Brazilian Journal of Botany (2026) 49:19
https://doi.org/10.1007/s40415-026-01145-3

SYSTEMATICS & PHYLOGENY - SHORT COMMUNICATION

Genetic and spatial data on the conservation of the critically endangered *Paepalanthus longiciliatus* (Eriocaulaceae)

Marcelo Trovó[1,2] · Mylena Cabrini[2,3] · Renato Ramos[4] · Yoshihisa Suyama[5] · Daiki Takahashi[6] · Catarina Lira[3]

Received: 29 October 2025 / Revised: 27 February 2026 / Accepted: 12 March 2026
© The Author(s) 2026

Abstract

We provide new genetic and spatial data on the conservation of *Paepalanthus longiciliatus* (≡*Coracoralina longiciliata* (Trovó) Andrino, Eriocaulaceae), a narrowly distributed species from Goiás, Brazil, officially categorized as Critically Endangered (CR). Despite identifying potential occurrence sites surrounding the type locality, which still harbors a population of a few hundred individuals, efforts to locate new populations were unsuccessful. Most of these potential areas are indeed unprotected private properties. Herbarium searches also failed to yield additional specimens; consequently, the species is known only from three records at the type locality (1996, 2009, and 2024). The species occurs in typical dystrophic cambisoils of the *Cerrado*, with a clayey-silty texture, generally considered less suitable for large-scale monoculture. However, land-use changes observed over time indicate the transformation of native vegetation into a mosaic of diverse uses, including a paved road, monoculture plantations, and pastures, the latter often involving the use of fire and invasive grasses. Genetic data suggest low genetic diversity and high inbreeding, although the relatively high nucleotide diversity suggests that some genetic variation is still retained. These patterns likely reflect the effects of genetic drift in an isolated species restricted to a small population with limited dispersal capacity. The species' rhizome and sprouting reproduction mode likely explain its survival under moderate adverse conditions. Given these findings, the species should remain categorized as Critically Endangered. Additional botanical explorations, the implementation of a Private Natural Heritage Reserve (RPPN), and ex-situ conservation techniques are essential efforts to ensure the preservation of this species.

Keywords Genetic diversity · IUCN · MIG-seq · Niquelândia · Poales

1 Introduction

Eriocaulaceae (Poales) is a Pantropical family widely distributed throughout the Neotropical Region, especially in Brazil, which harbors about half of the ca. 1400 known species (Giulietti and Hensold 1990; Stützel 1998; Giulietti et al. 2012). Species within this family often have narrow distributions, with many being microendemic and found only on one or a few adjacent mountains (Giulietti and Hensold 1990; Giulietti et al. 2005). This restricted distribution pattern is associated with a strong substratum specialization and a limited dispersion capacity. As a consequence, these species are highly vulnerable to habitat disturbances, loss, or fragmentation (Giulietti and Hensold 1990; Stützel 1998; Costa et al. 2008, 2018; Trovó and Stützel 2011). Therefore, it is not surprising that numerous species of Eriocaulaceae appear on the Brazilian Red Lists, with many classified as

✉ Marcelo Trovó
martrovo@gmail.com

1 Departamento de Botânica, Instituto de Biologia, Universidade Federal Do Rio de Janeiro, Cidade Universitária, Rio de Janeiro, RJ 21941-590, Brazil

2 Programa de Pós-Graduação Em Botânica, Escola Nacional de Botânica Tropical, Instituto de Pesquisas Jardim Botânico Do Rio de Janeiro, Rio de Janeiro, RJ 22460-036, Brazil

3 Diretoria de Pesquisa, Instituto de Pesquisas Jardim Botânico Do Rio de Janeiro, Rio de Janeiro, RJ 22460-040, Brazil

4 Departamento de Botânica, Instituto de Biociências, Universidade de São Paulo, Cidade Universitária, sao paulo, SP 05508-090, Brazil

5 Kawatabi Field Science Center, Graduate School of Agricultural Science, Tohoku University, 232-3 Yomogida, Naruko-Onsen, Osaki, Miyagi 989-6711, Japan

6 Faculty of Agriculture, Kyushu University, 744, Motooka, Nishi-Ku, Fukuoka 819-0395, Japan

Published online: 24 March 2026

endangered or critically endangered (Martinelli and Moraes 2013; Martinelli et al. 2014).

One of the threatened species from the Eriocaulaceae listed in the Brazilian Red List is *Paepalanthus longiciliatus* Trovó (≡*Coracoralina longiciliata* (Trovó) Andrino). This species is a narrow endemic plant, found only in the vicinity of Niquelândia (Goiás state, Brazil) (Trovó et al. 2013; Negrão et al. 2016). Since its original description, it has been recognized as a threatened species (Trovó and Sano 2011). It was officially categorized as Critically Endangered a few years later (Negrão et al. 2016) and subsequently included in the Brazilian National Plan for the Conservation of the Threatened Flora of the Alto Tocantins Basin (Verdi and Oliveira 2025). As with most other evaluated Eriocaulaceae species, data on population genetics and demography are absent. Consequently, their conservation status assessments are based primarily on the limited documentation of their geographic distribution. In this note, we revisit the conservation of *P. longiciliatus* based on new genetic and spatial data.

2 Material and methods

Field trips were dedicated to locating additional populations of *Paepalanthus longiciliatus* in the surrounding areas of the type locality (14°26′17"S, 48°09′51"W) over the last decade. Visits to the most relevant herbarium collections for the Eriocaulaceae from Goiás (acronyms CEN, HEPH, IBGE, SPF, UB, UFG) and searches on online databases (Species Link and Reflora) also aimed to locate additional specimens and collection sites. In the type locality, we collected eight individuals from the species aggregated population for genetic analysis, maintaining a minimum distance of five meters between them (Table S1) and estimated the number of flowering and vegetative individuals by visual inspection. Voucher specimens are deposited at RB (barcode RB 885460). It is worth to mention that within the different classification systems available (Christenhusz et al. 2020; Andrino et al. 2023, 2025; Stützel et al. 2024) the species may be positioned in different genera, *Paepalanthus* Mart. or *Coracoralina* Andrino and Sano. Here we adopt a broad *Paepalanthus* concept and treat the species in its original genus.

Spatial data – Species distribution maps were prepared using QGis software, including political boundaries, elevation, and relief. The conservation status was evaluated using standard methods (IUCN 2024), following the recent framework used for new species (Zavatin et al. 2023a; 2023b). Area of Occupation (AOO) was estimated with GeoCat (Bachman et al. 2011). Georeferenced data related to the historical series of vegetation transformation (MapBiomas 2024), impacts of fire, and mining were obtained using fire frequency raster (MapBiomas 2025), SIGMINE database (ANM 2025), and fieldwork observations.

Genetic data – DNA was extracted from silica gel-dried leaf tissue using Nucleo Spin™ Plant kit (Marchery-Nagel™, Germany) with slight modifications. The integrity of DNA was assessed using 1% agarose gel and DNA concentration was estimated with a Nanodrop™ 2000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). To obtain genome-wide single nucleotide polymorphisms (SNPs), we employed the Multiplexed ISSR genotyping by sequencing (MIG-seq) method, as described by Suyama and Matsuki (2015), and followed library preparation protocol described by Suyama et al. (2022). Sequencing was conducted on the Illumina MiSeq platform (Illumina, San Diego, CA, USA) using the MiSeq Reagent Kit v3 (150-cycle; Illumina).

After merging the forward and reverse reads of each sample following Suyama and Matsuki (2015), low-quality reads were removed using Trimmomatic v.0.32 (Bolger et al. 2014) with the following commands: HEADCROP:6, CROP:77, SLIDINGWINDOW:10:30, and MINLEN:51. The filtered reads were then assembled using Stacks v.2.41 pipeline (Rochette et al. 2019). The minimum depth was set to 6 (-m 6), and default values were employed for the other options. Using the populations program in Stacks, we extracted SNPs retaining only loci with no missing data across samples. To eliminate paralogous loci and possible PCR errors, loci exhibiting observed heterozygosity > 0.6 and SNPs with minor allele count < 0.3 were removed. A total of 195 SNPs from the eight individuals were obtained, following stringent quality control measures. Finally, VCFtools and PGDSpider 2 were used to generate input files for subsequent genetic analysis (Danecek et al. 2011; Lischer and Excoffier 2012). The filtered SNP dataset (VCF file) is available at https://doi.org/10.5281/zenodo.18038937.

We estimated expected (H_E) and observed (H_O) heterozygosities using the "adegenet" R package (Jombart et al. 2018; R Core Team 2025). Significant differences in heterozygosity variances were tested with Bartlett's test of homogeneity (*bartlett.test* function) after arcsine-transforming heterozygosity values to ensure data normality (Masuda et al. 2022). The inbreeding coefficient (F_{IS}) and allelic richness (Ar) were calculated using the function from the "dartR" R package (Gruber et al. 2018), and nucleotide diversity (π) was estimated using DnaSP v.6 (Rozas et al. 2017).

3 Results & discussion

Our efforts to locate additional populations of *Paepalanthus longiciliatus* were unsuccessful, despite the high potential for occurrence sites inferred from satellite images of habitat

similarity. Most of the areas surrounding the type locality are entirely within unprotected private properties, many of these inaccessible. We were able to visit a few areas in a region locally known as the *Mantiqueira* Mountain Complex (14°41′44"S 48°30′42"W), where we registered only a few unusual specimens related to the *P. chiquitensis* Herzog species complex. Our herbarium searches were similarly unsuccessful. Two specimens (*Fonseca 175* SPF; *Fonseca* et al. *2632* IBGE) were identified in 2014 as *P. longiciliatus*. However, these are unfortunately misidentifications of teratogenic specimens also belonging to the *P. chiquitensis* species complex, which is currently under review. The information indicating the possible occurrence of the species (under *Coracoralina longiciliata*) in Piauí (Flora e Funga do Brasil 2025), a state of North-Western Brazil, is inaccurate. Therefore, *P. longiciliatus* (Fig. 1) remains known exclusively from the type locality (Figs. 1 and 2), based on three different collections made in 1996, 2009, and 2024.

The only known population of *Paepalanthus longiciliatus* is composed by a few hundreds individuals occurring as an

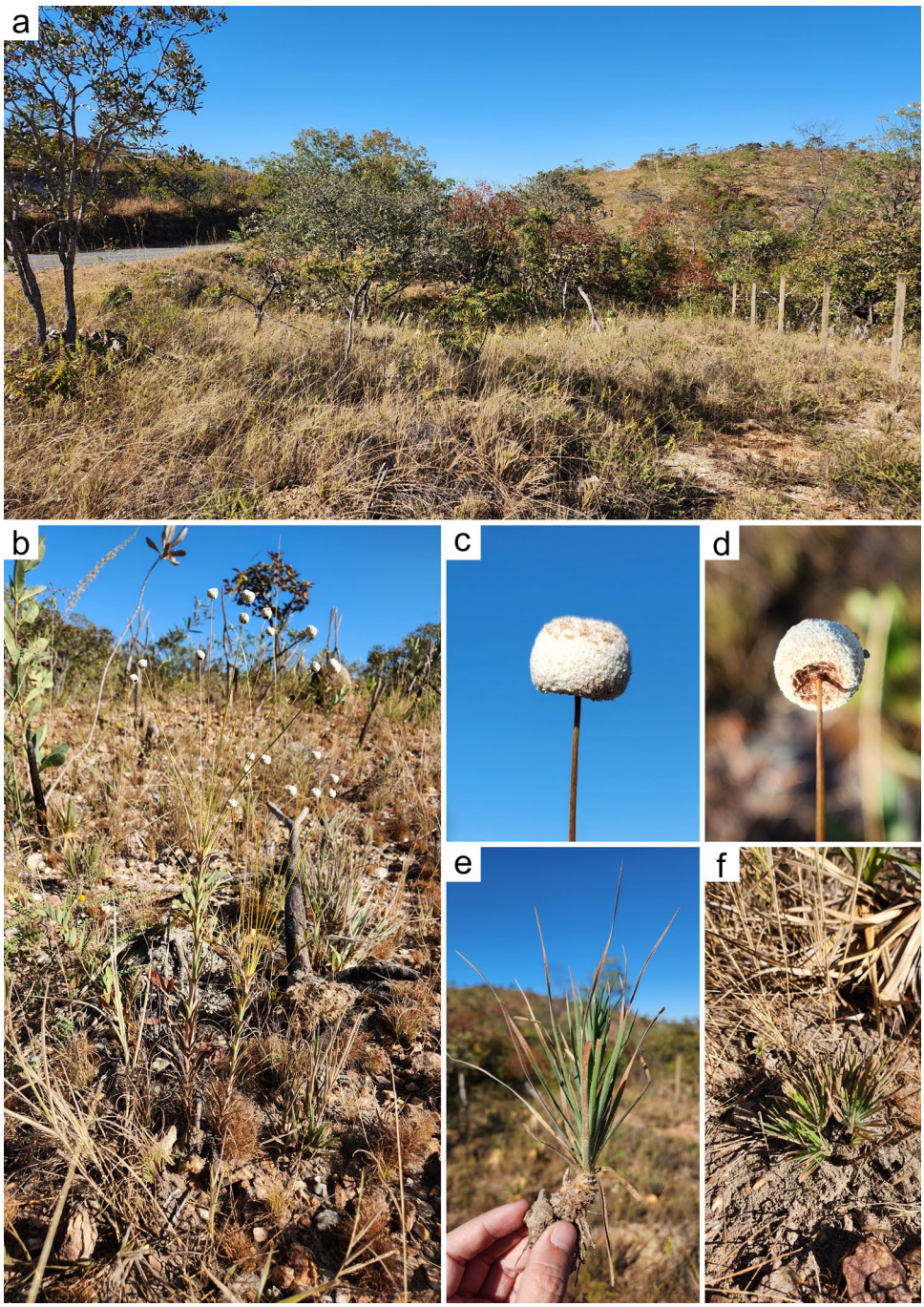


Fig. 1 *Paepalanthus longiciliatus* Trovó at the type locality in 2024. **a** Habitat. **b** Habit. **c** Capitulum seen from the side. **d** Capitulum seen from below, evidencing the involucral bracts. **e** Rosette, evidencing the subterraneous rhizome. **f** Sprouting rosettes. Photos: Marcelo Trovó

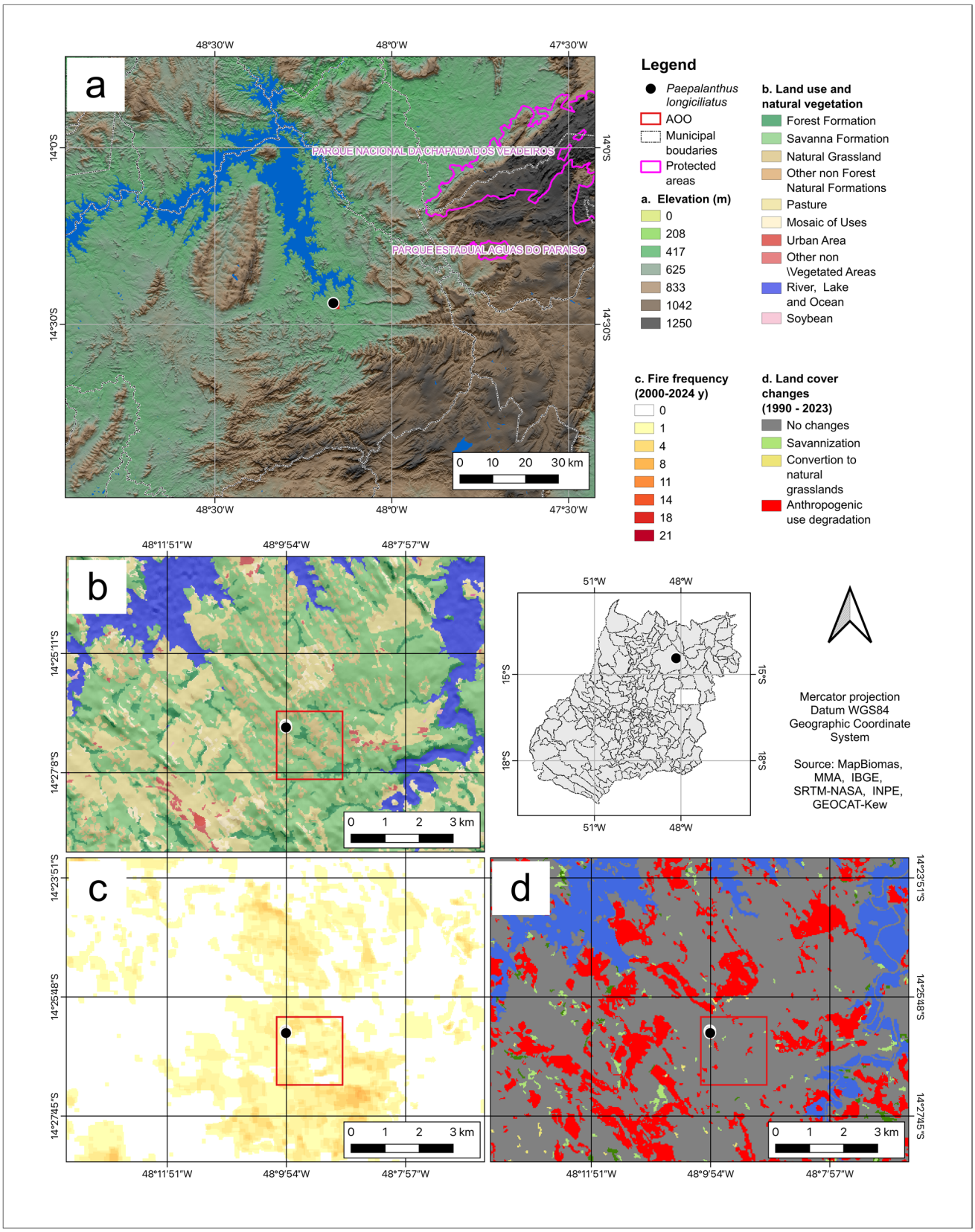


Fig. 2 Occurrence, including environmental and conservation spatial assessment of *Paepalanthus longiciliatus*. **a** location of the known population in the municipality of Niquelândia. **b** 2023's land use and natural vegetation. **c** Fire Frequency. **d** Natural vegetation and land-use transformations between 1990 and 2023. Elaborated by R. Ramos, September 2025

aggregated patch restricted to the municipality of Niquelândia, Goiás State (Central Brazil), along the GO-132 highway, at an altitude of 509 m (Fig. 2a). The species occurs in typical dystrophic cambisoils of the *Cerrado*, characterized by a clayey-silty texture, which is generally less suitable for monoculture plantations. The vegetation exhibits an herbaceous-shrubby savanna physiognomy, typical of the *Cerrado* biome (Fig. 2b). The environment in this area displays signs of disturbances in the vegetation caused by the construction and maintenance of a paved road. Additionally, the area is suitable for managing and consequently for the expansion of the existing pastures through the use of fire (Fig. 2c). The plant possesses rhizomes and vegetative reproduction (Fig. 1e–f) that allow it to survive during sporadic fire events, but recurrent fires can reduce population size. On the other hand, the complete absence of fire may alter competitive dynamics, as observed in *P. fonsecae* Trovó & Picanço (Trovó et al. 2025), favoring other herbaceous and shrubby species. In these dynamics, the use of exotic grass species has been noted as a significant factor as widely documented in the biome. Over time, changes have been observed in the native vegetation, which has transformed into various land-uses originally consisting of grasslands and savanna formations (*cerrado s.s.*). This transformation has led to the creation of diverse mosaics, including monoculture plantations and pastures (Fig. 2d).

Paepalanthus longiciliatus is officially classified as a threatened species (Negrão et al. 2016). The original assessment of its threat status was based on the scarce field data collected at the time of the species' description (Trovó and Sano 2011). Our field re-evaluation, conducted 14 years later, indicates that the species distribution and demographics have not changed significantly. Therefore, the area of occupancy (AOO) remains at 4 km^2, also maintaining the criteria A2bc; B2ab(ii, iii, iv), which qualifies for the Critically Endangered (CR) status. The primary threat to the species appears to be the impact of activities related to land-use conversion in the region, particularly given that it is not found in any protected area. Although genetic parameters are not explicitly addressed in the IUCN (2024) guidelines, our findings provide valuable insights for conservation efforts, representing a new contribution to the knowledge about this species, as seen below.

Genetic data revealed an overall low diversity within the species. The observed heterozygosity ($H_O = 0.2102$) was significantly lower than the expected heterozygosity ($H_E = 0.2492$; Bartlett's test, $p < 0.001$), suggesting a deficit of heterozygotes in the population. In contrast, nucleotide diversity was relatively high ($\pi = 0.1487$), allelic richness was moderate ($Ar = 0.8199$), and the inbreeding coefficient ($F_{IS} = 0.2209$) indicated high levels of inbreeding. This pattern of low genetic diversity and high inbreeding is consistent with the species' limited dispersal capacity, small population size, and restricted distribution. As such, the genetic results obtained here may be similar for other Eriocaulaceae (Cabrini et al. 2024, 2025), as most of the species of the family are narrowly distributed in the *Cerrado* (Giulietti and Hensold 1990; Giulietti et al. 2005). Congruent patterns have been observed throughout the *Cerrado*, where plant populations exhibiting particularly low genetic diversity are found in the central and southern regions, while genetic diversity tends to increase with distance from the center of the biome (Ballesteros-Mejia et al. 2020). This spatial trend likely reflects both historical and contemporary processes shaping genetic variation, including significant landscape modifications (Ballesteros-Mejia et al. 2020).

Although the *Cerrado* is the largest savanna in the world harboring a highly complex mosaic of habitats, large portions of its landscape have undergone massive transformations in recent decades. This is mainly due to the conversion of natural areas into agricultural fields, pastures, and urban zones (Sano et al. 2010; Strassburg et al. 2017). These land-use changes have resulted in habitat loss and fragmentation, disrupting population connectivity and reducing effective population sizes (Aguilar 2008; Diniz-Filho et al. 2009). In this context, limited gene flow among individuals can intensify the effects of genetic drift, leading to the random loss of alleles and a gradual increase in homozygosity (Anderson et al. 2010; Holderegger and Di Giulio 2010; Leimu et al. 2010). These processes are especially pronounced in small, isolated populations, where individuals tend to become more related to each other over time, reducing genetic variation and increasing the risk of inbreeding depression (Frankham et al. 2002; Frankham 2019). As a consequence, higher homozygosity and inbreeding depression may reduce fitness, and rapid environmental changes can further heighten the likelihood of extinction in populations that lack the genetic diversity necessary for an effective evolutionary response (Frankham 2005; Ouborg et al. 2006; DeWoody 2021).

We emphasize that the conservation of the microendemic species *Paepalanthus longiciliatus* depends largely on protecting the natural environment around its only known population, the type locality. Unfortunately, this area is under severe human pressure, as it is entirely enclosed within private properties. Efforts to promote the creation of a Private Natural Heritage Reserve (RPPN) are highly desirable in this region. Additionally, attempts to locate additional populations are crucial, as the low genetic diversity observed in the existing small population of the species could threaten its long-term survival facing environmental changes, highlighting the species' vulnerability and the importance of preserving genetic diversity. In this sense, efforts to generate rapid and low-cost genetic data, as those deriving from MIG-seq techniques (Suyama and Matsuki 2015), were highly useful for species conservation. Moreover, ex-situ conservation strategies may also help in the conservation of the species.

We point out that similar situations likely apply to many other species in the area, which is home to numerous micro-endemic and threatened species (Verdi and Oliveira 2025). A related species, *Paepalanthus flexuosus* Trovó, faces similar threats; as it is restricted to the nickel mining areas of Niquelândia (Trovó and Sano 2011), and was not located during our recent field trips.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s40415-026-01145-3.

Acknowledgements MT thank Alexander von Humboldt Foundation, FAPERJ (E-26/210.739/2024—APQ1) and CNPq (proc. 303866/2022-5—Pq2). MC thanks the CAPES and JBRJ for awarding a Msc. scholarship (proc. 88887.837683/2023–00).

Author contributions All authors contributed to the study conception and design. Field experiments were conducted by MT and MC. Material preparation, data collection and analysis were performed by MT, MC, RR, YS, DT, and CL. The first draft of the manuscript was written by MT, MC, and RR. Writing—review and editing, resources acquisition, and supervision were provided by MT, YS, DT, and CL. All authors read and approved the final manuscript.

Funding The Article Processing Charge (APC) for the publication of this research was funded by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) (ROR identifier: 00x0ma614).

Data availability All data generated or analyzed during this study are included in the supplementary material file and in a public repository at https://doi.org/10.5281/zenodo.18038937.

Declarations

Conflict of interest The authors declare that they have no conflict of interest.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by/4.0/.

References

Aguilar R, Quesada M, Ashworth L, Diego YH, Lobo J (2008) Genetic consequences of habitat fragmentation in plant populations: susceptible signals in plant traits and methodological approaches. Mol Ecol 17:5177–5188. https://doi.org/10.1111/j.1365-294X.2008.03971.x

Anderson CD, Epperson BK, Fortin MJ et al (2010) Considering spatial and temporal scale in landscape-genetic studies of gene flow. Mol Ecol 19:3565–3575. https://doi.org/10.1111/j.1365-294X.2010.04757.x

Andrino CO, Costa FN, Simon MF, Missagia RV, Sano PT (2023) Eriocaulaceae: a new classification system based on morphological evolution and molecular evidence. Taxon 72:515–549. https://doi.org/10.1002/tax.12915

Andrino CO, Barbosa-Silva R, Siniscalchi C et al (2025) Phylogenomic evidence reveals non-monophyly of Paepalanthoideae (Eriocaulaceae) and challenges the broad concept of *Paepalanthus*. Taxon. https://doi.org/10.1002/tax.13359. ((**in press**))

ANM (Agência Nacional de Mineração) (s.d.) SIGMINE – Sistema de Informações Geográficas da Mineração. ANM, Brasília. Available from https://geo.anm.gov.br/portal/apps/webappviewer (accessed 10 Sep 2025).

Bachman S, Moat J, Hill AW, de la Torre J, Scott B (2011) Supporting red list threat assessments with GeoCAT: geospatial conservation assessment tool. Zookeys 150:117–126. https://doi.org/10.3897/zookeys.150.2109

Ballesteros-Mejia L, Lima JS, Collevatti RG (2020) Spatially-explicit analyses reveal the distribution of genetic diversity and plant conservation status in Cerrado biome. Biodivers Conserv 29:1537–1554. https://doi.org/10.1007/s10531-018-1588-9

Bolger AM, Lohse M, Usadel B (2014) Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/BIOINFORMATICS/BTU170

Cabrini M, Lira C, Suyama Y, Takahashi D, Ishikawa N, Paglia I, Trovó M (2024) Genomic and morphological data reveal a critically endangered new species from the Atlantic Forest, *Paepalanthus salimenae* (Eriocaulaceae). Phytotaxa 655:173–186. https://doi.org/10.11646/phytotaxa.655.2.5

Cabrini M, Trovó M, Takahashi D, Suyama Y, Ramos R, Lira C (2025) Lithobiomes heterogeneity and geographic distance shape the landscape genomics within Brazilian mountain systems. Ecol Evol 15:e72476. https://doi.org/10.1002/ece3.72476

Christenhusz MJM, van den Berg C, Byng JW, Chase MW (2020) Proposal to conserve *Paepalanthus* nom. cons. against the additional name, *Tonina* (Eriocaulaceae). Taxon 69:1109–1110. https://doi.org/10.1002/tax.12333

Costa FN, Andrino CO, Sano PT, Trovó M, Echternacht L (2018) *Paepalanthus* (Eriocaulaceae) in the Central Espinhaço Range in Minas Gerais, Brazil: checklist, endemism, and nomenclatural changes. Phytotaxa 367:133–144. https://doi.org/10.11646/phytotaxa.367.2.3

Costa FN, Trovó M, Sano PT (2008) Eriocaulaceae na Cadeia do Espinhaço: riqueza, endemismos e ameaças. Megadiversidade 4:89–97

Danecek P, Auton A, Abecasis G et al (2011) The variant call format and VCFtools. Bioinformatics 27:2156–2158. https://doi.org/10.1093/bioinformatics/btr330

DeWoody JA, Harder AM, Mathur S, Willoughby JR (2021) The long-standing significance of genetic diversity in conservation. Mol Ecol 30:4147–4154. https://doi.org/10.1111/mec.16051

Diniz-Filho JAF, Nabout JC, Bini LM, Soares TN, Telles MPC, de Marco JP Jr, Collevatti RG (2009) Niche modelling and landscape genetics of *Caryocar brasiliense* ("pequi" tree: Caryocaraceae) in Brazilian Cerrado: an integrative approach for evaluating central–peripheral population patterns. Tree Genet Genomes 5:617–627. https://doi.org/10.1007/s11295-009-0214-0

Flora e Funga do Brasil (2025) *Coracoralina* in Flora e Funga do Brasil. Jardim Botânico do Rio de Janeiro. Available from https://floradobrasil.jbrj.gov.br/FB635670 (accessed 20 Oct 2025).

Frankham R (2005) Genetics and extinction. Biol Conserv 126:131–140. https://doi.org/10.1016/j.biocon.2005.05.002

Frankham R (2019) Conservation genetics. In: Fath BD (ed) Encyclopedia of ecology. Elsevier, Amsterdam, pp 382–390

Frankham R, Briscoe DA, Ballou JD (2002) Introduction to conservation genetics. Cambridge University Press, Cambridge

Giulietti AM, Andrade MJG, Scatena VL et al (2012) Molecular phylogeny, morphology and their implications for the taxonomy of Eriocaulaceae. Rodriguésia 63:1–19. https://doi.org/10.1590/S2175-78602012000100001

Giulietti AM, De Queiroz LP, Wanderley MDGL, van den Berg C (2005) Biodiversidade e conservação das plantas no Brasil. Megadiversidade 1:52–61

Giulietti AM, Hensold N (1990) Padrões de distribuição geográfica dos gêneros de Eriocaulaceae. Acta Bot Bras 4:133–159. https://doi.org/10.1590/S0102-33061990000100010

Gruber B, Unmack PJ, Berry OF, Georges A (2018) Dartr: an R package to facilitate analysis of SNP data generated from reduced representation genome sequencing. Mol Ecol Resour 18:691–699. https://doi.org/10.1111/1755-0998.12745

Holderegger R, Di Giulio M (2010) The genetic effects of roads: a review of empirical evidence. Basic Appl Ecol 11:522–531. https://doi.org/10.1016/j.baae.2010.06.006

IUCN Standards and Petitions Committee (2024) Guidelines for using the IUCN red list categories and criteria, ver 16. IUCN, Gland

Jombart T, Kamvar ZN, Collins C, Lustrik R, Beugin MP, Knaus BJ, Jombart MT (2018) Package 'adegenet'. Available from https://cran.r-project.org/web/packages/adegenet/index.html (accessed 02 Sep 2025).

Leimu R, Vergeer P, Angeloni F, Ouborg NJ (2010) Habitat fragmentation, climate change, and inbreeding in plants. Ann N Y Acad Sci 1195:84–98. https://doi.org/10.1111/j.1749-6632.2010.05450.x

Lischer HE, Excoffier L (2012) PGDSpider: an automated data conversion tool for connecting population genetics and genomics programs. Bioinformatics 28:298–299. https://doi.org/10.1093/bioinformatics/btr642

Martinelli G, Messina T, Filho LS (2014) Livro Vermelho da Flora do Brasil: Plantas Raras do Cerrado. Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, p 320

Martinelli G, Moraes MA (2013) Livro Vermelho da Flora do Brasil. Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, p 1100

Masuda K, Setoguchi H, Nagasawa K et al (2022) Rear-edge daylily populations show legacies of habitat fragmentation due to the Holocene climate warming. J Biogeogr 50:551–563. https://doi.org/10.1111/jbi.14552

MapBiomas (2024) Coleção 9 da Série Anual de Mapas de Cobertura e Uso da Terra do Brasil. Projeto MapBiomas – Instituto de Pesquisa Ambiental da Amazônia. Available from https://mapbiomas.org (accessed 09 Sep 2025).

MapBiomas (2025) Coleção 4: Mapeamento anual da área queimada no Brasil (1985–2024). Projeto MapBiomas – Instituto de Pesquisa Ambiental da Amazônia. Available from https://mapbiomas.org (accessed 18 Oct 2024).

Negrão R, Amaro R, Oliveira MTL (2016) *Coracoralina longiciliata* (Trovó) Andrino (Eriocaulaceae) in Lista Vermelha da Flora Brasileira: Centro Nacional de Conservação da Flora / Instituto de Pesquisas Jardim Botânico do Rio de Janeiro. Available from https://cncflora.jbrj.gov.br/ficha/635670 (accessed 20 Oct 2025).

Ouborg NJ, Vergeer P, Mix C (2006) The rough edges of the conservation genetics paradigm for plants. J Ecol 94:1233–1248. https://doi.org/10.1111/j.1365-2745.2006.01167.x

R Core Team (2025) R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna. Available from https://www.r-project.org/ (accessed 17 Oct 2025).

Rochette NC, Rivera-Colon AG, Catchen JM (2019) Stacks 2: analytical methods for paired-end sequencing improve RADseq based population genomics. Mol Ecol 28:4737–4754. https://doi.org/10.1111/mec.15253

Rozas J, Ferrer-Mata A, Sánchez-DelBarrio JC, Guirao-Rico S, Librado P, Ramos-Onsins SE, Sánchez-Gracia A (2017) DnaSP 6: DNA sequence polymorphism analysis of large data sets. Mol Biol Evol 34:3299–3302. https://doi.org/10.1093/molbev/msx248

Sano EE, Rosa R, Brito JLS, Ferreira LG (2010) Land cover mapping of the tropical savanna region in Brazil. Environ Monit Assess 166:113–124. https://doi.org/10.1007/s10661-009-0988-4

Strassburg BB, Brooks T, Feltran-Barbieri R et al (2017) Moment of truth for the Cerrado hotspot. Nat Ecol Evol 1:0099. https://doi.org/10.1038/s41559-017-0099

Stützel T (1998) Eriocaulaceae. In: Kubitzki K (ed) Flowering Plants Monocotyledons. The Families and Genera of Vascular Plants, Springer, Berlin, Heidelberg.

Stützel T, Trovó M, Echternacht L, Coan AI, de Lima Silva A, Watanabe MTC, Hensold N (2024) In support of a broad concept of *Paepalanthus* (Eriocaulaceae). Taxon 73:1117–1129. https://doi.org/10.1002/tax.13221

Suyama Y, Hirota SK, Matsuo A, Tsunamoto Y, Mitsuyuki C, Shimura A, Okano K (2022) Complementary combination of multiplex high-throughput DNA sequencing for molecular phylogeny. Ecol Res 37:171–181. https://doi.org/10.1111/1440-1703.12270

Suyama Y, Matsuki Y (2015) MIG-seq: an effective PCR-based method for genome-wide single-nucleotide polymorphism genotyping using the next-generation sequencing platform. Sci Rep 5:1–12. https://doi.org/10.1038/srep16963

Trovó M, Echternacht LA, Sano PT (2013) Distribution and conservation of *Paepalanthus* Mart. sect. *Diphyomene* Ruhland (Eriocaulaceae) in Neotropical savannas. Adansonia 35:195–206. https://doi.org/10.5252/a2013n2a2

Trovó M, Picanço LW, Sayuri Tajima A, de Mathias Tessari G, Ramos R, Gonçalves-Esteves V, Ike Coan A (2025) Taxonomy, anatomy and palynology of *Paepalanthus fonsecae* (Eriocaulaceae), a new species from Central Brazil. Nord J Bot 2025:e04528. https://doi.org/10.1111/njb.04528

Trovó M, Sano PT (2011) Five new and narrowly distributed species of *Paepalanthus* section *Diphyomene* (Eriocaulaceae) from Central Brazil. Syst Bot 36:610–620. https://doi.org/10.1600/036364411X583600

Trovó M, Stützel T (2011) Diaspores in Eriocaulaceae: morphology, mechanisms, and implications. Feddes Repert 122:456–464. https://doi.org/10.1002/fedr.201200003

Verdi M, Oliveira JA (2025) Plano de Ação Nacional para a conservação da flora ameaçada de extinção da Bacia do Alto Tocantins: PAN Bacia do Alto Tocantins. Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, p 106

Zavatin DA, Ramos R, Watanabe MTC, Pedrosa LG, de Lírio EJ (2023a) A new species of *Mollinedia* (Monimiaceae, Laurales) from the Quadrilátero Ferrífero, Brazil. PhytoKeys 234:189–201. https://doi.org/10.3897/phytokeys.234.109804

Zavatin DA, Almeida RBP, Ramos R, Lombardi JA (2023b) *Chionanthus monteazulensis* (Oleaceae), a new species from the campo rupestre of Espinhaço Range, Brazil. Phytotaxa 603:289–296. https://doi.org/10.11646/phytotaxa.603.3.8

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.