



## COMPARATIVE GENOMIC ANALYSIS AND PHYLOGENOMICS OF THE GALAPAGOS PINK IGUANA, *Conolophus marthae*

*Ph.D. Student:* Mohd Syafiq Abd Rahim / *Supervisor:* Prof. Gabriele Gentile

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The Galápagos Islands are situated in an extremely isolated area of the Pacific Ocean; the habitat to various unique animal and plant life that has inspired Charles Darwin's theory of evolution by natural selection in 1835. Although this archipelago has been discovered over two centuries ago, new species are still being discovered in these islands. One relevant example is the Galápagos pink land iguana (*Conolophus marthae*) described by Dr. Gabriele Gentile and his group from University of Rome, Tor Vergata. Before the discovery of this new iguanid species, two other iguanid species have been found, which are the yellowish herbivorous land iguana (*Conolophus subcristatus* and *Conolophus pallidus*) and the marine iguana (*Amblyrhynchus cristatus*).

The new species of pink land iguana *C. marthae* can be found only at Volcan Wolf at northernmost Isabela island and they are clearly distinguished from *C. pallidus* and *C. subcristatus*, by morphology, behavior and genetically. The differences of these three species raise the question of why they differ from each other even in the same cluster of isolated islands that make up the Galápagos. A study of their genomes is an avenue to answer deeper questions of the evolution of different species in a relatively close area that is otherwise not in contact with other iguanid or lizard species. The nuclear and mitochondrial genomes can be an important resource to understand the diversity of Galápagos iguanas specifically and perhaps evolution in general due to the archipelago's isolation.

By completing the sequence and annotation of the nuclear and mitochondrial genomes of Galápagos iguanas, the project aims at tackling questions related to adaptation to diving and other evolutionary trajectories, such as hemoglobin genes arrangement, driven by selection or drift. Next generation technologies, including single molecule real time (SMRT) sequencing will be used for genome sequencing of the different iguana species. Nuclear DNA genome data will allow for the investigation of among other things, the hemoglobin subunit genes and their possible roles in determining rates of molecular evolution along different lineages. Methylation data from SMRT sequencing of mitochondrial DNA will provide insights on the level of expression and regulation of mitochondrial genes and possible links with metabolic rates that may ultimately reflect on the rates of molecular evolution of mitochondrial DNA.