

## Assessing the role of transposable elements in the evolution of host genomic complexity

### Supervisory team:

**Main supervisor:** Dr Alex Hayward (University of Exeter)

**Second supervisor:** Prof Jason Wolf (University of Bath)

Dr Karl Wotton (University of Exeter)

**Collaborators:** Dr Konrad Lohse (University of Edinburgh), Prof Mark Blaxter (University of Edinburgh)

**Host institution:** University of Exeter (Penryn)

### Project description:

Transposable elements (TEs) and eukaryotic organisms share an ancient co-evolutionary history, and it is now clear that TEs comprise considerable proportions of eukaryote genomes. While active TEs have long been considered to be genomic parasites, it has recently become apparent that TE sequences have been extensively utilised by host genomes for diverse beneficial host functions, and that they have exerted a significant influence on host biology. However, little is known about the features that predispose a given TE to being harnessed for host purposes, or how TEs interact to contribute to the evolution of host genomic complexity. Improved knowledge of these aspects is crucial for a better understanding of the mutational processes that give rise to the evolution of genomic complexity. Correspondingly, novel insights into the role of TEs in host genome evolution offer to provide important evolutionary insights, as well as findings of direct potential benefit for applications in medicine and biotechnology.

This project 'Assessing the role of transposable elements in the evolution of host genomic complexity' seeks to use genomic data from a large number of newly sequenced European butterfly species pairs to quantitatively investigate the exciting question of the extent to which TEs are important in host genome evolution. The project will involve the application of cutting-edge approaches to identify and catalogue TEs, and the development of bioinformatics analyses to test for patterns in host gene-associated TEs. Additionally, the project will include a simulation-based approach to exploring the impact of varying TE and host dynamics on the recruitment of TEs during host genomic evolution.

This cross-disciplinary project will involve training at several prestigious universities, in cutting-edge bioinformatic and genomic approaches (Dr Alex Hayward, University of Exeter), mathematical modelling within an evolutionary genetics framework (Professor Jason Wolf, University of Bath). Additionally, the project involves collaboration with researchers at the University of Edinburgh (Dr Konrad Lohse, Professor Mark Blaxter), for data generation and analysis, and it is anticipated that the successful candidate will have the opportunity to also be involved in research visits to the University of Edinburgh.