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Digest: Multiple factors influence mountain orchid diversity and distribution

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This article corresponds to Fiorini, C.F., Borba, E. L., Resende-Moreira, L.C., de Camargo Smidt, E., & Knowles, L. L. (2023). Geographic isolation alone does not explain divergence of a group of orchid species across Brazil's campos rupestres sky-islands. *Evolution*. <https://doi.org/10.1093/evolut/qpaa010>

Abstract

How have orchid species diversified in the *campos rupestres*, Brazil? Fiorini et al. (2023) use genomic data sets and multidisciplinary approaches, including phylogenetics and population genomics, to investigate the diversity of *Bulbophyllum*. They demonstrate that geographic isolation alone does not explain diversification patterns in *Bulbophyllum* species throughout the sky forests. Some taxa show considerable evidence of gene flow, and lineages not previously identified as closely related could present a novel source of their genetic diversity.

Over time, topographical and related climatic changes have isolated and reunited populations (Alves & Kolbek, 1994), which both drives divergence by geographical isolation (allopatric speciation) and offers opportunity for gene flow, respectively. Mountainous areas are likely to form geographically isolated outcrops, resulting in disjunct plant populations with restricted distributions. Species' distributions are predicted to follow topographic and elevational patterns, a phenomenon that is particularly frequent in populations with localized seedling recruitment, such as orchids (Jersáková & Malinová, 2007).

In this study, Fiorini et al. (2023) sequenced reduced representations (ddRAD-Seq) of the genomes of six different *Bulbophyllum* orchid species from the section *Didactyle* distributed in the *campos rupestres* (Figure 1), a shrubby, herbaceous vegetation mosaic located within the Espinhaço/Chapada-Diamantina mountain chain in southeastern Brazil. They sampled 46 populations, collected across 36 localities to understand species' biogeography, potential interbreeding, and evolutionary relationships.

The authors investigate the following questions: (a) Are morphologically recognized species reciprocally monophyletic (i.e., do multiple populations of each species share a most recent common ancestor)? (b) Does geographic isolation reflect common divergence patterns? (c) Does geographic isolation drive genetic differences, within a species? and finally, (d) Is there genetic evidence of isolated populations interbreeding (i.e., gene flow), and if so, does this affect proposed species boundaries and morphological traits?

Three of the species were found to be monophyletic, whereas the remaining three had strong signatures of interspecific

gene flow or were paraphyletic or polyphyletic. All six species exhibited strong geographic patterns within their genetic variation, including clear genetic differences in northern and southern populations for widely distributed species. Furthermore, although populations within species share similar morphological characteristics, the evidence of gene flow in some species suggests a potential source of genetic diversity, possibly from other species from the *Didactyle* group or even from more distantly related species. While some genetic differences are influenced by geographic isolation, not all can be explained by this variable alone.

These findings highlight the importance of population genetics in understanding evolution at very recent timescales, especially the role of geographic isolation in microevolution. It also shows the importance of high-throughput sequencing data sets, as relying purely on morphological traits to determine relatedness is insufficient to test species boundaries (Pérez-Escobar et al., 2020) and tease apart the influence of important genetic events in the shaping of such lineages (Pérez-Escobar et al., 2022).

Studies, such as Fiorini et al. (2023) founded on comparative morphology and population genomics, pave the way for future research addressing the impact of geographical isolation, gene flow, and genetic diversity on speciation. Such factors have been repeatedly hypothesized to be responsible for the hyperdiversity of orchids in mountainous landscapes (Dodson, 2003), but have rarely been investigated in such detail.

Lastly, as climate change increases temperatures at a faster rate within higher elevations than lowlands (Verrall & Pickering, 2020), species adapted to mountain top

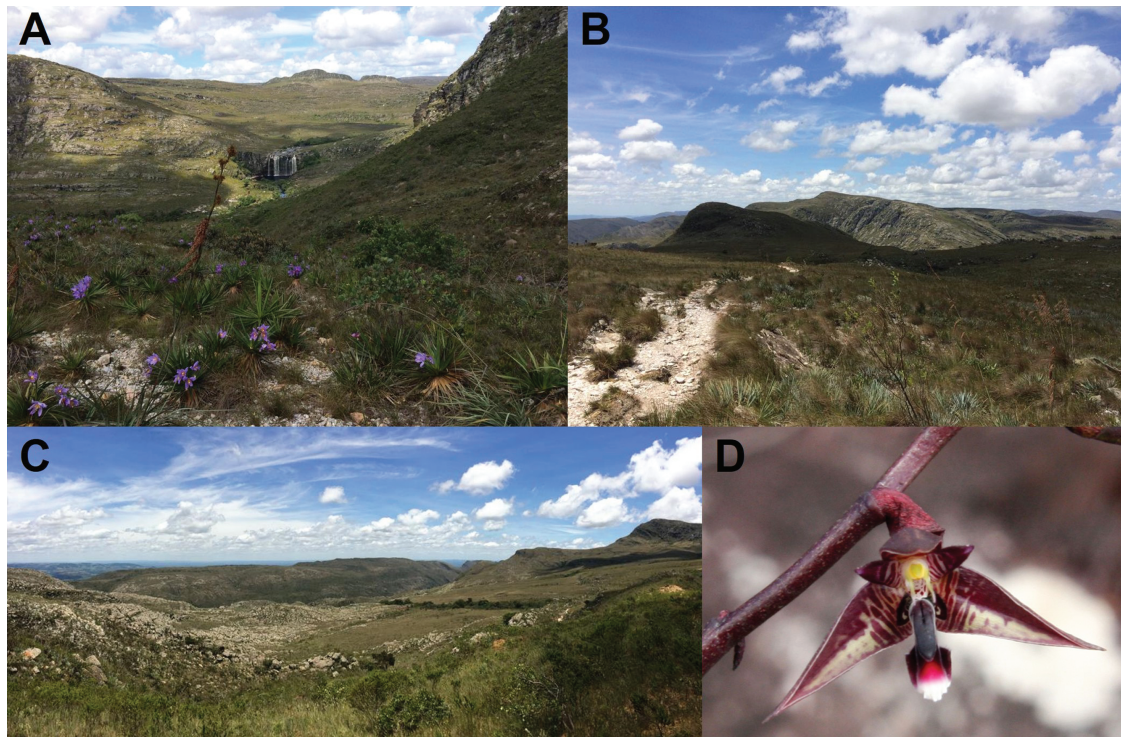


Figure 1. (A–C) Grasslands and rocky outcrops in the campos rupestres, Brazil. Photograph credit: Cassia Bitencourt. (D) Flower of *Bulbophyllum involutum* Borb. & F. Barros, an endemic orchid that inhabits the rocky outcrops of Minas Gerais and Bahia states in Brazil. Photograph credit: Daniela Zappi, used with the permission of the Board of Trustees of the Royal Botanic Gardens, Kew.

environments could be particularly vulnerable. However, species' adaptability to climatic change is still largely unknown. Utilizing population genomics in conjunction with functional trait analyses may uncover specific genes with adaptive potential to help overcome dramatic climate fluctuations and help predict which populations might have higher chances of survival.

Conflict of interest: The authors declare no conflict of interest.

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