Quantifying the evolution of multi-fungicide resistance and its effects on pathogen fitness and virulence

Supervisory team:
Main supervisor: Prof Ivana Gudelj (University of Exeter)
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Host institution: University of Exeter (Streatham/St Luke's)

CASE partner: Syngenta

Project description:

To feed the growing human population, we must double food production by 2050. Plant pathogens pose a major threat to food security and are responsible for significant crop losses. Therefore, farmers rely on antimicrobials to control pathogen outbreaks. However, pathogens can rapidly evolve resistance and threaten the effectiveness of these treatments. Improving our understanding of the evolutionary processes that drive resistance selection and its influence on disease virulence is critical for the development of resistance management strategies for sustainable crop protection. The proposed PhD CASE studentship in collaboration with the industrial partner Syngenta will tackle the challenge of understanding resistance evolution through an experimental, laboratory-based project that will be carried out in close collaboration with mathematical modellers.

Studentship goals: (1) Empirically assess the relevance of single- and multi-fungicide resistance for pathogen fitness and virulence; (2) Generate data to support overarching mathematical models of antifungal resistance evolution

Outcome and impact: The student will generate new and precise knowledge on the interactions between fungicide resistance, pathogen fitness and virulence. This is essential to accurately predict fungicide resistance evolution. This project can therefore contribute to building science-based resistance management strategies and to developing more sustainable agriculture.

Training: This PhD studentship will provide a unique opportunity to gain a range of experimental and quantitative skills essential to thrive in the modern fields of biology. To achieve this, we have put together a truly interdisciplinary team with expertise in modelling (Le Gros, Syngenta; Gudelj, Exeter), fungal genetics & antifungal resistance (Scalliet, Syngenta); quantitative evolutionary biology (Beardmore, Exeter) and plant pathology & synthetic fungal biology (Lindsay, Exeter). We will deploy our extensive expertise in a tractable laboratory experimental system with the fungus Magnaporthe oryzae, responsible for rice blast disease, the most severe and widespread disease of cultivated rice. It is also an ideal system for investigating the fundamental principles of antimicrobial resistance penalties as its genome, lifecycle and physiology are well understood and it is amenable to genetic engineering.