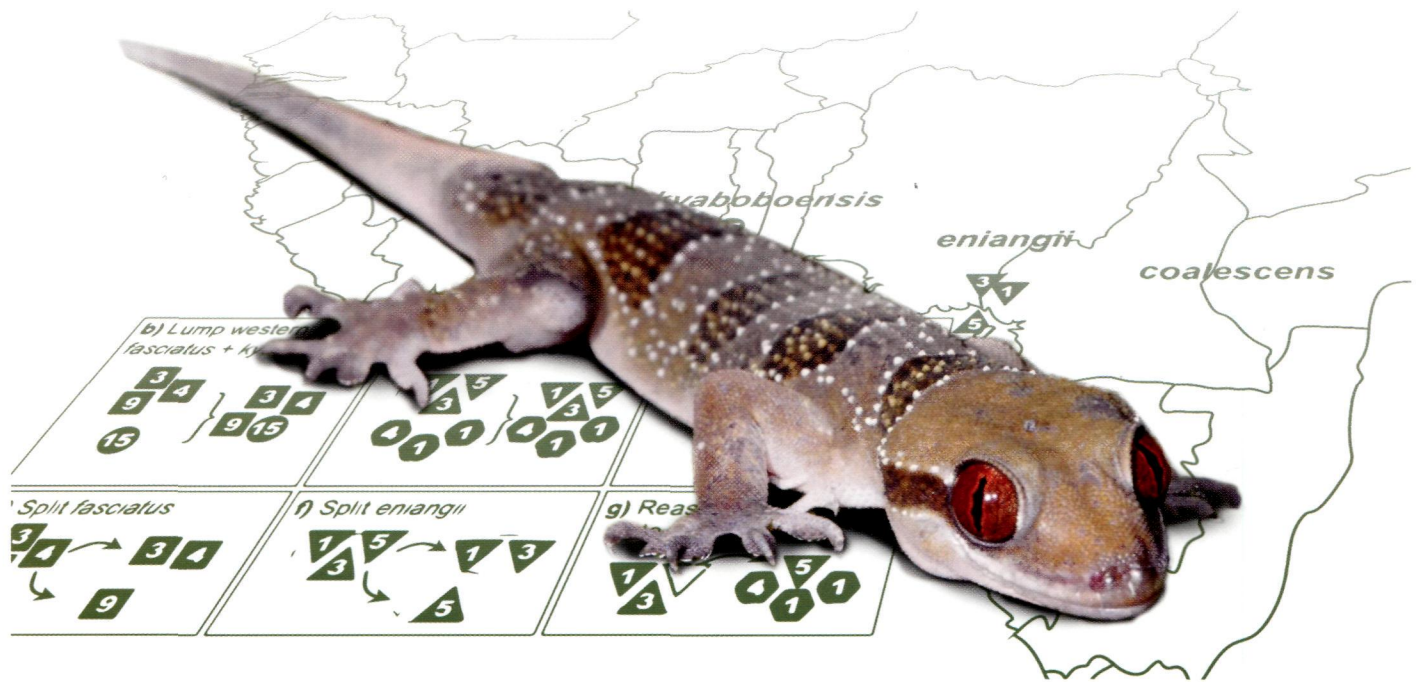


TM
598/6

Systematic Biology

A JOURNAL OF THE
Society of Systematic Biologists



VOLUME 63
NUMBER 4

JULY 2014

ONLINE ISSN 1076-836X
PRINT ISSN 1063-5157

Systematic Biology

Volume 63, Number 4 July 2014

CONTENTS



Scan to view this journal on your mobile device

REGULAR ARTICLES

- The Emergence of Lobsters: Phylogenetic Relationships, Morphological Evolution and Divergence Time Comparisons of an Ancient Group (Decapoda: Achelata, Astacidea, Glypheidea, Polychelida)
Heather D. Bracken-Grissom, Shane T. Ah Yong, Richard D. Wilkinson, Rodney M. Feldmann, Carrie E. Schweitzer, Jesse W. Breinholt, Matthew Bendall, Ferran Palero, Tin-Yam Chan, Darryl L. Felder, Rafael Robles, Ka-Hou Chu, Ling-Ming Tsang, Dohyup Kim, Joel W. Martin, and Keith A. Crandall457
- Competitive Release Leads to Range Expansion and Rampant Speciation in Malagasy Dung Beetles
Andreia Miraldo and Ilkka A. Hanski480
- Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography
Filip Bielejec, Philippe Lemey, Guy Baele, Andrew Rambaut, and Marc A. Suchard 493
- Incorporating Color into Integrative Taxonomy: Analysis of the Varied Tit (*Sittiparus varius*) Complex in East Asia
Bailey D. McKay, Herman L. Mays Jr., Cheng-Te Yao, Dongmei Wan, Hiroyoshi Higuchi, and Isao Nishiumi505
- Global Biodiversity Assessment and Hyper-Cryptic Species Complexes: More Than One Species of Elephant in the Room?
Mark Adams, Tarmo A. Raadik, Christopher P. Burridge, and Arthur Georges518
- Species Delimitation using Genome-Wide SNP Data
Adam D. Leaché, Matthew K. Fujita, Vladimir N. Minin, and Remco R. Bouckaert534
- Ribosomal DNA Sequence Heterogeneity Reflects Intraspecies Phylogenies and Predicts Genome Structure in Two Contrasting Yeast Species
Claire West, Stephen A. James, Robert P. Davey, Jo Dicks, and Ian N. Roberts543
- The Impact of the Rate Prior on Bayesian Estimation of Divergence Times with Multiple Loci
Mario Dos Reis, Tianqi Zhu, and Ziheng Yang 555
- Supertrees Based on the Subtree Prune-and-Regraft Distance
Christopher Whidden, Norbert Zeh, and Robert G. Beiko566
- Integrating Incomplete Fossils by Isolating Conflicting Signal in Saturated and Non-Independent Morphological Characters582
Liliana M. Dávalos, Paúl M. Velazco, Omar M. Warsi, Peter D. Smits, and Nancy B. Simmons
- Standard Sister Clade Comparison Fails when Testing Derived Character States
Jos Käfer and Sylvain Mousset601
- Analysis and Visualization of Complex Macroevolutionary Dynamics: An Example from Australian Scincid Lizards
Daniel L. Rabosky, Stephen C. Donnellan, Michael Grundler, and Irby J. Lovette610

POINTS OF VIEW

- Is the Tree of Life the Best Metaphor, Model, or Heuristic for Phylogenetics?628
David A. Morrison
- A Preliminary Framework for DNA Barcoding, Incorporating the Multispecies Coalescent639
Mark Dowton, Kelly Meiklejohn, Stephen L. Cameron, and James Wallman

Cover Illustration: Species delimitation, the process of estimating the boundaries and numbers of species, has become increasingly statistical with a greater reliance on genetic data. Current species delimitation methods rely on computationally-demanding approaches intended for small to moderate numbers of loci. On pages 534–542, Leaché and colleagues present a new species delimitation method that can accommodate genome-wide SNP data, which is becoming increasingly common in studies of non-model organisms. Using computer simulations and new empirical data for West African forest geckos (*Hemidactylus fasciatus* complex) they demonstrate that the method has the desirable properties of maintaining accuracy despite limitations in sample size or violations of model assumptions. This new genomically-enabled approach helps mitigate a growing demand for statistical and objective methods for delimiting species. Photo and artwork by Philipp Wagner.