



Using numerous contact zones to delimit species and calibrate a reference-based taxonomy in a challenging lizard group (*Heteronotia*).

Stephen M. Zozaya (Australian National University); Scott A. Macor (James Cook University); Conrad J. Hoskin (James Cook University); Megan Higgie (James Cook University); Craig Moritz (Australian National University).

What happens where divergent populations come into secondary contact? Is there evidence of reproductive isolation and restricted gene flow, or do they gradually intergrade into each other? Assessing where populations sit along this continuum is useful for species delimitation in sexually reproducing organisms, as nearly all species concepts agree that populations that remain distinct in sympatry represent species. Furthermore, by sampling many contact zones one can understand how divergence across genomes and phenotypic traits correlate with contemporary gene flow. This information can then be used to calibrate thresholds of divergence that inform a reference-based taxonomy when working with allopatric or poorly sampled populations. Here we aim to resolve species boundaries in *Heteronotia* geckos using RAD sequencing and dense geographic sampling to assess contemporary gene flow across ~20 contact zones. We then assess how gene flow between populations correlates with genomic divergence, thus calibrating divergence thresholds to inform taxonomic decisions for populations that lack contact zone sampling. This species delimitation approach combines direct assessment of evolutionary independence among candidate species while also calibrating a reference-based taxonomy to apply more broadly. Among other lessons, we highlight how accurate species delimitation of taxonomically difficult animal groups might often require data from contact zones.

Stephen Zozaya: stephen.zozaya@anu.edu.au