Constrained evolution – possibilities and impediments in pigment patterning

Supervisory team:
Main supervisor: Prof Robert Kelsh (University of Bath)
Second supervisor: Dr Christian Yates (University of Bath)
Prof Phil Donoghue (University of Bristol), Prof Matthew Wills (University of Bath)

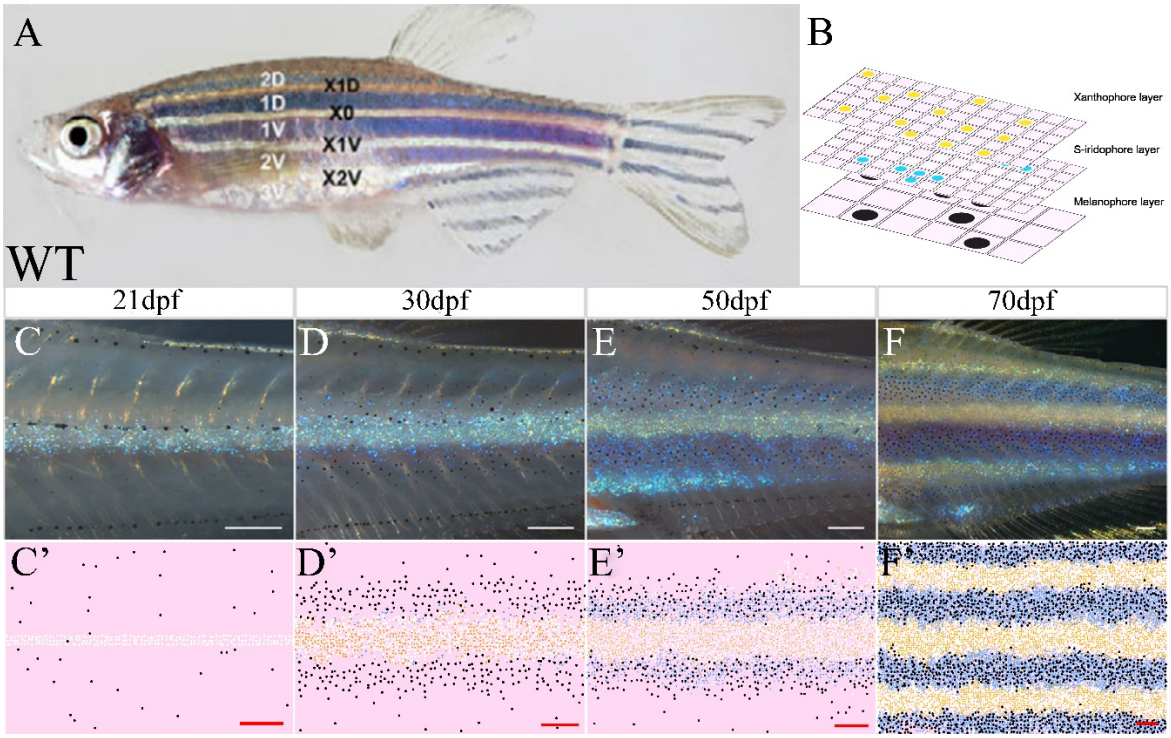
Host institution: University of Bath

Project description:
Evolution is popularly believed to be a gradual process typified by slow morphological change. In fact, the rate of change is highly variable, and can be very fast. How are such rapid changes in morphology achieved? Pigment patterns are biologically vital for both camouflage and sexual signalling, yet can differ markedly between sister species (those species pairs with the most recent divergences). There is a long tradition of both in silico and in vivo investigation of the underlying mechanisms. Pigment pattern formation is thus an excellent system for exploring the mechanisms and constraints underlying evolutionary novelties.

We have developed a detailed in silico representation of pigment stripe formation in the vertebrate developmental model, zebrafish (Danio rerio). Our computer model successfully simulates the patterns seen in wild-type fish (stripes), but also patterns seen in the lab in mutant zebrafish (thinner/thicker stripes and a diversity of spot patterns). Other species of Danio show a rich variety of other pigment patterns, and we propose the hypothesis that these have all evolved by modifying an otherwise conserved pattern formation process. Comprehensive exploration of our in silico model to simulate such changes will allow comparison of the model's outputs to the patterns seen in real fish. To explore such a large region of parameter space we will develop robust metrics to allow automated comparison of real pigment patterns as measured from fish to those produced in the model. Thus, we will identify the likely cellular bases for pattern diversification. Where the model outputs generate a pattern akin to that of a natural species, the underlying parameter values will indicate which biological aspects of the pattern formation process might be altered in that species. Conversely, where an extant species' pattern fails to be replicated within the model's morphospace, that will indicate where extra evolutionary novelty may be being utilised. In both these ways, this project will make important contributions to the understanding of a central problem in pattern formation and its evolution.

They should be excited by the prospect of joining an interdisciplinary team to use a mathematical modelling approach to explore a fundamental question in evolutionary biology.

Informal enquiries should be directed to Prof. Robert Kelsh, bssrnk@bath.ac.uk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