

This cave is mine: potential competitive exclusion between two species of *Rowlandius* (Schizomida: Hubbardiidae) in the Caatinga

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Abstract

The order Schizomida comprises small arachnids, with the genus *Rowlandius* being the most diverse, including 66 described species. In Brazil, two species, *Rowlandius potiguar* and *Rowlandius* sp. n. 1, are both endemic to the Caatinga biome and inhabit the caves of the Jandaíra Formation, exhibiting similar morphologies. Preliminary observations suggested that each cave hosts only one of these species. Based on an extensive sample size, molecular data, and morphological identification, we hypothesized a pattern of competitive exclusion between these species. This study employed phylogeographic, phylogenetic, and ecological niche modeling approaches to investigate whether there is a high degree of niche overlap between the two species or if they exhibit significant niche specialization. Specimens were collected from 27 caves, including 14 newly recorded locations. Molecular analyses, utilizing mitochondrial and nuclear markers, revealed no instances of cave sympatry among the different lineages. Ecological niche modeling indicated that *R. potiguar* demonstrates greater specialization in restricted habitats, while *Rowlandius* sp. n. 1 shows higher ecological flexibility and adaptability to varying environmental conditions. Furthermore, the soil water index emerged as the most significant environmental variable influencing the distribution of both species, consistent with their hygrophilic nature. The findings strongly support the hypothesis of competitive exclusion, with no sympatry observed between the species based on morphological, molecular, and ecological data. This pattern likely reflects an eco-evolutionary process of niche partitioning, where the two species may have evolved divergent strategies to reduce competition in resource-limited environments like caves. While some caves are located within the Furna Feia National Park, the majority lie outside protected areas. As a result, most populations of both species face ongoing threats, highlighting the urgent need for conservation efforts.

1. Introduction

The order Schizomida comprises small arachnids, with the genus *Rowlandius* being the most speciose, encompassing 66 described species (World Arachnida Catalog, 2025). These species exhibit a predominantly Neotropical distribution and are found in diverse habitats such as leaf litter, soil, and caves, particularly in the Caatinga, a semi-arid biome.

In Brazil, two *Rowlandius* species are endemic to the Jandaíra Formation (spanning Rio Grande do Norte and Ceará), including caves located within the Furna Feia National Park (FFNP). The park is a significant spot for troglotic species in the Caatinga. The two species, *Rowlandius potiguar* (Fig. 1A) and *Rowlandius* sp. n. 1 (Fig. 1B, currently under description), share similar distributions and exhibit comparable external morphologies. Notably, these species have never been recorded coexisting in the same cave, suggesting a possible case of competitive exclusion. Based on this observation, we hypothesize that there is either a high degree of niche overlap between these two species or that both exhibit pronounced niche specialization.

To investigate this, we employed a phylogeographic and phylogenetic approach, sampling schizomids across their known distribution. Additionally, we conducted ecological niche modeling (ENM), a method that integrates known occurrence data with environmental variables to characterize species' ecological niches. ENM is widely applied to both terrestrial and aquatic organisms and has been increasingly explored for cave-dwelling fauna. However, studies of this kind remain scarce in Brazil, particularly for schizomids (Peterson *et al.*, 2011).

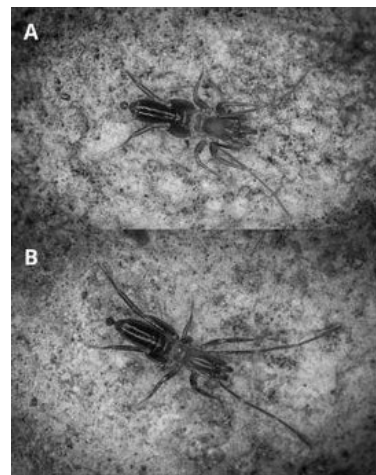


Figure 1: Specimens observed live in Felipe Guerra, Rio Grande do Norte, Brazil. (A) Male of *Rowlandius potiguar*, Carrapateira Cave; (B) Male of *Rowlandius* sp. n. 1, Pinga Cave. Source: Diego Bento, 2024.

2. Materials and methods

We collected schizomids from 27 caves, including 14 new records. The specimens were deposited in the Natural History Collections of the Federal University of Piauí (CHNUFP) and the Subterranean Invertebrates Collection of Lavras (ISLA) at the Federal University of Lavras.

For molecular analyses, total DNA was extracted from 97 specimens using the DNeasy Blood & Tissue Kit (Qiagen). Two molecular markers, cytochrome c oxidase I (cox1) and rDNA 28S, were sequenced following amplification via polymerase chain reaction (PCR). *Rowlandius ubajara* was used as the outgroup for phylogenetic analyses.

Consensus sequences were assembled using Geneious Prime software and aligned with ClustalW (Thompson et al., 1994) implemented in MEGA 11.0 (Tamura et al., 2021). Phylogenetic relationships were inferred through multilocus Bayesian inference (BI) analysis performed in BEAST (Drummond et al., 2012).

3. Results

The multilocus phylogenetic tree constructed using Bayesian inference (BI) revealed three major clades with strong branch support values (Fig. 2). The clade originating from the type locality of *Rowlandius potiguar* (Carrapateira Cave) also included specimens from 13 additional localities. This clade was identified as the sister group to a second clade comprising individuals of *Rowlandius sp. n. 2*, collected from Casa de Pedra Cave in Martins. Together, these two clades formed the sister group to the third clade, representing *Rowlandius sp. n. 1*, which included individuals from nine different caves. Notably, no sympatry was observed among the distinct lineages.

The ecological niche modeling results demonstrated strong predictive

Ecological niche modeling (ENM) was performed using Maxent models in R to evaluate the habitat suitability of both species. Occurrence data were obtained from the literature, biological collections, and the results of morphological and molecular analyses. A total of 30 occurrence points for *R. potiguar* and 16 for *Rowlandius sp. n. 1* were included in the modeling. Bioclimatic, soil, and vegetation variables were used, with a Pearson correlation filter ($P > 0.7$) applied to select four final variables. Calibration parameters were optimized using AIC, AUC, and omission rate values. The best-performing models were then used to generate species distribution maps in QGIS.

Additionally, a Principal Component Analysis (PCA) was conducted to examine similarities and differences in the relationships between species and the selected environmental variables, providing further insights into their habitat preferences.

accuracy (AUC > 0.8), highlighting similarities in habitat suitability between *R. potiguar* and *Rowlandius sp. n. 1* (Fig. 3). However, *Rowlandius sp. n. 1* exhibited a broader niche amplitude and greater adaptability to varying environmental conditions, whereas *R. potiguar* showed higher habitat specialization, resulting in a more restricted distribution.

The Soil Water Index emerged as the most influential variable in model construction, contributing over 50% to the results. Temperature and precipitation variables played key roles in defining niche partitioning between the species, while cation exchange capacity (CEC) was less significant and primarily highlighted differences in microhabitat preferences (Fig. 4).

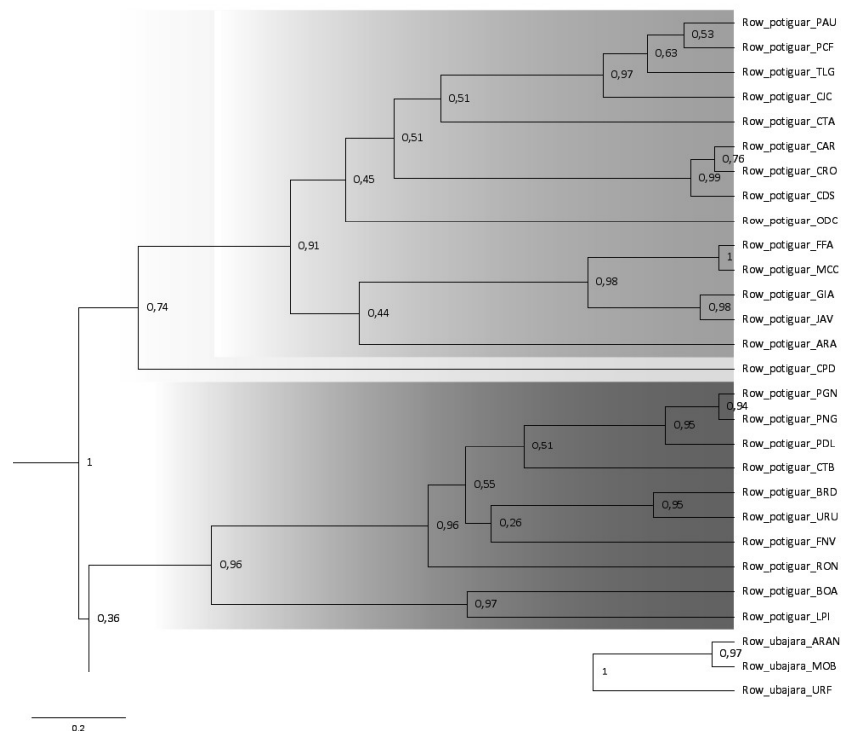


Figura 2: Multilocus consensus phylogenetic tree resulting from Bayesian inference. The colors represent each clade: blue for *R. potiguar*, yellow for *Rowlandius sp. n. 2*, and red for *Rowlandius sp. n. 1*. Each branch of the tree displays the posterior probability.

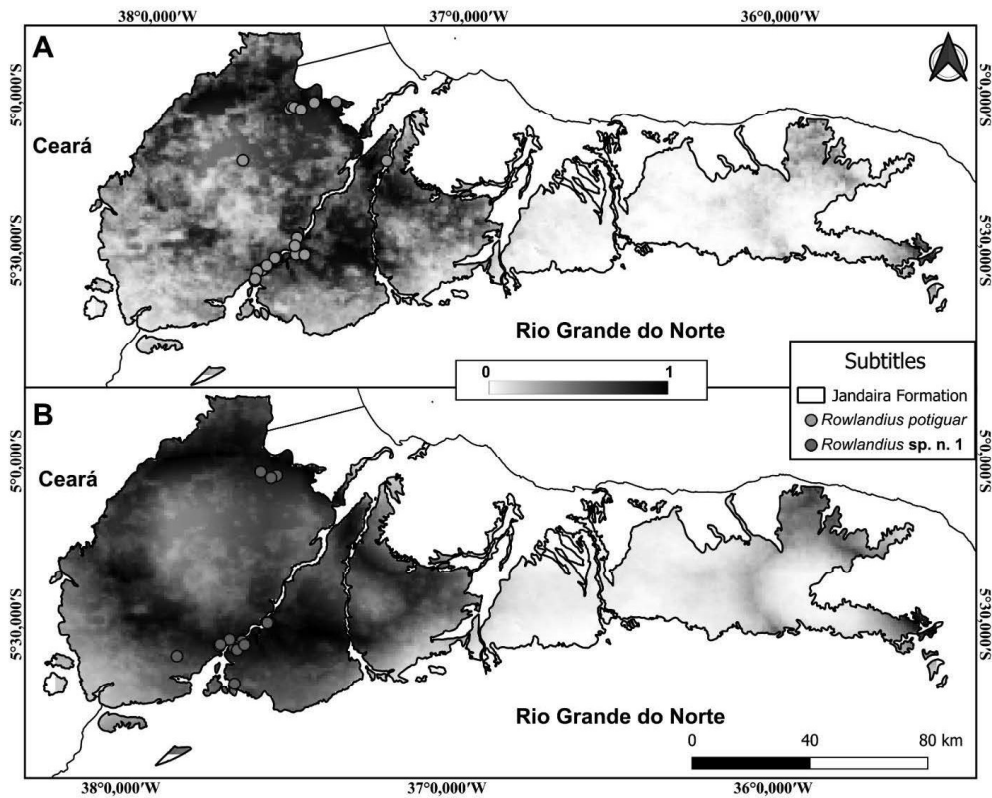


Figure 3: Habitat suitability, with the gradient representing the degree of suitability. (A) *R. potiguar*; (B) *Rowlandius sp. n. 1*.

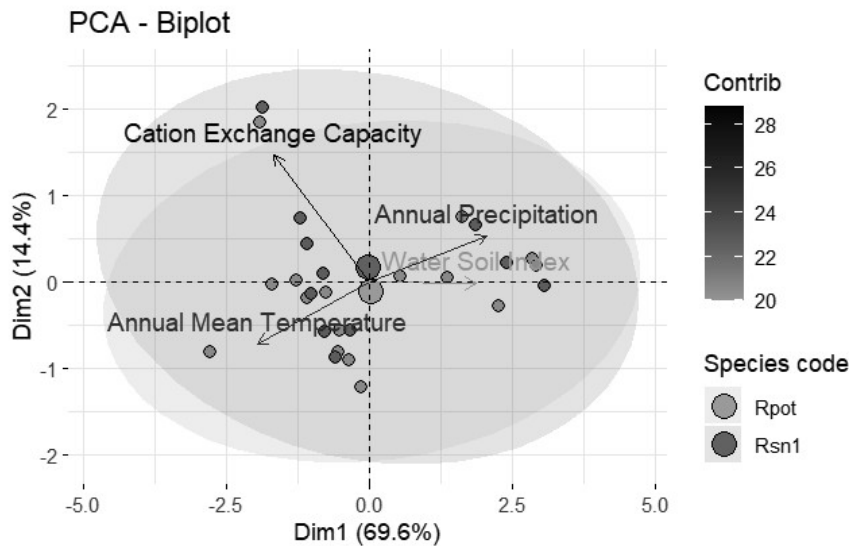


Figure 4: Principal Component Analysis (PCA), with larger circles representing the centroids, which are very close to each other. Contribution: Gradient of environmental variable contributions, where darker shades indicate higher contributions.

4. Discussion

The expanded collections of *Rowlandius* from Caatinga caves, including new records, have provided a more comprehensive understanding of the genus's geographic distribution, significantly enhancing the knowledge base beyond what was previously reported in the literature (Santos *et al.*, 2013; Bento *et al.*, 2021).

Molecular and morphological analyses consistently revealed the existence of a species complex, further emphasizing the diversity of this genus in the semi-arid region. The lack of a clear geographic pattern between the two species found in the Jandaíra Formation (*R. potiguar* and *Rowlandius sp. n. 1*) suggests population isolation driven by geological

fragmentation of the rocky outcrops in which they occur. This pattern aligns with observations of the troglitic planthopper *Kinnapotiguara troglobia* in the western Jandaíra Formation (Bento *et al.*, 2024). Caves within the same rocky outcrop may function as interconnected systems, offering refuge and higher humidity compared to the external environment, contributing to the isolation of cave-dwelling populations.

The absence of sympatry between the studied species and the niche modeling results suggest highly similar environmental suitability, reinforcing the hypothesis of competitive exclusion in resource-limited environments such as caves.

Niche modeling further indicated that *Rowlandius sp. n. 1* exhibits greater ecological flexibility and adaptability to varying environmental

conditions, while *R. potiguar* displays more specialized habitat requirements, favoring restricted environments. This pattern suggests a potential dominance of *Rowlandius sp. n. 1* in overlapping areas, which may highlight the ecological vulnerability of *R. potiguar* to environmental changes and competitive pressures.

Although some populations of *R. potiguar* and *Rowlandius sp. n. 1* are located within caves protected by the Furna Feia National Park (FFNP), the majority of localities and populations lie outside protected areas. This makes them vulnerable to numerous threats, including unregulated visitation, mining, deforestation, and agricultural expansion (Bento *et al.*, 2024).

5. Conclusion

This study revealed a broader geographic distribution of the genus *Rowlandius* in Caatinga caves. Molecular analyses uncovered a species complex, including two new species, highlighting the genus's remarkable diversity in the region. The absence of sympatry between *R. potiguar* and *Rowlandius sp. n. 1*, combined with niche modeling results, supports the hypothesis of competitive exclusion between the two species.

Rowlandius sp. n. 1 demonstrated a more generalist ecological niche, while *R. potiguar* exhibited a more specialized ecological niche. Niche

partitioning appears to be influenced by gradients of temperature and precipitation, with cation exchange capacity (CEC) playing a key role in microhabitat differentiation.

Although some caves within the Furna Feia National Park (FFNP) offer protection to both species, the majority of localities are situated outside protected areas. This leaves the species vulnerable to various threats, including mining, deforestation, and agricultural activities, emphasizing the need for expanded conservation efforts.

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