Telling tall tales: Evolutionary, functional, and genetic underpinnings of mammalian tail diversity

Project ID: 3649

Supervisory team

Main supervisor: Dr Katrina Jones (University of Bristol)
Second supervisor: Prof Matthew Wills (University of Bath)
Other supervisors: Prof Emily Rayfield (University of Bristol)
Collaborators: Prof. Mary O'Connell (University of Manchester)

Host institution: University of Bristol



Project description: Serial structures are a fundamental feature of animal body plans, from teeth and vertebrae to digits, feathers and scales. Their diversity can arise through changes in three parameters: the number, size and morphological complexity of repeated elements. However, we have a limited understanding of the biological mechanisms that generate this variation or how alternative developmental and morphological pathways influence function.This project will establish how genetic variation, morphological organisation and biomechanical function interact to generate diversity in a serial system. Despite remarkable diversity structure, all mammal tails consist of repeating caudal vertebrae that vary in number, length, and complexity. The student will examine whether these aspects of serial variation represent distinct routes through which functional phenotypic diversity is generated.The goals of this project are:1.Define the phenotypic architecture of a serial system by quantifying how variation in the three serial parameters (vertebral number, length and morphological complexity) generates tail diversity across mammals.2.Establish a morphological design space for tail diversity by modelling how independent and interacting variation in serial parameters determines achievable phenotypes.3.Identify genomic correlates of alternative routes to phenotypic diversification by comparing phenotypes with genomic data from the Vertebrate Genome Project, to test whether changes in regulatory genomic architecture predict distinct components of serial phenotype.4.Determine how serial organisation influences biological function using finite element analysis and 3D printed models of whole tail sequences to quantify the biomechanical consequences of variation in serial variation.By integrating genomic, morphological and biomechanical data, the project will establish how variation at different biological scales combines to generate functional phenotypic diversity. The student will test whether similar functional outcomes can be achieved through alternative morphological routes, whether these routes occupy predictable regions of phenotypic parameter space, and whether distinct components of serial-system organisation are associated with different genomic mechanisms. This will provide a general framework for understanding how genotype generates functional phenotype in complex serial structures.The student will work with a diverse supervisory team with expertise on vertebral anatomy (Jones, Bristol), complexity of serial structures (Wills), biomechanics (Rayfield), and comparative genomics (O'Connell). They will be equipped with a diverse set of quantitative skills including shape analysis, phylogenetic comparative methods, comparative genomics, and mechanical modelling. They

will work within a highly active research group (Bristol Palaeobiology) and across two world-leading institutions (Bristol, Bath).

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.