



# XIX International Botanical Congress

July 23-29, 2017 | Shenzhen China

Abstract ID#: T2-02-14

## A panmictic Amazonian world? Bryophytes testify

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### Introduction

The Amazonian rainforest has experienced dramatic climate change due to Pleistocene oscillations and its recent human-induced fragmentation. In this context, epiphytic bryophytes, with their foreshortened life-cycles and poikilohydric condition, offer an ideal model to investigate the impact of past, present and future fragmentation events on patterns of genetic structure and diversity. Using null model analyses based on metacommunity concepts for Amazonian epiphytic bryophyte communities, Mota & ter Steege<sup>1</sup> concluded that “dispersal did not show geographical structure across the area”. Metacommunity analyses thus raise the intriguing notion that Amazonian epiphytic assemblages might, due to their high dispersal capacities, behave as basin wide panmictic populations.



### Objectives

(i) Do Amazonian epiphytic bryophytes exhibit spatial genetic structure (SGS)?

If there is a significant SGS,

(iia) At which spatial scale does it occur?

(iib) What are the mechanisms shaping its underlying structure?

In particular, do neutral (isolation-by-distance, IBD) or ecological (isolation-by-ecology) processes shape patterns of genetic variation?

### Data analysis and results

Mantel tests between kinship coefficients (Fij) and geographic distance among individuals were computed to test for IBD (iib).

Although, in some species such as *Syrrhopodon hornschuchii*, intra-populational kinship coefficients were higher than the coefficients among populations, the slope of the regression analyses between kinship coefficients and geographic distance were not significant (Fig. 1).

### Discussion

Although the higher Fij observed within than among populations in some species point to the higher diaspore density in the vicinity of the mother gametophyte, the absence of a significant isolation-by-distance pattern suggests that Amazonian species are not constrained by dispersal at the regional scale investigated. Although further analyses are required, this lends support to the striking hypothesis derived from the application of neutral ecological models (Mota & ter Steege<sup>1</sup>) that “Amazonian epiphytic bryophytes behave as one single metacommunity”.

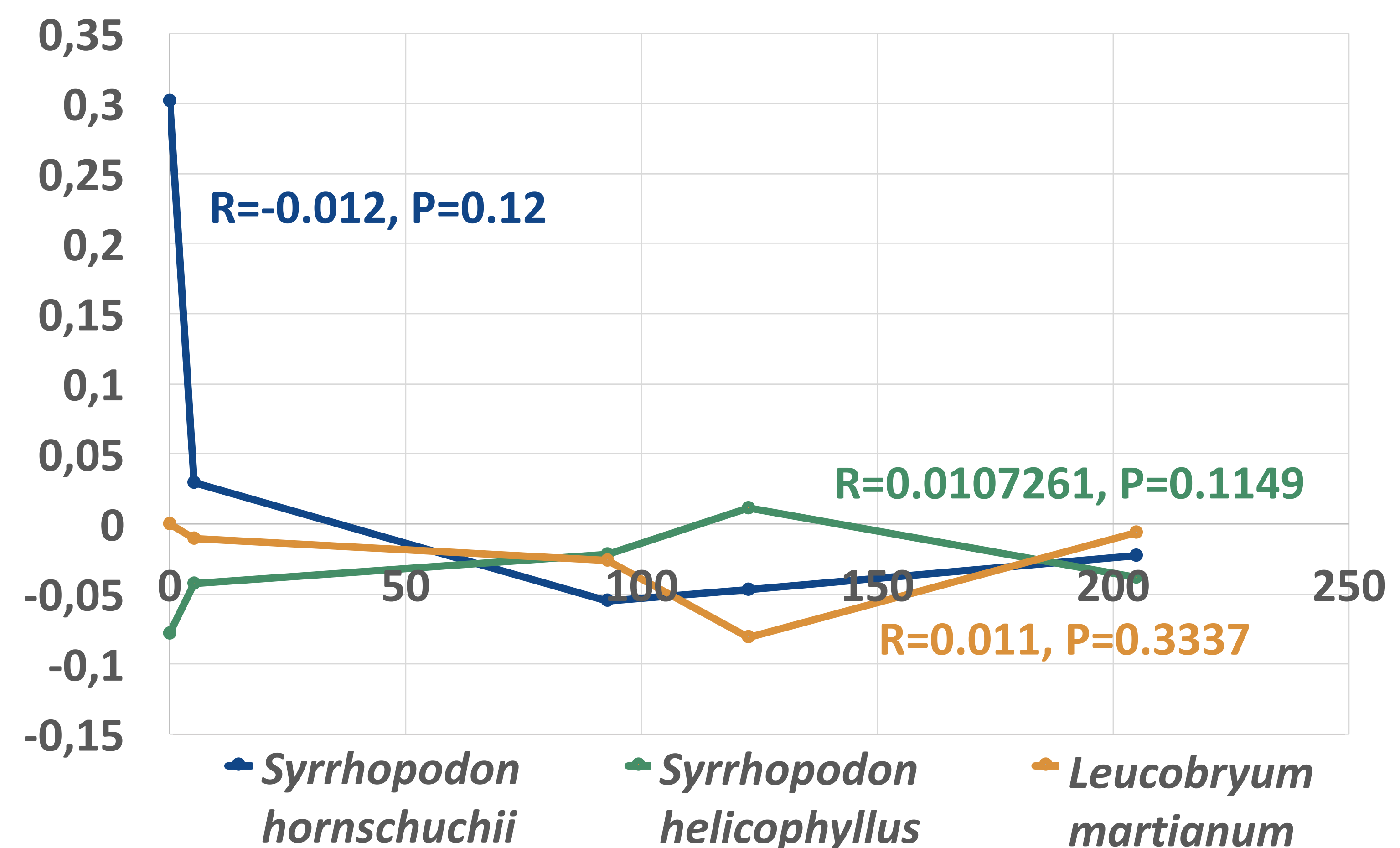
### Conclusion and perspectives

The study will provide key information on the populations dynamics of highly mobile species integral to the iconic Amazonian forest. Data on dispersal capacities will be coupled to Species Distribution Models (SDMs) to determine whether species migration rates are sufficient to maintain genetic connectivity among increasingly fragmented populations in the ongoing context of anthropogenic-mediated deforestation and accelerating climate change. Those results may further be employed to refine conservation policies.

### Material and Methods

11 epiphytic bryophyte species were sampled in a 50,000 km<sup>2</sup> area in the middle *Rio Negro*. 15-50 individuals were collected by species. Preliminary analyses using Sanger sequencing at traditional cpDNA and nDNA *loci* were completely monomorphic among populations at the spatial scale considered. Therefore, genome-wide genetic data were produced using Genotyping By Sequencing (GBS). We followed the GBS procedure as described in Elshire *et al.*<sup>2</sup> The software *Stacks* were used for bioinformatic analysis.

**Fig. 1.** Spatial autocorrelograms between average kinship coefficients (Fij) and geographic distance class (km) along with value and P-value of the slope (R) in Amazonian bryophytes



<sup>1</sup> Mota de Oliveira S. & ter Steege H. 2015. J. Ecol. 102: 441-450.

<sup>2</sup> Elshire R. *et al.* 2011. PLoS ONE. 6(5): 1-10.

Photographs by Ledent D. 2016. Brazil.