

Let's fight antimicrobial resistance and infectious diseases together

University of Antwerp

Laboratory of Medical Microbiology Vaccine and Infectious Disease Institute



By 2050, the death toll could be a staggering one person every three seconds if AMR is not tackled now. Antimicrobial resistance (AMR) is a global health threat, causing 1.27 million deaths in 2019 alone. By 2050, annual deaths could reach 10 million. The WHO Bacterial Priority
Pathogens List highlights key resistant bacteria, including Gram-negative strains resistant to last-resort antibiotics and major pathogens like *Salmonella*, *P. aeruginosa*, *Acinetobacter, S. pneumoniae* and *S. aureus* (UN Antimicrobial report 2023, WHO 2024).



Phenotypic functional assays

Biofilm models, evolution experiments, MIC testing and more



Molecular methods & sequencing

Illumina MiSeq sequencing, MinION long-read sequencing, qPCR and more

Research line 1: How do bacterial pathogens evolve towards

Research line 2: What drives the interactions between host cells

more invasive disease?

Salmonella and E. coli are major causes of gastrointestinal and life-threatening bloodstream infections. Salmonella is a leading cause of bloodstream infections in young children in sub-Saharan Africa, with mortality rates up to 20% and over 600,000 deaths annually. E. coli is the most common cause of bloodstream infections globally, particularly in the elderly. We are examining the genetic evolution of these pathogens, their immune evasion, spread, antimicrobial resistance, and vaccine target coverage.

Read more: Van Puyvelde S., Nature Commun. 2023



and pathogens?

Functional assays using organoids and cell culture models are key to studying bacterial infections and treatment responses. *Pseudomonas aeruginosa* and *Streptococcus pneumoniae*, which can cause severe infections, will be examined using these models to understand their behavior with the host and other microbiota, and resistance mechanisms. <u>These studies aim to reveal how bacterial components interact with the host, other microbiota, antimicrobial treatments and contribute to persistent infections.</u>

Read more: Van Averbeke V, Front. Immunol., 2022; Vlaeminck J, Front. Microbiol,2022, Wheatley R, Nat. Comm, 2021





Research line 3: How does antibiotic resistance spread in the One Health context?

Globally, 300 km³ of wastewater annually, with high levels of antimicrobial resistance genes (ARGs), may spread resistance due to ecological factors. <u>We will</u> <u>screen wastewater from hospitals, urban areas, and</u> <u>farms in three countries with varying antibiotic use to</u> <u>catalogue prevalent transmissible ARGs and their</u>



Research line 4: How can we use WGS to understand bacterial population biology and emergence of antibiotic resistance?

Rising antibiotic resistance among pathogenic bacteria is a major global health issue. Whole genome sequencing (WGS) helps track and understand outbreaks of priority pathogens like *Streptococcus pneumoniae*, methicillin-resistant *Staphylococcus aureus*, extended-spectrum beta-lactamase-producing *E. coli*, and carbapenem-resistant *Klebsiella pneumoniae*. Our global collections use WGS to study serotypes, resistomes, virulomes, and mobile elements, aiming to understand bacterial transmission and resistance gene spread across humans, animals, and the environment under the One-Health approach, and to track serotype evolution within populations.



mobile elements.

Premature births, occurring in 10% of live births, often lead to NICU admissions for 8% of these infants, who are highly vulnerable to resistant bacteria. We aim to study the rates and transmission of antibiotic-resistant bacteria in European NICUs by sampling both infants and their environments, which may harbor antibiotic-resistant bacteria.



Read more: NeoIPC website, Russell NJ, Plos Med, 2023; Lin Q, Comms. Biol, 2022

Read more: Kakaraskoska-Boceska, Nat. Comm. 2024; Diaz Caballero J, Nat. Comm., 2023, Nguyen MN, Clin Microbiol Infect. 2021, Berkell M, Nature Commun. 2021

Read more about LMM and scan the QR code!

Prof. dr. Surbhi Malhotra-Kumar Surbhi.malhotra@uantwerpen.be Prof. dr. Sandra Van Puyvelde (research line 1) Sandra.vanpuyvelde@uantwerpen.be