

UNIVERSIDADE FEDERAL DO PARANÁ

RENATTHO NITZ OLIVEIRA

PADRÕES GLOBAIS DE BETA DIVERSIDADE FILOGENÉTICA EM ANUROS

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Dissertação apresentada ao Programa de Pós-Graduação em Ecologia e Conservação como requisito parcial para obtenção do grau de Mestre em Ecologia e Conservação, Setor de Ciências Biológicas, Universidade Federal do Paraná.

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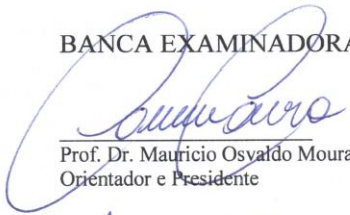
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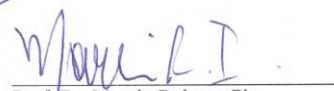
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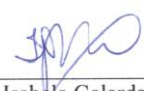
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RESUMO

Os estudos envolvendo beta diversidade são fundamentais para se compreender os processos que geram e mantêm os padrões atuais de biodiversidade. Atualmente, as raízes históricas dos processos ecológicos têm sido estudadas dentro de uma abordagem filogenética. Nessa dissertação, os principais objetivos foram identificar quais os mecanismos responsáveis pelos padrões global e regional de beta diversidade filogenética em anuros. Para isso, foi calculada a Filobetadiversidade entre regiões biogeográficas e entre ecoregiões neotropicais. Ainda, como a dissimilaridade filogenética pode ser resultado tanto da substituição de linhagens entre as comunidades, quanto por diferenças na diversidade filogenética, foi aplicado um método de partição da Filobetadiversidade em seus componentes. Além disso, foram analisadas as contribuições relativas da distância geográfica e de variáveis climáticas históricas na explicação dos padrões observados entre as ecoregiões. Em qualquer uma das escalas analisadas, a substituição de linhagens foi o principal componente gerador dos padrões atuais, indicando que a fragmentação e subsequente isolamento dos continentes é o principal processo responsável pela dissimilaridade filogenética observada entre as regiões biogeográficas. Já, em escalas menores, a distância tende a ser a principal causa dos padrões observados entre as ecoregiões embora, em alguns casos, as mudanças climáticas que ocorreram no passado foram mais importantes do que a distância geográfica em si. Em conjunto, os resultados obtidos sugerem que os padrões de beta diversidade filogenética em anuros são resultado da substituição espacial de linhagens associado a processos climáticos históricos.

Palavras-chave: Partição da Filobetadiversidade, Substituição de Linhagens, Regiões biogeográficas, Ecoregiões.

ABSTRACT

In this paper, we explore the mechanisms related to global and regional patterns of Phylogenetic Beta Diversity (PBD) in anurans. To achieve this, we measured PBD at two geographical scales: between biogeographic realms and between Neotropical ecoregions using the complement of PhyloSor index. We also decomposed PBD into their two components, accounting for phylogenetic turnover (PBD_{Turn}) and differences in Phylogenetic diversity (PBD_{PD}). Additionally, we evaluated the relative effects of geographic distance and historical variables to test which mechanism best explains the phylogenetic turnover among Neotropical ecoregions. We hypothesized that the isolation between biogeographical realms should represent a strong barrier to anurans, leading to lineage turnover. Thus, we expected high PBD_{Turn} values between them. Moreover, for ecoregions pairwise comparisons we expected phylogenetic turnover to be explained by geographic distance and history of climate-change. At both scales, the PBD_{Turn} component of PBD was the mostly important component. For biogeographic realms, it seems that vicariance processes are the main driver of lineage turnover, whereas for ecoregions, the observed phylogenetic turnover was mainly related to geographic distance and, in some occasions, the Historical variables were a more important predictor of lineages turnover than geographic distance. Together, our results show that phylogenetic dissimilarity patterns are the result of spatial turnover of lineages in combination with historic processes.

Keywords: Phylobetadiversity components, PhyloSor, turnover of lineages, biogeographic regions, Neotropical ecoregions.

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1 INTRODUCTION

The changes in species composition across geographic space is defined as beta diversity (WHITAKER, 1960). This concept has been used by ecologists to quantify the dissimilarity between biological communities and as a way to explore how ecological communities are assembled as well as which mechanisms are responsible for the uneven spatial distribution of biodiversity on earth (HILLEBRAND, 2004). However, dissimilarity between communities can be the result of two different processes: species turnover and dissimilarity associated with species losses, in which a poorest community assemblage is a subset of the richest one (BASELGA, 2010). In this context, Baselga (2010) proposed an additive partitioning framework to decompose the taxonomic beta diversity index into its two components, which enabled to quantifying the role of these two processes. The first component (replacement component) represents the dissimilarity resulting from the differences in species composition or species turnover between communities while the second one, represents the dissimilarity caused by differences in species richness (a nestedness-resultant component).

The composition of biological communities results from the interplay between ecological and evolutionary processes (RICKLEFS, 1987). However, taxonomic beta diversity does not take into account that species do not represent independent units due to shared evolutionary history (QIAN et al, 2013). The incorporation of evolutionary history within the beta diversity concept leads to an evolutionary approach to explore spatial patterns of biodiversity, the concept of Phylogenetic Beta Diversity or Phylobetadiversity (PBD, GRAHAM & FINE, 2008). PBD measures how the relationships between species change along a geographic space in the same way as beta diversity measure changes in species composition. (GRAHAM & FINE, 2008). Also, PBD metrics can be partitioned into two components (PBD_{TURN} and PBD_{PD}) which account for the turnover of lineages or differences in phylogenetic diversity, respectively (LEPRIEUR, 2012).

Anurans exhibited numerous distinct radiations and they are a globally distributed vertebrate class (ROELANTS, 2007), occurring in all biogeographic

realms except for Antarctica (PYRON, 2014). Due to their physiological constraints, they are tightly associated with environmental conditions (DUELLMAN & TRUEB, 1986). Moreover, they have a well-resolved hypothesis of relatedness (PYRON & WIENS, 2013) which makes them a good model to study PBD patterns and to test the role of ecological and historical processes associated with these patterns.

Once different variables can act and generate dissimilar patterns at different scales (GOUVEIA et al., 2013), in this study we explore the patterns of phylogenetic beta diversity of anurans between biogeographic realms and Neotropical ecoregion (OLSON et al., 2001). In addition, we aim to investigate the relative importance of processes that might be related with observed PBD patterns among ecoregions. We expected high PBD_{Turn} values at both global and regional scales because biogeographic realms are spatially isolated and anurans have weak dispersal ability (BLAUSTEIN et al., 1994) coupled with environmental specialization. As the assembly of biological communities might be affected by both ecological and evolutionary processes (RICKLEFS, 1987), we expected that PBD_{Turn} between Neotropical ecoregions should result from a combination of geographic distance and past climate changes.

2 MATERIAL AND METHODS

We used the global distribution maps of anurans (IUCN, 2014) and a phylogeny (PYRON & WIENS, 2011) which includes the phylogenetic relationships and divergence times for 2394 anurans species. The distribution maps were used to produce a species list for each biogeographic realm, except for Antarctica, which have no records, and Oceania because there are few species records available. These maps were obtained from International Union for Conservation of Nature database (IUCN, 2014). We used only distributions of species in their native ranges.

The taxonomic status of all species included in the Peron & Wiens (2011) were updated according to Frost (2015). We only included in subsequent analyses species included in the phylogeny and from which the geographic distribution was available. The final dataset comprised 2329 species representing 35% of currently valid anurans species (FROST, 2015). The percentage of species that did not match the inclusion criteria among biogeographic regions was 63% of species from Australasian regions, 60% of species from Neotropical, 58% of species from Afrotropical, 57% of species from Indo-Malay, 34% of species from Palearctic and 18% of species from Nearctic.

To test for drivers of phylogenetic beta diversity between ecoregions, we used two sets of variables representing the past climatic changes and geographic distance between ecoregions. As historic variables may have contributed to generate phylogenetic patterns, by allowing or preventing species occurrence, the velocity of climate change (SANDEL et al, 2011) was included in the analysis to represent the effect of past climate conditions over lineages.

2.1 Phylobetadiversity among biogeographic regions

We calculated PBD between biogeographic realms using 1 minus the PhyloSor index to determine global patterns of Anura phylogenetic beta diversity. PhyloSor (BRYANT et al., 2008) is one of the most commonly used

metrics and measures the phylogenetic similarity between two communities by comparing the sum of branch lengths shared between these communities to the total branch lengths of the communities. There are other metrics to compute phylogenetic dissimilarity but they are very redundant among each other (SWENSON, 2011).

Because phylogenetic dissimilarity might result from differences in phylogenetic diversity, we decomposed the overall PBD into two components, turnover and nestedness (LEPRIEUR et al., 2012). The turnover-resultant component (PBD_{Turn}) represents the phylogenetic dissimilarity that is not caused by PD differences (PBD_{PD} component). Thus, without decoupling PBD, we could overestimate the degree of lineage differentiation between communities (LEPRIEUR et al., 2012). We did this partition following the phylogenetic additive partitioning framework proposed by Leprieur et al. (2012), which was based on an approach for compositional beta diversity (BASELGA, 2010). Although there are other methods to partition beta diversity (e.g. CARVALHO et al., 2012), Baselga's original approach is the only one where the replacement of species is not constrained by variation in species richness (BASELGA & LEPRIEUR, 2015).

In order to test whether the PBD between biogeographic realms are different from expected by chance alone, we compared the observed values with those obtained by a null model. To achieve this we generate a null distribution of expected PBD values randomizing the species names across the phylogeny 999 times and calculating PBD and its components each run. Then, we calculate the standard effect size (SES) for the PhyloSor and their components using the mean and standard deviation of null distribution and compared to mean of observed PBD values. If the observed values do not differ from expected values the phylogenetic dissimilarity among communities might be explained by the compositional beta diversity.

Furthermore, we performed a cluster analysis based on PBD_{Turn} values using unweighted pair-group method with arithmetic mean (UPGMA). We use cluster analysis to represent the pattern of turnover between all biogeographic regions. All analyses were performed using R 3.1.2 (R Development Core Team 2014). Species list for each biogeographic realm were obtained with ArcMap 10.0 (ESRI, 2015).

2.2 Phylobetadiversity among ecoregions

To determine the PBD patterns among Neotropical ecoregions, we calculate the PhyloSor index in the same way as we did for biogeographic realms. First, we pruned the phylogeny to include only branch lengths of species present in the Neotropics. Additionally, we performed a partial redundancy analysis (pRDA) to evaluate the relative contribution of two sets of explanatory variables (geographic distance and historical effects) on the Lineage turnover (PBDTurn). This analysis was done using Vegan 2.3-0 R package (OKSANEN et. al 2015).

This analysis was done first for the all Neotropical ecoregions and then dividing the Neotropical realm into 9 latitudinal bands (FIGURE 1) of ten degrees (0-10°N, 52 ecoregions; 10-20°N, 70 ecoregions; 20-30°N, 23 ecoregions; 0-10°S, 48 ecoregions; 10-20°S, 32 ecoregions; 20-30°S, 24 ecoregions; 30-40°S, 15 ecoregions, 40-50°S, 5 ecoregions, 50-60°S, 2 ecoregions). We use this approach as a way to limit the distance between communities and avoid possible spurious effects of large distances between communities on our analysis. We only include in analysis, pairwise comparisons for which the turnover component was different from expected by chance. As most comparisons within latitudinal zones 40-50°S and 50-60°S did not differ from random variations, these bands were excluded from the analysis.

The geographic distance was measured as the geodesic distance between all ecoregions centroids. However, for adjacent ecoregions we set the distance to zero. To represent the effects of historic climate-change, we classified each ecoregion into stable (low climate-change velocity) or unstable (High climate-change velocity) (FIGURE 1) based on the median value for Global climate-change velocity and used the type of comparison (stable-stable, unstable-unstable or stable-unstable) as an explanatory variable.

All analysis were carried out on R 3.1.2 (R DEVELOPMENT CORE TEAM, 2015). Maps and latitudinal bands were produced using ArcMap 10.0 (ESRI, 2015).

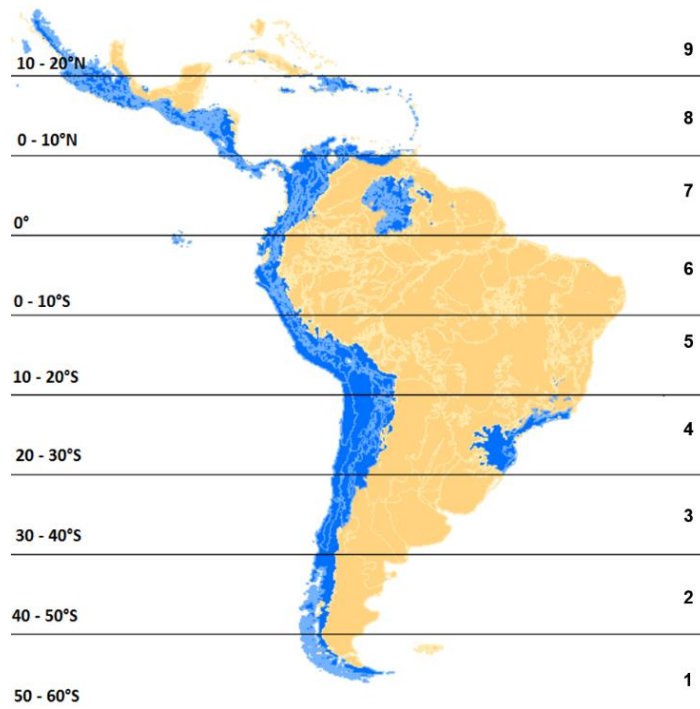


FIGURE 1. MAP SHOWING THE 169 NEOTROPICAL ECOREGIONS NINE LATITUDINAL ZONES. BLUE ECOREGIONS REPRESENT STABLE ECOREGIONS (LOW CLIMATE-CHANGE VELOCITY) AND YELLOW ECOREGIONS REPRESENT UNSTABLE ECOREGIONS (HIGH CLIMATE-CHANGE VELOCITY).

3 RESULTS

3.1 Phylogenetic Beta Diversity patterns among biogeographic regions

All pairwise comparisons between biogeographic realms showed high levels of phylogenetic beta diversity. In general, PBD values were higher than 0.90 (TABLE 1), except for the pairwise comparisons between Indo-Malay/Palearctic and Neotropical/Nearctic realms for which Phylobetadiversity were slightly lower (0.52 and 0.80 respectively). In addition, we found high values of compositional beta diversity among all pairwise comparisons between Biogeographic realms (APPENDIX 1).

All PBD values were higher than expected by taxonomic beta diversity (TABLE 1). When accounting for dissimilarity caused by differences in phylogenetic diversity, the turnover component of PBD was the main component explaining the phylogenetic dissimilarity among communities (mean PBD_{Turn} : 0.84 ± 0.21 , TABLE 1). However, the comparison between Nearctic/Neotropical showed a contrasting result after controlling by PD differences. The high PBD value observed (0.80) were most explained by the nestedness component rather than by the turnover component (0.25, TABLE 1) suggesting that if we consider only a broad measure of PBD we could overestimate the lineage turnover. All PBD_{Turn} component values were greater than expected by chance. While PBD_{PD} component had, in general low values and lower than expected by chance.

The results of the cluster analysis showed a great phylogenetic dissimilarity between the New World and Old World (PBD_{Turn} : 0.87; FIGURE 2). The Afrotropical realm had the most distinct lineages compared to all other regions (FIGURE 2). Furthermore, the comparisons between Nearctic/Neotropical and Indo-Malay/Palearctic showed that these realms were phylogenetically close to each other (FIGURE 2).

TABLE 1. DECOMPOSITION OF PBD INTO TURNOVER (PBD_{TURN}) AND NESTEDNESS COMPONENTS (PBD_{PD}) BETWEEN BIOGEOGRAPHIC REALMS. STANDARD EFFECT SIZES (SES) VALUES ARE ALSO SHOWED. IN BOLD, SES VALUES THAT DID NOT DIFFER FROM NULL EXPECTATION.

Pairwise comparisons	PBD	PBD_{TURN}	PBD_{PD}	SES.PBD	SES. PBD_{TURN}	SES. PBD_{PD}
Australasian - Afrotropical	0.97	0.95	0.01	20.43	19.78	-8.33
Australasian - Indo-Malay	0.91	0.86	0.05	17.11	15.81	-4.90
Australasian - Nearctic	0.95	0.93	0.02	13.63	12.92	-5.80
Australasian - Neotropical	0.98	0.96	0.02	25.65	29.97	-23.06
Australasian - Palearctic	0.92	0.91	0.01	15.65	14.72	-0.12
Afrotropical - Indo-Malay	0.96	0.96	0.00	24.05	23.13	-1.05
Afrotropical - Nearctic	0.96	0.92	0.04	15.14	15.83	-11.11
Afrotropical - Neotropical	0.98	0.97	0.01	34.05	36.27	-20.69
Afrotropical - Palearctic	0.91	0.88	0.02	18.86	18.49	-7.03
Indo-Malay - Nearctic	0.96	0.91	0.06	15.36	15.44	-10.08
Indo-Malay - Neotropical	0.98	0.98	0.01	32.74	35.81	-21.49
Indo-Malay - Palearctic	0.52	0.37	0.15	6.03	3.48	2.09
Nearctic - Neotropical	0.80	0.25	0.54	7.14	5.42	-1.10
Nearctic - Palearctic	0.94	0.91	0.04	12.90	12.11	-5.39
Neotropical - Palearctic	0.98	0.96	0.02	25.24	29.37	-22.88

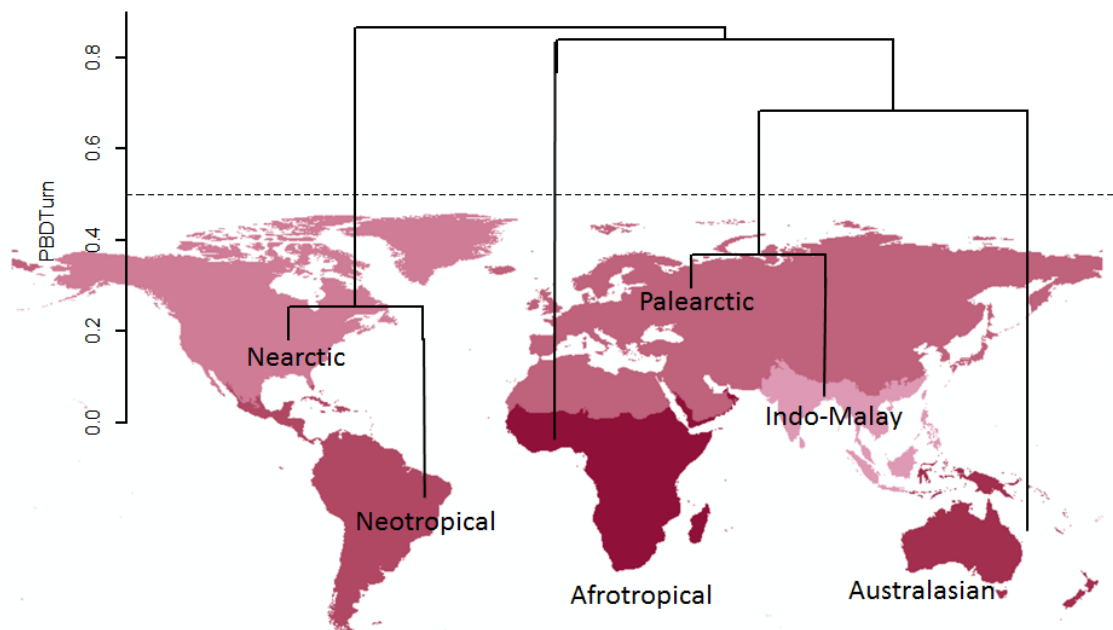


FIGURE 2. RESULTS OF AN UPGMA CLUSTER ANALYSIS AND PBD_{TURN} UNIQUENESS BETWEEN BIOGEOGRAPHIC REALMS. NODES UNDER THE DASHED LINES HAVE VALUES LESS THAN 0.5. PHYLOGENETIC UNIQUENESS ARE MEASURED AS THE MEAN PBD_{TURN} VALUES BETWEEN FOCAL REALM AND ALL OTHERS. COLORS INDICATE THE DEGREE TO WHICH THEY ARE PHYLOGENETICALLY UNIQUE COMPARED WITH ALL OTHER REALMS (THE DARKER THE COLOR, THE LARGER THE DIFFERENCE).

3.2 Phylogenetic Beta Diversity patterns among ecoregions

The phylogenetic dissimilarity between Neotropical ecoregions was strong explained by the turnover component (FIGURE 3). The mean PBD was 0.69 ± 0.19 with turnover component explaining an average of 75% of phylogenetic dissimilarity. However, more than a half of PBD_{Turn} values were not different from expected by the null model, that is a random turnover of lineages.

The partition of variance analysis for all Neotropical ecoregions showed that geographic distance was the only predictor that has an explanatory power although the largest amount of variation remains unexplained (FIGURE 4).

When analyzing by latitudinal bands, the geographic distance still explained the largest part of phylogenetic turnover (FIGURE 4). But, the pure effect of geographic distance was not the most important effect in three of seven latitudinal bands analyzed, even so, in two of these bands (0° - 10° S and 30° - 40° S) it had a shared effect with other variables. In these two zones, the pure effect of historic variables explained most of the phylogenetic turnover with geographic distance ranking as the second strongest explanatory predictor either by their pure effect or by the shared effect with historic variables. Another band where geographic distance had a small effect was the 20° - 30° N latitudinal zone. However, none of analyzed variables had a strong explanatory power at this band.

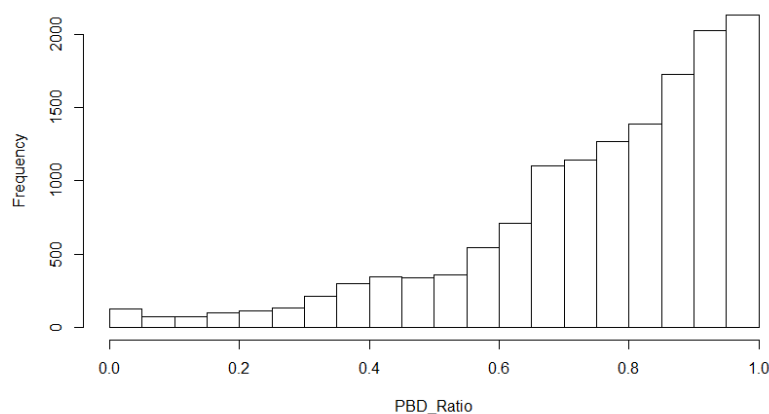


FIGURE 3. FIGURE 3. PBD_{RATIO} (PBD_{TURN}/PBD) BETWEEN ECOREGIONS. VALUES GREATER THAN 0.5 INDICATE THAT THE PHYLOGENETIC DISSIMILARITY BETWEEN ECOREGIONS PAIRWISE WAS MOST EXPLAINED BY THE LINEAGE TURNOVER (PBD_{TURN} COMPONENT) RATHER THAN DIFFERENCES IN PHYLOGENETIC DIVERSITY (PBD_{PD}).

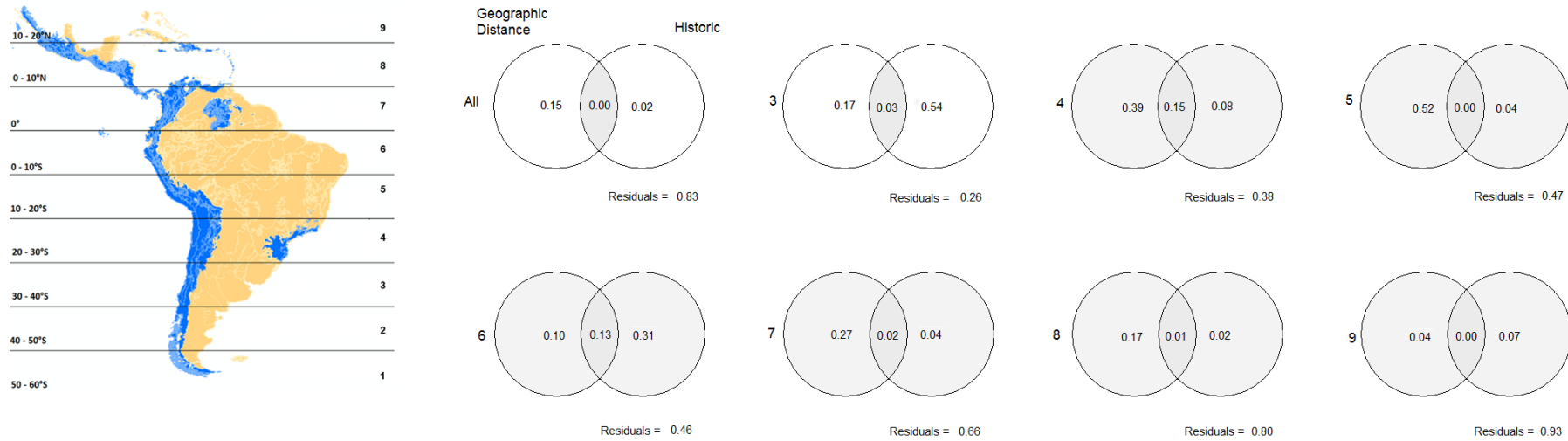


FIGURE 4. NEOTROPICAL ECOREGIONS AND LATITUDINAL BANDS (LEFT). PARTITION OF THE VARIANCE OF TURNOVER COMPONENT (PBD_{TURN}) EXPLAINED BY PURE AND JOINT EFFECTS OF GEOGRAPHIC AND HISTORIC DISTANCES FOR ALL NEOTROPICAL ECOREGIONS (ALL) AND EACH OF SEVEN LATITUDINAL BANDS ANALYZED (NUMBERS 3 TO 9).

4 DISCUSSION

4.1 Global patterns

Both phylogenetic and compositional beta diversity values were high, showing that isolation among biogeographic realms could be the mechanism leading to lineage differences. After we decomposed phylogenetic beta diversity we obtained the same pattern, where PBD_{Turn} were the most important component accounting for the phylogenetic dissimilarities between biogeographic realms. Also, PBD_{Turn} values were higher than expected by the null model showing a non-random turnover of lineages. In other words, the observed lineage turnover is not only a result of species changes between communities.

The comparison in which the PBD_{PD} component was the most important component (between Nearctic and Neotropical realms) showed that phylogenetic dissimilarities were mainly caused by differences in phylogenetic diversity rather than to turnover of lineages. As this component did not differ from what is expected by chance, the differences in phylogenetic diversity between these two biogeographic realms were due only for differences in species richness. This pattern is probably the outcome of a high rate of speciation in the tropics (PYRON & WIENS, 2013; WIENS, 2007) together with high extinction rates in Nearctic region that can be caused by quaternary glaciation events (DOBROVOLSKI et al., 2012).

Coupled with a high nestedness component of phylogenetic dissimilarity between Nearctic and Neotropical regions, there was, also, a low turnover rate (PDB_{Turn}), suggesting that these realms are phylogenetically similar. However, this low value of PBD_{Turn} was greater than expected by the null model, meaning that Nearctic and Neotropical realms share less evolutionary history than the mean evolutionary history shared by random communities (GRAHAM, 2009). This can be explained by the fact that Nearctic region was colonized by anurans around 200 Ma and has more ancient lineages than South America, which has a high speciation rate and younger clades (PYRON & WIENS, 2013, WIENS, 2007). The net outcome of this scenario would lead to a turnover of lineages composed by distant related species and greater than expected by chance as we have found.

The low PBD_{Turn} observed among Nearctic and Neotropical realms (TABLE 1, FIGURE 2) could also result from dispersion events or faunal exchange events since these exchanges occurred after the formation of Panamanian Isthmus, a land bridge connecting these two realms by 3.5 – 3.1 Ma (COATES & OBANDO, 1996). However, this route of dispersion are more associated with mammals' distributions (COX, 2000) than for other groups, such as anurans. Pyron & Wiens (2013) showed that anurans have limited dispersion to temperate regions from tropical regions but a much higher colonization of tropics by temperate regions. This might be explained by niche conservatism with few lineages being able to tolerate cold climatic conditions whereas lineages from temperate regions will be released from physiological constraints when colonizing the tropics (WIENS & DONOGUE, 2004; SMITH et al., 2012.). Therefore, the low turnover between Nearctic and Neotropical realms are possibly associated with asymmetrical dispersions between these realms due to niche conservatism.

The results of the cluster analysis based on PBD_{Turn} component for anurans were similar to the pattern obtained for bats (PEIXOTO et al., 2013). These authors argued that the separation between New World and Old World by the Atlantic Ocean could have prevented bat dispersion. This might be even more restrictive for anurans that have low dispersion ability and low physiological tolerances than bats. In this way, only some lineages would be able to cross the Bering Strait (e.g. some species of genus *Hyla*; LI et al., 2015).

Besides the Nearctic/Neotropical comparison, the cluster analysis also showed that the Indo-Malay and Palearctic realms were grouped together. These areas are thought to be transition zones, without defined boundaries (PEIXOTO et al., 2013). However, contrary to Nearctic/Neotropical pairwise, for the Indo-Malay/Palearctic comparison, the PBD_{Turn} was the most important component (TABLE 1). So, it is possibly that the PBD_{Turn} component result from the uplift of Himalayas Mountains that ceased the faunal exchange between these two regions (LI et al., 2013).

Our results also showed that the Afrotropical realm had the greatest phylogenetically distinctiveness (FIGURE 2). This can be explained by the Afrotropical origin of many lineages (PYRON, 2014) together with strong isolation of that realm which could result in high lineage endemism.

4.2 Regional patterns

Phylogenetic dissimilarities among ecoregions were mainly driven by turnover component. Probably as result of the larger spatial extent analyzed and the restrict dispersion ability of anurans (BLAUSTEIN et al., 1994). However, more than a half of these PBD_{Turn} pairwise ecoregions comparisons did not differ from the expected by the null model. Overall, it implies that the observed differences in the evolutionary history between ecoregions could be assigned to differences in species composition (beta diversity). Despite this, PBD_{Turn} component were also the most important component for comparisons, which PBD differ from the expected by chance, suggesting a non-random turnover of lineages.

The pronounced importance of geographic distance as a driver of PBD_{Turn} changes observed within latitudinal zones was related with the potential influence of distance to generate isolation, similarly to distance-decay process, thus acting as a filter based on dispersal or even habitat specialization (NEKOLA & WHITE, 1999; HUBBELL, 2001). Nonetheless, the explanatory power of historic variables was higher than geographic distance for some latitudinal bands, which suggest that the historic climate also have an important contribution to lineage turnover. This role of historic climate arises through comparisons between ecoregions with low climate change velocities and between ecoregions with different climate velocities (low-high) tend to exhibit greater PBD_{Turn} values than comparisons among unstable ecoregions as showed in a previous study (DA SILVA et al, 2014). In addition, the importance of climatic-change velocity depends of dispersal abilities of the group (SANDEL et al, 2011). Therefore, it seems that historic variables and spatial isolation act jointly to generate lineage differentiation between ecoregions within latitudinal bands. Although, we did not observe a clear pattern for all latitudinal bands.

5 CONCLUSION

We demonstrated that dissimilarity between biogeographic regions are most driven by turnover of lineages. This close link implies a major role of geologic events determining the current position of continents along with past events such as glaciations. This suggests that at coarser spatial scales, the geographic or environmental isolation of continents may have a strong dispersion barrier to anurans, leading to differential speciation and lineage turnover.

Among ecoregions, the geographic distance between areas was the main factor explaining phylogenetic dissimilarities. Such a pattern was expected due to the restricted dispersal ability of Anura. Nonetheless, as predicted, historic variables represented by the climate velocity change also have an important role. Therefore, the incorporation of historic processes into analysis should increase our understanding about current biodiversity patterns. Although there is a strong relationship between anurans and environmental conditions, at least in the scale analyzed, current climate descriptors did not explain the changes in lineage turnover between ecoregions.

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APPENDIX

APPENDIX 1 - COMPOSITIONAL DISSIMILARITY BETWEEN BIOGEOGRAPHIC REALMS (BETA.SOR) AND ITS COMPONENTS (BETA.SIM AND BETA.SNE). THESE VALUES ARE MEASURED FOLLOWING BASELGA (2010) AND ARE CALCULATED IN R USING BETAPART PACKAGE (BASELGA ET AL., 2012).

Pairwise comparisons	beta.sor	beta.sim	beta.sne
Australasian - Afrotropical	1.00	1.00	0.00
Australasian - Indo-Malay	0.97	0.96	0.01
Australasian - Nearctic	1.00	1.00	0.00
Australasian - Neotropical	1.00	1.00	0.00
Australasian - Palearctic	0.99	0.99	0.00
Afrotropical - Indo-Malay	1.00	1.00	0.00
Afrotropical - Nearctic	1.00	1.00	0.00
Afrotropical - Neotropical	1.00	1.00	0.00
Afrotropical - Palearctic	0.96	0.95	0.01
Indo-Malay - Nearctic	1.00	1.00	0.00
Indo-Malay - Neotropical	1.00	1.00	0.00
Indo-Malay - Palearctic	0.63	0.51	0.12
Nearctic - Neotropical	0.89	0.44	0.45
Nearctic - Palearctic	1.00	1.00	0.00
Neotropical - Palearctic	1.00	1.00	0.00