EVOLUTIONARY GENETICS RESEARCH GROUP (EG)

Brief description of research lines

3) Molecular evolution and adaptation

To investigate the mechanisms involved in molecular evolution and/or environmental adaptation and stress our group is studying different vertebrate species living in distinct environments.

a. Genetic basis of the migratory behavior and life-history traits in lamprey paired species

We are investigating the long-standing question in lamprey research about the validity of paired species, namely *Lampetra fluviatilis* and *L. planeri*, and the possibility that these are instead two ecotypes of the same species. We will use next-generation sequencing to identify candidate loci with putative fixed differences, namely those responsible for the marked shift in morphology and life-history.

CBA researchers: C Mateus, MJ Alves.

International collaborators: W Salzburger (Univ. Basel, Switzerland).

b. Molecular basis for olfaction in Procellariiform seabirds

The molecular basis of avian olfaction has received little attention, reflecting the belief that avian species lack a functionally well-developed sense of smell. We are extending the understanding of the evolution of avian olfactory receptor genes (ORG) using Procellariiform seabirds as a model system. We have built and screened a cosmid library to isolate ORG in *Calonectris diomedea*. The resulting 96 ORG containing clones have been sequenced and assembled with *Illumina* and 454 reads, and are presently being annotated to characterize ORG and surrounding genomic regions. We will investigate whether evolutionary patterns of Procellariiformes OR genes support the hypothesis that this group relies on the sense of smell. Using cytogenomics approaches, we will investigate the genomic organization of *C. diomedea* OR genes.

CBA researchers: MC Silva, MJ Collares-Pereira, MM Coelho.

International collaborators: JC Silva (Institute for Genome Sciences, USA); D Griffin (Univ. of Kent, UK).

c. Adaptive capacity and distribution responses of species with different thermal ranges under climate change: an investigation using two sister-species of Australian skinks

This project intends to investigate the adaptive capacity and distribution responses of two Australian skink sister species that have different thermal ranges to climate change. Phylogeographic, demographic and selection analysis of genomic data, and physiological information, will be combined

with past, current and future species distribution models under several climate scenarios, in an original approach to understand how species with different thermal constraints will respond to predicted future climate.

CBA researchers: AC Silva, C Fernandes (EG/ADC), MM Coelho.

International collaborators: C Moritz (Australian Nat. Univ., Australia).

d. RAD-seq genome scan to detect candidate loci under selection for local adaptation in weasel populations from latitudinal extremes

Given the increased interest, in the context of climate change, in local adaptation to thermally contrasting environments, we are comparing weasel populations between two latitudinal extremes of the species' distribution in Europe. Specifically, we are analyzing RAD-seq data from populations in Portugal and Finland with multiple approaches to detect loci potentially under selection, as a first step in identifying genes involved in climate adaptation.

CBA researchers: C Fernandes (EG/ADC), M Rodrigues (ADC), M Santos-Reis (ADC).

International collaborators: J Merilla (Univ. of Helsinki, Finland).

e. Adaptive potential of freshwater fish environmental stress

Fish of the Iberian Peninsula and Amazon are exposed to daily and seasonal variations in water parameters, yet these variations are somewhat different in the two contexts. Aiming to discover and characterize a large set of genes involved in thermal and hypoxic stress, transcriptome sequencing will be performed for two species of *Squalius* genus and other two of *Paracheirodon* genus, both in control and stress conditions. Furthermore, expression profiles of the genes of interest will be achieved using qPCR, in *in-situ* conditions in order to provide a more comprehensive view of the mechanism that allows fish to adapt in harsh environments. Finally, this study is expected to enhance our understanding on how fish can cope with the increasing severity of climate changes.

CBA researchers: T Jesus, MM Coelho.

International collaborators: A Val & V Val (INPA, Brazil); C Moritz, (Australian Nat. Univ., Australia).

f. Impacts of heavy metals in freshwater fish

We are initiating a study where contamination by heavy metals may have a significant impact on the viability of endemic fish populations. We intend to explore this study at metabolomic, transcriptomic and epigenomic levels in order to gain a better understanding of the stress response. In this project we will have the support of the economically relevant Portuguese company SOMINCOR, that explores the biggest European mine of copper and zinc. We will also collaborate with the Institute of Nature and Forests

Conservation, a governmental Institution that is responsible for the implementation of conservation policies.

CBA researchers: A Inácio, MJ Collares-Pereira, MM Coelho.