

## EVOLUTIONARY GENETICS RESEARCH GROUP (EG)

### Brief description of research lines

#### 1) Evolutionary history and speciation in natural populations

Our central goal is to understand the evolutionary mechanisms and environmental constraints that drive the history of natural populations and the course of speciation in wild vertebrates.

##### a. Phylogeography, phylogeny and speciation of dolphin species

Using a multi-locus approach, in combination with the latest analytical methods, we have been studying the evolutionary history of dolphin species of the subfamily Delphininae. We have recently used paleoceanographic data to elucidate the demography and speciation of the genus *Delphinus* and, using a seascape genetics approach we suggested that environmental features such as sea surface temperature and chlorophyll concentration are currently playing a role in driving and maintaining population divergence in these species. In the near future we aim to expand these results by studying a sympatric genus of dolphins (*Stenella*), to further clarify the patterns and processes involved in population divergence and speciation not only in these animals, but also in the marine environment.

*CBA researchers: AR Amaral, MM Coelho.*

*International collaborators: LM Möller & L Beheregaray (Flinders Univ., Australia); H Rosenbaum (Wildlife Conservation Society, USA); G Amato (American Museum of Natural History, USA); KM Robertson & WF Perrin (Southwest Fisheries Science Center, NOAA, USA); S Siciliano (Marine Mammal Group Study, GEMM-Lagos and FIOCRUZ, Rio de Janeiro, Brazil).*

##### b. Phylogeography and historical demography of Procellariiform seabirds

Using a multi-locus coalescent-based approach, we aim to characterize the evolutionary relationships among populations of co-distributed pelagic seabird species, and discuss divergence scenarios in light of geological barriers. Results to date indicate that the Isthmus of Panama did not act as a major barrier to dispersal in these species. Conversely, Pleistocene paleo-oceanographic changes may have acted as strong vicariant mechanisms of population divergence. Non-physical barriers, such as allochronic breeding seasons between hemispheres and local adaptation, may act as reinforcing mechanisms of population divergence. In the future, we would like to expand our population sampling and explore the role of evolutionary forces, such as natural selection, in the genomic divergence of sympatric species of *Oceanodroma*.

*CBA researchers: MC Silva, MM Coelho.*

*International collaborators: VL Friesen (Queens University, Canada); R Wanless (Percy Fitzpatrick Institute of African Ornithology, South Africa); B Robertson (University of Otago, New Zealand).*

c. Phylogeography of the endemic subspecies of fire salamander from Southwest Portugal

We are carrying out a phylogeographic study of the endemic subspecies of fire salamander from SW Portugal, *Salamandra salamandra crespoides*, to clarify its evolutionary history and its geographic boundaries with neighboring subspecies. We are analyzing mitochondrial and nuclear DNA to identify possible contact zones and admixture among subspecies.

*CBA researchers: AC Silva, MM Coelho, C Fernandes (EG/ADC), R Rebelo, L Simões (ADC).*

d. Phylogeography and population genetics of Eurasian mustelids

We are investigating the phylogeography and population genetics of three Palearctic mustelid carnivores (European polecat, stone marten and weasel) to elucidate their evolutionary history and assess the role of historical and contemporary factors in shaping their population structure and gene flow across Eurasia. We are using the control region of mitochondrial DNA and species-specific microsatellite loci developed in our lab as molecular markers. These studies will help identifying evolutionarily significant units for conservation and increase our current knowledge of European phylogeography.

*CBA researchers: C Fernandes (EG/ADC), AC Silva (EG); M Costa, M Rodrigues, M Basto, M Santos-Reis (ADC).*

*International collaborators: J Merilla (Univ. of Helsinki, Finland - weasels); B Gómez-Moliner (Univ. of the Basque Country, Spain - stone martens); J Michaux (Univ. of Liège, Belgium - European polecats).*

e. Evolutionary processes underlying genetic diversity in endemic freshwater fish

We seek to infer the speciation history of Iberian Cyprinids in Western Iberia, taking into consideration the geological and environmental history of the region. We also have recently initiated the study of the impact of short-term events, like human induced habitat changes and severe droughts, in the genetic variability of threatened cyprinid species using natural populations and Natural History Collection specimens. In the next triennium, we will continue looking at the influence of landscape heterogeneity in shaping genetic structuring of endemic cyprinid species, both large-scale paleohistorical factors and also local landscape and environmental factors.

*CBA researchers: T Jesus, C Fernandes (EG/ADC), MJ Alves, N Mesquita, J Anjos, MM Coelho.*

f. Evolutionary process and taxonomic uncertainties in genets

The genus *Genetta* is one of the most controversial of the family Viverridae (Carnivora). We recently assessed the first comparative chromosome maps of *G. maculata* and two *G. genetta* subspecies with *Felis catus*. Results allowed to understand their karyotypic differentiation. We intend to

investigate in the near future more *Genetta* species, to help disentangling the evolutionary process underlying *Genetta* speciation.

*CBA researchers: MM Oom, RM Silva, J Kjällerström, MJ Collares-Pereira, C Fernandes (EG/ADC).*

*National collaborators: R Chaves & F Adegá (University of Trás-os-Montes e Alto Douro, Portugal).*

*International collaborators: T Raudsepp (Texas A&M University, USA).*