

Elucidating transposon-fungus pathogenomics to deliver more productive, sustainable, and resilient agriculture

Supervisory team:

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Project description:

Fungi are among the most damaging human, animal, and plant pathogens. Fungal phytopathogens (plant fungal pathogens), especially those attacking cereals, are of particular concern to safeguard global food security. These decrease crop yields and contaminate food chains with harmful mycotoxins, threatening food production and necessitating careful management and monitoring programmes. Consequently, advancing understanding of fungal phytopathogens is a major international research priority.

The ongoing genomic revolution offers great scope in the fight against fungal phytopathogens, to improve the productivity, resilience, and sustainability of global agriculture. Two outstanding fundamental challenges where genomic approaches present significant promise are:

- 1. Elucidating underlying mechanisms that shape key host-fungal interactions (e.g. host specificity, virulence, pathogenicity)
- 2. Characterising evolutionary processes leading to a switch in fungal lifestyle from harmless freeliving saprotrophs to damaging pathogens

A particularly promising emerging research area is fungal host-transposon interactions. Transposons are mobile selfish genetic elements that can transpose (move position) within the genome. Transposition can be harmful if a transposon jumps into an essential genomic region. However, transposition can also generate selectively beneficial genomic novelty, for example where insertions facilitate adaptive regulatory mutations. This project will leverage the combined power of expertly curated phenotypic databases, extensive genomic datasets, detailed bioinformatic analyses, and largescale evolutionary experiments, to test the role of transposons in shaping the dynamic genomes of fungal pathogens.

Firstly, a largescale expertly-curated database of fungal sequences with demonstrated relevance in pathogenhost interactions (PHI-base.org) will be analysed. Transposons at genomic locations of known pathogenicity, virulence, and sensitivity to chemicals will be interrogated, considering fungi with different infection biologies and disease-causing abilities.



Secondly, transposon landscapes will be analysed among diverse strains in the genus Fusarium, which contains many of the most damaging plant and animal fungal pathogens. Of particular interest are: (a) The origin and evolution of strain-specific accessory chromosomes, often rich in transposons and implicated in switches to pathogenicity; (b) The extent of transposon horizontal transfer and associated propensity for among-strain transfer of fungal sequences, especially of pathogenic relevance.

Thirdly, evidence suggests that physiological stress may release transposons from repression in fungal genomes. Increased rates of transposition may in turn boost genomic evolvability, with selection favouring novel advantageous mutations for traits such as pathogenicity, virulence, or fungicide resistance. Such effects are particularly likely under conditions of repeated high selection.

We will test the stress-induced transposon mobilisation hypothesis using a combination of experimental evolution, high resolution genome sequencing, and powerful bioinformatic analyses.

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.