Peer Community In
Evolutionary Biology

A genomic perspective is needed for the re-evaluation of species boundaries, evolutionary trajectories, and conservation strategies of the Galápagos giant tortoises

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doi: 10.24072/pci.evolbiol.100031

Cite as: Fontaine MC. 2017. A genomic perspective is needed for the re-evaluation of species boundaries, evolutionary trajectories, and conservation strategies of the Galápagos giant tortoises. *Peer Community in Evolutionary Biology*, 100031. doi: 10.24072/pci.evolbiol.100031

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A recommendation of

Loire E, Galtier N. 2017. **Lacking conservation genomics in the giant Galápagos tortoise.** *BiorXiv*, 101980, ver. 4 of 26th September 2017. doi: 10.1101/101980

Published: 26th September 2017

Genome-wide data obtained from even a small number of individuals can provide unprecedented levels of detail about the evolutionary history of populations and species [1], determinants of genetic diversity [2], species boundaries and the process of speciation itself [3]. Loire and Galtier [4] present a clear example, using the emblematic Galápagos giant tortoise (*Chelonoidis nigra*), of how multi-species comparative population genomic approaches can provide valuable insights about population structure and species delimitation even when sample sizes are limited but the number of loci is large and distributed across the genome.

Galápagos giant tortoises are endemic to the Galápagos Islands and are currently recognized as an endangered, multi-species complex including both extant and extinct taxa. Taxonomic definitions are based on morphology, geographic isolation and population genetic evidence based on short DNA sequences of the mitochondrial genome (mtDNA) and/or a dozen or so nuclear microsatellite loci [5-8]. The species complex enjoys maximal protection. Population recoveries have been quite successful and spectacular conservation programs based on mitochondrial genes and microsatellites are ongoing. This includes for example individual translocations, breeding program, "hybrid" sterilization or removal, and resurrection of extinct lineages).

In 2013, Loire et al. [9] provided the first population genomic analyses based on genome scale data (~1000 coding loci derived from blood-transcriptomes) from five individuals, encompassing three putative "species": *Chelonnoidis becki*, *C. porteri* and *C. vandenburghi*. Their results raised doubts about the validity/accuracy of the currently accepted designations of "genetic distinctiveness". However, the implications for conservation and management have remained unnoticed.

In 2017, Loire and Galtier [4] have re-appraised this issue using an original multi-species comparative population genomic analysis of their previous data set [9]. Based on a comparison of 53 animal species, they show that both the level of genome-wide neutral diversity (πS) and level of population structure estimated using the inbreeding coefficient (F) are much lower than would be expected from a sample covering multiple species. The observed values are more comparable to those typically reported at the "among population" level within a single species such as human (*Homo sapiens*). The authors go to great length to assess the sensitivity of their method to detect population structure (or lack thereof) and show that their results are robust to potential issues, such as contamination and sequencing errors that can occur with Next Generation Sequencing techniques; and biases related to the small sample size and sub-sampling of individuals. They conclude that published mtDNA and microsatellite-based assessment of population structure and species designations may be biased towards over-splitting.

This manuscript is a very good read as it shows the potential of the now relatively affordable genome-wide data for helping to both resolve and clarify population and species boundaries, illuminate demographic trends, evolutionary trajectories of isolated groups, patterns of connectivity among them, and test for evidence of local adaptation and even reproductive isolation. The comprehensive information provided by genome-wide data can critically inform and assist the development of the best strategies to preserve endangered populations and species. Loire and Galtier [4] make a strong case for applying genomic data to the Galápagos giant tortoises, which is likely to redirect conservation efforts more effectively and at lower cost. The case of the Galápagos giant tortoises is certainly a very emblematic example, which will find an echo in many other endangered species conservation programs.

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Appendix

Reviews by four anonymous referees: http://dx.doi.org/10.24072/pci.evolbiol.100031