

Plant Endemism and Diversity of the Guiana Shield

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- What is the genetic and spatial distribution of 30 years' worth of data collection across the Guiana Shield? • How are related species distributed?
- What are the patterns of richness and endemism across the shield? • How does sampling bias influence collection/results?

Introduction

- The Guiana Shield is one of the least explored areas in the world spanning 2,287,859 km² across parts of Venezuela, Brazil, Colombia, Guyana, French Guiana, and Surinam (Hammond, 2005).
- It is best known for the prominent 'tepui'—sheer sided mountains found in the highlands—and high biodiversity and endemism (Maguire, 1970).
- Here, we present results from a preliminary investigation of the nature and sources of this diversity using specimen data collected by the Biological Diversity of the Guianas Program and DNA sequence data from Genbank.

- (1) Location of the Shield
- (2) Shield outline
- (3) Distribution of herbarium samples from the Shield

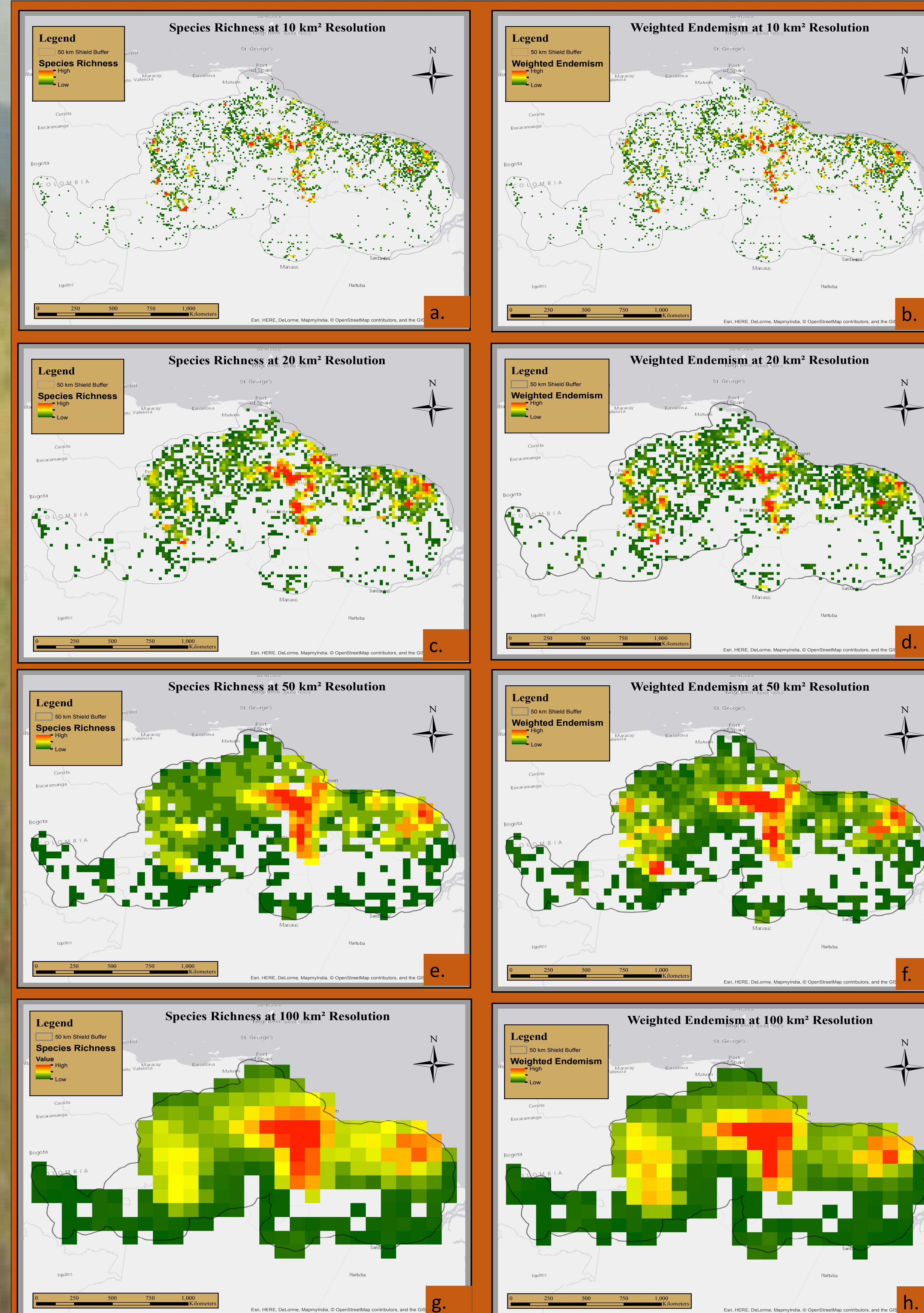


Methods

- The geographic extent of the shield used in these analyses follows Gibbs and Baron, 1994.
- DNA sequences from NCBI Genbank (atpB, trnK, matK, ndhF, rbcL, rps4, trnL) were aligned with MAFFT and manually edited with AliView.
- Phylogenies were generated with RaxML
- Spatial data were cleaned using a custom R-based spatial data cleaning pipeline, OpenRefine and Excel, then analyzed using ArcGIS and Biodiverse.



(4) matK Phylogeny of taxa from the Shield



Figures 5: Distribution of species richness within the Guiana Shield at decreasing resolutions: (a) 10km²; (c) 20km²; (e) 50km²; (g) 100km²; and species endemism at (b) 10km²; (d) 20m² resolution; (f) 50km² (h) 100km²

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Results

- The matK phylogeny (Fig. 4) shows high confidence in relationships between taxa; the data represents 148 unique families.
- Sub-regions of western Venezuela, west-central Guyana, and eastern French Guiana show high endemism and richness at all resolutions.
- The patterns of richness/endemism in the tepui regions are not as distinct as expected.
- First exploratory approach to data analysis reveals some correlation between the number of samples and richness at 100 km², R²= 0.64.

Discussion

- High confidence in the phylogeny: our data is strong and will be useful for ongoing analyses.
- There is a tradeoff between cell size and distribution: higher resolution is more precise but loses the broader scope of diversity data. However lower resolution can skew data, and is especially prone to sampling bias.
- Samples per cell are not even across the shield, sampling bias is prevalent; botanists collect in interesting places/easy to get to/politically stable.
- However, the analyses are likely robust to bias at broader scales as low sampling effort tends to underestimate endemism and richness (Baldwin, 2017).

Ongoing Research

- Concatenate "fast genes" (ITS) with current alignment and further analyze the genetic relationships and spatial distribution of this large data set.
- Continue to explore how richness and endemism are concentrated in the Guiana Shield. Specifically:
 - how does the terrain/environments/habitats influence the diversity on the shield? Are highlands more diverse?
- Work out an uneven sampling structure.
- Analyze the correlation between biological/geological factors and endemism/richness.



Piriqueta cistoides

Passiflora candida

Paullinia pinnata

Tepui compositae

References

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