

Poster



Phylogenetic structure of White-sand Forest and Slope Forest tree communities of Brazilian Coastal Rainforest

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Introduction

The Atlantic Rainforest is a large biome that extends along the latitudinal axis of the Brazilian coast. The White-sand Forest (WF) and Slope Forest (SF) are two of its main environments. They are geographically close (Fig 1) and share the species pool and similar climatic conditions. The main difference between these environments are their edaphic conditions: in the White-sand Forests the soils are sandy and nutrient poor, conditions that are often considered stressful and more restrictive to tree development. Only species with specific traits and physiological mechanisms that can develop under these abiotic conditions should occur in communities with sandy soils. Therefore, it was expected that environmental filtering would be stronger on White-sand Forest tree communities than on those in the Slope Forest.

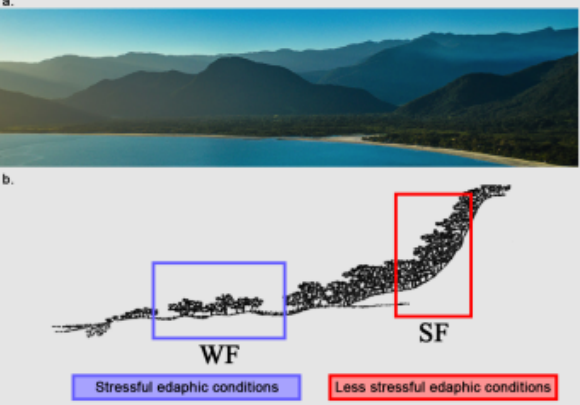


Fig. 1 - Picture of Brazil's coast, closer to the sea in the coastal plain region is the White-sand Forest and in the lower mountain region is the Slope Forest (a). Schematic drawing depicting the transition between White-sand Forest (red) and Slope Forest (blue) (b).

Assuming that in Angiosperms there is niche conservatism, it is expected that in communities under strong environmental filtering the phylogenetic pattern would be clustered and in communities with strong limiting similarity the pattern would be overdispersed (Fig 2). Since it was expected that environmental filtering would be stronger in the White-sand Forest tree communities, their phylogenetic structure was expected to be more clustered than the communities in the Slope Forest. To access this hypothesis, this study aimed to relate phylogenetic patterns to ecological processes driving the community assembly of these environments.

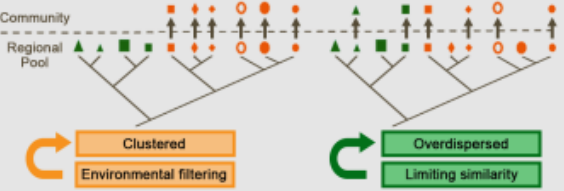


Fig. 2 - Phylogenetic tree of the regional pool under environmental filtering (left) resulting in a phylogenetically clustered local community with taxa with similar traits (same color). The same phylogenetic tree of the regional pool under limiting similarity (right) resulting in a phylogenetically overdispersed local community with taxa with different traits (different shapes and colors).

Methods

We used a subset of the Neotropical Tree Communities database (TreeCo 2.0) and analyzed 80 sites, 16 in the White-sand Forest and 44 in the Slope Forest (Fig 3).

The phylogenetic tree was constructed with the 363 genus that occur in at least one site (Fig 4). Genus from Cyatheaceae and Podocarpaceae were excluded from the phylogenetic tree because they were rare and too evolutionarily distant from Angiosperms. The phylogeny was obtained through the package V.Phylomaker.

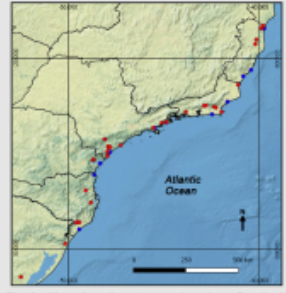


Fig. 3 - Map of southwestern and southern Brazil with the 16 locations of White-sand Forest sites (blue) and the 44 Slope Forest sites (red).

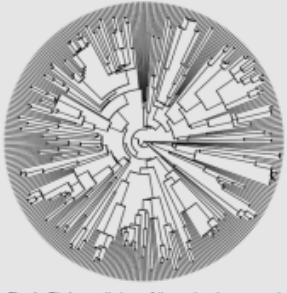


Fig. 4 - Phylogenetic tree of the regional genus pool.

Results

To access the phylogenetic structure we measured the alpha phylogenetic diversity of each site with the standardized effect size of the Mean Phylogenetic Distance (sesMPD) and Mean Nearest Taxon Distance (sesMNTD). We used the standardized effect size because MPD and MNTD are sensitive to site richness and the sites had different values of richness. Communities with sesMPD or sesMNTD values lower than -1.96 were considered phylogenetic clustered, values over 1.96 were considered phylogenetic overdispersed and communities with values between -1.96 and 1.96 were not different than expected by the null model.

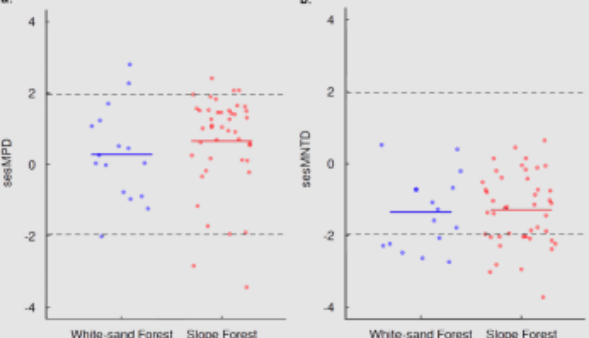


Fig. 5 - Variation in the standardized effect size of (a) mean phylogenetic distance (sesMPD) and (b) mean nearest neighbor distance (sesMNTD) for the White-sand Forest (blue) and the Slope Forest tree communities (red), each point represents a site and the horizontal line represents the mean for that environment .

For both sesMPD and sesMNTD the phylogenetic structure did not differ between the White-sand and Slope Forests communities (Fig 5) (t test: 0.975, P-value: 0.338; t test: -0.205, P-value: 0.839, respectively) and the community phylogenetic structure in each environment was not, on average, different than expected by chance (White-sand Forest mean sesMPD: 0.28 and mean sesMNTD: -1.35; slope forest mean sesMPD: 0.66 and mean sesMNTD: -1.28).

Discussion

Contrary to our expectations, the pattern of alpha phylogenetic diversity observed in the White-sand Forest and in the Slope Forest tree communities was not different. The main proposed explanations for these results are:

- i) Most plants present in the Atlantic Forest pool could be tolerant to sandy and nutrient poor soils. Consequently, the environmental filtering would not be a strong process for determining which genus from this regional pool can occur in the White-sand Forest tree communities.
- ii) In these communities, the environmental filter is important but interacts with other structuring processes, such as limiting similarity or neutral processes, and does not leave a clear phylogenetic clustered pattern.
- iii) Plants can have different traits and strategies to survive in sandy and nutrient poor soils, therefore, the environmental filter would not result in a clustered phylogenetic pattern.

Due to the great variation in sesMPD and sesMNTD observed between communities of the same environment, we conducted an additional analysis to assess if this variation was related to the latitudinal gradient. This analysis was done through a multiple linear model (Fig 6).

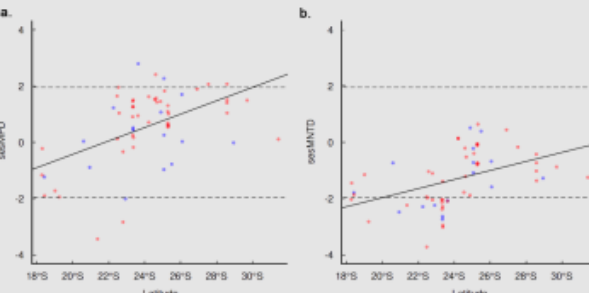


Fig. 6 - Relationship between latitude and (a) the standardized effect size of the mean phylogenetic distance (sesMPD) or (b) mean nearest neighbor distance (sesMNTD) for the White-sand Forest (blue) and the Slope Forest tree communities (red). Each point represents a site and the black line represents the predicted values by the linear model.

We found a strong positive relationship between sesMPD and latitude (r^2 : 0.2569, p-value: 0.00003589) (Fig 6a), we also found a positive relationship between sesMNTD and latitude (r^2 : 0.202, p-value: 0.0003156) (Fig 6b). These results highlight that there could be factors that vary along the latitudinal gradient, such as the climatic conditions or biogeographic history, that can be important to determine the phylogenetic structure of these communities in the Atlantic Forest.

In future research efforts, the positive relation between sesMPD and sesMNTD with the latitude gradient could be better understood by distinguishing how constituent to this results are the components of climatic variation and biogeographic history, respectively.

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