

Looking for evidence of co-evolution between nuclear and mitochondrial genomes in a situation of interspecific hybridization

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Although the mitochondrial genome is the most studied in biodiversity surveys, the relationship between its sequence variation and functional evolution, as well as its co-evolution with the nuclear genome, remain little documented and tested. We here take advantage of a peculiar biological situation to tackle this question. In northern but not in southern Iberian Peninsula, the Iberian hare, *Lepus granatensis*, harbors high frequencies of mtDNA from *L. timidus*. Since the latter is an arctic/boreal species and there is evidence in other species for a role of mtDNA in adaptation to cold, some functional differences may exist between the mtDNAs of the two species. We therefore ask whether the strong north-south differentiation for mtDNA in *L. granatensis* is paralleled by differentiation at some nuclear genes, as a result of either co-introgression with mtDNA or evolution after mtDNA introgression. If genes with such patterns were preferentially involved in interactions with mitochondrial genes, we would have a strong case for coevolution between the two genomes, for the functional role of mtDNA variation, and perhaps the adaptive nature of interspecific mtDNA introgression. We collected transcriptome sequencing data from 5 *L. granatensis* sampled in northern and 5 in southern populations, and also from *L. timidus*. Mapping of the *Illumina* sequence reads onto a de novo assembly of hares' transcripts was performed using *bwa*, and SNP and genotype calling was done using *samtools*. Preliminary analyses suggest that F_{ST} values between northern and southern samples based on over 3000 nuclear genes are generally very low, with an average close to zero. However, a small number of genes present high levels of geographic structure, and some of these have variation consistent with introgression from *L. timidus*. These results suggest that introgression of nuclear genes co-occurred with mtDNA but affected a small number of genes. Interestingly, a gene ontology analysis revealed a significant excess of functions related with mitochondria in the 1% of nuclear genes with the highest F_{ST} (irrespective of evidence for introgression) which may indicate adaptive co-evolution between the mitochondrial and nuclear genomes, accompanying introgression of mtDNA.

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