THE GIS
SPEAKER SERIES

Genome Institute of Singapore
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Antibiotic resistance in the human gut microbiome

Prof. Willem van Schaik

Chair of Microbiology and Infection, Head of Research of the School of Infection, Inflammation and Immunology
University of Birmingham

Host: Niranjan Nagarajan

Thursday 14 August 2025
1.30pm – 2.30pm

GIS L2 – Seminar Room
60 Biopolis Street, Genome, Singapore 138672

About The Speaker

Professor Willem van Schaik studied for a PhD in microbiology under the supervision of Professor Tjakko Abee and Professor Willem de Vos at Wageningen University (the Netherlands), followed by post-doctoral studies on an EMBO Long-Term Fellowship at the Pasteur Institute (Paris, France) on the regulation of virulence gene expression of Bacillus anthracis in the laboratory of Dr Agnès Fouet. He then moved to the University Medical Center Utrecht in the Netherlands, where he worked on the comparative and functional genomics of several multi-drug resistant opportunistic pathogens, including Enterococcus faecium, Escherichia and Klebsiella pneumoniae, and the gut microbiome as a reservoir of antibiotic resistance genes.

In 2017, he moved to the University of Birmingham, where he was appointed as professor in Microbiology and Infection. In the same year, he was awarded a Royal Society Wolfson Research Merit Award. From 2020 to 2024 he was Director of the University of Birmingham's Institute of Microbiology and Infection and has been Head of Research in the School of Infection, Inflammation and Immunology since 2024.

About The Seminar

The human gut harbours a complex microbial ecosystem with hundreds of different species. The vast majority of these contribute positively to our health but the gut microbiome also contains multidrug-resistant opportunistic pathogens, like Escherichia coli and Enterococcus. In addition, commensals also frequently carry antibiotic resistance genes in their genomes and it is not clear to what extent these can be transferred to other members of the gut microbiome.

In this seminar, I will present recent, mostly unpublished, work from the group in which we used a range of genomic approaches to characterise novel microbial reservoirs of antibiotic resistance, and to quantify the role of bacteriophages in mediating horizontal gene transfer of antibiotic resistance genes in the gut microbiome.