

Digest: Massive mixing and merging of Madagascar Gemsnakes

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Abstract

Introgressive hybridization can give rise to reticulated patterns in a phylogeny. In a recent study, DeBaun et al. detected 12 reticulation events across the phylogeny of the Madagascar Gemsnakes, suggesting that their evolutionary history cannot be captured in a bifurcating tree. Moreover, identifying the true network of a group is difficult when using only available extant data. The evolution of these snakes might thus be even more tangled than we currently think.

Introgression—the transfer of genetic material through hybridization and backcrossing—is prevalent in nature. Advances in genome sequencing techniques and statistical methods have allowed researchers to document numerous cases in a diverse collection of taxa (Taylor & Larson, 2019). Introgression can often be inferred from particular genetic signatures, such as gene trees that deviate from the species tree. However, these patterns of gene tree discordance can also be explained by other evolutionary processes (e.g., incomplete lineage sorting) or a weak phylogenetic signal in certain genes (Degnan & Rosenberg, 2009). Additional analyses are thus warranted to determine whether introgression is the cause of gene tree discordance.

In a recent study, DeBaun et al. (2023) analyzed patterns of gene tree discordance across the phylogeny of the Madagascar Gemsnakes (Pseudoxyrhopiidae, Lamprophiidae), an adaptive radiation of 109 species in 17 genera, to pinpoint potential instances of introgression. After accounting for phylogenetically uninformative genes, the researchers inferred phylogenetic networks in clades with conflicting gene trees. These analyses uncovered 12 reticulation events and suggested that at least 30 species are the result of one or more hybridization events. Hence, the evolutionary history of the Madagascar Gemsnakes can better be represented by a network rather than a bifurcating tree.

Most reticulation events involved younger species. This temporal pattern is partly due to the accumulation of species on the island, providing more opportunities for hybridization. However, older reticulation events are harder to detect because the introgression signal decays over time as introgressed regions are purged from the genome (Moran et al., 2021). In addition, older reticulation events might have involved now-extinct species (Ottenburghs, 2020). The

genetic signatures of these “ghost introgression” events are difficult to detect in modern-day genomes, leading to a potential underestimation of ancient introgression events (Tricou et al., 2022). In addition, current methods are only able to identify low-complexity reticulations (Solís-Lemus & Ané, 2016). The evolution of the Madagascar Gemsnakes might be even more reticulated than we imagined.

References

- DeBaun, D., Rabibisoa, N., Raselimanana, A. P., Raxworthy, C. J., & Burbrink, F. T. (2023). Widespread reticulate evolution in an adaptive radiation. *Evolution*, 77(4), 931–945. <https://doi.org/10.1093/evolut/qp011>
- Degnan, J. H., & Rosenberg, N. A. (2009). Gene tree discordance, phylogenetic inference and the multispecies coalescent. *Trends in Ecology & Evolution*, 24(6), 332–340. <https://doi.org/10.1016/j.tree.2009.01.009>
- Moran, B. M., Payne, C., Langdon, Q., Powell, D. L., Brandvain, Y., & Schumer, M. (2021). The genomic consequences of hybridization. *eLife*, 10, e69016. <https://doi.org/10.7554/eLife.69016>
- Ottenburghs, J. (2020). Ghost introgression: Spooky gene flow in the distant past. *Bioessays*, 42(6), 2000012. <https://doi.org/10.1002/bies.202000012>
- Solís-Lemus, C., & Ané, C. (2016). Inferring phylogenetic networks with maximum pseudolikelihood under incomplete lineage sorting. *PLoS Genetics*, 12(3), e1005896. <https://doi.org/10.1371/journal.pgen.1005896>
- Taylor, S. A., & Larson, E. L. (2019). Insights from genomes into the evolutionary importance and prevalence of hybridization in nature. *Nature Ecology & Evolution*, 3(2), 170–177. <https://doi.org/10.1038/s41559-018-0777-y>
- Tricou, T., Tannier, E., & de Vienne, D. M. (2022). Ghost lineages highly influence the interpretation of introgression tests. *Systematic Biology*, 71(5), 1147–1158. <https://doi.org/10.1093/sysbio/syab011>