



## RECONSTRUCTING EVOLUTION AND ADAPTATIONS OF GALÁPAGOS IGUANAS: A GENOMIC APPROACH

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Galápagos iguanas have always been a source of fascination and interest for researchers, becoming icons of ancient and modern evolutionary biology. The evolution of this taxon is dominated by a combination of local extinctions and colonizations and, in this process, selection, genetic drift, and hybridization may have played and may still be playing a crucial and complex role. The main goal of this project will be to understand the relative importance of all these processes, studying and analysing genomes and transcriptomes of all the four species of Galápagos iguanas, in order to shed light on their evolution and adaptations.

Initially we will conclude the analyses on the already available data by completing sequencing, assembly and annotation of all the iguanas' genomes: there will be at list one genome at high coverage and high depth for each species, used as the reference genome. Then, other individuals for each species will be sequenced at a lower coverage in order to reconstruct, with higher resolution, the demographic histories of species particularly important for conservation, such as *Conolophus marthae* (the pink iguana) and *C. pallidus* (Santa Fe land iguana), both known to have a single population endemic to single islands. Disentangling long lasting histories at small population size, caused by severe bottlenecks occurred in just a few generations, is fundamental to understand the impact of demography on the evolutionary potential of the species. Taking advantage of demographic reconstruction by coalescence, such as Sequentially Markovian Coalescent Methods (PSMC or MSMC), it will be possible to investigate demographic histories and evolution patterns from genomic data. In details, these methods infer past changes in effective population size ( $N_e$ ), including the timing of bottleneck events or population expansions/reduction in the past. Addressing demography will be fundamental to understand which has been the most powerful agent of change of the allele frequencies of specific genome's regions involved in actual or supposed adaptations: natural selection or genetic drift. Comparative genomic, transcriptomic analyses of different tissues and molecular evolutionary approaches will be used to detect signatures of selection and drift at a genome-wide scale, in order to identify genetic sequences related to specific adaptations. Some examples are the diving adaptations of the marine iguana (*Amblyrhynchus cristatus*) or the possible behavioural, ecological and physiological adaptations to avoid DNA damages and Vitamin D downregulation in the depigmented pink iguana.

In conclusion, it is fundamental to fill the current lack of knowledge and develop a strong genetic and genomic background on Galápagos iguanas. In fact, knowing which has been past populations trends that shaped current demography, the actual genetic variability in relation to population dimensions, the level of inbreeding, hybridization and local adaptations in the different species will really help to formulate an effective and successful conservation and management plan for these vulnerable and threatened species.

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