# A genomic perspective on the origins, evolution and adaptation of Galapagos Iguanas

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## Project summary

The revolution in sequencing technology and genomic science in recent years is now allowing evolutionary biologists to dissect the genetic basis of adaptation and population histories of non-model organisms in unprecedented detail. Key questions related to adaptation include, the type and number of genetic changes which underpin the evolution of new phenotypes, the strength and time scales for selection, the extent of parallel and convergent evolution among different taxa, and the nature of environmental and ecological factors which drive natural selection. Understanding these mechanisms not only provides fundamental insights into the process of evolution, but is also important for assessing species vulnerability and responses to potential future environmental change.

This project provides a unique opportunity to examine adaptation and evolutionary history in an iconic set of species for evolutionary biologists, the marine (*Amblyrhynchus cristatus*) and land iguanas (*Conolophus* sp) of the Galapagos archipelago. Both genera of Galapagos iguanas originate from the same common ancestor, diverging around 4.5-10.5 million years ago, with both groups subsequently spreading across the archipelago. Land iguanas diversified to form 3 species - *Conolophus subcristatus*, native to six islands, and *Conolophus pallidus*, which is restricted to Santa Fe. The third species *Conolophus marthae*, known as the pink iguana, is only found on Volcan Wolf at the northern end of Isabela. It was only recently recognised as forming a genetically and ecologically distinct species and is now considered endangered due to its small population size and restricted distribution.



Marine iguana - *Amblyrhynchus cristatus*



Land iguana - *Conolophus subcristatus*

Santa Fe land iguana - *Conolophus pallidus*



Pink iguana - *Conolophus marthae*



The process of divergence and diversification among these iguanas has generated many novel adaptations over relatively short evolutionary timescales – most strikingly adaptation to diving and the marine environment in *Amblyrhynchus cristatus*, which is the world's only fully marine lizard. Land iguanas have their own adaptations to the harsh terrestrial environment in the Galapagos, including diet, tolerance of arid conditions and fluctuating resources, as well as various differences in morphology and pigmentation. This provides an amazing natural model system for evolutionary biologists to characterise the genomic basis of adaptation and novel phenotypes; the process of speciation, including mechanisms that prevent hybridization and genetic introgression; as well as characterising the origins and history of iguana populations. These can be linked with palao- and present environmental data to yield a better understanding of the environmental and ecological conditions which drove the evolution of these species.

The project is a part of a collaborative iguana genome and evolution consortium led by Dr Gabriele Gentile at the University of Rome Tor Vergata. Dr Gentile has been pioneering the study and conservation of pink iguanas for many years. The student will spend time working in both Leeds and Rome.

Multiple genome sequences for all land and marine iguana species are currently being generated, as a result of a collaboration between the University of Rome Tor Vergata and the Universiti Kebangsaan Malaysia (Prof. Mohd Firdaus Raih) and will be completed shortly. The aims for the PhD project include:

1. Complete the annotation of the nuclear and mitochondrial genomes of Galapagos iguanas.
2. Use comparative genomic and molecular evolutionary approaches to detect signatures of selection at a genome-wide scale.
3. Identify genes and other sequence variation related to adaptation to diving and other evolutionary trajectories, such as patterns of pigmentation, and DNA repair driven by selection or drift.
4. Identify sequence variation associated with speciation of iguanas in Galapagos.

5. Use nuclear genome data to investigate the interaction between pigmentation, DNA repair system genes and their possible role in determining rates of molecular evolution along different lineages.
6. Use mtDNA and its methylation patterns to provide insights on the level of expression and regulation of mitochondrial genes and its possible link with metabolic rates, which may ultimately influence rates of molecular evolution of mtDNA.
7. There is potential to generate additional data at a population scale to conduct high resolution analyses of population history in land and marine iguanas.

### Expected outcomes:

New knowledge on the molecular adaptions underpinning the evolution of iguanas in Galapagos, and phenotypic novelty more generally; a detailed understanding of the way environmental factors drive the evolution of novel adaptations; insights into the population demographic history of Galapagos iguanas in relation to past environmental change; generation of data relevant to the conservation management of Galapagos iguana populations.

### Methodologies

This is essentially a bioinformatics/computation project, but there may be opportunities to gain hands on laboratory experience of associated DNA sequencing techniques. The project will use data from a range of Next Generation Sequencing (NGS) approaches including de novo sequencing on Illumina and other platforms to build and annotate de novo assemblies of iguana genomes. Data will be then be analysed with a range of bioinformatics, population genomics and molecular evolution tools in high performance computing environments, as appropriate to the research questions.

### Requirements

Hons degree and/or Masters in a topic relating to Biology, Zoology, Ecology, Genetics, Biodiversity, Evolution, Bioinformatics, Maths & Biology etc. An interest in working at the interface of ecology, biodiversity and population/evolutionary genomics is desirable. Prior experience of bioinformatics is helpful but not essential. However interest in developing skills in bioinformatics and computing is important.

### Training

Amongst other topics, training will be provided in population and evolutionary genetics/genomics, comparative genomics, phylogenetics, bioinformatics, genome assembly, genome wide analysis of molecular evolution, statistical modelling in R, and use of high performance computing facilities. As well as on the job training within our research groups, the student will have chance to participate in national and international training workshops on these topics, and to present results at various conferences at home and overseas.

### Research context and partners

This project is part of a consortium involving researchers from the University of Leeds, University of Rome, Tor Vergata, and Universiti Kebangsaan, Malaysia. The student will join the Ecology and Evolution group in the School of Biology, Leeds, and will be integrated with the LIDA and Leeds Omics, virtual institutes which encompass a large group of researchers working on genomics and bioinformatics related projects. The student will also spend significant time working with Dr Gentile in Rome, and visiting other collaborating institutions across Europe and further afield.

## How to apply

For details on how to apply, please see our graduate school website here:
https://studentservices.leeds.ac.uk/pls/banprod/bwskalog_uol.P_DispLoginNon

Faculty of Biological Sciences Graduate School site is here:
https://biologicalsciences.leeds.ac.uk/research-degrees

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