Origin, diversification and evolution of the family Fanniidae (Diptera)

The incredible diversity found in the Tree of Life has long fascinated scientists, prompting investigations into the factors that drive species diversification and the varying richness of species across habitats, regions, and taxonomic groups. One prominent pattern, the latitudinal diversity gradient (LDG), traditionally shows a decline in species richness from the equator to the poles. Despite being a fascinating pattern that has been studied for decades, a satisfactory explanation for it remains elusive. A challenge to understanding the standard LDG is the discovery of a small but growing number of lineages that deviate from this pattern, lineages exhibiting inverse LDGs with peak species richness in extratropical regions. An important goal is to identify and characterise such contrarian clades and understand the ecological and evolutionary processes that contribute to their differences. By studying these groups, we can improve our understanding of diversity gradients by seeking explanations for these non-standard cases using the same fundamental mechanisms that underlie speciation, extinction, and dispersal—three processes that ultimately impact species richness and diversity gradients.

This project focuses on the dipteran family Fanniidae as a model group to evaluate scenarios that aim to explain the latitudinal diversity gradient. Fanniidae are found in all biogeographic regions of the world, with the highest species diversity observed in temperate areas of both hemispheres, revealing an inverse LDG. However, a crucial first step for exploring evolutionary questions using phylogenies is establishing robustly resolved taxonomic relationships. As the relationships within Fanniidae remain questionable, this project will employ state-of-the-art molecular methods to construct a large-scale phylogeny of Fanniidae. This study will provide new and highly desirable insights into the phylogenetic relationships within the Fanniidae family—an insect group of medical, sanitary, and veterinary importance to humans and animals. Secondly, leveraging the global distribution of Fanniidae, we will infer the centre of origin for the family and examine scenarios that potentially explain its diversity gradient. We will explore whether patterns of Fanniidae species richness can be explained by mechanisms associated with time for species accumulation, species diversification rates, available regional energy, or combination of these three explanations. Finally, through sampling genomes from Fanniidae lineages exhibiting distinct ecological, physiological, or behavioural traits, we will conduct a comparative genomics study. This analysis will uncover potential genetic and genomic mechanisms underlying the biological adaptations of Fanniidae, exploring specific rapidly evolving gene families responsible for their successful adaptation to local habitats.

The outcomes of this study will contribute to a deeper understanding of Fanniidae and hold relevance for specialists, the broader scientific community, and society at large. We will establish a robust phylogenetic framework for Fanniidae, shedding light on the evolutionary relationships within the family. Additionally, by investigating mechanisms underlying the LDG and the genetic adaptability of Fanniidae, we will advance our knowledge of biodiversity patterns and the genetic processes driving species adaptation.