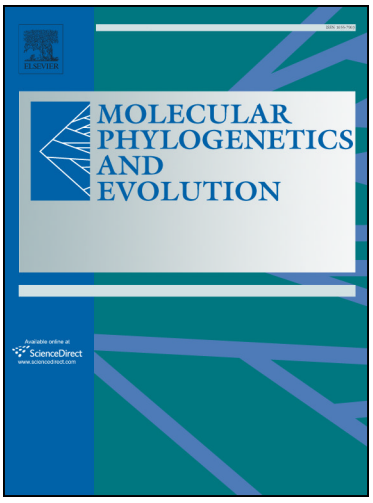

Exon-based phylogenomics strengthens the phylogeny of Neotropical cichlids and identifies remaining conflicting clades (Cichliformes: Cichlidae: Cichlinae)

Katriina L. Ilves, Dax Torti, Hernán López-Fernández

PII: S1055-7903(17)30521-3
DOI: https://doi.org/10.1016/j.ympev.2017.10.008
Reference: YMPEV 5944

To appear in: *Molecular Phylogenetics and Evolution*

Received Date: 13 July 2017
Revised Date: 5 October 2017
Accepted Date: 6 October 2017

Please cite this article as: Ilves, K.L., Torti, D., López-Fernández, H., Exon-based phylogenomics strengthens the phylogeny of Neotropical cichlids and identifies remaining conflicting clades (Cichliformes: Cichlidae: Cichlinae), *Molecular Phylogenetics and Evolution* (2017), doi: https://doi.org/10.1016/j.ympev.2017.10.008

Exon-based phylogenomics strengthens the phylogeny of Neotropical cichlids and identifies remaining conflicting clades (Cichliformes: Cichlidae: Cichlinae)

Katriina L. Ilves[1,2*], Dax Torti[3,4], and Hernán López-Fernández[1,5]

[1] Department of Natural History, Royal Ontario Museum, 100 Queen's Park, Toronto, ON M5S 2C6 Canada

[2] Current address: Biology Department, Pace University, 1 Pace Plaza, New York, NY 10038

[3] Donnelly Sequencing Center, University of Toronto, 160 College Street, Toronto, ON M5S 3E1 Canada

[4] Current address: Ontario Institute for Cancer Research, MaRS Center, 661 University Avenue, Toronto, ON M5G 0A3 Canada

5 Department of Ecology and Evolutionary Biology, University of Toronto, 25 Willcocks Street, Toronto, ON M5S 3B2 Canada

*Corresponding author at: Biology Department, Pace University, 1 Pace Plaza, New York, NY 10038; email: katriina.ilves@gmail.com

Abstract

The phenotypic, geographic, and species diversity of cichlid fishes have made them a group of great interest for studying evolutionary processes. Here we present a targeted-exon next-generation sequencing approach for investigating the evolutionary relationships of cichlid fishes (Cichlidae), with focus on the Neotropical subfamily Cichlinae using a set of 923 primarily single-copy exons designed through mining of the