



Editorial: Assessing Biodiversity in the Phylogenomic Era

Michael G. Campana^{1*}, Melissa T. R. Hawkins² and Susana Caballero³

¹ Center for Conservation Genomics, Smithsonian National Zoological Park and Conservation Biology Institute, Smithsonian Institution, Washington, DC, United States, ² Department of Vertebrate Zoology, Division of Mammals, National Museum of Natural History, Smithsonian Institution, Washington, DC, United States, ³ Laboratorio de Ecología Molecular de Vertebrados Acuáticos, Departamento de Ciencias Biológicas, Universidad de Los Andes, Bogotá, Colombia

Keywords: biodiversity, phylogenomics, taxonomy, species delimitation, population structure, hybridization, conservation

Editorial on the Research Topic

Assessing Biodiversity in the Phylogenomic Era

Over the last 15 years, rapid advances in high-throughput sequencing technology and bioinformatics have permitted the generation of phylogenomic datasets across the tree-of-life. Ongoing phylogenomic analyses range in scope from in-depth analyses of single species in time and space to attempts to sequence the genomes of every species on earth (Earth BioGenome Project: Lewin et al., 2018). These projects are necessary and timely due to the ongoing mass extinction known as the “Anthropocene” (Ceballos et al., 2020). Assessments of extant and extinct biodiversity is required to understand the evolution of life on earth, guide environmental policies, and inform species conservation efforts.

In this Research Topic, we collect nine research articles using current phylogenomic techniques to (re)assess patterns of biodiversity across the tree-of-life. Articles range in content from new bioinformatic tools to combine disparate genomic datasets (Fountain et al.) to species delimitation (Leaché et al.), disentangling reticulate speciation (Grummer et al.; Nge et al.), population structure and demographic analyses (Timm et al.; Martínez-García et al.), and metagenomics and microbiomics (Kaufmann and Cassin-Sackett; Lozano Mojica and Caballero; O’Rourke et al.). The breath of subjects covered in this Research Topic illustrates the wide utility of phylogenomic methods for assessing biodiversity.

Due to the proliferation of phylogenomic techniques, one of the current challenges is the combination of datasets from disparate sequencing technologies ranging from traditional single gene Sanger sequencing to the multitude of different high-throughput approaches. Additionally, sequencing technologies are often developed for specific model organisms, necessitating their adaptation to non-model organisms. Fountain et al. illustrate that iScan microarrays can be adapted to non-model organisms for high-throughput single nucleotide polymorphism (SNP) discovery. They also develop a script to combine SNP datasets from multiple sequencing technologies to make the best use of novel and existing data. By using these methods, Fountain et al. are able to genotype great apes at a far higher resolution than previously possible.

The increased resolution of phylogenomic methods have revealed fine-scale population structure (e.g., Cortes-Rodriguez et al., 2019; Gallego-García et al., 2021) and possible cryptic species in previously designated species and populations (e.g., Jin et al., 2020). The taxonomic significance of this structure needs further evaluation to determine whether these populations are significantly reproductively isolated. Here, Leaché et al. use double digest Restriction-Associated sequencing (ddRADseq) and a reference-based taxonomy to delimit species in the Greater Short-horned Lizard species complex (*P. hernandesi*).

OPEN ACCESS

Edited and reviewed by:

Rodney L. Honeycutt,
Pepperdine University, United States

*Correspondence:

Michael G. Campana
campanam@si.edu

Specialty section:

This article was submitted to
Phylogenetics, Phylogenomics, and
Systematics,
a section of the journal
Frontiers in Ecology and Evolution

Received: 27 October 2021

Accepted: 31 October 2021

Published: 03 December 2021

Citation:

Campana MG, Hawkins MTR and
Caballero S (2021) Editorial: Assessing
Biodiversity in the Phylogenomic Era.
Front. Ecol. Evol. 9:803188.
doi: 10.3389/fevo.2021.803188

Additionally, phylogenomic analyses routinely detect population admixture and hybridization, which can both generate and reduce biodiversity (e.g., Lamichhaney et al., 2015; Grossen et al., 2016; Kearns et al., 2018; Lavretsky et al., 2019). Introgression can be a frequent source of cytonuclear discordance via plastid capture (e.g., Hawkins et al., 2016), necessitating the analysis of both nuclear and plastid sequences to reconstruct the species tree. Using hybridization enrichment, Nge et al. identified repeated introgression and chloroplast capture in the Australian endemic plant genus *Adenanthos*. Similarly, Grummer et al. identified repeated hybridization between four species of *Liolaemus* lizards in Argentina using ddRADseq and mitochondrial DNA. These hybridization events necessitate revisions to taxonomic and conservation units, especially in legal systems where species protection is predicated on taxonomic distinctiveness (e.g., Waples et al., 2018).

Beyond redefinition of taxonomic units, phylogenomic techniques have critical implications for practical population management. Lozano Mojica and Caballero analyze environmental DNA from Colombian water bodies to assess vertebrate species richness and revise species ranges in this critically understudied biodiversity hotspot. Both Timm et al. and Martínez-García et al. use phylogenomic methods to inform fisheries management for commercially important species that underwent recent severe population collapses. Timm et al. use ddRADseq to identify previously unknown population structure in the Gulf of Mexico pink shrimp (*Farfantepenaeus duorarum*) and largely confirm an existing model of larval transport (Criales et al., 2000). By comparing whole mitogenomes obtained from 48 archaeological cod (*Gadus morhua*) specimens to 496 recent samples, Martínez-García et al. show that cod mitogenomic diversity reflects past demographic history rather than recent and historical overfishing. Analysis of nuclear

genomes and greater sample sizes may better resolve impacts of overexploitation by humans.

Moreover, phylogenomics has expanded beyond the host organisms—investigations now routinely include analyses of associated microbiomes, pathogens, and diets. Kaufmann and Cassin-Sackett investigate patterns of microbial succession in sedimentary DNA found in Black-tailed prairie dogs (*Cynomys ludovicianus*) burrows. Black-tailed prairie dogs have undergone significant die-offs due to outbreaks of sylvatic plague (*Yersinia pestis*). Microbial communities in the burrows reflect usage patterns of the prairie dogs and the deposition of corpses due to plague infection. Using fecal DNA, O'Rourke et al. analyze the diet and foraging ecology of the endangered Indiana bat (*Myotis sodalis*). Their analyses revealed that Indiana bats were generalist consumers that most frequently foraged within riparian habitats. Their results indicate that conservation of the Cypress Creek National Wildlife Refuge's riparian habitat is critical to the Indiana bat's conservation.

Phylogenomic techniques are rapidly displacing earlier single genetic marker analyses. As sequencing throughputs continue to increase and costs continue to drop, we anticipate that these methods will only become more important. The articles in this Research Topic provide a snapshot of the current state-of-the-art.

AUTHOR CONTRIBUTIONS

MC drafted the manuscript. All authors revised and approved the final manuscript.

FUNDING

The Smithsonian Institution supported MC and MH.

REFERENCES

- Ceballos, G., Ehrlich, P. R., and Raven, P. H. (2020). Vertebrates on the brink as indicators of biological annihilation and the sixth mass extinction. *Proc. Natl. Acad. Sci. U.S.A.* 117, 13596–13602. doi: 10.1073/pnas.1922686117
- Cortes-Rodriguez, N., Campana, M. G., Berry, L., Faegre, S., Derrickson, S. R., Ha, R. R., et al. (2019). Population genomics and structure of the critically endangered Mariana Crow (*Corvus kubaryi*). *Genes* 10:187. doi: 10.3390/genes10030187
- Criales, M. M., Bello, M. J., and Yeung, C. (2000). Diversity and recruitment of penaeoid shrimps (Crustacea: Decapoda) at Bear Cut, Biscayne Bay, Florida, USA. *Bull. Mar. Sci.* 67, 773–788. Available online at: <https://www.ingentaconnect.com/content/umrsmas/bullmar/2000/00000067/00000002/art00007>
- Gallego-García, N., Caballero, S., and Shaffer, H. B. (2021). Are genomic updates of well-studied species worth the investment for conservation? a case study of the Critically Endangered Magdalena river turtle. *J. Hered.* esab063. doi: 10.1093/jhered/esab063
- Grossen, C., Seneviratne, S. S., Croll, D., and Irwin, D. E. (2016). Strong reproductive isolation and narrow genomic tracts of differentiation among three woodpecker species in secondary contact. *Mol. Ecol.* 25, 4247–4266. doi: 10.1111/mec.13751
- Hawkins, M. T. R., Leonard, J. A., Helgen, K. M., McDonough, M. M., Rockwood, L. L., and Maldonado, J. E. (2016). Evolutionary history of endemic Sulawesi squirrels constructed from UCEs and mitogenomes sequenced from museum specimens. *BMC Evol. Biol.* 16:80. doi: 10.1186/s12862-016-0650-z
- Jin, M., Zwick, A., Słipiński, A., and de Keyser, R., Pang, H. (2020). Museomics reveals extensive cryptic diversity of Australian prionine longhorn beetles with implications for their classification and conservation. *Syst. Entomol.* 45, 745–770. doi: 10.1111/syen.12424
- Kearns, A. M., Restani, M., Szabo, I., Schröder-Nielsen, A., Kim, J. A., Richardson, H. M., et al. (2018). Genomic evidence of speciation reversal in ravens. *Nat. Commun.* 9:906. doi: 10.1038/s41467-018-03294-w
- Lamichhaney, S., Berglund, J., Almén, M. S., Maqbool, K., Grabherr, M., Martínez-Barrio, A., et al. (2015). Evolution of Darwin's finches and their beaks revealed by genome sequencing. *Nature* 518, 371–375. doi: 10.1038/nature14181
- Lavretsky, P., McInerney, N. R., Mohl, J. E., Brown, J. I., James, H. F., McCracken, K. G., et al. (2019). Assessing changes in genomic divergence following a century of human-mediated secondary contact among wild and captive-bred ducks. *Mol. Ecol.* 29, 578–595. doi: 10.1111/mec.15343
- Lewin, H. A., Robinson, G. E., Kress, W. J., Baker, W. J., Coddington, J., Crandall, K. A., et al. (2018). Earth BioGenome Project: sequencing life for the future of life. *Proc. Natl. Acad. Sci. U.S.A.* 115, 4325–4333. doi: 10.1073/pnas.1720115115
- Waples, R. S., Kays, R., Fredrickson, R. J., Pacifici, K., and Mills, L. S. (2018). Is the red wolf a listable unit under the US Endangered species act? *J. Hered.* 109, 585–597. doi: 10.1093/jhered/esy020

Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's Note: All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

At least a portion of this work is authored by Michael G. Campana and Melissa T. R. Hawkins on behalf of the U.S. Government and, as regards Dr. Campana, Dr. Hawkins, and the U.S. Government are not subject to copyright protection in the United States. Foreign and other copyrights may apply. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC-BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.