

**Digest: *Liolaemus* lizards as an emerging model system to study hybridization as a driver of rapid radiations**

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**Author note:** This article corresponds to Sánchez, K., Recknagel, H., Elmer, K.R., Avila, L.J. and Morando, M. 2024. Tracing evolutionary trajectories in the presence of gene flow in South American temperate lizards (Squamata: *Liolaemus kingii* group). *Evolution*, 78(4), qpae009.

<https://doi.org/10.1093/evolut/qpae009>

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## Abstract

Recent perspectives on speciation genomics emphasize the pivotal role of hybridization in driving rapid radiations. The *Liolaemus* lizard genus displays impressive species richness with around 290 species widely distributed across southern South America. Sánchez et al. (2024) conducted a comprehensive study on the 5-million-year-old *Liolaemus kingii* group, which includes 14 species. The research provides new key insights to enhance our understanding of this rapid radiation, including its diversification in space and time and consequences of hybridization in its morphological evolution and taxonomy.

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## Main text

The *Liolaemus* lizard genus is roughly 20 million years old and includes about 290 species, making it the second most diverse amniote genus globally (Olave et al., 2018). Notably, it includes species able to live in the driest nonpolar desert, the Atacama Desert (*L. montanus* group), as well as species adapted to salt pans (*L. anomalus* group). Furthermore, it encompasses the world's highest-altitude reptile, which lives at 5,400 meters (Cerdeña et al., 2021), plus *L. magellanicus*, the only herpetofauna species living at the southernmost tip of the world at 52 degrees latitude. (Jaksic, 2022). Over the past 15 years, numerous *Liolaemus* species have been described, with predictions suggesting it may surpass the diversity of the 60-million-year-old *Anolis* lizards, which include 440 species and are a textbook example of adaptive radiation (Morando et al., 2003).

In a recent article, Sánchez et al. (2024) presented a comprehensive study focused on the 5-million-year-old *Liolaemus kingii* group, a clade of 14 species within the herps from the "end of the world" clade (*L. lineomaculatus* section). From a micro to a macro perspective, the study leverages genomic, phenotypic, spatial, and climatic data based on specimens collected over 20 years of fieldwork across ~450,000 km<sup>2</sup> in Patagonia. Using cutting-edge methodological approaches, the research provides new key insights to enhance our understanding of this spectacular rapid radiation.

The key to *Liolaemus* diversification may lie in an exceptionally low extinction rate, rather than a high speciation rate (Olave et al., 2020a; 2020b). In other words, the genus seems to have an extraordinary ability to survive through time. In contrast to the evolutionary patterns of *Anolis* lizards, *Liolaemus* species do not develop such extreme morphological specializations to microenvironments. A generalist morphology is considered a better strategy, given heterogeneous and fluctuating environmental conditions in southern South America over time, including glacial cycles, oceans incursions and retreats, the Andes uplift, and severe volcanism. Preventing specialization may enhance *Liolaemus* survival by allowing species to shift niches in response to changing environmental conditions (Olave et al., 2020a; 2020b).

In line with these predictions, Sánchez et al. (2024) reconstructed spatial and temporal distribution shifts during glacial cycles affecting the *L. kingii* group. Their findings indicate repetitive niche shifts during glaciations, promoting divergence events, but also secondary contact among *L. kingii* group lineages. Their results also promoted a taxonomic rearrangement of the group by identifying distinct evolutionary trajectories.

Hybridization may be a key mechanism for driving radiation in the *Liolaemus* genus by rapidly reassembling genetic variation in novel combinations on which natural selection can work (Marques et al., 2019). Sánchez et al. (2024) demonstrate a new case of extensive hybridization among *Liolaemus* species, a phenomenon that was first suggested in Morando et al. (2004) and has been repeatedly proven to be rampant in these lizards (Olave et al., 2011; 2018; Araya-Donoso et al.,

2019; Grummer et al., 2021; Morando et al., 2020b; Esquerré et al., 2022; Sánchez et al., 2023). Hybridization has occurred even between species that diverged more than 5 million years (or 2.5 million generations) ago, as well as between species having significant differences in morphology and habitat use (Olave et al., 2011; 2018). Most of the hybrid zones among *Liolaemus* species are located in center-southern Patagonia (reviewed in Morando et al., 2020a), at a hotspot of the genus diversity with peaks of increased speciation and reduced extinction rates (Skeels et al., 2023). Evidence of hybrids retaining intermediate phenotypes to parental species across generations has been detected in this area as well (Olave et al., 2011; 2018).

Now, for the first time, Sánchez et al. (2024) has delivered an invaluable missing piece in this puzzle: hybridizations events are associated with significant signals of transgressive evolution of phenotypes. In other words, phenotypic evolution in *Liolaemus* has been impacted by hybridization. Whether hybridization plays a role in reducing phenotypic divergence across taxa by generating offspring with intermediate phenotypes, and, consequently, contributes to the conservation of a successful generalist morphology, remains an interesting hypothesis gradually gaining support. Unlikely to be a neutral process, pervasive hybridization among these lizards breaks conventional understanding of species diversification, and presents a living laboratory to study the driving forces behind accelerated evolutionary diversification.

**Conflict of interest:** The author declares no conflict of interest.

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