

Evaluating the contribution of transposons to agricultural domestication

Supervisory team:

Main supervisor: Dr Alex Hayward (University of Exeter)

Second supervisor: Dr Pablo Orozco Ter Wengel (Cardiff University)

Prof Chris Bass (University of Exeter)

Host institution: University of Exeter (Penryn)

Project description:

Vertebrates and transposons share an ancient co-evolutionary history. Indeed, the whole of vertebrate evolution has occurred within the context of transposon interactions, since the origin of transposons is believed to significantly predate the origin of the vertebrates. Consequently, vertebrate genomes typically contain very large proportions of both active transposons and mutated transposon remnants (e.g. transposons account for ~50% of total genome content in humans).

Until recently, transposons were largely considered to be 'junk DNA' that littered the host genome. While active elements were known to cause insertional mutagenesis, there was very little appreciation that transposons played a meaningful role in host evolution. However, since the genomics revolution, it has become apparent that transposons are highly important players in the evolution of host genomic complexity, playing key regulatory roles as well as directly contributing protein coding sequence as raw material for novel host functions.

Given an abundance of high quality genomes from across vertebrate phylogeny, we are now in a powerful position to learn more about the intricacies by which transposons are harnessed by host genomes during evolution. This offers great potential for developing novel applications across a range of important areas in biology. This project will address the exciting question of the contribution of transposons to agricultural domestication, using a detailed comparative genomics analysis of important livestock breeds and their wild ancestors.

In this project, genomic data from a large number of agriculturally important livestock species, will be complemented with data from high and low producing breeds and wild ancestral species, to perform cutting-edge bioinformatic analyses of transposon content, integration history, and interactions with host gene ontology. This will provide a new and detailed picture of transposon activity and the contribution of transposons during domestication. Of particular interest will be transposon involvement in genomic regions linked to production traits, and regions identified to contain transposon hotspots, where nested insertions have provided the substrate for evolutionary processes such as adaptive walks and the expression of new host phenotypes.

This cross-disciplinary project will involve training at several prestigious universities, including cutting-edge bioinformatic and phylogenetic approaches at Exeter (Dr Alex Hayward, University of Exeter), and population genomics and livestock genomics at Cardiff (Dr Pablo Orozco ter Wengel). The project will provide highly novel insights into the genetic architecture and evolutionary basis of domestication, with considerable potential for applications in agriculture, to increase the resilience and sustainability of livestock production systems.