

# Is genome evolution accelerating at speciation time?

## Supervisory team:

**Main supervisor:** Prof Davide Pisani (University of Bristol)

**Second supervisor:** Prof Philip Donoghue FRS (University of Bristol)

Prof Mike Beaumont (University of Bristol), Prof Michael J. Benton FRS (University of Bristol)

**Collaborators:** Dr Mark Wilkinson (Natural History Museum), Dr David Gower (Natural History Museum)

**Host institution:** University of Bristol

## Project description:

The fossil record and DNA both record information about the history of life<sup>1,2</sup>. However, fossils often suggest a significantly younger age for the same event<sup>3</sup>. One possible explanation for these discrepancies is that the first individuals belonging to a new species have low fossilization potential. Alternatively, it is possible that DNA evolves faster during radiations. If speciation happens in small populations, bottlenecks should precede the origins of new species, and this should lead to relaxed negative selection, and an associated increase in the rate of evolution. DNA may be going through long periods of slow change, followed by brief periods of rapid evolution.

Here, we will test whether DNA evolves faster at speciation time. We will focus on recent radiations whose age can be well constrained. The student will investigate, among others, the radiation of Seychelles (limbless) Caecilian amphibians, Caribbean anoles, the lacertid lizards of Sicily and the Sulawesi and Philippines fanged frogs. The student will use real data, statistical modeling, and simulations. They will estimate rates of evolution, and compare them against “background” rates estimated from related, non-insular lineages (e.g. continental European lacertids Vs Sicilian ones). They will model rate of evolution at speciation and test whether rates of genomic evolution change at speciation.

We seek a student with background in evolution or computing and willing to learn computational techniques or evolution. During year one, two rotations will be organized. With these rotations we shall study a model radiation, that of the Seychelles (limbless) Caecilians. (1) The student will join the Palaeobiology Research Group in Bristol where, under the guidance of Profs Pisani, Donoghue and Benton to carry out molecular clock analyses of Caecilian from the Seychelles, and learn about phylogenetics, bioinformatics and palaeontology. During this period the student will regularly visit the Natural History Museum during this first rotation to work with Dr Gower and Wilkinson (world leading experts in Caecilian biogeography and taxonomy). They will then join Professor Beaumont to (2) model how rates of DNA evolution change at speciation times. During the rotations training will be provided in fossil data analysis; Comparative genomics and bioinformatics; Taxonomy and molecular methods; Statistical modeling and computer programming in “R”. In the remaining years the student will further develop these skills and investigate other radiations, emerging as a multidisciplinary evolutionary biologist with computational and taxonomic skills, and a detailed knowledge of genomics and paleontology.

- 1- Erwin et al. 2011 Science. DOI: 10.1126/science.1206375
- 2- Dos Reis et al. 2015 Current Biology. 25:2939-2950
- 3- Rota-Stabelli et al. 2013 Current Biology 23:392-398.