

HR926-10 Microbiomics and Metagenomics

22/23

Department

Life Sciences

Level

Taught Postgraduate Level

Module leader

Hendrik Schaefer

Credit value

10

Module duration

2 weeks

Assessment

100% coursework

Study location

University of Warwick main campus, Coventry

Description

Introductory description

The aim of this module is to provide students with an understanding of the role of environmental and host-associated microbial communities in driving processes in the environment and affecting the physiology and health of plants, animal and human hosts. High throughput methodologies including next generation sequencing approaches have revolutionised the study of microbial diversity and function by metagenomics approaches.

[Module web page](#)

Module aims

This module will provide students with the understanding of microbial diversity, the functional roles that microorganisms have both in the environment and in association with plant, animal and human hosts (microbiomics) and how the knowledge gained from studying microbiota can aid understanding of global change, or be exploited to achieve progress in agriculture, biotechnology and human health.

Outline syllabus

This is an indicative module outline only to give an indication of the sort of topics that may be covered. Actual sessions held may differ.

Microbial diversity, and systematics; ribosomal RNA as a conserved phylogenetic marker

Culturability (and non-culturability) of microorganisms; the case for microbial community analysis using molecular biological, cultivation-independent approaches

Distribution of microorganisms in the environment and role in biogeochemical cycling (case studies)

Diversity of plant, animal, human-associated microbiomes (case studies)

Establishing gene function in model organisms and translation of findings to microbial communities (incl tutorial case study)

Stable isotope and radioisotope approaches to linking microbial identity and function

Metagenomics approaches for studying composition and metabolic potential (metagenomics, metatranscriptomics, metaproteomics)

IT workshop: practical examples of databases, online resources used for diversity and metagenomics studies; gene finding and annotation of DNA sequence data.

Learning outcomes

By the end of the module, students should be able to:

- After taking this module, students should be able to critically evaluate how different methodological approaches can help to dissect structure/function relationships in microbial communities and identify the biases associated with different methods.
- After taking this module, students should be able to autonomously interpret original research outputs of advanced microbiomics studies and critically evaluate the findings.
- After taking this module, students should be able to discuss the role of microbial consortia in diverse environments, including the human gut, industrial processes, and the natural environment.
- After taking this module, students should be able to discuss the diverse roles that microorganisms have in the functioning of the biosphere, both as 'free-living' environmental microorganisms, in engineered systems, as well as in association with plant, animal and human hosts.

Indicative reading list

Madigan, M. T. et al. (2018) Brock biology of microorganisms. Fifteenth edition. NY, NY: Pearson. Available at: http://encore.lib.warwick.ac.uk/iii/encore/record/C_Rb3229767.

Vorholt, J. A. (2012) 'Microbial life in the phyllosphere', Nature Reviews Microbiology, 10(12), pp.

828–840. doi: 10.1038/nrmicro2910.

Brown, C. T. et al. (2015) 'Unusual biology across a group comprising more than 15% of domain Bacteria', *Nature*, 523(7559), pp. 208–211. doi: 10.1038/nature14486.

Bulgarelli, D. et al. (2012) 'Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota', *Nature*, 488(7409), pp. 91–95. doi: 10.1038/nature11336.

Caporaso, J. G. et al. (2012) 'Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms', *The ISME Journal*, 6(8), pp. 1621–1624. doi:10.1038/ismej.2012.8.

Chen, Y. and Murrell, J. C. (2010) 'When metagenomics meets stable-isotope probing: progress and perspectives', *Trends in Microbiology*, 18(4), pp. 157–163. doi:10.1016/j.tim.2010.02.002.

Davide Bulgarelli (2015) 'Structure and Function of the Bacterial Root Microbiota in Wild and Domesticated Barley', *Cell Host & Microbe*. Elsevier, 17(3). doi: 10.1016/j.chom.2015.01.011.

Escobar-Zepeda, A., Vera-Ponce de León, A. and Sanchez-Flores, A. (2015) 'The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics', *Frontiers in Genetics*, 6. doi: 10.3389/fgene.2015.00348.

Eyice, Ö. et al. (2018) 'Bacterial SBP56 identified as a Cu-dependent methanethiol oxidase widely distributed in the biosphere', *The ISME Journal*, 12(1), pp. 145–160. doi: 10.1038/ismej.2017.148.

Hug, L. A. et al. (2016) 'A new view of the tree of life', *Nature Microbiology*, 1(5). doi: 10.1038/nmicrobiol.2016.48.

Lundberg, D. S. et al. (2012) 'Defining the core Arabidopsis thaliana root microbiome', *Nature*, 488(7409), pp. 86–90. doi: 10.1038/nature11237.

Meyer, F. et al. (2008) 'The metagenomics RAST server – a public resource for the automatic phylogenetic and functional analysis of metagenomes', *BMC Bioinformatics*, 9(1). doi: 10.1186/1471-2105-9-386.

Parks, D. H. et al. (2017) 'Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life', *Nature Microbiology*, 2(11), pp. 1533–1542. doi: 10.1038/s41564-017-0012-7.

Valles-Colomer, M. et al. (2019) 'The neuroactive potential of the human gut microbiota in quality of life and depression', *Nature Microbiology*, 4(4), pp. 623–632. doi: 10.1038/s41564-018-0337-x.

Yarza, P. et al. (2014) 'Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences', *Nature Reviews Microbiology*, 12(9), pp. 635–645. doi: 10.1038/nrmicro3330.

[View reading list on Talis Aspire](#)

Subject specific skills

Identify the role that microbiota associated with animals, plants and humans have for host physiology and understand how knowledge of the microbiome may be exploitable in order to bring about beneficial changes to host physiology, health and — in case of crop plants, to crop yield and

disease resistance.

Transferable skills

Autonomously interpret original research

Critically evaluate different methodological approaches

Study

Study time

Type	Required
Lectures	14 sessions of 1 hour (19%)
Tutorials	4 sessions of 1 hour (5%)
Practical classes	6 sessions of 1 hour (8%)
Private study	51 hours (68%)
Total	75 hours

Private study description

Self-directed study.

Costs

No further costs have been identified for this module.

Assessment

You do not need to pass all assessment components to pass the module.

Assessment group A4

	Weighting	Study time	Eligible for self-certification
Data analysis and summary	100%	25 hours	Yes (extension)
A microbiomics/metagenomics related data analysis (drawing on a case study or experimental data) with a short executive summary of 500 words defining the context and scope of the analyses presented as well as key conclusions.			

Feedback on assessment

Feedback given formally through Moodle.

Availability

Courses

This module is Core for:

- Year 1 of THRA-D4A1 Postgraduate Taught Environmental Bioscience in a Changing Climate

This module is Core optional for:

- Year 1 of TLFS-J7N2 Postgraduate Medical Biotechnology and Business Management
- THRA-D4A3 Postgraduate Taught Food Security
 - Year 1 of D4A3 Food Security
 - Year 1 of D4A3 Food Security
- Year 1 of THRA-D4A2 Postgraduate Taught Sustainable Crop Production: Agronomy for the 21st Century

This module is Optional for:

- Year 1 of TBSS-C5N2 Postgraduate Taught Biotechnology, Bioprocessing and Business Management
- Year 1 of ULFA-C1A1 Undergraduate Biological Sciences (MBio)

This module is Unusual option for:

- Year 1 of TCHA-F1PE Postgraduate Taught Scientific Research and Communication