Microbiology series; Thursday 27th of February 2025

The speaker Dr Conor Feehily:

https://www.gla.ac.uk/schools/infectionimmunity/staff/conorfeehily/#

Title: Strainspotting in the vaginal microbiome

Bio: Dr Feehily's PhD was obtained from University of Galway (NUI Galway) where he investigated the role of the glutamate decarboxylase system in stress response of Listeria monocytogenes under the supervision of Prof Conor O'Byrne. He then moved to University College Cork and APC Microbiome Ireland as a postdoctoral researcher to work with Prof Paul Cotter and Prof Paul Ross, searching for strains of Lactobacillus that could inhibit the pathogens involved in bacterial vaginosis. A subsequent funded postdoctoral fellowship saw him continue and extend this work at Teagasc and the APC and develop research into the role of the vaginal microbiome in preterm birth. He now teaches at University of Glasgow and the School of Infection and Immunity as a lecturer in Bacteriology.

Abstract: Within the vaginal microbiome, Lactobacillus species are important members that maintain health and prevent pathogen colonization. The depletion of these health-associated lactobacilli has consistently been linked to adverse gynaecologic and obstetric outcomes, including an increased risk of preterm birth (PTB). To date, much of our research in this area has relied on taxonomic surveys that compare communities at a genus and species level. While the protective role of Lactobacillus spp. is well recognized, the functional mechanisms driving strain-level variations and the impact of these on vaginal health remain underexplored. Using whole-genome sequencing and metagenomics, we recently identified strain-specific differences in the vaginal microbiome with potential implications for host-microbe interaction. Notably, we demonstrated that Lactobacillus jensenii strains isolated from vaginal swabs of preterm pregnancies were phylogenetically distinct from those isolated from full-term pregnancies. Several genetic signatures were identified that distinguished the PTB and full-term birth (FTB)-associated strains, including genes predicted to be involved in cell wall synthesis, lactate and acetate metabolism, and DNA repair. Importantly, preliminary data has confirmed that these genetic differences are reflected in functional phenotypes related to low pH survival and lactate metabolism. These findings underscore the importance of moving beyond species-level classifications to better understand how specific bacterial strains influence pregnancy outcomes and vaginal health.