

Integrating knowledge and approaches across microbiomes: From plants to humans and soil to sea

Charles Darwin House, London
19th September 2018

9:00 am: Registration opens

9:30 am: **KEYNOTE TALK: Thorunn Helgason**, University of York
TBC

10.10 am: **Alfred Burian**, University of Derby
TBC

10.25 am: **Lesley Hoyles**, Nottingham Trent University
**Pangenome and metapangenome analyses reveal the relevance of
Klebsiella michiganensis to the preterm infant gut microbiome**

10.40 am: **Antonella Succurro**, University of Cologne
TBC

10.55 am: Tea break

11.30 am: **KEYNOTE TALK: Penny Hirsch**, Rothamsted Research
Chicken and egg: relationship between crop plant and soil microbiomes

12.10 pm: **Sarah Worsley**, University of East Anglia
The chemical ecology of *Actinobacteria*-host interactions

12.25 pm: **James Doonan**, Bangor University
**The gene expression landscape of host-beetle-microbiota interactions
in a complex tree disease**

12.40 pm: Lunch

1.30 pm: **KEYNOTE TALK: Petra Louis**, The Rowett Institute, University of Aberdeen
Carbohydrate metabolism of the human intestinal microbiota

2.10 pm: **Geertje van Keulen**, Swansea University
TBC

2.25 pm: **Kelly Redeker**, University of York

TBC

2.40 pm: **KEYNOTE TALK:** Julian Marchesi, Cardiff University and Imperial College London

TBC

2.55 pm: Tea break

3.30 pm: **KEYNOTE TALK:** Matthew Ryan, Centre for Agriculture and Biosciences International (CABI)

TBC

4.10 pm: Ellen Decaestecker, KU Leuven

Host genotype and microbiome structure the environmental microbial community: a freshwater case study from Daphnia and bacterioplankton

4.25 pm: Peter Graystock, Imperial College London

Shaping microbiomes for optimum host phenotypes

4.40 pm: Final comments and end

POSTER PRESENTATIONS

4D microbial cartography: modelling the spatial, compositional and functional dynamics of a tree microbiome.

Jake M. Robinson, Harry Watkins, Martin Breed.

Archaea in agriculture: Investigating the role of ammonia oxidising archaeon Candidatus Nitrosocosmicus franklandus C13 within the root associated microbiome.

Sam Prudene, Sarah F. Worsley, Lucas Balis, Colin J. Murrell, Laura Lehtovirta-Morley, Matthew I. Hutchings.

Post-mortem translocation analysis using 16S sequencing.

Lily Gates, Neil Sebire, Nigel Klein, Dagmar Alber.

Microbiota linked to spatial distribution of the visceral leishmaniasis vector in Bihar, India

Poppy Stevens, Ian Goodhead, Rachael Antwis, Gala Garrod, Mike Coleman, Geraldine Foster.

Specific Microbial Sampling Methods Across the Female Reproductive Tract Could Alter Our Understanding of the Underlying Composition

Liisa Veerus, Shorok B Mombrikotb, Emma Ransome, Thomas Bell, Tommaso Pizzari.