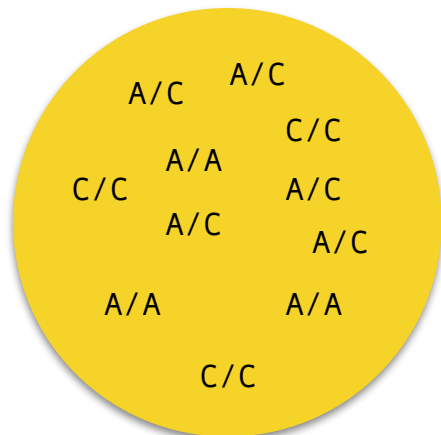


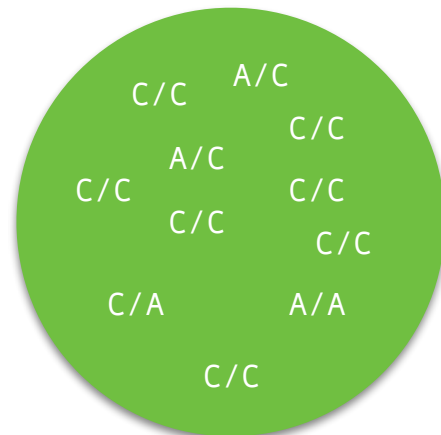
Population Genetics



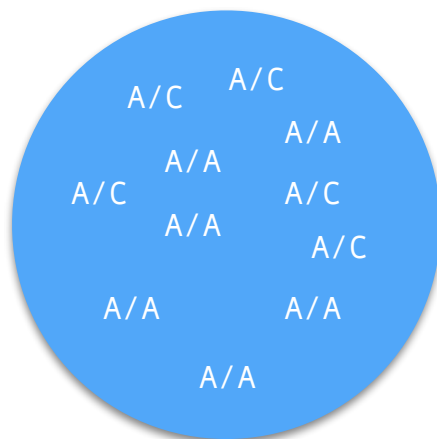
Phylogenetics



Population 1



Population 2



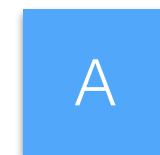
Population 3



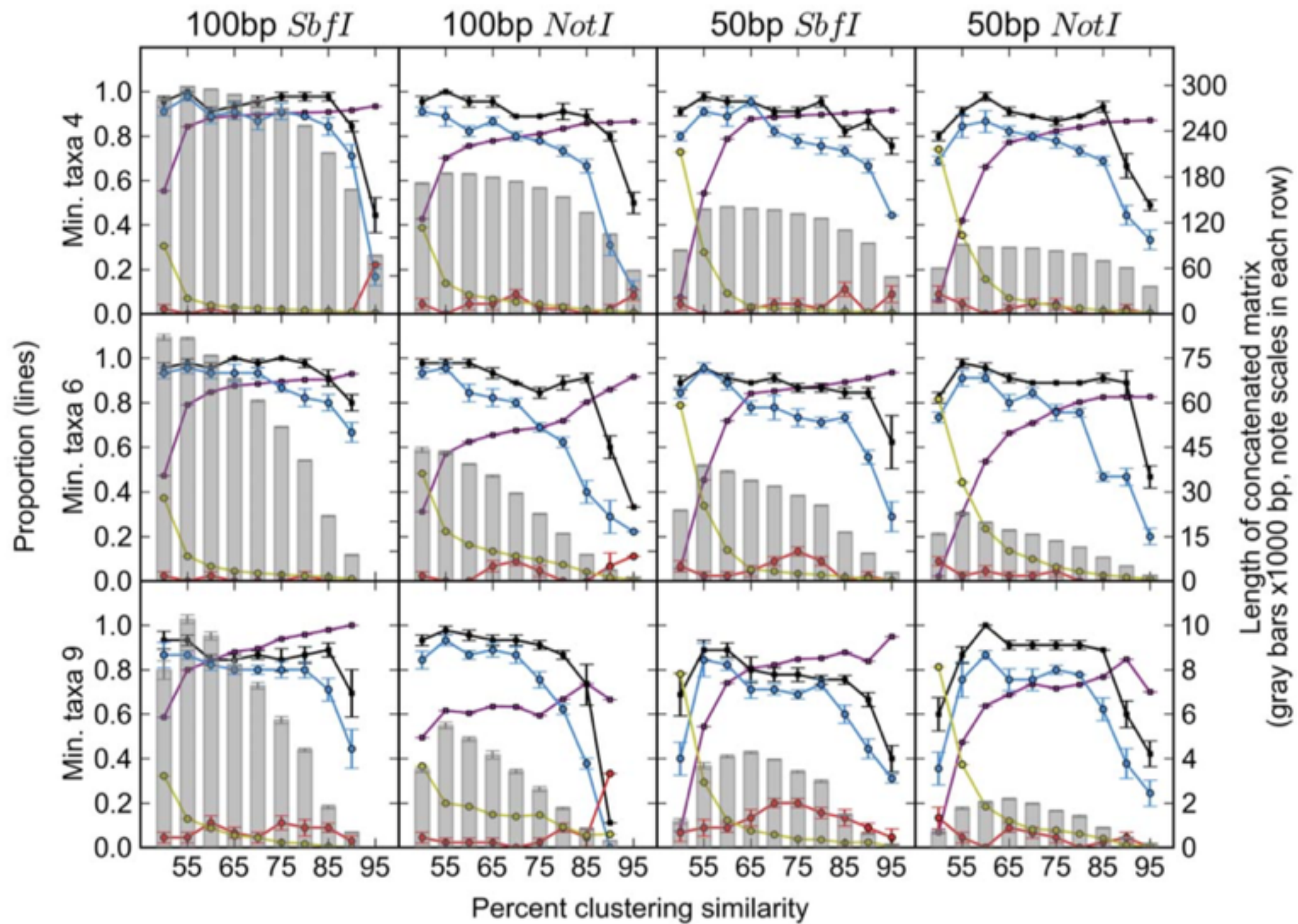
Species 1



Species 2



Species 3

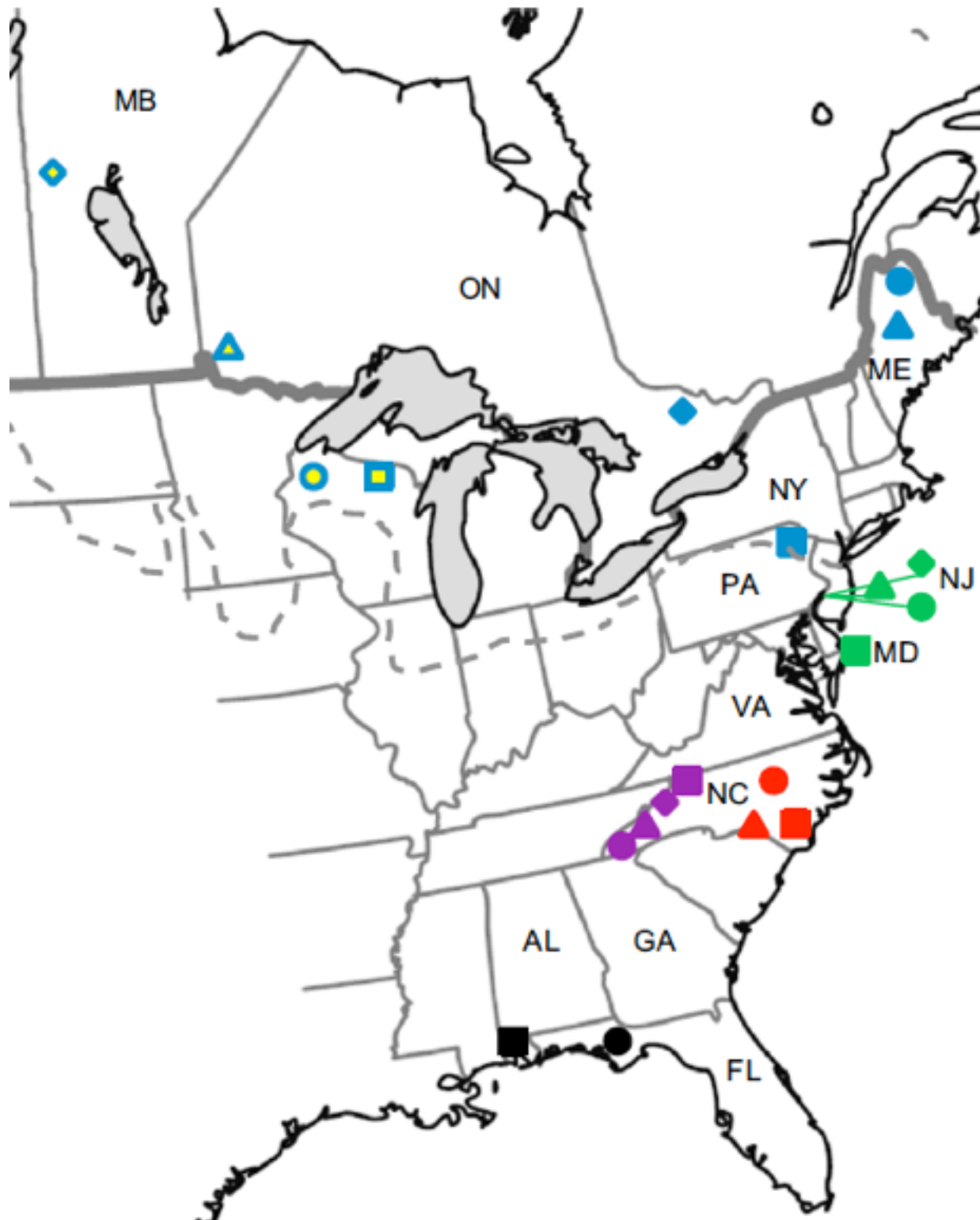


Inferring Phylogenies from RAD Sequence Data

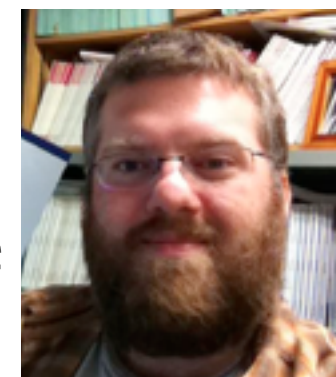
Benjamin E. R. Rubin^{1,2*}, Richard H. Ree³, Corrie S. Moreau³

¹ Committee on Evolutionary Biology, University of Chicago, Chicago, Illinois, United States of America, ² Department of Zoology, Field Museum of Natural History, Chicago, Illinois, United States of America, ³ Department of Botany, Field Museum of Natural History, Chicago, Illinois, United States of America

The pitcher plant mosquito, *Wyeomyia smithii* a model for evolution due to climate change

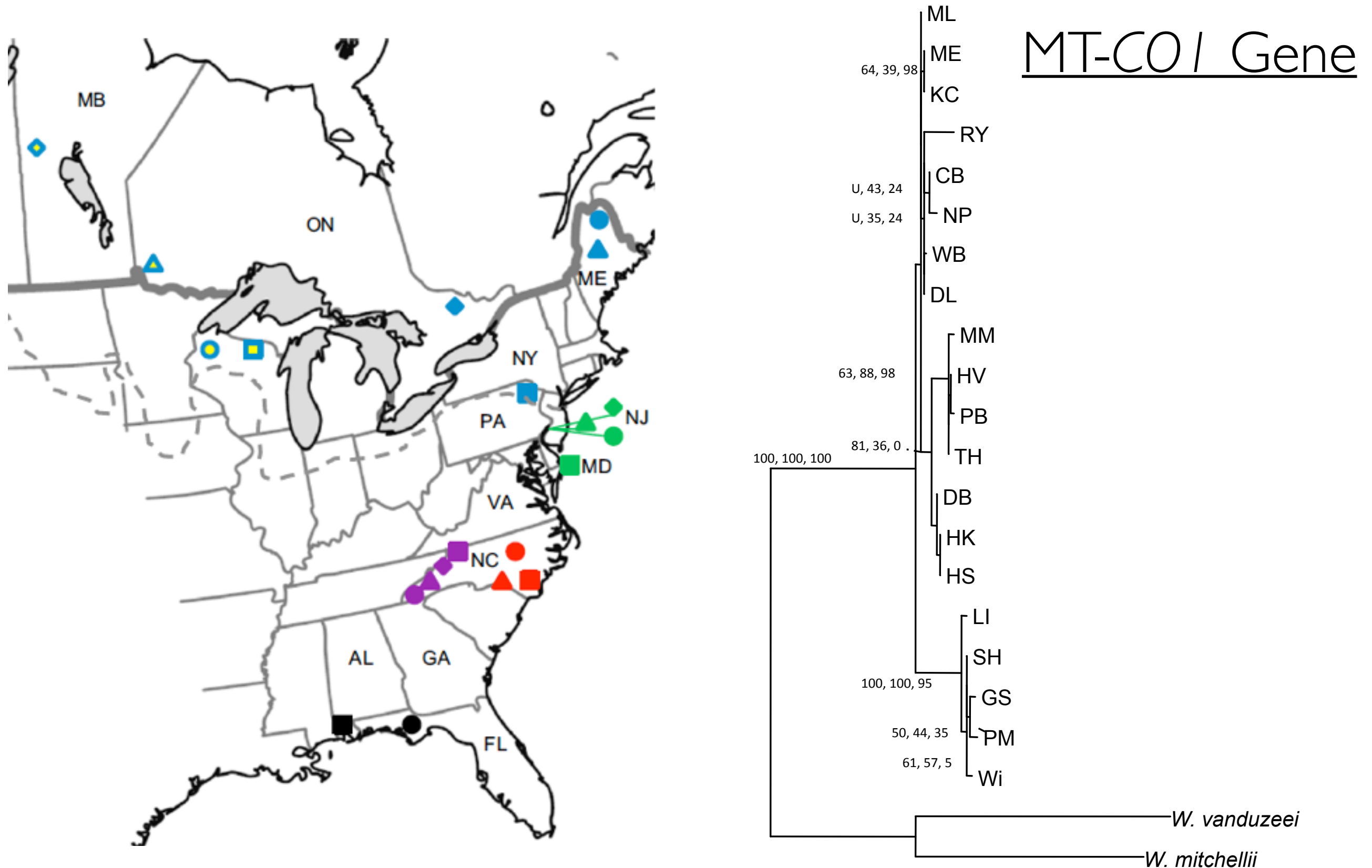


Paul
Hohenlohe

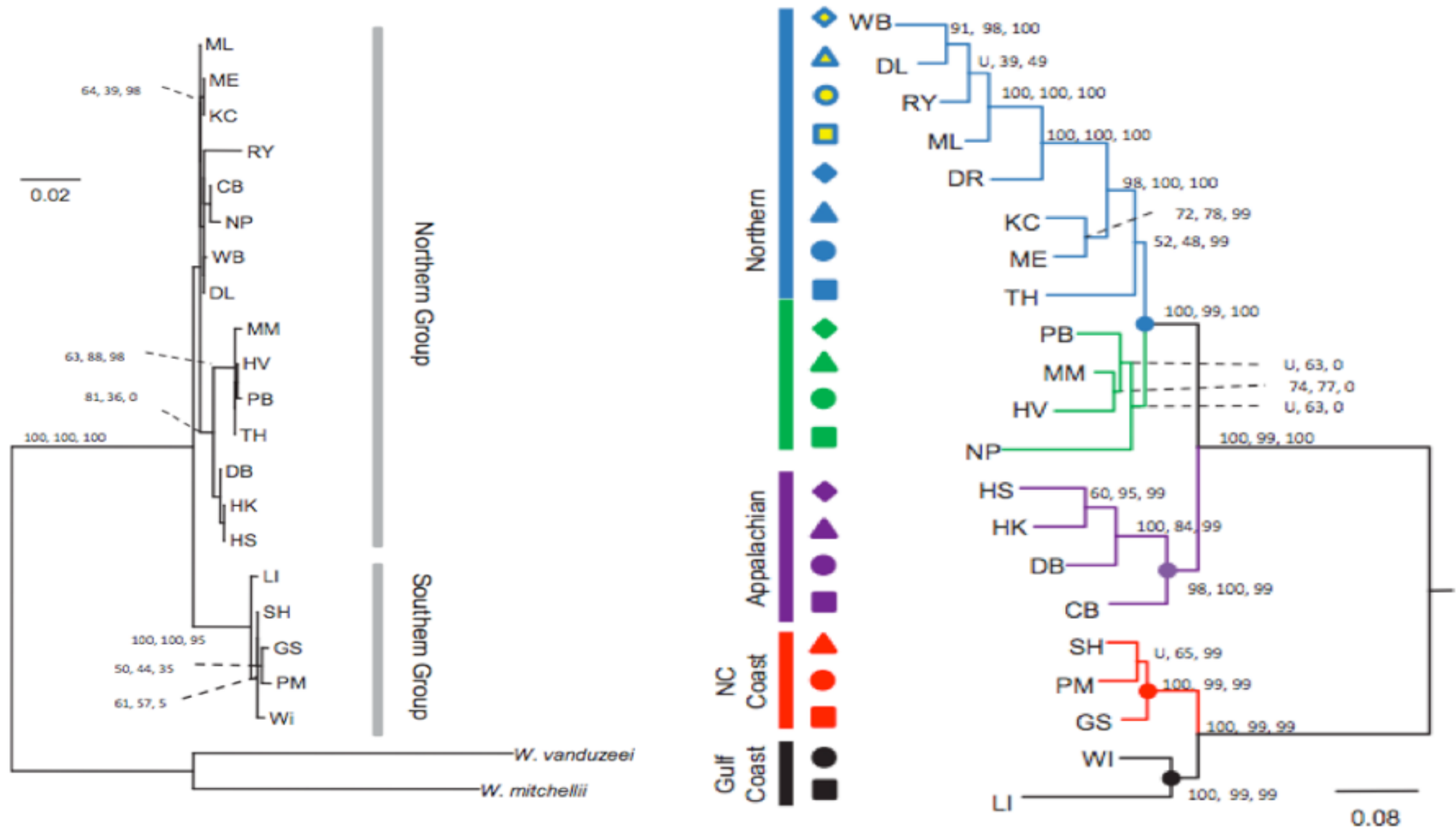


Kevin
Emerson

Resolving post-glacial phylogeography in *Wyeomyia smithii*



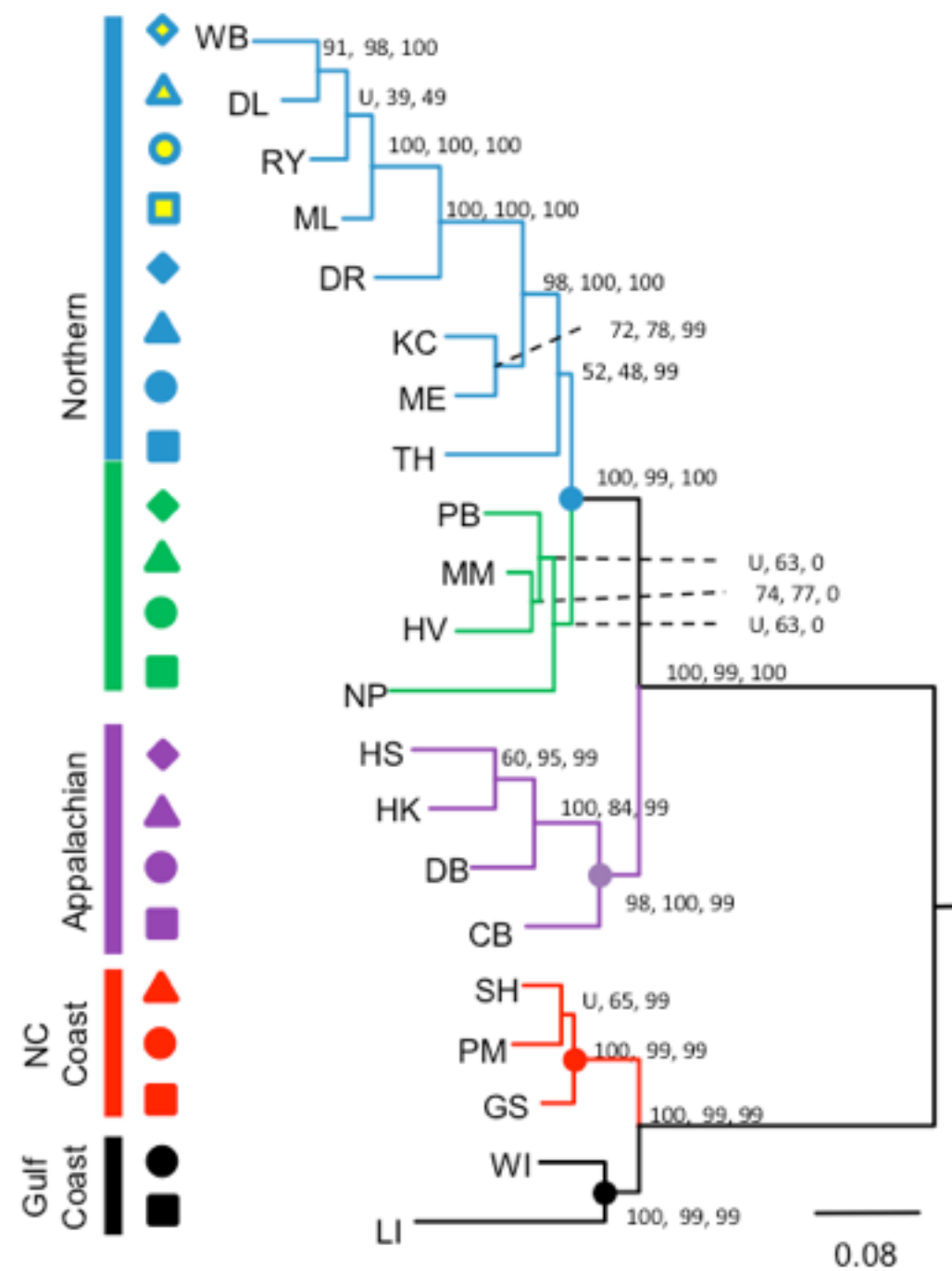
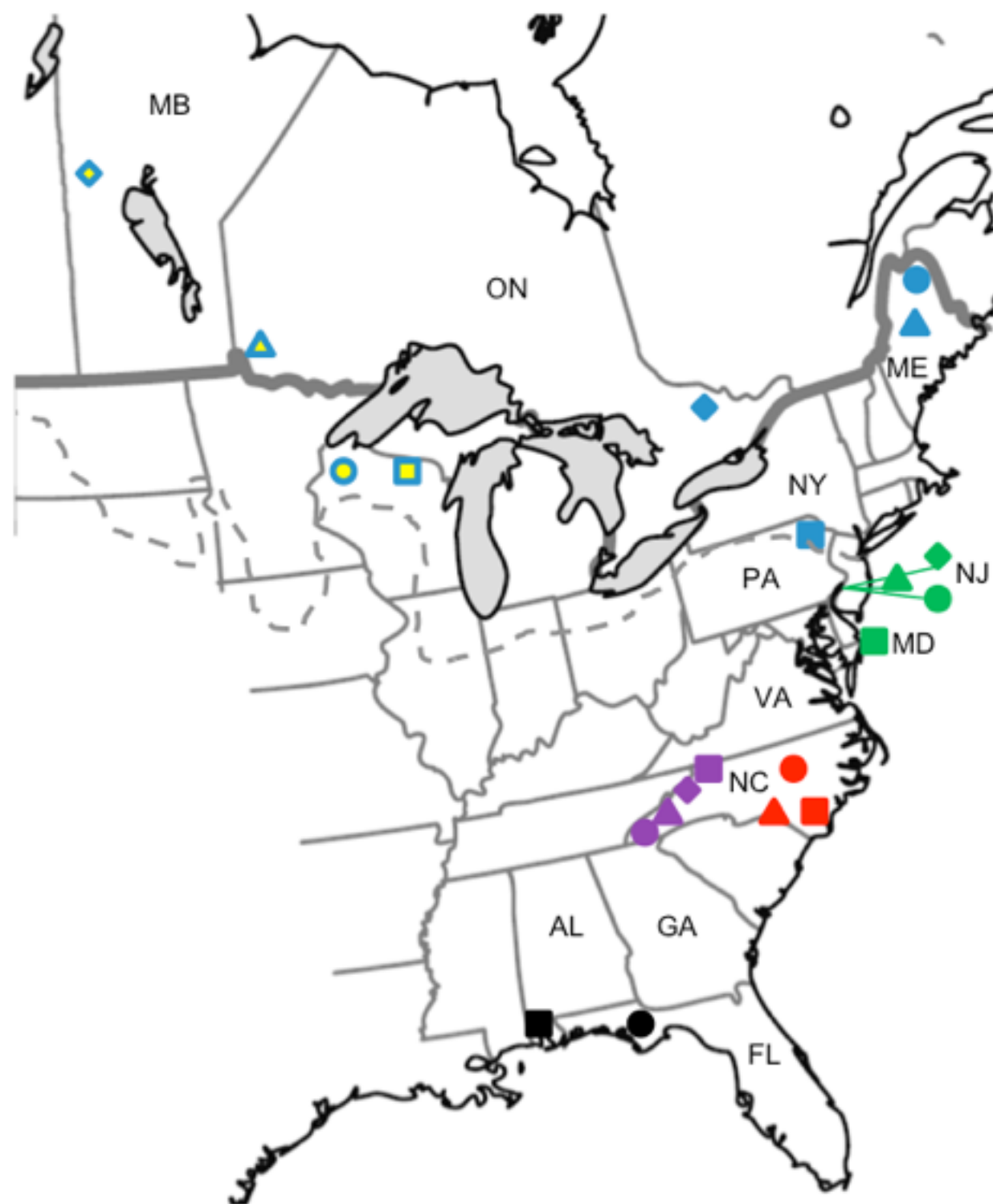
Genomic Data Improves Resolution



Resolving postglacial phylogeography using high-throughput sequencing

Kevin J. Emerson¹, Clayton R. Merz, Julian M. Catchen, Paul A. Hohenlohe, William A. Cresko, William E. Bradshaw, and Christina M. Holzapfel

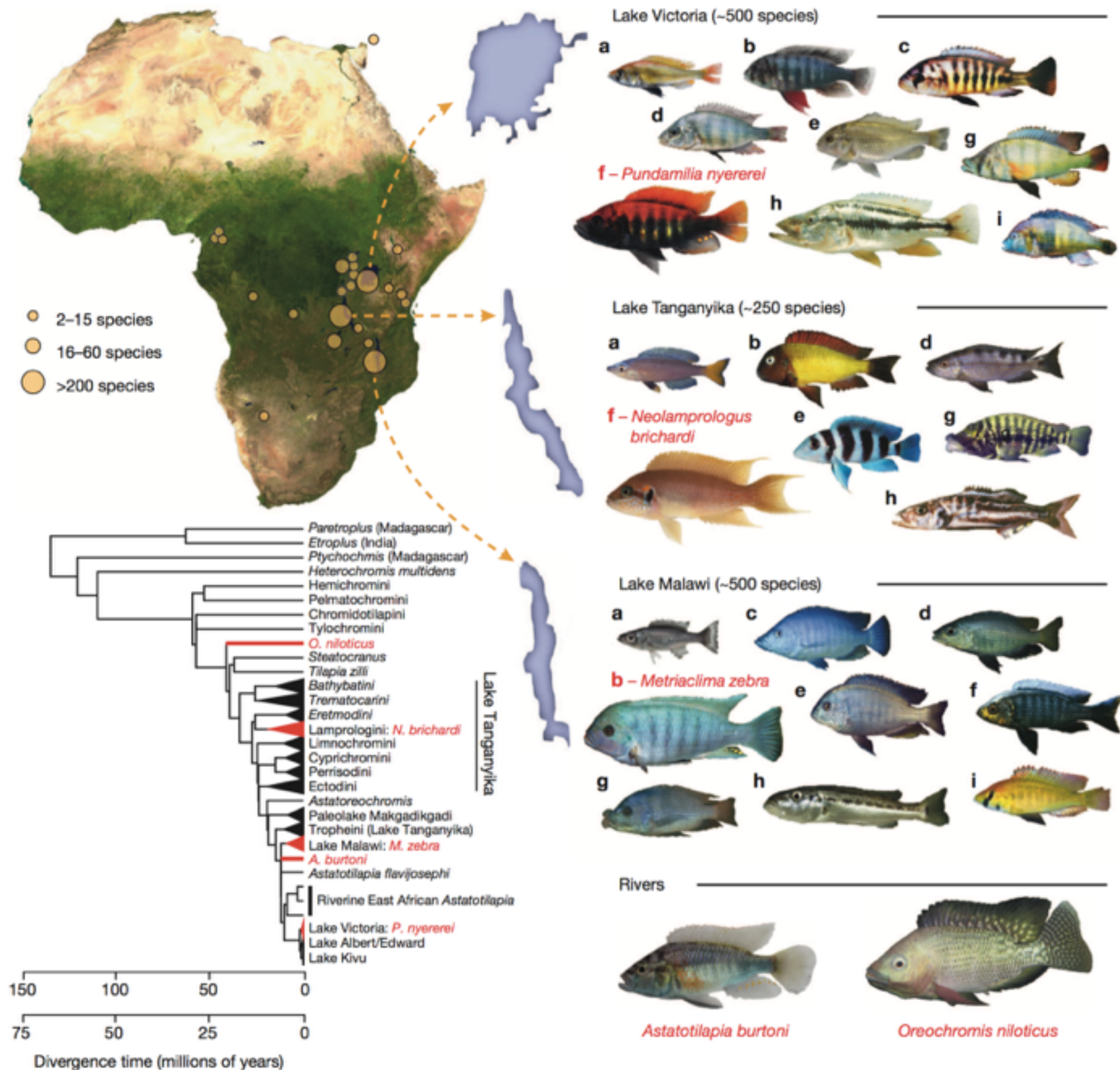
¹Center for Ecology and Evolutionary Biology, University of Oregon, Eugene, OR 97403-5289



Resolving postglacial phylogeography using high-throughput sequencing

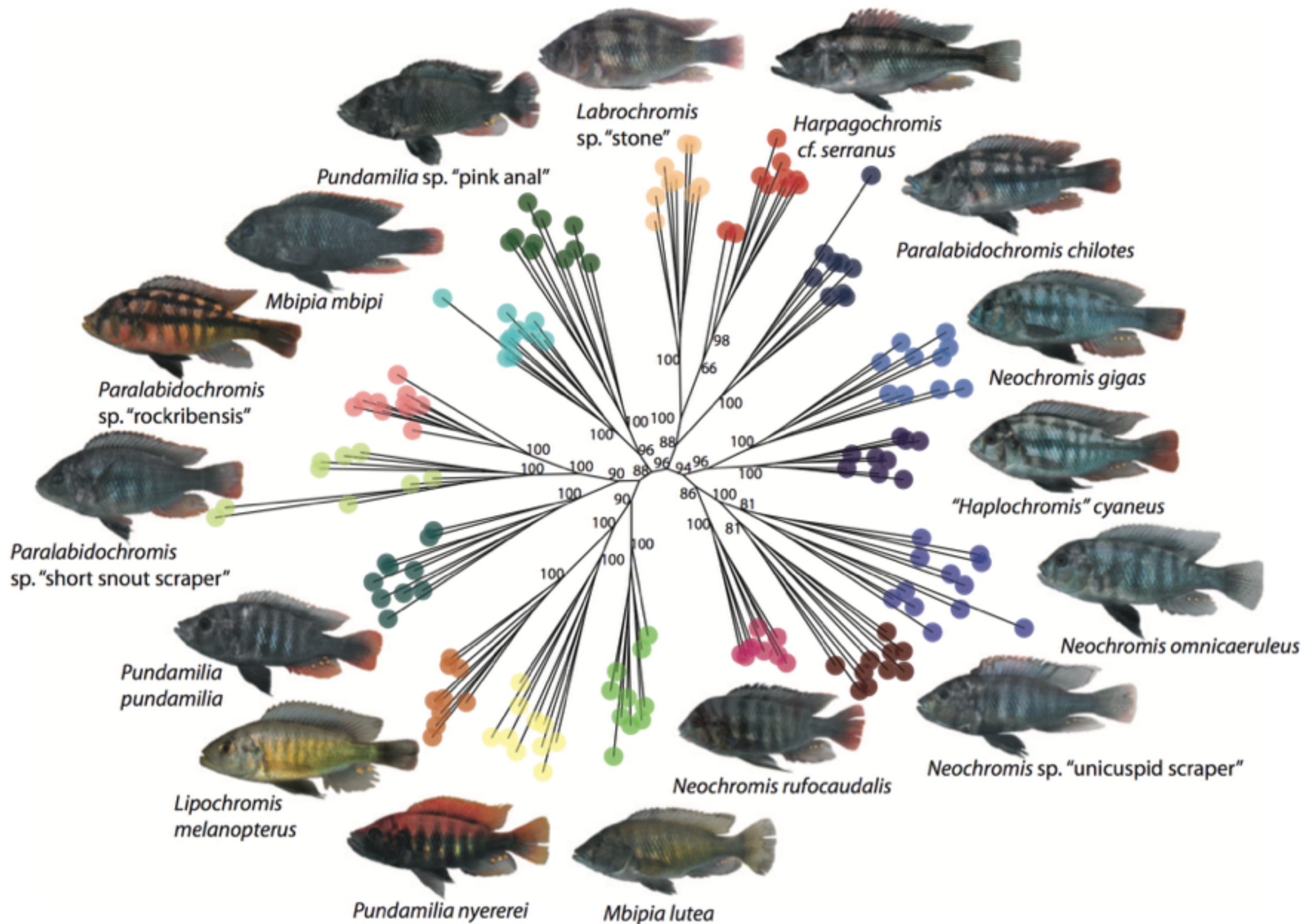
Kevin J. Emerson¹, Clayton R. Merz, Julian M. Catchen, Paul A. Hohenlohe, William A. Cresko, William E. Bradshaw, and Christina M. Holzapfel

Center for Ecology and Evolutionary Biology, University of Oregon, Eugene, OR 97403-5289



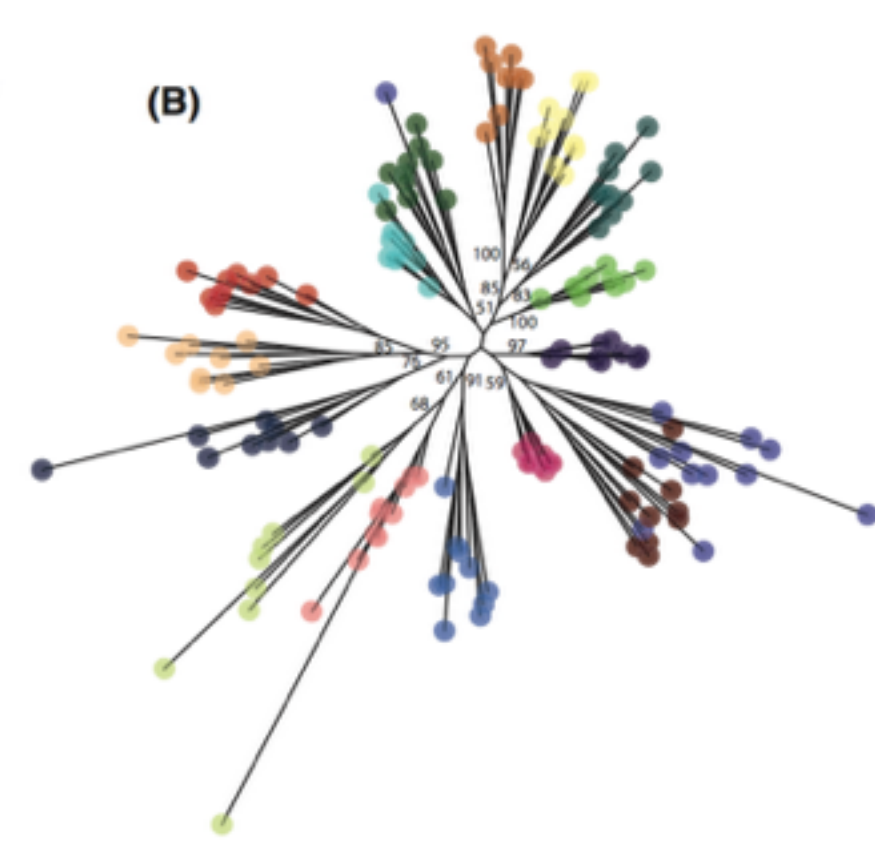
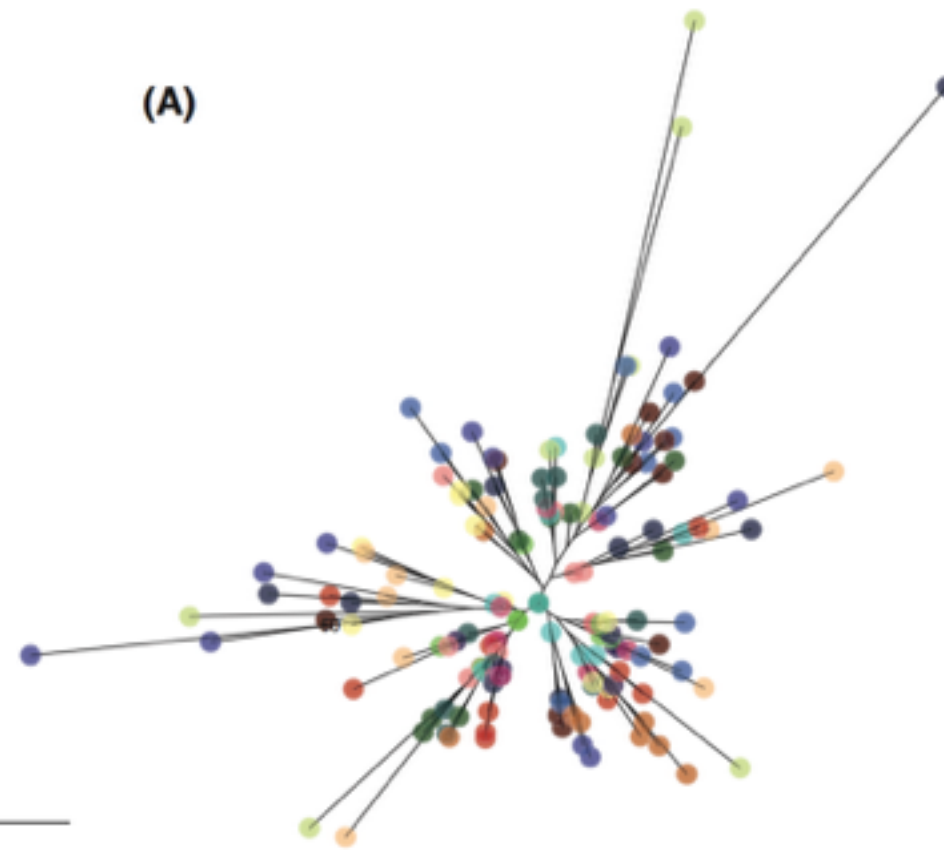
The genomic substrate for adaptive radiation in African cichlid fish

David Streelman^{1,2,3,4}, Catherine E. Wagner^{1,2,3,4}, Yang L. Li^{1,2,3,4}, Milan Malinsky^{1,2,3,4}, Jesse Koller^{1,2,3,4}, Shaoxian Fan^{1,2,3,4}, Qing Shao^{1,2,3,4}, Kevin Y. Ng^{1,2,3,4}, Zhi Wei Lim^{1,2,3,4}, Eriqne Soudry^{1,2,3,4}, Jason Turner-Matney^{1,2,3,4}, Jeremy Johnson^{1,2,3,4}, Rosa Alcazar^{1,2,3,4}, Bryan B. Smith^{1,2,3,4}, Francisco Reyes^{1,2,3,4}, Benjamin Auer^{1,2,3,4}, Jessica Allard^{1,2,3,4}, Chris Amemiya^{1,2,3,4}, Nanshi Auer^{1,2,3,4}, Jean-François Babin^{1,2,3,4}, Frederique Bayle^{1,2,3,4}, Hubert^{1,2,3,4}, Aaron Bertha^{1,2,3,4}, Ryan Branstetter^{1,2,3,4}, James L. Cauley^{1,2,3,4}, Katherine A. Coates^{1,2,3,4}, Rebecca D'Amico^{1,2,3,4}, Oly Ekel^{1,2,3,4}, Linda Galloway^{1,2,3,4}, Francisco Gauthier^{1,2,3,4}, Hugo J. Gass^{1,2,3,4}, Santa Guzman^{1,2,3,4}, Lucie Guzman^{1,2,3,4}, Richard Guyon^{1,2,3,4}, Natalie S. Haddad^{1,2,3,4}, William Hargreaves^{1,2,3,4}, Remy M. Hargreaves^{1,2,3,4}, Hyeon A. Hoffmann^{1,2,3,4}, Thomas Houlder^{1,2,3,4}, Catherine Houlder^{1,2,3,4}, David S. Jaffe^{1,2,3,4}, Wanda Jara^{1,2,3,4}, Adam P. Lee^{1,2,3,4}, John MacCollum^{1,2,3,4}, Salome Mawdsley^{1,2,3,4}, Maura Nilsson^{1,2,3,4}, Håkan Nilsson^{1,2,3,4}, Catherine O'Neil^{1,2,3,4}, David J. Pennell^{1,2,3,4}, Barbara Prentiss^{1,2,3,4}, Richard Robinson^{1,2,3,4}, Gary C. P. Rowe^{1,2,3,4}, Hilary S. Satterthwaite^{1,2,3,4}, Michael S. Satterthwaite^{1,2,3,4}, John Sanchez-Julian^{1,2,3,4}, M. Emily Santos^{1,2,3,4}, Steve Searle^{1,2,3,4}, Ted Shreeve^{1,2,3,4}, Ross Sutherland^{1,2,3,4}, Frederick T. Tey^{1,2,3,4}, Louise Williams^{1,2,3,4}, Sarah Young^{1,2,3,4}, Shuangyue Yin^{1,2,3,4}, Northern Okada^{1,2,3,4}, Thomas D. Kocher^{1,2,3,4}, Eric A. Miska^{1,2,3,4}, Eric S. Lander^{1,2,3,4}, Rikako Furukawa^{1,2,3,4}, Kiyoshi D. Furukawa^{1,2,3,4}, Axel Meyer^{1,2,3,4}, Chris P. Ponting^{1,2,3,4}, J. Todd Streelman^{1,2,3,4}, Kenneth S. Todd^{1,2,3,4}, Ole Seehausen^{1,2,3,4} & Frederica D. Palm^{1,2,3,4}

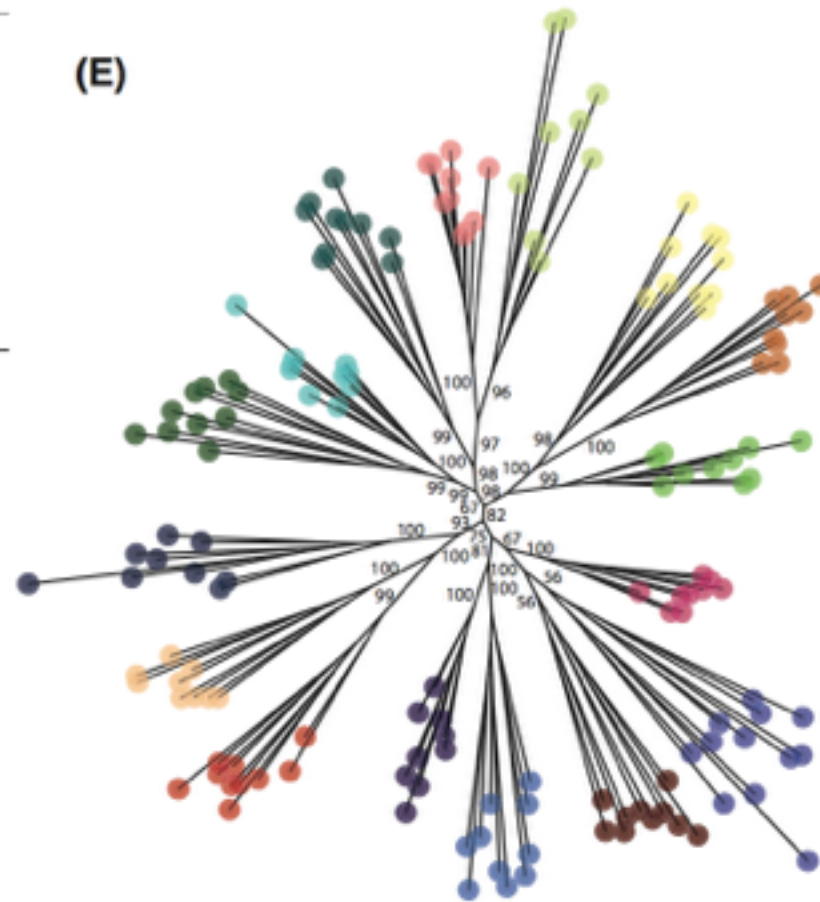


Genome-wide RAD sequence data provide unprecedented resolution of species boundaries and relationships in the Lake Victoria cichlid adaptive radiation

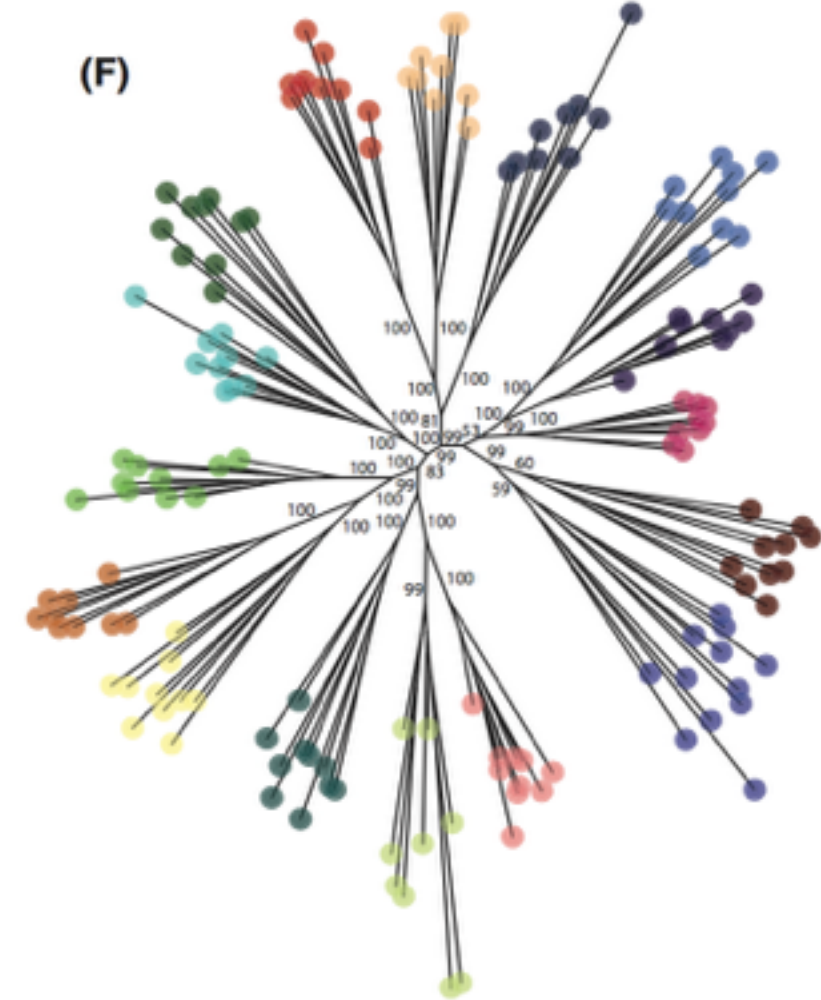
CATHERINE E. WAGNER,*† IRENE KELLER,*† SAMUEL WITTEW,*† OLIVER M. SELZ,*† SALOME MWAIKO,*† LUCIE GREUTER,*† ARJUN SIVASUNDAR,*† and OLE SEEHAUSEN,*†
 *Department of Fish Ecology & Evolution, EAWAG Centre for Ecology, Evolution and Biogeochemistry, Seestrasse 79, 6047, Kastanienbaum, Switzerland, †Institute of Ecology and Evolution, Aquatic Ecology, University of Bern, Baltzerstrasse 6, 3012, Bern, Switzerland



(E)



(F)

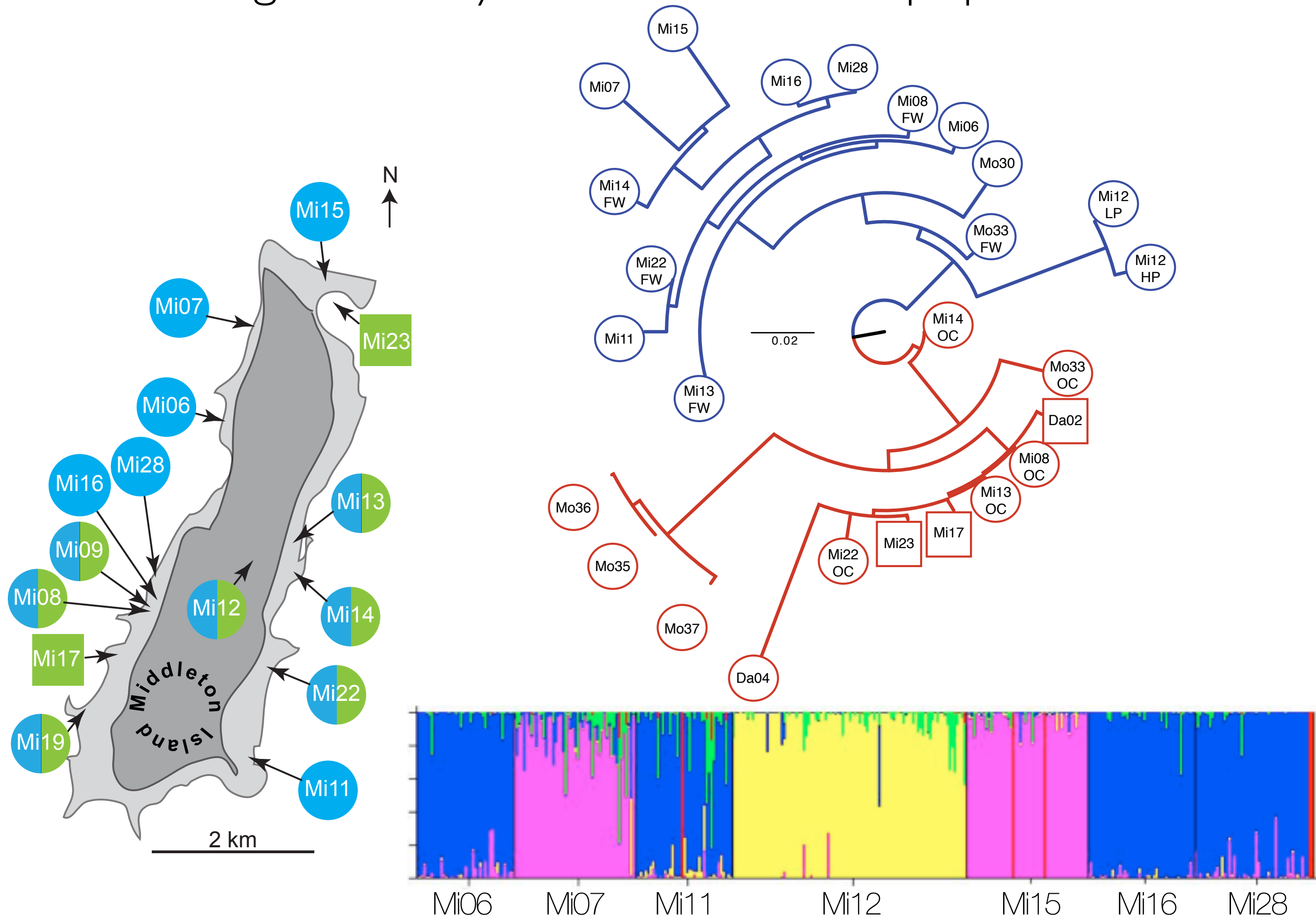


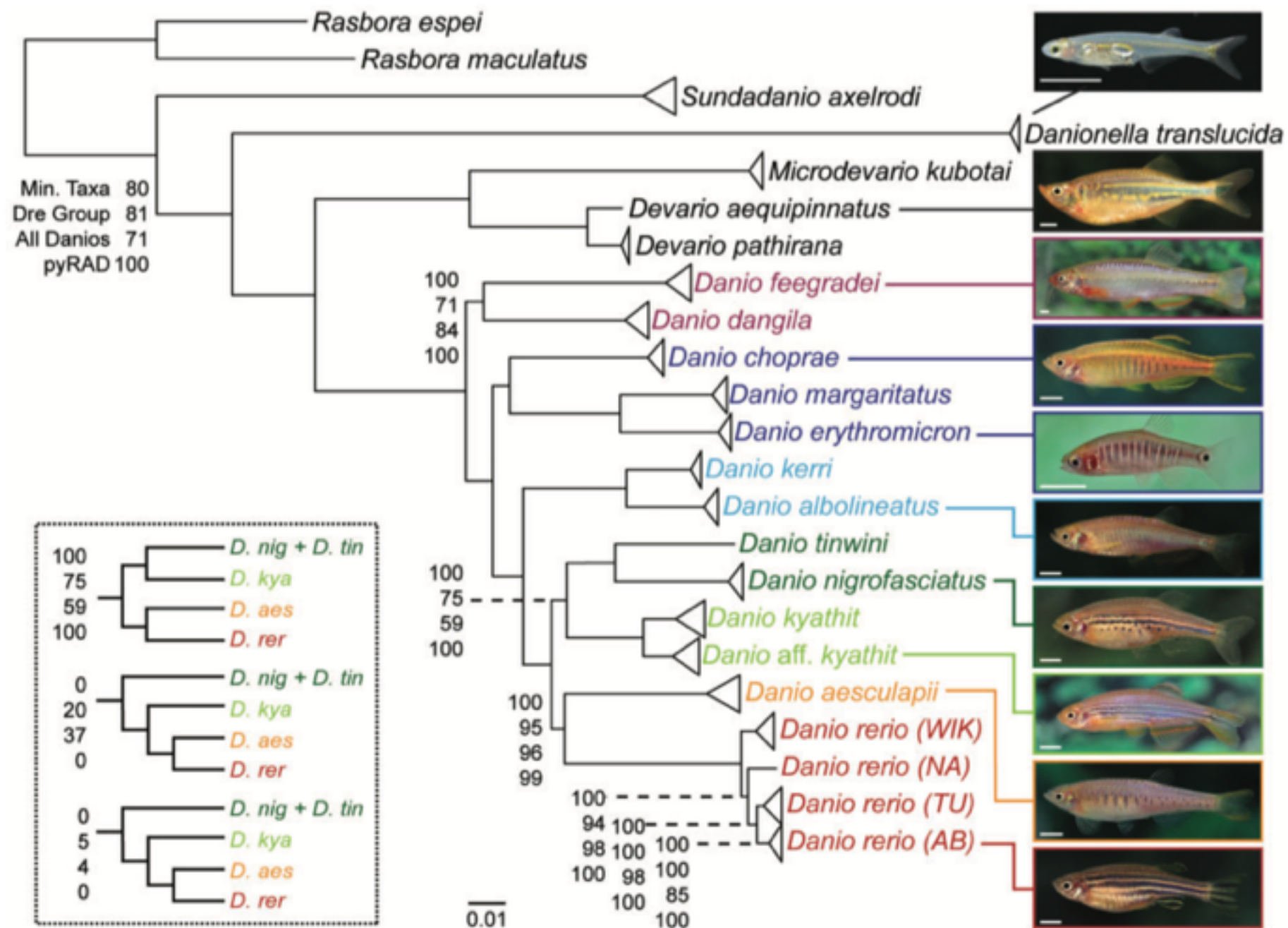
	Min individuals	<i>n</i> base pairs	<i>n</i> loci	<i>n</i> variable loci
a	145	33 953	406	406
b	125	370 024	4418	4095
c	115	1 360 153	16 233	14 580
d	110	2 030 538	24 230	21 516
e	100	3 141 515	37 476	32 886
f	75	4 224 048	50 380	43 618
g	15	5 820 379	69 426	56 385

Genome-wide RAD sequence data provide unprecedented resolution of species boundaries and relationships in the Lake Victoria cichlid adaptive radiation

CATHERINE E. WAGNER,^{1,2} IRENE KELLER,^{1,2} SAMUEL WITTWER,^{1,2} OLIVER M. SELZ,^{1,2} SALOME MWAIKO,^{1,2} LUCIE GREUTER,^{1,2} ARJUN SIVASUNDAR,^{1,2} and OLE SEEHAUSEN^{1,2}
¹Department of Fish Ecology & Evolution, EAWAG Centre for Ecology, Evolution and Biogenetics, Seestrasse 79, 6047, Kastanienbaum, Switzerland, ²Institute of Ecology and Evolution, Aquatic Ecology, University of Bern, Baltzerstrasse 6, 3012, Bern, Switzerland

Origins of 50 year old freshwater populations





Phylogeny of Zebrafish, a “Model Species,” within *Danio*, a “Model Genus”