Institute of Zoology and Biomedical Research

**Topic: The influence of interspecific gene flow on the integrity of mitonuclear coadaptation**

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**Background information:**

Proteins encoded by interacting mitochondrial and nuclear genes catalyze essential metabolic processes such as oxidative phosphorylation (OXPHOS) in the mitochondria of eukaryotic cells. The direct interaction of these proteins requires cooperation between mitonuclear allele combinations. However, the two genomes have different modes of inheritance, recombination and mutation rates. These differences have the potential to coerce reciprocal changes in interacting OXPHOS genes (mitonuclear coadaptation). In hybridizing species, mismatched combinations (mitonuclear incompatibilities), i.e. OXPHOS protein complexes with subunits from both of the parental species, could result in inferior enzymatic performance and reduced fitness of hybrid progeny. Selection for the maintenance of integrity of coadaptedmitonuclear gene complexes may have major consequences for local adaptation, reproductive isolation and speciation. However, apart from a few systems, little is known of the role of mitonuclear match and mismatch on speciation. In particular, the extent of mitonuclear coadaptation among closely related species and the dynamics of mitonuclear associations in hybridizing species are not well understood. Moreover, the fitness effects of mitonuclear incompatibilities have been assessed in very few species.

**The main question to be addressed in the project:**

What is the effect of gene flow via hybridization on co-adapted mitonuclear gene complexes? Do co-adapted complexes flow more freely between hybridizing species than randomly chosen nuclear loci?

The 1st aim of the project will be an assessment of mitonuclear co-adaptation across a broad panel of hybridizing species, including deeply divergent lineages within species. We will focus primarily on vertebrates, especially amphibians and reptiles.

The 2nd stage of the project will take advantage of several amphibian species complexes in which the mtDNA of one species has introgressed onto the nuclear background of a different species, with purportedly little or no nuclear gene flow. We will test the hypothesis that mtDNA replacement has entailed the introgression of coadapted nuclear genes due to strong selection for mitonuclear integrity.

The third aim of the project, contingent on the results of stage 2, will check for differential performance of lineages with mismatched mitochondrial and nuclear OXPHOS components, with an aim to assess whole organism (i.e. tadpole) fitness. We hypothesize that mismatched individuals will have lower fitness under a range of environmental gradients.

**Information on the methods/description of work:**

**A major component of the project will involve labwork and bioinformatics using targeted sequencing approaches after establishing gene models from transcriptome/genomic data for each of the species complexes. Samples from some systems, as well as transcriptomes, will be available from collaborators. In other systems, the project will involve *de novo* collection of data, including field work (collection of tissue samples from selected species complexes including *Pelophylax*, *Lissotriton*, *Ichthyosaura*). New transcriptomes will be generated if necessary. Hypothesis tests will be centered around the assumptions that, if there is selection maintaining the integrity of co-adapted OXPHOS complexes across species boundaries, then genetic differentiation between hybridizing species at OXPHOS genes should be lower compared to a random sample of nuclear genes. On the other hand, we should observe higher linkage disequilibrium among OXPHOS genes as well as genealogical discordance between OXPHOS genes and a randomly selected set of nuclear genes. Further work will involve the husbandry of amphibian larvae for experimental fitness assays.**

**Additional information (e.gSpecial requirements from the student):**Candidates are expected to have a strong interest in evolutionary biology and a basic knowledge of molecular ecology.

**Place/name of potential foreign collaborator:** CIBIO - Research Center in Biodiversity and Genetic Resources, InBIO Associate Laboratory, University of Porto, Portugal

**References:**

Gershoni, M., Templeton, A. R., &Mishmar, D. (2009). Mitochondrial bioenergetics as a major motive force of speciation. *Bioessays*, 31(6), 642-650.

Morales, H. E., Pavlova, A., Amos, N., Major, R., Kilian, A., Greening, C., &Sunnucks, P. (2018). Concordant divergence of mitogenomes and a mitonuclear gene cluster in bird lineages inhabiting different climates. *Nature Ecology & Evolution*2(8), 1258.

Hill, G. E. (2019). Reconciling the mitonuclear compatibility species concept with rampant mitochondrial introgression. *Integrative and Comparative Biology*, [doi: 10.1093/icb/icz019](https://doi.org/10.1093/icb/icz019)