Hares, turtles, and the race to unravel genetic diversity

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Iberian Hare. Credit: Pedro Moreira, 2009

If you thought the only way to solve a puzzle was by looking at a picture of its end result as you go, guess again. Using an innovative approach to the study of genetic diversity, an international research team, comprising three researchers from the Research Center in Biodiversity and Genetic Resources – CIBIO/InBIO Laboratório Associado, in Portugal, demonstrated that it is possible to unveil the mechanisms underlying genetic diversity and evolutionary change, by focusing on species that are not commonly used as model-organisms.

In the age of genome analysis, most of the strategies put forth to tackle

genetic diversity have focused on a very limited number of species, for which well-annotated reference genomes are available, as for instance, fruit flies and humans. However, in a recent study, published in the latest issue of *PLOS Genetics*, Gayral, Melo-Ferreira and colleagues overcome the traditional paradigms of genomic analysis and their potential limitations, and show that it is possible to explore a broad range of organisms for whom that information is still incomplete or unavailable, as is the case of hares, turtles, oysters or even termites.

In a time when full genome sequencing has become quite popular in well-developed countries, José Melo-Ferreira and colleagues suggest a strategy based in next-generation sequencing, which allows obtaining insightful and reliable data from new information that is largely unknown. In spite of the inevitable challenges it presents, this approach is very stimulating, as sustained by the researcher from CIBIO, who states that "... it is almost like solving a puzzle without having access to the final picture. We have shown that, instead of attempting to reconstruct the genetic profile and evolutionary history of the individuals it is possible to efficiently attain that information, without having those data to begin with. This opens new opportunities for the study of the genomes of a wide range of species, which is likely to provide a deeper understanding of the evolutionary process".

In addition to this extraordinary technological advancement, it is important to highlight the important contribution of this study for he understanding of biological diversity. A hypothesis that is now widely accepted by the research community suggests that population size is the most determining aspect of a species' ability to retain beneficial genetic information and remove harmful information. For instance, it is though that the diversity and adaptive capacity of invertebrates, whose populations are exceedingly numerous, are above those observed in vertebrates, typically with lower population sizes. Nevertheless, this study reveals that this is not at all a straightforward issue. As José Melo-

Ferreira explains, "... in a way, our results show that this line of reasoning is too simplistic. Actually, the utter discrepancy that until now was thought to exist between the adaptive capacity of vertebrates and invertebrates, is substantially lessened if we turn our attention to species that are usually not considered". Hence, this study paves the way to new and promising perspectives on the study of major determinants of evolution, which bare significant implications for biodiversity research and the outline of conservation strategies.

More information: Gayral, P. et al. (2013) Reference-Free Population Genomics from Next-Generation Transcriptome Data and the VertebrateInvertebrate Gap. *PLoS Genet* 9(4): e1003457. doi:10.1371/journal.pgen.1003457

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