

Can we predict and optimise the assembly and succession of host microbiomes?

Supervisory team:

Main supervisor: Dr Elze Hesse (University of Exeter)

Second supervisor: Prof Tiffany Taylor (University of Bath)

Non-academic (CASE) supervisor: Dr Paul Rutten (Concert Bio)

Prof Angus Buckling (University of Exeter), Dr Daniel Padfield (University of Exeter)

Collaborators: Dr Stacey Vincent (Concert Bio), Dr Andrew Matthews (University of Exeter)

Host institution: University of Exeter (Penryn)

CASE partner: Concert Bio

Project description:

With the future prospect of growing crops under harsher environmental conditions, the use of hydroponics is projected to increase over the next few decades (20% over the next 5 years, with industry currently being estimated at \$100Bn). Lettuce – an economically important crop – is often grown hydroponically. Under these simplified growing conditions, lettuce crops are commonly destroyed by large-scale devastating outbreaks of root-rot caused by species of the parasitic oomycetes *Pythium*. This typically results in a 10-20% total annual loss. Host microbiomes play a key role in determining pathogen invasion success. For example, bacteria often compete for limiting resources, which could suppress successful colonisation of the host by the pathogen. On the other hand, bacteria can also produce compounds that facilitate the growth of others (metabolic cross-feeding) with the potential to enhance successful pathogen invasion. This raises an important question – can we predict and optimise host-microbiome interactions to limit disease incidence? This project will combine mathematical, experimental evolution and genomic approaches to understand and manipulate the microbiome in a lettuce hydroponic system with the aim of preventing pathogen invasion.

We will track the assembly and succession of root-associated and free-living microbial communities in an experimental hydroponic lettuce-microbiome system. Plant-microbe communities will be cultivated under different resource regimes, half of which will be experimentally invaded with *Pythium*. We will use flux-balance analyses (FBA) to calculate the flow of metabolites in the system and predict bacterial growth rates under different growing conditions. The outcome of FBA will be compared to experimental data to determine whether single-species metabolic fluxes can be used to predict community assembly, succession, and *Pythium* invasion. In microbial communities, temporal changes can result from both ecological and evolutionary selection acting over similar timeframes, as well as physiological changes mediated by gene regulation. To determine the genetic changes underpinning community interactions, we will sequence a subset of bacterial genomes before and after long-term evolution with and without *Pythium*. We will determine the relative roles of mutation and gene regulation in determining species interactions and invasion resistance using a combination of genomics and transcriptomics.

We will achieve these aims using a highly interdisciplinary approach. Depending on the preference of the candidate, these will include microbiome research (Elze Hesse), molecular evolution (Tiffany Taylor), statistical modelling (Daniel Padfield) and experimental evolution (Angus Buckling). We will closely work together with Concert Bio (Paul Rutten) – a new company that both monitors and enhances hydroponic microbiomes.

Our aim as the SWBio DTP is to support students from a range of backgrounds and circumstances. Where needed, we will work with you to take into consideration reasonable project adaptations (for example to support caring responsibilities, disabilities, other significant personal circumstances) as well as flexible working and part-time study requests, to enable greater access to a PhD. All our supervisors support us with this aim, so please feel comfortable in discussing further with the listed PhD project supervisor to see what is feasible.