FUTURE OAK

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Characterising and engineering the oak microbiome to future-proof an arboreal icon

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SYLVA FOUNDATION

ActionOak PROTECTING OUR OAK TREES

Forest Research The Research agency of the Forestry Commission

PRIFYSGOL ABERYSTWYTH UNIVERSITY

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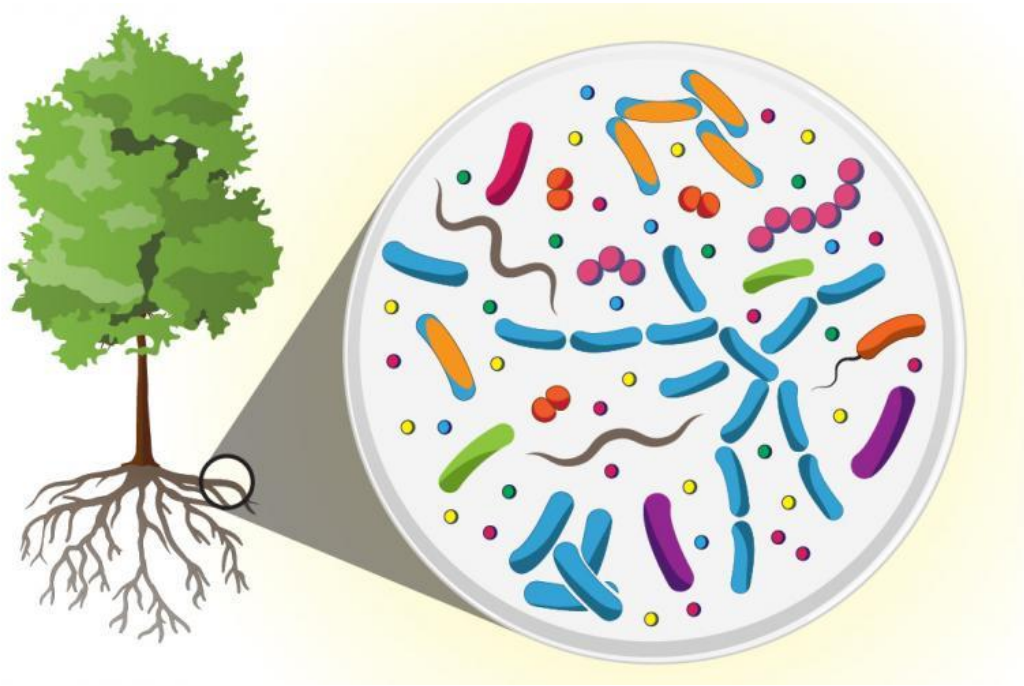
The microbiome: the collection of microbes, and their interactions within the habitat where they are found

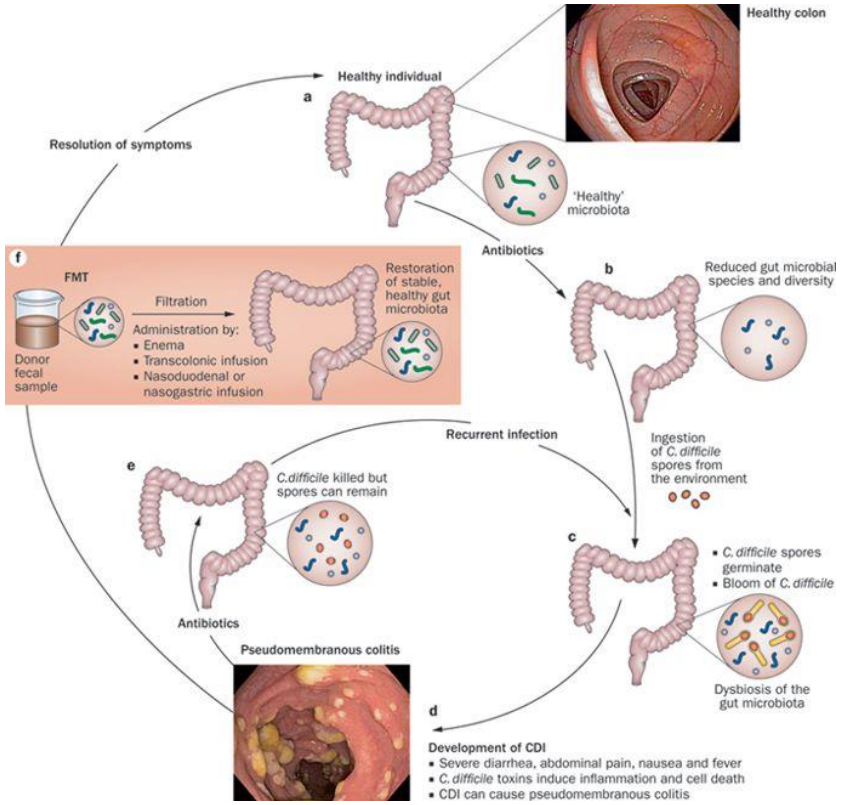
- Provision of important resources
- Bioconversion of nutrients
- Stimulating immune responses
- Protection against pathogens



Engineering microbiomes for disease suppression

nature biotechnology

Faecal Microbiota Transplants

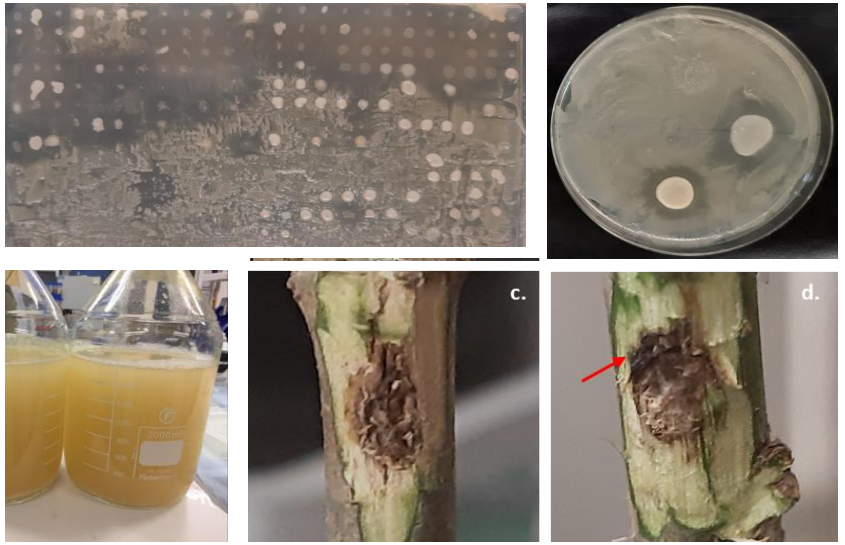


Rhizosphere microbiome structure alters to enable wilt resistance in tomato

Min-Jung Kwak[1,8], Hyun Gi Kong[2,8], Kihyuck Choi[2,8], Soon-Kyeong Kwon[1,8], Ju Yeon Song[1,8], Jidam Lee[1], Pyeong An Lee[2], Soo Yeon Choi[2], Minseok Seo[3,7], Hyoung Ju Lee[2], Eun Joo Jung[2], Hyein Park[1], Nazish Roy[2], Heebal Kim[3,4], Myeong Min Lee[1], Edward M Rubin[5,7], Seon-Woo Lee[2] & Jihyun F Kim[1,6]

Tomato variety Hawaii 7996 is resistant to the soil-borne pathogen *Ralstonia solanacearum*, whereas the Moneymaker variety is susceptible to the pathogen. To evaluate whether plant-associated microorganisms have a role in disease resistance, we analyzed the rhizosphere microbiomes of both varieties in a mesocosm experiment. Microbiome structures differed between the two cultivars. Transplantation of rhizosphere microbiota from resistant plants suppressed disease symptoms in susceptible plants. Comparative analyses of rhizosphere metagenomes from resistant and susceptible plants enabled the identification and assembly of a flavobacterial genome that was far more abundant in the resistant plant rhizosphere microbiome than in that of the susceptible plant. We cultivated this flavobacterium, named TRM1, and found that it could suppress *R. solanacearum*-disease development in a susceptible plant in pot experiments. Our findings reveal a role for native microbiota in protecting plants from microbial pathogens, and our approach charts a path toward the development of probiotics to ameliorate plant diseases.

Engineering oak microbiomes



Research questions:

Which microorganisms are beneficial to oak?

How do host and environmental factors affect their presence?

Can they be used to suppress disease and promote health in oak?

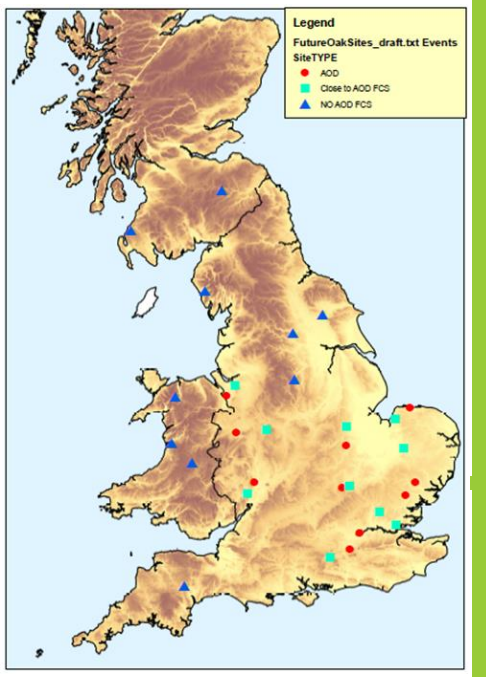
FUTURE OAK: Characterising and engineering the oak microbiome to future-proof an arboreal icon

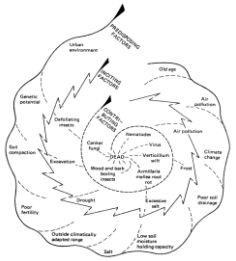
Objective 1: Characterise the landscape-scale multidimensional interactions that influence the oak microbiome in health and disease

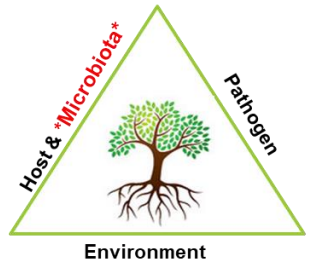
Objective 2: Identify disease suppressive microbiota in the oak microbiome

Objective 3: Engineering the oak microbiome for disease suppression

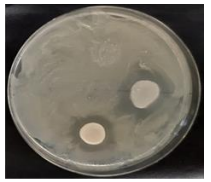
Objective 4: explore the management context of engineered microbiome approaches to tree health



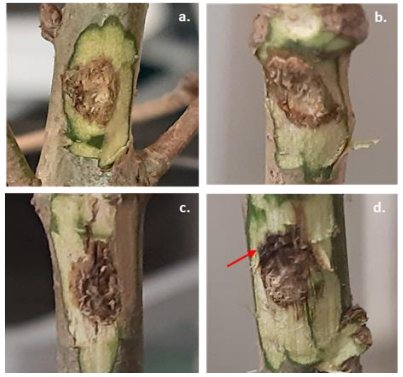




Screen disease suppressive microbiota for bacterial agents of Acute Oak Decline



Apply engineered microbiomes for disease suppression

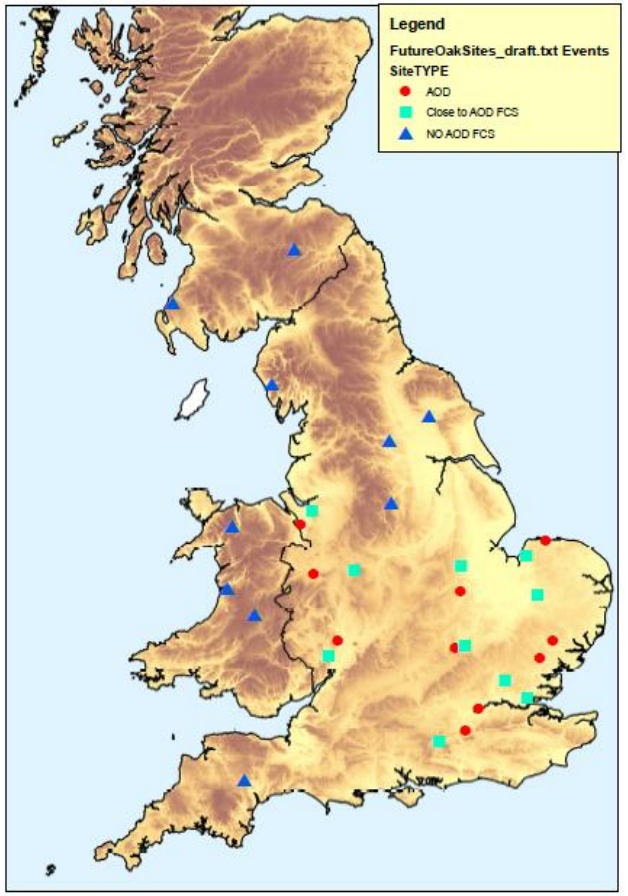


FUTURE OAK

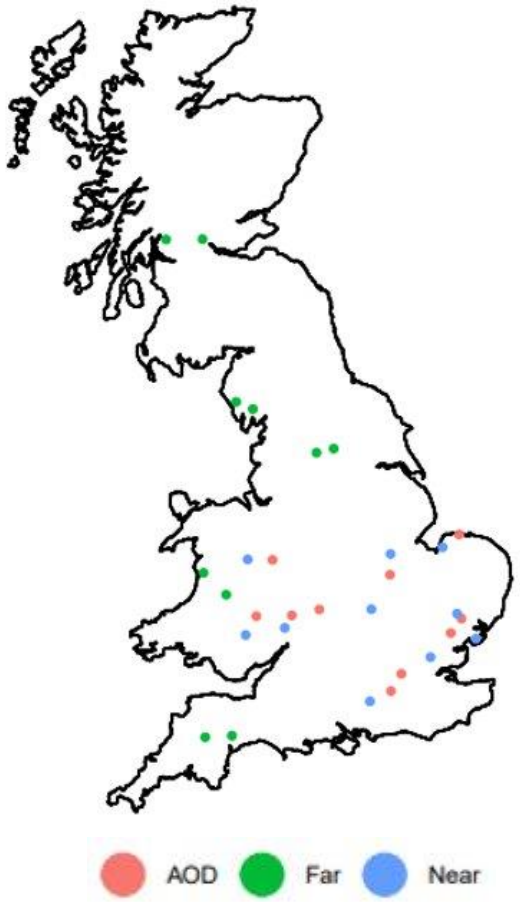
Objective 1: Microbiome-wide and metabolome-wide association ***(MWAS)*** study of native British oak

1. Landscape-scale MWAS (300 trees)
2. Phenotypic decline index
3. Microbiome and metabolome analysis
4. Environmental metadata
5. Machine learning (biomarker discovery, ecological analysis)

Characterise the landscape-scale multidimensional interactions that influence the oak microbiome in health and disease.



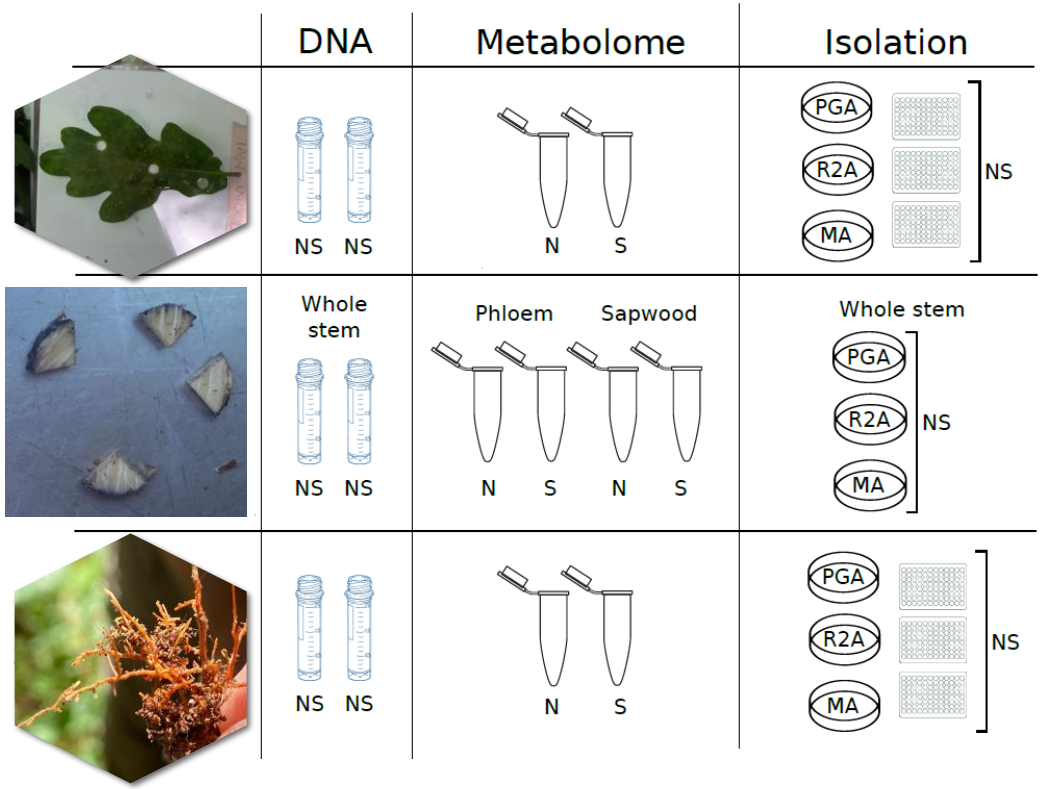
Microbiome-wide association study ***(MWAS)*** of native British oak



30 sites across the UK

350 oak trees

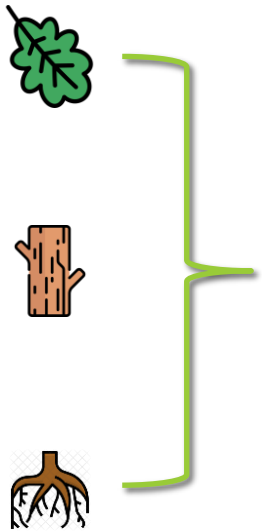
Leaf, stem and root.



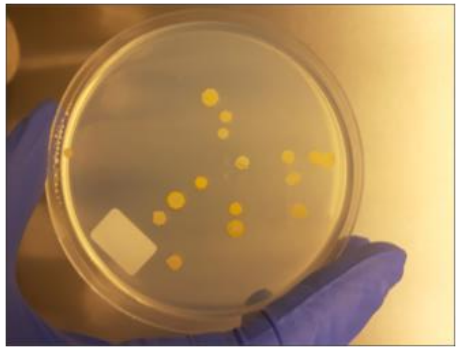
Microbiome: 1050 samples | 16S rRNA gene & ITS profiling | metagenomics
Metabolome: 1200 samples

Isolating oak leaf, stem and rhizosphere microborganisms

Alejandra Ordoñez

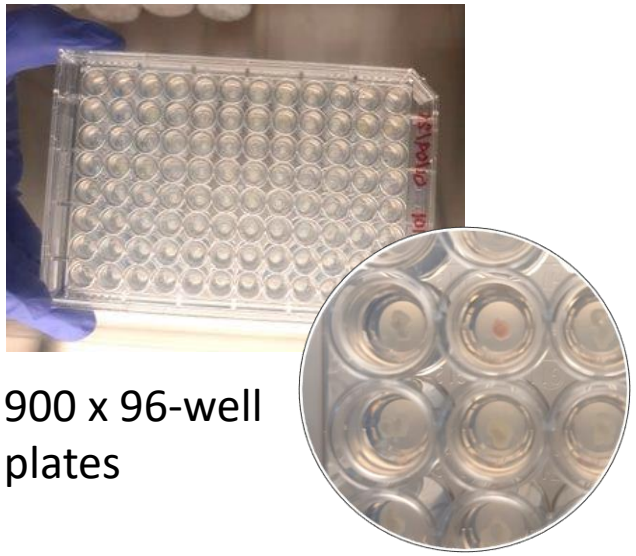


1. Serial dilution and streak plating on agar



1350 agar plates – 3 growth media

2. Dilution to extinction in 96 well plates



900 x 96-well plates

Microbial isolation:

- 150 trees
- 14,400 isolates on agar
- 86,400 dilution to extinction wells
- Estimate >30,000 isolates

Objective 1: Microbiome-wide and metabolome-wide association *(MWAS)* study of native British oak

Sampling:

350 trees | 30 sites | 3 countries | in 7 weeks

Microbiome:

1050 samples | 16S rRNA gene & ITS profiling | DNA sequencing

Microbial isolation:

150 trees |14,400 isolates on agar | 86,400 dilution to extinction wells

Metabolome:

1200 samples

Thanks to all team members at Forest Research, Bangor, Aberystwyth, FR Technical services unit (TSU), tree climbers and land owners/managers.

Thanks for listening