

Runaway sexual selection- catching the genes.

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Sexual selection has generated an incredible amount of biodiversity. The idea that exaggerated male traits and female choice for those traits become associated to produce runaway sexual selection is widely accepted. In the nearly 90 years since Fisher proposed this though, the genetic mechanisms remain elusive, despite the genomics revolution of the last ten years or so. A major challenge in biology is therefore evaluating the wealth of models which predict how biodiversity could be generated by sexual selection, with empirical examples using known “sexual selection loci”. Understanding the genetic changes which can lead to runaway sexual selection would allow us to better understand how a substantial proportion of life on earth evolved.

A well established model for studying genetics, evolution and behaviour are the cichlid fish of Lake Malawi. Approximately 1000 species of fish have evolved in less than 5 million years, showing an incredible array of ecologically and sexually selected adaptations, and there are many genomic resources available. Studies in our lab have identified a genomic region associated with a fascinating sexually selected behaviour - the shape of underwater sand-castles (“bowers”) that male fish build in order to impress females, and we are now in a position to explore and verify this experimentally. There are about 200 species of bower building fish, each bower is species specific and females’ preference is based on different aspects of bower shape, such as height or diameter, which themselves might be constrained by both male condition, and environmental heterogeneity with respect to sediment type available.

This system is ideal for studying sexual selection and mate choice because i) fish build bowers and mate in large pools in captivity ii) individuals can be identified using PIT tags iii) bower manipulation or substitution is possible iv) cichlid fish are maternal mouth brooders and offspring can be DNA paternity tested v) genomic studies have identified candidate genes responsible for varying bower shapes vi) we already have 15 genomes from 3 related species waiting to be analysed vii) we are developing CRISPR-cas9 gene editing in these species.

This PhD will be multidisciplinary and allow the candidate to explore the genetic basis of these behaviours experimentally in the lab, along with the roles that condition dependence and environmental heterogeneity could play in shaping biodiversity through sexual selection. There is scope to shape the project to the student’s interests, but ultimately, understanding how this ubiquitous genomic region is involved in the expression of both male trait and female preference will have far reaching implications for our understanding of vertebrate sexual selection and diversification.

