

EVOLUTIONARY GENETICS RESEARCH GROUP (EG)

Brief description of research lines

2) Hybridization in evolution and speciation

To understand the mechanisms involved in the persistence, diversification and speciation of hybrids, our group is currently studying different systems.

a. Evolutionary mechanisms behind hybridization in dolphins

We hypothesize that reticulate evolution either through ancient introgressive hybridization or hybrid speciation among two worldwide distributed species of the delphinid genus *Stenella* (*S. coeruleoalba* and *S. longirostris*) explain the origin of *Stenella clymene*, which is endemic to the Atlantic Ocean and the least known dolphin species. If proven, this will be one of the first cases of hybridization to be detected in wild marine mammals. We will use a wide array of molecular markers (mitochondrial DNA, microsatellites and SNPs; some of them obtained by NGS), to get a thorough genetic characterization of each putative parental and hybrid species. This study will provide insights on the evolutionary processes leading to species formation.

CBA researchers: AR Amaral, MM Coelho.

International collaborators: H Rosenbaum (Wildlife Conservation Society, USA); G Amato (American Museum of Natural History, USA); K Robertson & W Perrin (Southwest Fisheries Science Center, NOAA, USA); G Lovewell (Mote Marine Laboratory, USA).

b. Uncovering introgression processes in homoploid fish complexes

After the discovery of homoploid hybrid zones (HZs) involving the cyprinid (nase) species *Pseudochondrostoma duriense* or *P. polylepis* and *Achondrostoma oligolepis*, we are now concluding (i) the comparative cytogenetic analysis of almost all the "nase species" living in Portuguese inland waters; and (ii) the comparative genetic and cytogenetic analyses of fish from the three distinct HZs, using distinct molecular markers and CGH and WCP techniques. These approaches will help understanding introgression dynamics, namely which chromosome regions are preferentially involved in genomes' introgression. Thus, we expect to discover specific areas of genome compatibility and their role in speciation.

CBA researchers: C Pereira, MA Aboim, MJ Collares- Pereira.

International collaborators: P Rab (IAPG, Libechov – Czech Academy of Sciences, CR).

c. Uncovering hybridization processes in a unique allopolyploid fish complex

We are addressing questions of allopolyploid genome evolution using *Squalius alburnoides* complex as a model. This fish complex is characterized by a constant switch of genome composition in consecutive generations,

which very frequently involves a change in ploidy level. This leads to recurrent situations of potential genomic shock. Thus, we have been exploring: i) patterns of genome regulation, especially in dosage compensation; ii) mechanisms of gene silencing, namely methylation and miRNA's; iii) mechanisms of sexual determination and differentiation in hybrids of different genomic compositions and sex-genders; iv) the reproductive dynamics, including experimental sexual selection and mate-choice trials; and v) genome reshaping mechanisms. A parallel study with natural and artificial triploids and pentaploids *Poecilia formosa* and *Oryzias latipes* (medaka) is also ongoing, to achieve a deeper understanding of how genome expression regulation takes place in a hybrid genomic environment (allo genomic context) and in a system of multiple genome copies (polyploid).

CBA researchers: I Matos, M Machado, M Santos, A Inácio, MJ Collares-Pereira, MM Coelho.

National collaborators: V Barreto (Instituto Gulbenkian de Ciência, Oeiras); F Enguita & A R Grosso (Instituto de Medicina Molecular, Lisboa).

International collaborators: M Shartl & Y Wakamatsu (Univ. Würzburg, Germany); L Comai (UC Davis Genome Center, USA); J Bogart (Univ. Quebec, Canada); K Be (Univ. Berkeley, USA); N Cunado (Univ. Complutense, Spain); R Walter (Texas State University, USA).