The comparative biogeography of Philippine geckos challenges predictions from a paradigm of climate-driven vicariant diversification across an island archipelago

Jamie R. Oaks¹ Cameron D. Siler² Rafe M. Brown³

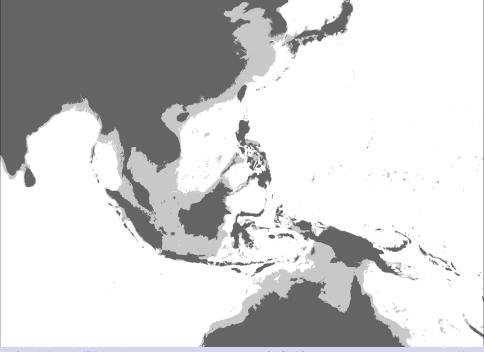
¹Department of Biological Sciences & Museum of Natural History, Auburn University, Auburn, Alabama 36849, USA

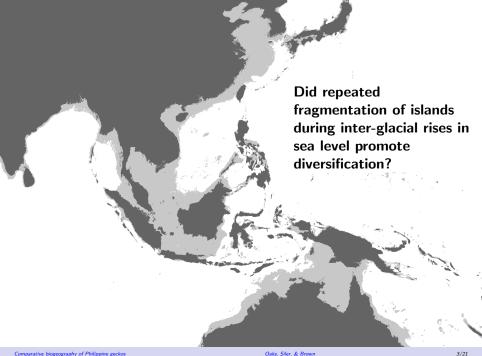
²Sam Noble Oklahoma Museum of Natural History and Department of Biology, University of Oklahoma, Norman, Oklahoma 73072-7029

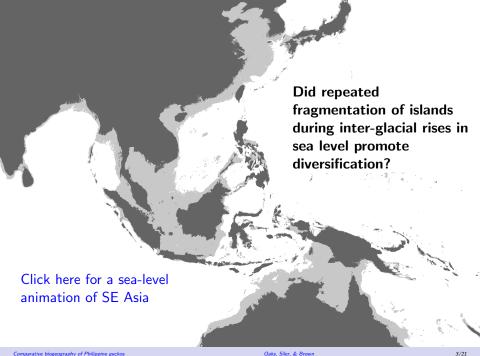
³Biodiversity Institute and Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, Kansas 66045, USA

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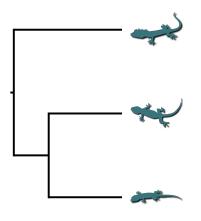




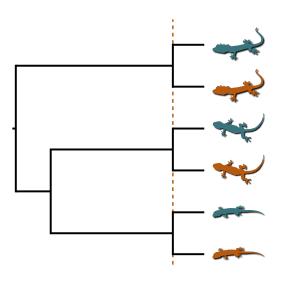
"Species-pump" Hypothesis Repeated climate-driven fragmentation of the Philippine Islands was a primary mechanism of speciation for terrestrial fauna

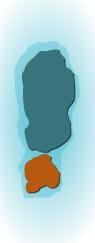
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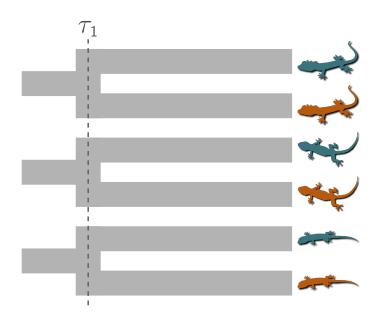
Prediction Taxa co-distributed across islands within the same Pleistocene aggregate island complex (PAIC) will have divergence times that tend to be clustered around times when sea levels fragmented the islands

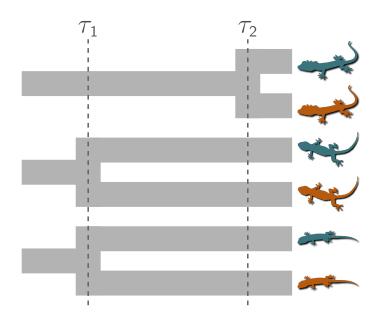


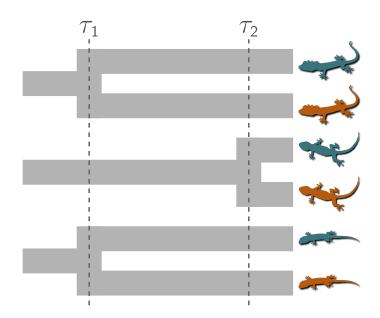


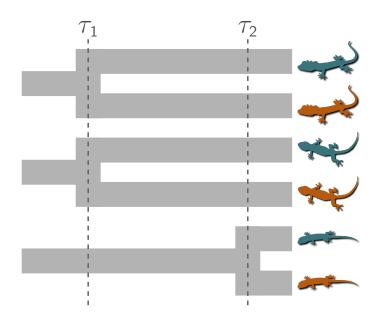


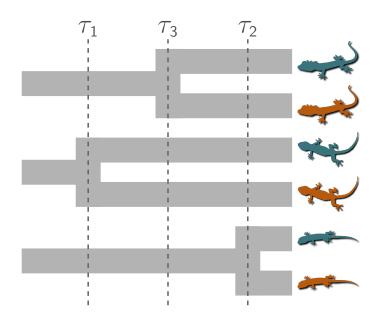


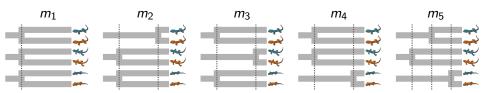


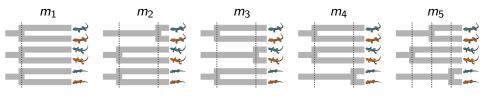












We want to infer the model and divergence times given genetic data

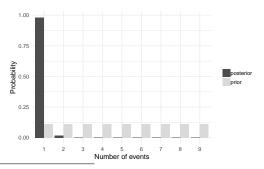
▶ Oaks et al. (2013)¹ collected mitochondrial DNA sequences from 22 pairs of populations (including bats, shrews, skinks, geckos, snakes, and frogs)

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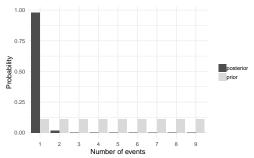
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 - But, method was very sensitive to prior assumptions and often biased toward estimating co-divergences

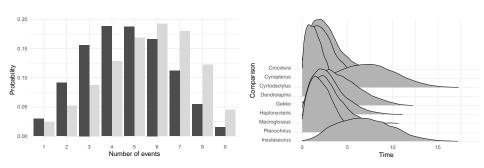


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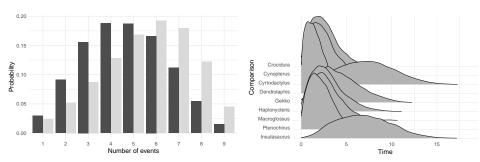
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 - New method was less biased, but little information in summary statistics to inform divergence times



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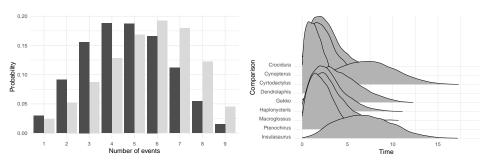
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What now? We need **more data** and/or an **improved method** that better utilizes the information in those data.

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What now? We need **more data** and/or an **improved method** that better utilizes the information in those data. **Our goal is to do both.**

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Cyrtodactylus (Gekkonidae)

- ▶ 265+ species across Asia
- ▶ 10+ species across Philippines
- Nocturnal, scansorial lizards that eat terrestrial invertebrates
- Specialized bent toes for climbing



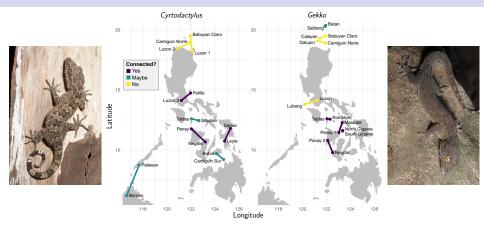
Gekko (Gekkonidae)

- ► 60+ species across Southeast Asia
- ▶ 14+ species across Philippines
- Nocturnal, scansorial lizards that eat terrestrial invertebrates
- Subdigital lamellae for climbing





Methods



- Sampled individuals from 8 pairs of populations for both Cyrtodactylus and Gekko
 - Sampled 2–5 individuals per population
- ► Collected genome-wide DNA sequence data from each individual
 - Restriction-site-associated DNA sequencing (RADseq)

Analyzed RADseq data with full-likelihood Bayesian comparative phylogeographic method:

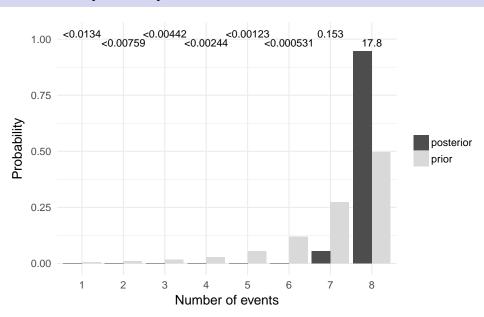
Ecoevolity: Estimating evolutionary coevality

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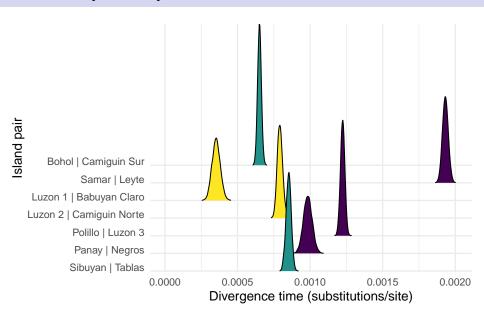
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 Used simulations to assess how well ecoevolity works given the gekkonid RADseq data sets

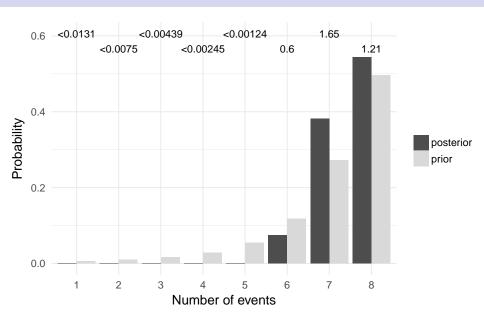
Results: Cyrtodactylus



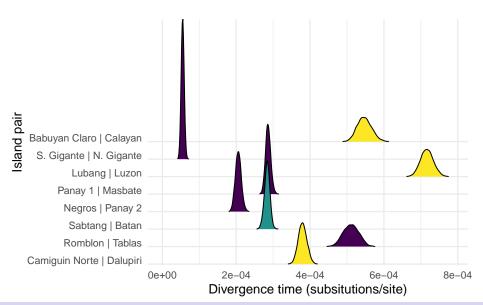
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Key findings

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Key findings

- Strong support that all 8 pairs of Cyrtodactylus populations diverged independently
- Weak support that all 8 pairs of Gekko populations diverged independently
- Simulation results suggest ecoevolity can accurately estimate the timing and number of divergences given the gekkonid RADseq data

Caveats

- ► Too few island pairs to rule out climate-driven vicariant speciation
- ▶ Differences in divergence times could be due to variation in fragmentation times among island pairs
- Differences in divergence could also be due to variation in mutation rates

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- Too few island pairs to rule out climate-driven vicariant speciation
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Seems safe to conclude that the "species-pump" is not the rule for gekkonids, but maybe the exception

Take home points

► Support against the "species-pump" hypothesis

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- ▶ Results suggest repeated cycles of climate-driven island fragmentation were not an important mechanism of speciation for gekkonid lizards in the Philippines

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- ► Support against the "species-pump" hypothesis
- Results suggest repeated cycles of climate-driven island fragmentation were not an important mechanism of speciation for gekkonid lizards in the Philippines
- ▶ Rare over-water dispersal via rafting on vegetation is likely an important mechanism responsible for the distribution of gekkonid lizards in the Philippines

Everything is on GitHub...

Software:

► Ecoevolity: https://github.com/phyletica/ecoevolity

Open-Science Notebook:

► Gecko RADseq: https://github.com/phyletica/gekgo

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- Auburn University Hopper Cluster

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Photo credits:

- Rafe Brown and Cam Siler
- PhyloPic!

Questions?

joaks@auburn.edu phyletica.org



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