i> fungi	Frank Schreiber	Germany
	> Predicting antifungal concentrations that select for resistance: An enhanced approach to establish environmental thresholds	Isobel Stanton	UK
	> Monitoring the frequency of fungicide resistant <i>Botrytis cinerea</i> in grapevine after selective removal of chemistries	Lincoln Harper	Australia
	> From field diagnostics to novel solutions for fungicide resistance	Joel Haywood	Australia
	> Coupling airborne spore trapping and molecular diagnostics to monitor fungicide resistance	Ismail Ahmed Ismail	Australia
	> Persistence and fitness costs of fungicide resistance in grapevine mildews	Cian Hoban	Australia
	> Environmental, ecological and evolutionary drivers of azole-resistant <i>Aspergillus fumigatus</i> in the UK	Rachel Payne	UK
	> Moderated panel discussion	TBA	Multinational
11:00am - 1:00pm	S4.2D CONCURRENT SESSION: One Health AMR genomics and surveillance		
	> The emergence and spread of hybrid <i>E.coli</i> pathogens and the capture of novel genetic elements that expand the repertoire of AMR	Steven Djordjevic	Australia
	> Genomic assessment of horizontal transfers of antibiotic resistance genes across bacterial taxa	Nicolas Godron	France
	> Systematic One Health <i>E. coli</i> surveillance across environmental, animal and clinical sectors	Veronica Jarocki	Australia
	> Genomic research and development initiative - a review of accomplishments of a One Health AMR program	Tim McAllister	Canada
	> Host-associated antimicrobial resistance dynamics in wastewater treatment revealed by single-cell genomics	Mardalisa	Indonesia
	> Environmental bacteria as vectors for the cross border transport of antimicrobial resistance: A multi-omics characterization	Peiying Hong	Saudi Arabia
	> EMAR Fiji: A program of deep sampling and bacterial whole-genome sequencing to understand antimicrobial resistance in Fiji	Ethan Wyrsh	Australia
	> Recycled water as an environmental interface for antimicrobial resistance: Genomic hazard profiling of <i>Escherichia coli</i>	Mika Dewi	Australia
	> Conjugative IncF, IncI, and IncB/O/K/Z plasmids in <i>Escherichia coli</i> carrying blaCTX-M-15 are widespread across European aquatic environments	Annie Justh De Neczpal	Sweden
	> A One Health surveillance system on ESBL-producing <i>Escherichia coli</i> in an agricultural watershed	Xu Li	USA
	> Taxonomic, geographic, and horizontal gene transfer assessment of clinical, environmental, animal, and food isolates expressing blaIMP-27 and blaIMP-64 carbapenemase genes	Susan Vaughn	USA

Time	Title	Speaker	Country
9:00am - 10:30am	S5.1A CONCURRENT SESSION: Environmental AMR monitoring and public health > Monitoring of antimicrobial resistant faecal indicator bacteria in urban aquatic environments > Environmental selection of AMR in healthcare wastewater: Mechanisms, mobility, and public health implications > Early childhood exposure to antimicrobial-resistant organisms: environmental exposure pathways and household-level drivers in peri-urban Malawi > Impact of environmental AMR on built environment and public health > Environmental perturbations alter mobility and risk of clinically relevant ARGs: lessons from an in vitro gut reactor > A One Health approach to antimicrobial stewardship: Lessons learned from ten years of the National Centre for Antimicrobial Stewardship > Resistome surveillance as infrastructure science: building a One Health framework for environmental antimicrobial resistance monitoring	Qiyi Yuan Rietie Venter Emma Budden Gabriele Berg Fathima Afsal Lisa Hall Ulf Dahle	Singapore Australia USA Austria Canada Australia Norway
9:00am - 10:30am	S5.1B CONCURRENT SESSION: Frontiers in environmental AMR selective pressures > Chemical mixtures and physicochemical conditions in wastewater treatment plants as non-antibiotic drivers of antimicrobial resistance > Widespread on-site selection of antibiotic-resistant <i>E. coli</i> within hospital sewers driven by ciprofloxacin and β-lactams > A new method for prioritising aquatic pollutants that may select for antimicrobial resistance, using rationale from antibiotic drug design > Like parent, like metabolite: Antibiotic transformation products exert selective pressure for antimicrobial resistance comparable to parent compounds	Diana Aga D. G. Joakim Larsson Emma Louise Rossiter Pooja Lakhey	USA Sweden UK Australia
11:00am - 12:30pm	S5.2 CLOSING PLENARY SESSION > Integrating environmental risk assessment and climate resilience to combat the environmental dimension of AMR > Parallaxic Praxis for One Health AMR: Turning Multiple Viewpoints into Collective Action > EDAR: Where have we been, where are we going? > EDAR8 ECR Excellence Awards > EDAR9 Announcement	Jason Snape Pauline Sameshima Ed Topp Former EDAR Chairs and Lisa Kirkland It's a surprise!	United Kingdom Canada France Multinational Home of EDAR9