Leila Meyer

Macroecologia e distribuição geográfica da tribo Bignonieae (Bignoniaceae)

Orientador: Prof.º José Alexandre Felizola Diniz-Filho

Coorientadora: Prof.ª Lúcia G. Lohmann

Goiânia-GO

Fevereiro de 2019

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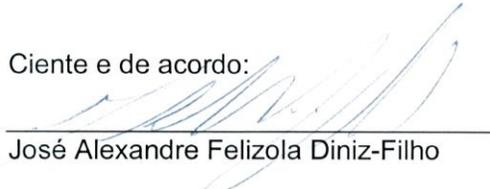
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Leila Meyer

Macroecologia e distribuição geográfica
da tribo Bignonieae (Bignoniaceae)

Tese apresentada à Universidade Federal de Goiás, como parte das exigências do Programa de Pós-graduação em Ecologia e Evolução para obtenção do título de doutora.

Orientador: Prof.º José Alexandre Felizola Diniz-Filho
Coorientadora: Prof.ª Lúcia G. Lohmann

Goiânia-GO
Fevereiro de 2019

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ATA DA SESSÃO PÚBLICA DE DEFESA DE TESE Nº 77

Aos vinte e seis dias do mês de fevereiro de 2019 (26/02/2019), às treze horas e trinta minutos (13h30min), no Auditório do ICB V, UFG, reuniram-se os componentes da banca examinadora: **Prof. Dr. José Alexandre Felizola Diniz-Filho, ICB/UFG; Prof. Dr. Matheus de Souza Lima Ribeiro, ICB/UFG; Profa. Dra. Levi Carina Terribile, ICB/UFG; Dra. Geiziane Tessarolo, UEG; Profa. Dra. Suzana de Fátima Alcântara; UFSC;** para, em sessão pública presidida pelo (a) primeiro(a) examinador(a) citado(a), procederem à avaliação da defesa de tese intitulada: **"Macroecologia e distribuição geográfica da tribo Bignonieae (Bignoniaceae)"**, em nível de doutorado, área de concentração em Ecologia e Evolução, de autoria de **Leila Meyer**, discente do Programa de Pós-Graduação em Ecologia e Evolução da Universidade Federal de Goiás. A sessão foi aberta pelo(a) presidente(a), que fez à apresentação formal dos membros da banca. A palavra, a seguir, foi concedida a(o) autor(a) da tese que, em cerca de __50__ minutos, procedeu à apresentação de seu trabalho. Terminada a apresentação, cada membro da banca arguiu a(o) examinada(o), tendo-se adotado o sistema de diálogo sequencial. Terminada a fase de arguição, procedeu-se à avaliação da tese. Tendo-se em vista o que consta na Resolução nº 1127 de dezembro de 2012 do Conselho de Ensino, Pesquisa, Extensão e Cultura (CEPEC), que regulamenta o Programa de Pós-Graduação em Ecologia e Evolução, a tese foi ___Aprovada___, considerando-se integralmente cumprido este requisito para fins de obtenção do título de Doutor(a) em Ecologia e Evolução pela Universidade Federal de Goiás. A conclusão do curso dar-se-á quando da entrega da versão definitiva da tese na secretaria do programa, com as devidas correções sugeridas pela banca examinadora, no prazo de trinta dias a contar da data da defesa. Cumpridas as formalidades de pauta, às __16__ h e __30__ min., encerrou-se a sessão de defesa e, para constar, eu, Suely Ana

Ribeiro, secretária executiva da Universidade Federal de Goiás - UFG, lavrei a presente ata que, após lida e aprovada, será assinada pelos membros da banca examinadora em três vias de igual teor.

Prof. Dr. José Alexandre Felizola Diniz-Filho
Presidente da banca
ICB/UFG

Prof. Dr. Matheus de Souza Lima Ribeiro
ICB/UFG

Profa. Dra. Levi Carina Terribile
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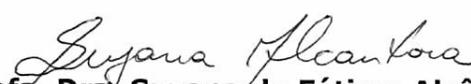
Profa. Dra. Suzana de Fátima Alcântara
UFSC

Dedico esta tese aos meus pais e aos meus queridos avós.

"O que vale na vida não é o ponto de partida e sim a caminhada.

Caminhando e semeando, no fim terás o que colher. "

Cora Coralina

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Sumário

Resumo

Um dos maiores desafios da biogeografia e macroecologia é entender os mecanismos subjacentes aos padrões de distribuição geográfica da diversidade. Esta tese contribui com esse tópico, uma vez que seu objetivo central foi investigar padrões e processos relacionados à distribuição da diversidade da tribo Bignonieae (Bignoniaceae), o maior clado de lianas neotropicais com ~ 400 espécies. Ao comparar dois métodos de polígonos usados para estimar a área de distribuição das espécies (i.e., mínimo polígono convexo e *alpha hull*) (**Capítulo 1**), observamos que eles podem ser usados em equivalência para gerar mapas de riqueza. No entanto, o *alpha hull* é uma escolha mais conservadora para evitar superestimativas da área de distribuição das espécies em comparação ao mínimo polígono convexo. Observamos que tanto a área de distribuição das espécies da tribo quanto a riqueza total de Bignonieae respondem de maneira similar às variáveis ambientais e espaciais (**Capítulo 2**), o que sugere que os mesmos processos estão atuando sobre os dois níveis. No entanto, alguns atributos das espécies diminuem tal congruência, a saber: (i) ausência de nectários extraflorais, (ii) área de distribuição geográfica pequena a intermediária, e (iii) tempo de divergência recente. Observamos também que a altura de dossel é um preditor importante da riqueza de espécies de lianas da tribo (**Capítulo 3**), além das variáveis climáticas e edáficas. Porém, a relação entre riqueza e altura de dossel depende do ambiente em que as lianas ocorrem. A riqueza de lianas de ambientes florestais e ripários aumenta com o aumento da altura de dossel, enquanto a riqueza de lianas de savana é maior em ambientes com vegetação mais baixa. Ao longo dos três capítulos, notamos que a distribuição geográfica da riqueza de espécies da tribo, em escala macroecológica, está associada à distribuição de ambientes florestais e savânicos pelo Neotrópico, com maior concentração de espécies em ambientes florestais, como a Amazônia e a Mata Atlântica.

Palavras-chave: *alpha hull*, altura de dossel, desconstrução da riqueza, lianas, padrão de riqueza.

Abstract

Understanding geographical patterns of species diversity and their underlying processes is one of the major goals of biogeography and macroecology. This thesis contributes to this topic as its main aim was to investigate patterns in the distribution of species richness of the tribe Bignonieae (Bignoniaceae), the largest clade of Neotropical lianas with almost 400 species. Comparing two hull methods used to build species ranges (i.e., convex hull and alpha hull) (**Chapter 1**), we found that both methods can be considered as equivalent for mapping species richness patterns. However, the alpha hull is a more conservative approach that tends to reduce the chance of species range overestimation in comparison to the convex hull. We found that species ranges and the overall Bignonieae richness pattern respond similarly to environmental and spatial variables (**Chapter 2**), which suggests that the same process are acting to determine both species ranges and species richness in Bignonieae. Nonetheless, some species attributes reduced the congruence in ranges and richness response, such as: (i) lack of extrafloral nectaries, (ii) small to medium range sizes, and (iii) late-diverging species. We also found that canopy height is a main driver of richness patterns of liana species of the tribe (**Chapter 3**), in addition to climate and soil variables. However, the relationship of liana richness and canopy height changes according to the habitat where species occur. Lianas from forest and riparian habitats increase in number in taller canopies, while savanna lianas increase in shorter canopies. We noticed the distribution of species richness of the tribe is associated with the current distribution of forest and savanna habitats in the Neotropics, with a great species accumulation in forest habitats such as the Amazon and the Atlantic rainforests.

Keywords: alpha hull, canopy height, richness deconstruction, lianas, richness patterns.

Introdução geral

Padrões espaciais de diversidade

Desde as viagens dos naturalistas ao redor do mundo, durante os séculos XVIII e XIX, se percebeu que a diversidade biológica não se distribui uniformemente pelo espaço geográfico (Brown 2014), mas que esta segue alguns padrões que, a partir de então, passaram a ser descritos e estudados. Por exemplo, a riqueza de espécies de diversos grupos de organismos é maior próximo à linha do equador e diminui em direção aos polos (i.e., o gradiente latitudinal de riqueza; Mittelbach et al. 2007; Brown 2014; Fine 2015). Além da descrição de padrões de distribuição da diversidade, grandes esforços também têm sido despendidos para que os mecanismos que geram e mantêm tais padrões sejam conhecidos, o que tem levado à formulação de diversas hipóteses. Para o gradiente latitudinal de riqueza, por exemplo, existem mais de 30 hipóteses propostas (Lomolino et al. 2010), muitas das quais não são mutuamente excludentes. Apesar dos esforços, uma formulação única que explique os padrões de riqueza ainda não foi alcançada. O que é esperado, considerando que se trata da distribuição geográfica de unidades biológicas distribuídas ao longo do tempo evolutivo, que foram influenciadas por eventos geomorfológicos e climáticos históricos, que sofrem com a dinâmica do clima e ambiente atual, e que interagem com a distribuição de outros organismos.

Dentre os possíveis promotores dos padrões de riqueza de espécies, a variação do clima ao longo do espaço aparece como mecanismo chave de várias hipóteses, e.g. hipótese de produtividade (Gillman et al. 2015), conservatismo de nicho (Wiens & Donoghue 2004), teoria metabólica (Brown 2014). Além do clima atual, eventos geomorfológicos (e.g., dinâmica das placas tectônicas, formação de montanhas) e mudanças climáticas que aconteceram no passado também exerceram influência sobre os padrões de riqueza, sobretudo por criar barreiras e limitar a dispersão das espécies (Fine 2015; Antonelli et al. 2018). Interações interespecíficas, por sua vez, parecem atuar

na distribuição da riqueza de espécies por aumentarem a chance de especialização e reduzirem a possibilidade de extinção devido à coexistência interespecífica (Gotelli et al. 2010; Henriques-Silva et al. 2019). De maneira semelhante, a heterogeneidade ambiental (e.g., heterogeneidade topográfica, edáfica ou da estrutura da vegetação) também promove o acumulo de espécies por contribuir com a especialização e coexistência das espécies (Kerr & Packer 1997; Oliveira & Scheffers 2019). Considerando as prováveis influências dos fatores mencionados, é possível perceber que os padrões de riqueza são resultado da atuação individual de diferentes fatores, assim como da interação entre esses fatores.

Além da atuação de múltiplos fatores, a própria natureza da variável 'riqueza de espécies' dificulta o entendimento de padrões de distribuição da riqueza. Segundo Marquet et al. (2004), a riqueza de espécies é uma variável agregada, pois representa, em um único número, toda variedade de espécies que coocorrem em um certo local e tempo. Diferenças ecológicas ou evolutivas entre as espécies são ignoradas, já que todas têm o mesmo peso sobre o somatório do número de espécies. Como a complexidade inerente às espécies pode ser um componente importante para o entendimento dos padrões de riqueza, Marquet et al. (2004) propuseram a ideia de 'desconstrução' do padrão de riqueza. Essa abordagem consiste em classificar as espécies em grupos de acordo com características ecológicas (e.g., síndrome de polinização, dispersão) ou evolutivas (e.g., clado, tempo de divergência) relevantes e, então, avaliar a relação entre a riqueza de espécies desses grupos e diferentes fatores (e.g., ambiente atual, clima passado) (Marquet et al. 2004). Tal abordagem permite observar mudanças na relação entre a riqueza de espécies e os fatores decorrentes de particularidades das espécies.

Uma dificuldade da desconstrução do padrão de riqueza é definir quais características serão usadas para classificar as espécies (Marquet et al. 2004). Neste sentido, Terribile et al. (2009) argumentam que cada espécie poderia ser considerada como um 'grupo' em decorrência da história

evolutiva e características ecológicas que são únicas. Assim, Terribile et al. (2009) propuseram a ideia de 'máxima desconstrução' do padrão de riqueza, que consiste em avaliar como determinados fatores atuam para delimitar a área de distribuição geográfica de cada espécie. Na sequência, a resposta de cada espécie aos fatores pode ser comparada à resposta do conjunto de espécies sintetizada pela riqueza de espécies (Terribile et al. 2009).

Além da complexidade inerente às espécies e processos dos quais emergem os padrões de distribuição da riqueza, conclusões a respeito de tais padrões dependem também da qualidade e completude da amostragem da biodiversidade (Fine 2015; Hortal et al. 2015), assim como da maneira que os dados disponíveis são processados (e.g., Graham & Hijmans 2006; Bombi et al. 2011). Em geral, não conhecemos todas as espécies existentes (i.e., lacuna de conhecimento Linneana), não sabemos qual é a distribuição geográfica completa das espécies já descritas (i.e., lacuna de conhecimento Wallaceana), e o conhecimento disponível não é homogeneamente distribuído pelo espaço (i.e., locais próximos às rodovias ou centros de pesquisa tendem a ser melhor amostrados que locais isolados) (Hortal et al. 2015; Oliveira et al. 2016). No entanto, conhecer quantas espécies existem e qual a distribuição geográfica delas é essencial para construir mapas de riqueza gerados pela sobreposição da área de distribuição geográficas das espécies (e.g., Stropp et al. 2016). Além disso, os mapas de riqueza podem variar de acordo com o método utilizado para representar a área de distribuição das espécies (e.g., somente pontos de ocorrência, polígonos, modelos de distribuição de espécies) (Graham & Hijmans 2006; Bombi et al. 2011).

Família Bignoniaceae e Tribo Bignonieae

Bignoniaceae é uma família botânica que pertece à ordem Lamiales e é composta por oito tribos (i.e., Bignonieae, Catalpeae, Coleeae, Crescentieae, Jacarandeae, Oroxyleae, Tecomeae e Tourrettieae), aproximadamente 800 espécies e 80 gêneros (Olmstead et al. 2009). As espécies da

família ocorrem predominantemente em florestas tropicais, sobretudo na região Neotropical, mas algumas espécies são encontradas em regiões temperadas (Olmstead et al. 2009). Árvores, arbustos e lianas são mais comuns na família Bignoniaceae, apesar de existirem algumas espécies herbáceas encontradas em altas altitudes. As espécies da família se caracterizam por apresentar (i) folhas compostas e opostas, (ii) flores gamossépalas e gamopétalas, com corola tubular, (iii) androceu epipétalo formado por quatro estames didínamos e um estaminódio dorsal, e (iv) frutos tipo cápsula loculicida, septícida ou síliqua, com sementes aladas (Fisher et al. 2004). Diversas espécies da família têm uso ornamental, madeireiro e medicinal (Gentry 1992). No Brasil são encontradas 416 espécies e 33 gêneros de Bignoniaceae, das quais 202 são endêmicas (Bignoniaceae in Flora do Brasil 2020).

A tribo Bignonieae apresenta cerca de 400 espécies e 20 gêneros (Lohmann & Taylor 2014), o que corresponde à metade das espécies da família Bignoniaceae. Tal diversidade faz com que Bignonieae seja considerada o maior clado de lianas Neotropicais, uma vez que quase 90% de suas espécies são lianas, enquanto o restante são arbustos (Lohmann 2006; Lohmann & Taylor 2014; Meyer et al. *in prep.*). Espécies da tribo Bignonieae são reconhecidas por apresentar (i) caule com crescimento secundário anômalo em que o floema é composto por quatro a 32 cunhas arranjadas em diferentes configurações entre o xilema, (ii) folhas opostas e compostas, geralmente com o folíolo terminal transformado em gavinha, e (iii) frutos do tipo cápsula septícida com grande variação de tamanho e formato (Lohmann et al. 2006; Lohmann & Taylor 2014). As flores são bastante vistosas, apresentam grande variação de coloração, e atraem diferentes polinizadores como abelhas, vespas, borboletas, mariposas, beija-flores e morcegos (Gentry 1974). As espécies frequentemente apresentam sementes aladas dispersas pelo vento, mas algumas espécies têm sementes não aladas dispersas pela água (Lohmann & Taylor 2014).

Todas as espécies da tribo Bignonieae ocorrem exclusivamente no Novo Mundo, desde o Sul dos Estados Unidos até o Norte do Chile e Argentina (Lohmann et al. 2013). As espécies se distribuem por uma ampla gama de ambientes, desde florestas tropicais úmidas, matas riparias até ambientes florestais e savânicos secos, mas com grande concentração de espécies na Amazônia e Mata Atlântica (Lohmann et al. 2013; Lohmann & Taylor 2014). A área de distribuição das espécies da tribo é variada com espécies de ocorrência restrita até amplamente distribuída (Lohmann et al. 2013; Meyer et al. 2018).

Bignonieae representa um dos grupos de plantas neotropicais mais bem conhecido graças aos vários estudos filogenéticos (e.g., Lohmann 2006; Kaehler et al. 2012; Medeiros & Lohmann 2015b), taxonômicos (e.g., Lohmann & Taylor 2014; Medeiros & Lohmann 2015a; Fonseca et al. 2017), evolutivos (e.g., Alcantara et al. 2013; Sousa-Baena et al. 2014; Nogueira et al. 2015; Pace et al. 2015) e biogeográficos (Lohmann et al. 2013) que já foram desenvolvidos. A alta diversidade de espécies e ampla distribuição geográfica do grupo, juntamente com um amplo e consistente conhecimento acumulado, fazem da tribo Bignonieae um excelente grupo para investigar padrões de diversidade em escala macroecológica.

Objetivos da tese

Esta tese de doutorado teve como objetivo geral avaliar padrões e mecanismos relacionados à distribuição geográfica da diversidade da tribo Bignonieae. Para cumprir com tal objetivo, estruturamos a tese em três capítulos:

No primeiro capítulo, investigamos se a área de distribuição geográfica das espécies de Bignonieae e o padrão de riqueza da tribo variam de acordo com o método de construção de polígonos utilizado para representar a área de distribuição das espécies. Avaliamos dois métodos de construção de polígonos: (i) o mínimo polígono convexo, que é o método tradicional e foi mais

utilizado na literatura científica, e (ii) o *alpha hull*, que é o método atualmente recomendado pela IUCN. Também avaliamos se as incongruências na área de distribuição das espécies entre os dois métodos estão associadas ao grau de conhecimento sobre a distribuição geográfica das espécies (i.e., a lacuna de conhecimento Wallaceana). Esperamos que espécies com a área de distribuição bem conhecida (i.e., espécies descritas a mais tempos ou com mais registros de ocorrência) tenham maior congruência nas estimativas da área de distribuição geradas pelos dois métodos de construção de polígonos.

No segundo capítulo, avaliamos se processos que atuam na delimitação da área de distribuição geográfica das espécies da tribo também são os processos que determinam o padrão geral de riqueza de Bignonieae. Para isso, definimos um conjunto de variáveis climáticas, edáficas e espaciais e avaliamos como a área de distribuição das espécies e a riqueza geral da tribo respondem a essas variáveis, conforme proposto pela abordagem de máxima desconstrução da riqueza. Também avaliamos se incongruências na resposta da área de distribuição das espécies e da riqueza de espécies estão associadas aos atributos das espécies. Para isso, utilizamos a abordagem de desconstrução do padrão de riqueza e agrupamos as espécies de acordo com atributos ecológicos, geográficos e evolutivos.

No terceiro capítulo, investigamos como a altura de dossel, clima e solo interagem para determinar padrões de riqueza de espécies de lianas da tribo Bignonieae. Avaliamos se a altura de dossel tem um efeito positivo sobre a riqueza de lianas, mesmo quando efeitos indiretos do clima e solo são controlados. A expectativa é que a riqueza de lianas aumente em florestas mais altas porque existe maior oferta de suporte físico (e.g., tronco de árvores) e habitat. Também testamos se a riqueza de lianas de ambientes com menor altura de dossel (e.g., ambientes ripários e savânicos) é menos relacionada à altura de dossel que a riqueza de lianas de ambientes florestais,

uma vez que ambientes ripários e savânicos oferecem menor disponibilidade de habitats em comparação às florestas neotropicais.

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Capítulo 1

Comparação entre métodos de polígonos usados para estimar área de distribuição geográfica das espécies e mapas de riqueza

A comparison of hull methods for estimating species ranges and richness maps

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Abstract

Aims: The combined analysis of species ranges allows the detection of overall species richness patterns. As such, the reliability of richness maps is directly related to the accuracy of individual range estimates. We compared how species ranges and richness patterns are influenced according to the use of different methods (convex hull and alpha hull) and evaluated if differences in range estimates are related to the Wallacean shortfall.

Methods: We used occurrence records of 386 species from the tribe Bignonieae (Bignoniaceae) to build richness maps by stacking species ranges, using the convex hull and alpha hull methods. We evaluated the behaviour of the richness estimates in relation to other variables (i.e., other richness measures, environmental and spatial variables). We correlated the differences in range estimates to proxies of Wallacean shortfall (i.e., species description date and variation of pseudo-ranges generated by jack-knife).

Results: Convex hull estimated larger ranges than alpha hull. The Wallacean shortfall affected range estimates equally regardless of the hull method used. Both hull methods generated similar richness maps. Richness estimates showed similar correlation patterns in relation to other variables regardless of the hull method used.

Conclusions: Despite the slight differences in range estimates, both hull methods can be used in equivalence to map species richness of the tribe Bignonieae.

Keywords: alpha hull, Bignonieae, convex hull, species richness patterns, Wallacean shortfall.

Introduction

A good understanding of the geographic ranges of taxa is essential for ecological and evolutionary studies (Graham & Hijmans 2006; Hawkins et al. 2007a; Tomašových & Jablonski 2016), and is critical for conservation planning and management (Bombi et al. 2011; IUCN 2014). Richness maps are usually produced by stacking the geographic ranges from multiple taxa (e.g., Hawkins et al. 2007a; Pereira & Palmeirim 2013; Qian et al. 2014). As such, the reliability of richness maps is directly related to the accuracy of species range estimates (Graham & Hijmans 2006; Bombi et al. 2011). However, species ranges can vary depending on the estimation method used (Graham & Hijmans 2006; Rocchini et al. 2011; Pena et al. 2014; Tsianou et al. 2016). While some methods only take into account the geographical aspect of species ranges (e.g., ranges estimated by minimum convex hull), others associate species occurrence records with environmental variables (e.g., species distribution modelling).

Many macroecological studies have correlated richness patterns with environmental variables, especially climatic variables (Hawkins et al. 2007a; Field et al. 2009; Braga et al. 2014). However, when richness patterns are determined by stacking species ranges that were estimated through approaches that take environmental variables into account (e.g., SDM), it becomes redundant to correlate the resulting richness patterns to environmental variables (Terribile et al. 2009). This redundancy can be avoided by reconstructing species ranges based on species occurrence points alone, such as ranges estimated by minimum convex hull. Apart from stacking species ranges, richness patterns can also be estimated by counting the number of species found in a particular locality based on occurrence records available from museum collections or biodiversity inventories (Graham & Hijmans 2006; Bombi et al. 2011; Ballesteros-Mejia et al. 2013; Mata et al. 2017). To avoid biases in richness estimates due to unequal sampling across areas, sampling effort can be standardised through rarefaction (Gotelli & Colwell 2010). However, simply counting

the number of species known to occur in various localities generally leads to underestimates of species richness (Graham & Hijmans 2006; Bombi et al. 2011; Raedig & Kreft 2011).

The minimum convex hull method (hereafter, convex hull method) has been broadly used to estimate species ranges and to infer richness patterns of different taxonomic groups (e.g., Diniz-Filho et al. 2008; Morueta-Holme et al. 2013; Roque et al. 2016). However, the convex hull often overestimates species ranges (Burgman & Fox 2003; Bombi et al. 2011; IUCN 2014). To deal with this bias, a generalisation of the convex hull method, known as the alpha hull method, has been proposed (Edelsbrunner et al. 1983; Burgman & Fox 2003). These methods differ in the estimation of the internal angles. While angles can be convex or concave in an alpha hull method, angles are exclusively convex under the convex hull method (Burgman & Fox 2003; IUCN 2014). The alpha hull method has been shown to be more efficient when real species ranges have a concave shape, while the convex hull method tends to overestimate those same ranges (Burgman & Fox 2003). However, both methods have been shown to be similarly good when the real shape of the range is convex (Burgman & Fox 2003).

Apart from the method used, range delimitation also depends on the knowledge of the geographical occurrence of each species (Rocchini et al. 2011; Meyer et al. 2016), which generally is discontinuous and unevenly distributed in space (Loiselle et al. 2008; Oliveira et al. 2016). It is broadly known that our knowledge on species occurrence is generally affected by the so-called 'Wallacean shortfall' (Bini et al. 2006; Hortal et al. 2015; Oliveira et al. 2016), especially in tropical regions (Hortal et al. 2015; Oliveira et al. 2016). Knowledge about species occurrences is not equal among taxa, especially because: (i) some species were described more recently than others, giving them less time to be studied and collected (Diniz-Filho et al. 2005; Meyer et al. 2016), and (ii) species have different levels of detectability, with inconspicuous or more narrowly distributed species being less detectable than conspicuous or widely distributed taxa (Diniz-Filho et al. 2005;

Sheth et al. 2008; Meyer et al. 2016). Furthermore, knowledge is also not equally distributed in geographic space because more accessible regions such as those close to universities and research centres generally concentrate greater sampling effort (Hopkins 2007; Schulman et al. 2007; Ballesteros-Mejia et al. 2013; Oliveira et al. 2016). The uncertainties associated with range estimates of individual species accumulate when ranges are stacked to construct overall richness maps (Graham & Hijmans 2006; Bombi et al. 2011), potentially biasing our understanding of the processes underlying richness patterns.

Even though species ranges estimated by convex hull and alpha hull methods have been evaluated through simulations of range shapes and biases in sampling effort (Burgman & Fox 2003), species ranges and richness patterns estimated by those methods have not been extensively evaluated using empirical data. The tribe Bignonieae (Bignoniaceae), the largest clade of Neotropical lianas (Lohmann 2006; Lohmann & Taylor 2014), is an excellent model for an empirical study of this nature. Bignonieae includes ca. 400 species and is well characterised based on morphological and molecular characters (Lohmann & Taylor 2014). The whole tribe is very important ecologically, contributing to the overall structure of tropical forests and providing resources for pollinators (Gentry 1991), and has been the subject of multiple phylogenetic (e.g., Lohmann 2006; Kaehler et al. 2012; Medeiros & Lohmann 2015a; Fonseca et al. 2015), taxonomic (e.g., Lohmann & Taylor 2014; Medeiros & Lohmann 2015b; Fonseca et al. 2017), evolutionary (e.g., Alcantara et al. 2013; Sousa-Baena et al. 2014; Nogueira et al. 2015; Pace et al. 2015), and biogeographical (e.g., Lohmann et al. 2013) studies. Moreover, species of Bignonieae have variable distribution patterns, ranging from narrowly to broadly distributed (Lohmann et al. 2013). However, knowledge of species occurrence varies among species because Bignonieae includes species that were described in the mid-eighteenth century, up to species that were only described very recently (e.g., Medeiros & Lohmann 2014; Zuntini et al. 2015a 2015b; Fonseca et al. 2016).

It is important to consider these variations in knowledge of species occurrence and their effects on estimating species ranges and richness patterns. Apart from the relevance of this clade for the understanding of the assembly of tropical forests as a whole, a richness map was not available for Bignonieae so far.

In this study, we evaluated how the estimates of geographical ranges of species of Bignonieae and the overall richness pattern for the tribe vary according to the use of convex hull and alpha hull methods. To better understand the behaviour of each hull method, we also compared the richness patterns generated by the two hull methods with rarefied richness estimates based on species occurrence records from museums and from local inventories. The behaviour of these different richness estimates was investigated by exploring the relationship between emergent richness patterns, environmental and spatial variables. We also evaluated whether differences in range estimates were related to the level of knowledge about the geographic occurrences of individual species (i.e., the Wallacean shortfall). We expected differences in range estimates to be lower for species with better known occurrences. Our analyses were intended to support studies that aim at reconstructing species ranges and richness patterns using databases with varying levels of knowledge of species occurrence.

Methods

Species occurrence records

For this study, we used a geo-referenced dataset of species occurrence records of the tribe Bignonieae compiled by LG Lohmann from her own collections and from herbarium records that she examined from multiple collections, especially the Missouri Botanical Garden (www.tropicos.org). For this database, the identification of each individual specimen was carefully checked by LG Lohmann. In addition, geographical coordinates were directly extracted from

specimens whenever available and subsequently verified to confirm that the coordinate really belonged to the described location. Whenever coordinates were not included in the specimen label, the most specific locality was identified and coordinates were searched using online gazetteers, especially the 'Getty Thesaurus of Geographic Names Online' (www.getty.edu/research/tools/vocabularies/tgn/). Georeferencing followed the best practices proposed by Chapman & Wieckzorek (2006).

We plotted occurrence records of each species individually and verified the distribution of each taxon using available taxonomic reviews and expert knowledge (LG Lohmann). For the genus *Adenocalymma* Mart. ex Meisn., species distribution ranges were verified by LG Lohmann and LHM Fonseca simultaneously. All occurrence records located outside known species geographic ranges were removed from the database. Whenever species had less than 10 occurrence records, additional occurrence records were retrieved from the following monographs: *Adenocalymma* (Fonseca 2017), *Amphilophium* Kunth (Pool 2007a 2007b 2008 2009), *Bignonia* L. (Zuntini 2015), *Dolichandra* Cham. (Fonseca et al. 2017), *Lundia* DC. (Kaehler 2011), *Mansoa* DC. (Silva-Castro 2010), *Pleonotoma* Miers (Gomes 2006), and *Tynanthus* Miers (Medeiros & Lohmann 2015b). For species with more than 10 records, we established that their known range (i.e., species geographic range described in taxonomic reviews) was well represented by the occurrence records already included in our database; therefore, we did not include additional records for those taxa. This dataset follows the species taxonomic delimitation of Lohmann & Taylor (2014), except from *Adenocalymma* for which a more recent synopsis is available (Fonseca 2017), and some taxa for which taxonomic updates were published recently (e.g., Zuntini et al. 2015a 2015b; Fonseca et al. 2016).

The final database included 386 species belonging to 20 genera, with a total of 28,763 occurrence records, out of which 21,138 records were used to carry out the analyses. The 7,625

records that were excluded represented duplicate localities (i.e., records of the same species in the same locality, but collected by different collectors or by the same collector at different times). Out of the 386 species, 30 (8%) had only one or two occurrence records, 80 (21%) had between three and nine records, and 276 species (71%) had more than 10 records (Table S1.1). Out of the 28,763 occurrence records, 24,079 (84%) had the collection date available: 1% was collected before 1900, 10% were collected between 1900 and 1949, 69% were collected between 1950 and 1999, and 4% were collected since 2000. All species have Neotropical distribution except from *Bignonia capreolata* L., which is restricted to southern United States (Lohmann & Taylor 2014).

Estimation of species ranges and richness maps

We constructed hulls to represent the range of all species with three or more occurrence records (356 of the 386 species). To estimate species ranges based on the convex hull method, we used the 'gConvexHull' function of the 'Rgeos' package (Bivand et al. 2016) implemented in R (R Core Team 2017). This method joins the outermost occurrence records of each species in a convex hull (i.e., a hull with all internal angles less than 180°) that encompasses all species records. We delimited each species range by one hull, except for 11 species that showed disjunct distributions (e.g., species with some isolated occurrence records in the Amazon rainforest and others in the Atlantic rainforest). For species with disjunct distributions, we represented their ranges by two disjoint hulls (Table S1.1).

To estimate species ranges based on the alpha hull method, we used the 'ashape' function of the 'alphahull' package (Pateiro-López & Rodríguez-Casal 2016) implemented in R (R Core Team 2017), which is based on the algorithm by Edelsbrunner et al. (1983). For each species, we established an alpha value as the smallest value that provided a single hull encompassing all species occurrence records but without any holes. For the 11 species with disjunct distributions, the alpha

value was calculated as the smallest value that gave two disjoint hulls while including all occurrence points (see alpha values of each species in Table S1.1). Under the alpha hull method, the alpha value determines which occurrence points have to be joined to delimit the species hull (Edelsbrunner et al. 1983; Burgman & Fox 2003; Pateiro-López & Rodríguez-Casal 2010). The first step of this method is to build a Delaunay triangulation that includes all species occurrence points (Burgman & Fox 2003; Pateiro-López & Rodríguez-Casal 2010). Thereafter, only some connections of the Delaunay triangulation are maintained according to the alpha value. Two points remain connected if there is an open circle of radius alpha with both points on its boundary that do not contain other occurrence points. The alpha hull results from the outermost Delaunay connections that are maintained according to the radius of the circle. This method allows variations in the resolution of the external surface of the hull so that low alpha values provide hulls with finer surface resolution, while increases in alpha lead to convergence between the alpha hull and convex hull ranges (Burgman & Fox 2003; Pateiro-López & Rodríguez-Casal 2010; IUCN 2014). By varying the alpha value, it is also possible to group occurrence points in multiple independent hulls and to represent species disjoint geographic distributions (Burgman & Fox 2003; IUCN 2014). A challenge of this method is to establish the alpha value given that the hull shape changes according to the choice of alpha (Capinha & Pateiro-López 2014).

We built two richness maps, one for each hull method (i.e., convex hull and alpha hull), by stacking the range of the 356 species on a grid of cells with 0.5×0.5 degrees across the entire occurrence area of the tribe Bignonieae. We projected the occurrence records of the 30 species with less than three records directly on the grid and summed these species to the stacked richness maps. All our geographic data were projected using Behrmann equal area projection.

Rarefied species richness

We generated two additional richness estimates based on the number of species estimated from museum occurrence records and from local inventories. Because the number of occurrence records varies among sample units, we used the rarefaction approach to standardise sample effort and avoid bias in richness estimates (Gotelli & Colwell 2010). The 'museum occurrence records' were represented by the occurrence records of each species of tribe Bignonieae (i.e., the same 21,138 occurrence records of the original database of the tribe used to build the hulls). We overlapped all museum occurrence records on the grid with 0.5 resolution degrees and calculated the number of records per grid cell, using the same approach used to build point-to-grid maps (Graham & Hijmans 2006). The 'occurrence records of local inventories' were obtained from species richness and abundance of 95 sites available from Alcantara (2010) and Alcantara et al. (2014). Most of these sites correspond to Alwyn Gentry's transect database (www.mobot.org/MOBOT/research/gentry/ transect.shtml). The sites have a sampled area around 0.1 ha and are distributed throughout the occurrence area of tribe Bignonieae (Alcantara et al. 2014). We also overlapped these sites on the grid to identify which grid cell corresponds to each site.

To estimate rarefied richness, we cumulatively and randomly selected occurrence records in each sample unit and counted the respective species number. The selection of occurrence records was conducted until all records had been considered. We repeated this procedure 1000 times and obtained the mean species richness for each amount of occurrence record per sample unit (Mata et al. 2017). We used grid cells as the sample unit of the richness estimated from museum occurrence records, and used the 95 sites as the sample units of the richness estimated from local inventories. We truncated the number of occurrence records per sample unit to estimate rarefied richness. We established the truncation threshold based on two criteria: (i) maximise the correlation between the rarefied richness and the richness generated by hull methods, and (ii) minimise the loss of

geographically effective degree of freedom according to Dutilleul's method to deal with spatial autocorrelation (SAC) (Legendre et al. 2002). This last approach was necessary because, as the truncation threshold increases, the set of sample units with a number of occurrence records that are equal or greater than the truncation threshold decreases. So does the degree of freedom, losing power to estimate the statistical significance of the correlation. For the rarefied richness from museum occurrence records, we truncated sample effort in 71 records per sample unit. As such, we retained only 14 grid cells that included 71 or more records in our richness estimates. For the rarefied richness estimated from local inventories, we truncated the sample effort in 30 records and considered 25 of the 95 sites in our richness estimates (Fig. S1.1).

Knowledge about geographic occurrence of individual species

Collection effort and knowledge of species ranges are cumulative over time (Diniz-Filho et al. 2005; Lobo et al. 2007; Meyer et al. 2016). As such, we considered that species described a long time ago have better known geographic occurrences than more recently described taxa. Therefore, we used the year of description of each species as a measure of knowledge about geographic occurrence of individual species. The date of description of each species was obtained from Lohmann & Taylor (2014) or from the original descriptions in the case of species that were described after 2014.

We also used the coefficient of variation (CV) of pseudo-values of species ranges generated by jack-knife as a proxy for the knowledge of species occurrences. To generate pseudo-values, we first identified the occurrence records that delimited the range of each species according to the convex hull method. We then excluded one record at a time, rebuilt the convex hull with the remaining species records and calculated the new range size.

Pseudo-values of ranges were calculated according to Sokal & Rohlf (1995), using the equation:

$$\emptyset_i = nSt - (n - 1)St_{-i}$$

where $\emptyset_i$ represents each pseudo-value, n is the number of records used to delimit each species range, St is the range size calculated considering all species records, and St_{-i} is the range size calculated by removing the i-th record of the species range. We then calculated the CV of the pseudo-values of each species. We considered that species with a good level of geographic occurrence knowledge should have lower CVs, because the removal of one occurrence record should not change range sizes significantly. On the other hand, species for which distribution knowledge was lower should have higher CVs because the removal of one record would lead to more drastic changes in range size.

Data analyses

Species ranges – we carried out an ordinary least squares (OLS) simple regression model, in which the response and predictor variables were the size of species ranges estimated by convex hull and alpha hull, respectively. Species range size was represented by the area of species' hull. To assess the similarity of species ranges estimated by the hull methods, we tested if the intercept and slope of the OLS model differed statistically from zero (i.e., $\alpha = 0$) or from one (i.e., $\beta = 1$), respectively. We represented incongruences in species range size by the CV of ranges estimated by each method. We used CV as our measure because the simple difference between ranges generated by each method is correlated with range size ($r_s = 0.89$ for range size estimated by convex hull and $r_s = 0.84$ for alpha hull). Because hull methods generate the same hull for species with three occurrence records, we only calculated incongruences in range estimates for species with more than three occurrence records (344 species). To evaluate whether the level of knowledge about species

geographic occurrences was related to incongruences in range estimates, we correlated the CV of ranges with the date of description of each species, as well as with the CV of pseudo-values of species ranges generated by jack-knife. We did not correct the degrees of freedom for phylogenetic autocorrelation in analyses with geographic range data because species ranges tend to have weak phylogenetic signal (Diniz-Filho & Tôrres 2002; Gaston 2003).

Species richness – we carried out an OLS regression for richness estimates to test whether the richness estimated by convex hull and alpha hull were significantly similar. However, as we detected SAC in OLS model residuals according to Moran's I correlogram (Legendre 1993), estimates of standard error of the model parameters and consequently type I error in significance tests may be biased (Legendre 1993; Hawkins et al. 2007b). We then used a spatially explicit simultaneous autoregressive (SAR) model to deal with SAC in richness regression models (Cressie 1993). We described the spatial relation among grid cells using a connectivity matrix that linked all grid cells to a distance less than 150 km. We tested if the intercept and slope of the SAR models differed statistically from zero (i.e., $\alpha = 0$) and from one (i.e., $\beta = 1$), respectively.

To evaluate the behaviour of each hull method in estimating richness maps, we correlated the richness generated by convex hull and alpha hull with the rarefied richness estimated from museum occurrence records and from local inventories, for grid cells in which rarefied richness were estimated. We also correlated these four richness estimates with the actual evapotranspiration (AET) to explore the relationship between the different richness estimates and this variable. AET is viewed as a general surrogate of energy-water balance in the environment and usually explains a large amount of variation in richness (Hawkins et al. 2003; O'Brien 2006). We obtained the AET data from Global Soil-Water Balance Database (Trabucco & Zomer 2010). For all correlations, we corrected the degrees of freedom (v^*) to deal with SAC and avoid biases in the significance tests using the Dutilleul's method (Legendre et al. 2002) available through the 'modified.ttest' function

of the 'SpatialPack' package (Osorio et al. 2014) implemented in R (R Core Team 2017). We also evaluated the overall spatial trends in the different richness estimates by performing an OLS regression for each richness estimate against latitude and longitude and their quadratic expansions, in a quadratic trend surface analysis. This spatial analysis was carried out to describe and compare broad-scale trends in richness patterns from different estimates.

Results

Species ranges

Species of the tribe Bignonieae showed large variability in their range sizes (Fig. 1), ranging from 18 km^2 according to the convex hull and alpha hull methods (for *Anemopaegma nebulosum* Firetti-Leggieri and L.G. Lohmann) to 16,811,048 km^2 according to convex hull method and 14,534,540 km^2 according to alpha hull method (for *Dolichandra unguis-cati* (L.) L.G. Lohmann). However, 40% and 42% of the species had range sizes smaller than 250,000 km^2 according to convex hull and alpha hull methods, respectively. Furthermore, half of the species had range sizes lower than 475,000 km^2 according to the convex hull method and lower than 375,000 km^2 according to the alpha hull method.

Overall, the convex hull overestimated range sizes in comparison to the alpha hull (Fig. 2). The regression of species ranges generated by the hull methods showed that the intercept was different from zero (α = 128400, t = 3.35, df = 355, p < 0.01) and the slope was different from one (β = 1.20, t = 15.78, df = 355, p < 0.01), against the expectation that both methods would provide the same species range estimates.
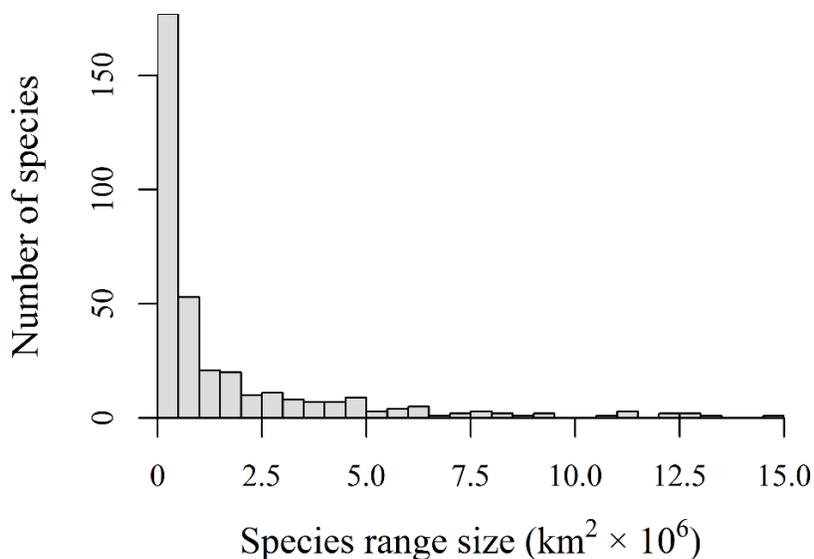
Figure 1. Range size distribution of the 356 species belonging to tribe Bignonieae estimated by the alpha hull method (histogram of ranges estimated by convex hull had the same distribution pattern and is not shown).
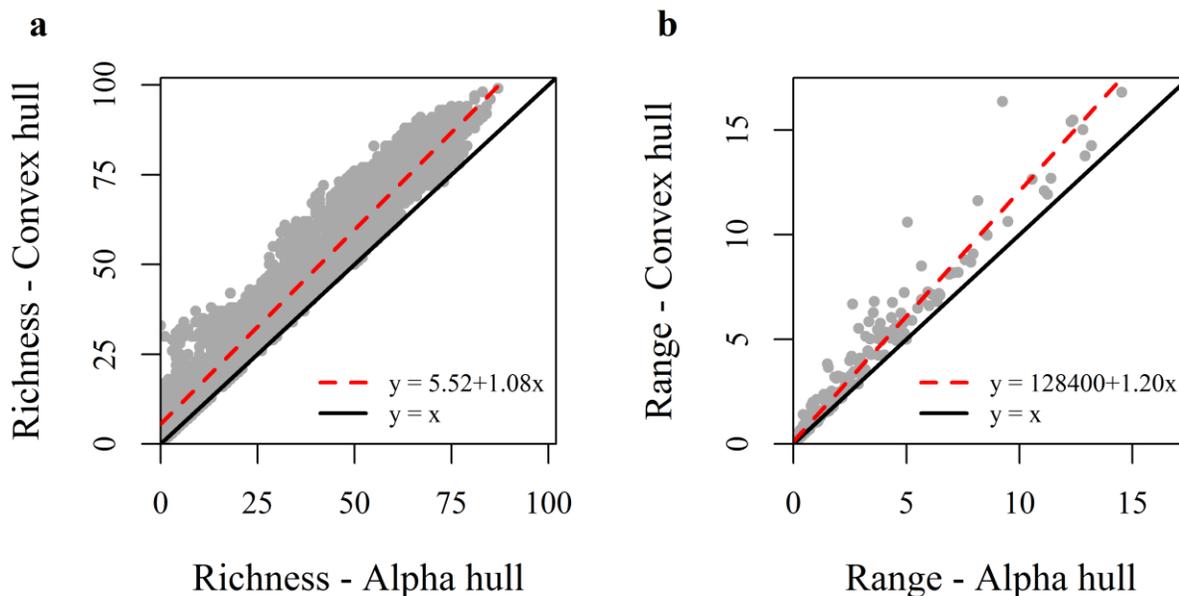
Figure 2. (a) Simultaneous autoregressive regression model of the species richness of tribe Bignonieae estimated by the convex hull and alpha hull methods; and (b) Ordinary least squares regression model of the range of 356 species estimated by each hull method. The range corresponds to the species range size in $km^2 \times 106$. Black lines represent the expectation if both hull methods provide the same range or richness estimates. Red lines represent the fit of the regression models.

The hull methods generated different range estimates for almost all species. However, 41% of the species had a CV of range estimates that was lower than 10%, while 69% of the species had a CV that was lower than 20% (Fig. 3a). The incongruences in range estimates did not appear to be strongly related to the knowledge about species' geographic occurrences. The correlation between the CV of species ranges and the CV of pseudo-values of ranges generated by the jack-knife approach was weak but significant (r_s = -0.20, df = 342, t = -3.66, p < 0.01; Fig. 3b). The same applied to the correlation between the CV of species ranges and the year of species description (r_s = -0.23, df = 342, t = -4.17, p < 0.01; Fig. 3c). The discovery and description of new species of the tribe Bignonieae have occurred gradually since the mid-eighteenth century (Fig. 3d).
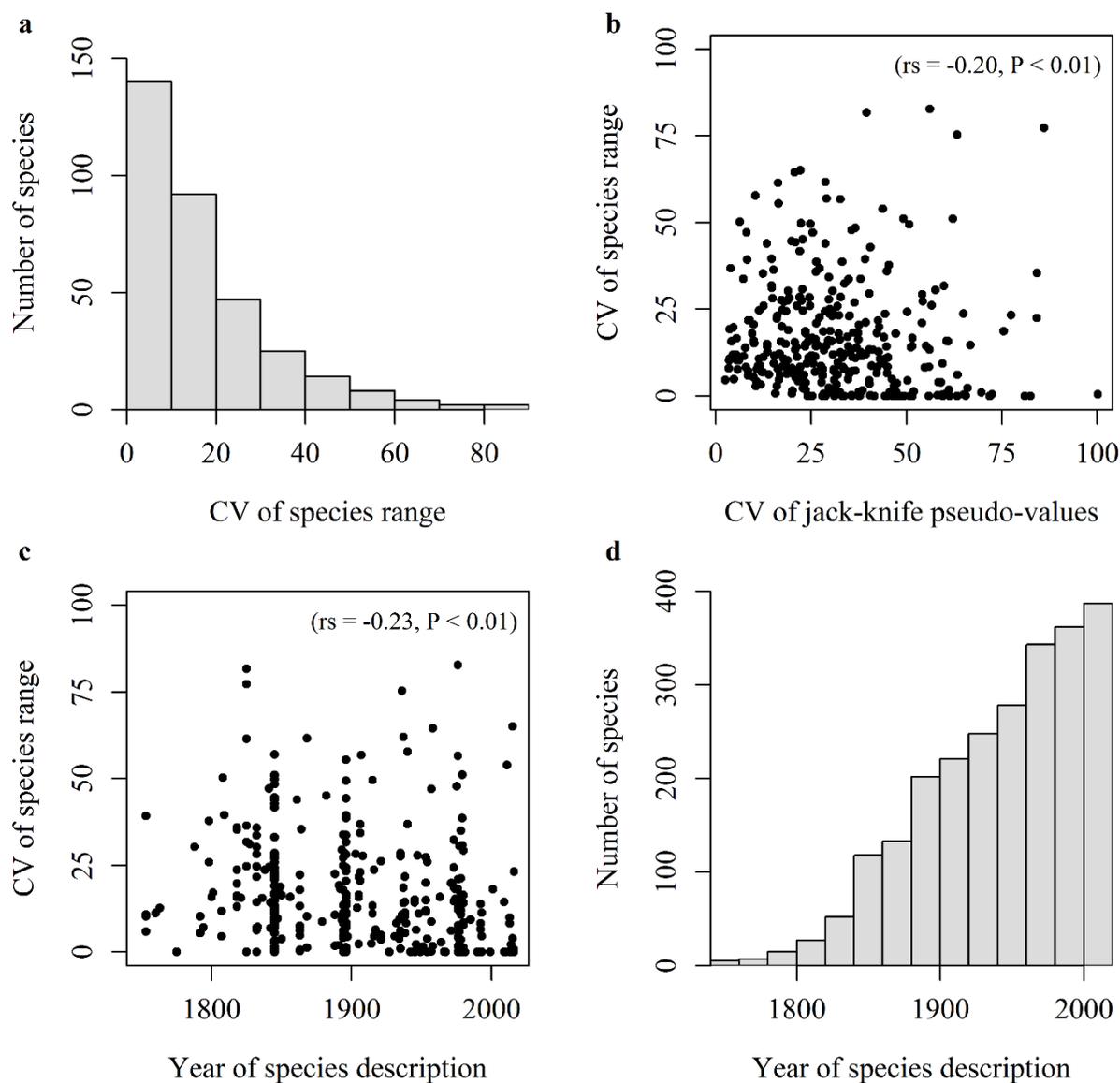
Figure 3. (a) Distribution of the coefficient of variation (CV) of species ranges of the tribe Bignonieae estimated by hull methods; (b) Relationship between the CV of species ranges estimated by hull methods and the CV of pseudo-values of ranges generated by jack-knife; (c) Relationship between the CV of species ranges estimated by hull methods and the year of species description; and (d) Distribution of the year of species description of all species of the tribe Bignonieae (386 species). For plots a, b and c, only species with more than three occurrence records were considered (344 species). The CV of jack-knife pseudo-values and the year of species description are the proxies for the knowledge of the geographic occurrence for each species.

Species richness

Both hull methods generated similar richness patterns for the tribe Bignonieae (Fig. 4). In the regression of species richness generated by each hull method, the intercept was not different from zero ($\alpha = 5.52$, t = 0.19, df = 1998, p = 0.85) and the slope was not different from one ($\beta = 1.08$, t = 0.10, df = 1998, p = 0.92) (Fig. 2), corroborating the similarities in both richness maps.

Species richness of members of tribe Bignonieae is concentrated in humid tropical regions, such as the Amazon and the Atlantic rainforests (Fig. 4a-b). In rain forests, richness reached 99 and 87 species per grid cell according to the convex hull and alpha hull methods, respectively. On the other hand, the minimum richness per grid cell was one species according to both methods. The average richness per grid cell was 40 species (SD = 28) according to the convex hull method and 32 species (SD = 24) according to the alpha hull method. The richness pattern cannot be considered a sampling artefact, as the correlation between species richness and the number of occurrence records per grid cell was weak for both hull methods (convex hull: $r_s = 0.13$, t = 1.38, $v^* = 107.70$, p = 0.17; alpha hull: $r_s = 0.18$, t = 1.96, $v^* = 112.11$, p = 0.05; see Fig. S1.2).
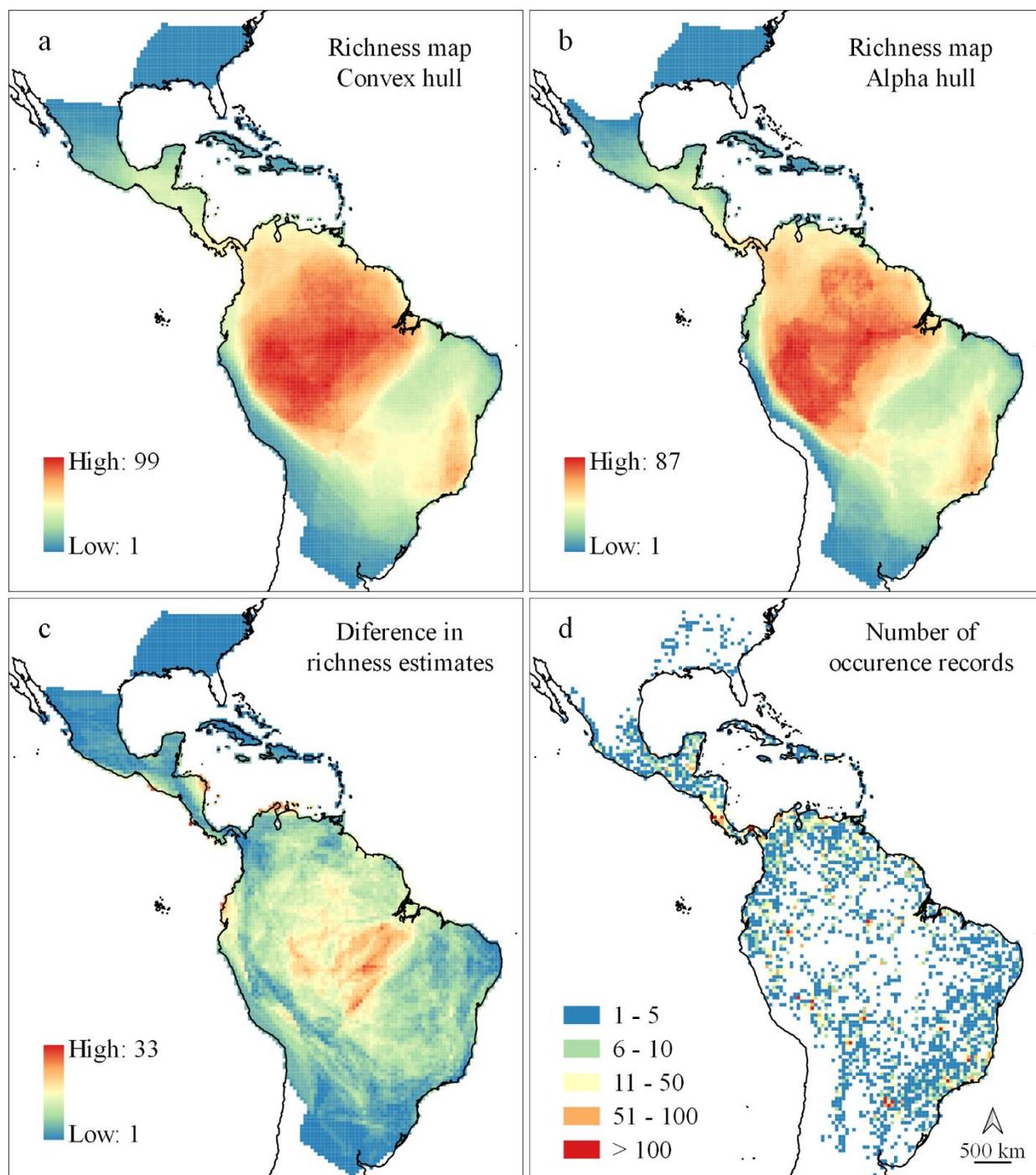
Figure 4. (a) Richness map of the tribe Bignonieae generated by the convex hull method; (b) Richness map of tribe Bignonieae generated by the alpha hull method; (c) Incongruences in richness maps estimated by each hull method; and (d) Number of occurrence records per grid cell.

The correlation between species richness estimated by both hull methods and the rarefied species richness generated from museum occurrence records or from local inventories showed the same pattern, regardless of the hull method used (Fig. 5; Table 1). The correlation of the richness generated by both hull methods and the rarefied species richness estimated from museum occurrence records was strong and significant ($r \approx 0.90$ for both hull methods; Table 1). The average rarefied richness per grid cell was 25 species (threshold of 71 museum occurrence records per grid cell), while the minimum and maximum richness were 15 and 38 species, respectively. The correlation between the richness estimated by hull methods and the rarefied richness estimated from local inventories was less strong but still significant ($r \approx 0.58$ for both hull methods; Table 1). The average richness in local inventories was eight species (sampling threshold of 30 plants per local inventory), while the minimum and maximum richness were one and 12 species, respectively.

Table 1. Correlations between the species richness of the tribe Bignonieae estimated by hull methods and rarefied richness generated from museum occurrence records (threshold of 71 records per grid cell) and rarefied richness generated from local inventories (threshold of 30 records per local inventory).

Rarefied richness	Convex hull richness				Alpha hull richness			
	r	F	$v*$	p	r	F	$v*$	p
Museum occurrence records	0.89	15.12	3.81	0.02	0.91	17.61	3.82	0.02
Local inventories	0.58	6.87	13.51	0.02	0.59	7.71	14.62	0.01
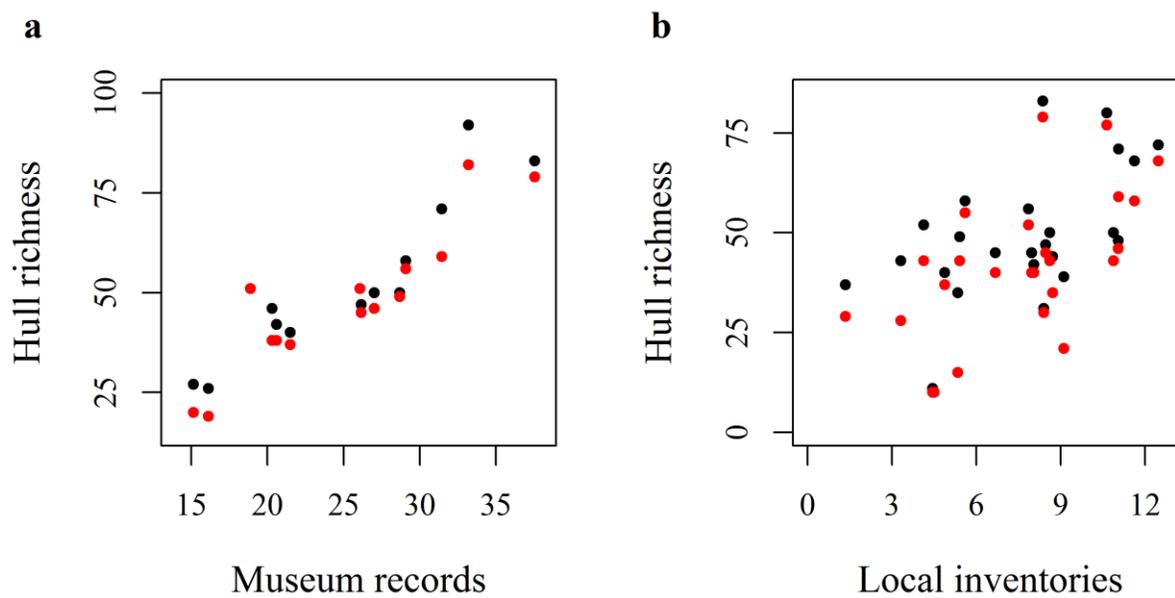
Figure 5. (a) Relationship between the richness of the tribe Bignonieae estimated by hull methods and rarefied richness generated from museum occurrence records (threshold of 71 records per grid cell); and (b) Richness estimated by hull methods and rarefied richness generated from local inventories (threshold of 30 records per local inventory). Red and black dots represent the richness of convex and alpha hull methods, respectively.

Species richness patterns generated by hull methods showed similar and strong environmental and spatial patterns, whereas the rarefied richness estimated from museum occurrence records and from local inventories showed a weaker relationship with these variables (Table 2 and 3). The correlations between AET and richness estimated by hull methods were significant and around r ≈ 0.68, whereas the correlations between AET and the rarefied richness were below r ≈ 0.45 and not significantly different from zero (Table 2). The quadratic trend surface (spatial variables) explained 73% and 67% of the richness patterns generated by convex and alpha hull methods, respectively (Table 3). The importance of each spatial variable of the trend surface was similar regardless of the hull method used. The explanatory power of the trend surface was

68% for rarefied richness from museum records and dropped to 20% for rarefied richness from local inventories; in the latter the pattern was not significant (Table 3).

Table 2. Correlation between actual evapotranspiration and different richness estimates for the species of the tribe Bignonieae.

	Actual evapotranspiration			
	r	F	v^*	p
Convex hull richness	0.69	8.04	8.64	0.02
Alpha hull richness	0.68	7.44	8.63	0.02
Rarefied richness – Museum occurrence records	0.44	1.45	6.17	0.27
Rarefied richness – Local inventories	0.30	1.33	13.77	0.27

Table 3. OLS regression models between different richness estimates for the species of the tribe Bignonieae and the quadratic trend surface.

	Convex hull	Alpha hull	Museum occurrence records	Local inventories
Intercept	< 0.01	< 0.01	< 0.01	< 0.01
Lat	-4.50	-3.95	-2.38	-3.06
Long	-6.14	-5.62	1.81	1.10
Lat²	-1.19	-1.12	-1.96	-1.13
Long²	-6.54	-5.89	1.54	0.82
Lat × Long	-5.02	-4.32	-0.91	-2.16
R² adj.	0.73	0.67	0.68	0.20
F	3471	2402	6.59	2.20
df	6286	6036	8	19
p	< 0.01	< 0.01	0.01	0.10

The main differences in richness estimates by both hull methods were concentrated in grid cells located on the edges of the continent (e.g., north and west of South America and east and west of Central America), as well as in the Amazon rainforest (Fig. 4c). The central portion of South America, which encompasses the Amazon rainforest, showed the greatest deficit in collection effort (Fig. 4d). On the other hand, Central America, the eastern and northern portions of South America showed the greatest collection effort for Bignonieae. The relationship between the difference in richness estimates and the number of occurrence records per grid cell showed that cells with the highest collection efforts also have lower incongruence in richness estimates (Fig. 6).
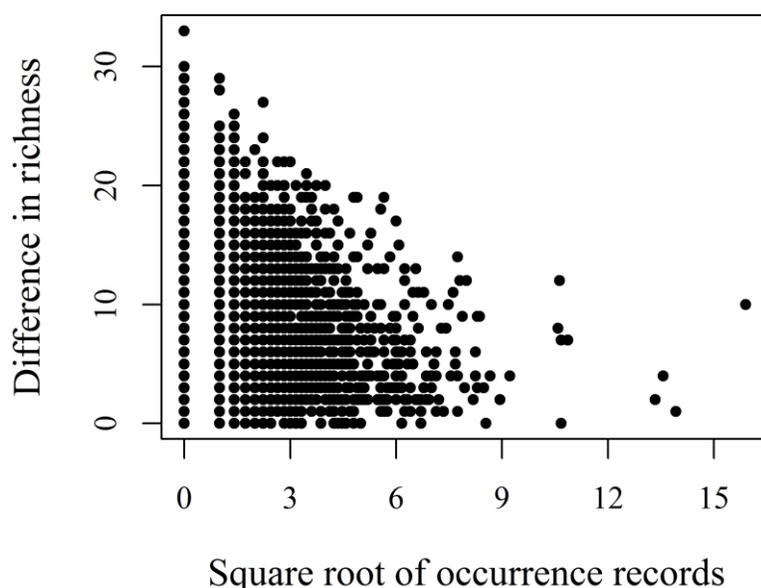
Figure 6. Relationship between the number of occurrence records per grid cell and the difference in richness of the tribe Bignonieae estimated by the convex hull and alpha hull methods.

Discussion

In this study we showed that both convex hull and alpha hull methods generated similar richness maps for the tribe Bignonieae. However, species range estimates differed between hull methods, as the convex hull estimated larger species ranges than the alpha hull. Furthermore, the Wallacean

shortfall affected species range estimates equally regardless of the hull method used, indicating that differences in range estimates are not related to the knowledge of species occurrences.

Hull method evaluation

Our estimates of the geographic species ranges of the species of the tribe Bignonieae based on the convex hull and alpha hull methods led to similar patterns of species richness distribution, despite differences in the individual species range estimates. Richness maps generated by stacking species ranges reconstructed on occurrence records exclusively are useful to understand the relationship between richness patterns and environmental variables (e.g., Hawkins et al. 2007a; Diniz-Filho et al. 2008; Braga et al. 2014), especially because this method does not take environmental variables into the species range estimates such as species distribution modelling.

The correlation between the richness generated by each hull method and the rarefied richness (generated from museum occurrence records and local inventories) were almost identical, independently of the hull method used. This pattern also applied to correlations between the richness estimated by each hull method and the AET and the quadratic trend surface. These results also support that, despite the differences in range estimates, the richness response pattern to other variables remains the same independently of the hull method considered.

Species richness estimates

The richness maps of tribe Bignonieae shown here represent the first compilation of richness pattern of the largest clade of Neotropical lianas. Lianas are often neglected in ecological studies, even though they comprise up to 35% of the species richness and 25% of the woody plant density in tropical forests (Schnitzer et al. 2012). The richness maps of Bignonieae showed a higher concentration of species in the Amazon and the Atlantic rainforests, and a lower number of species

distributed through drier areas and extratropical zones. The pattern of richness distribution of Bignonieae may be related to contemporary environmental variables, as indicated by the high correlation between richness and AET, as well as to other historical and evolutionary processes (Lohmann et al. 2013).

The species richness estimated by the hull methods and rarefaction led to similar richness gradients (i.e., species rich grid cells showed higher richness independently of the method used to estimate richness). However, richness estimates generated by hull methods were higher than richness estimated by rarefaction (Fig. 5). The rarefied richness estimated from museum occurrence records is expected to be lower because sampling effort per grid cell may not be sufficient to record all species whose ranges should overlap in a particular cell according to the hull methods (see Bombi et al. 2011). Moreover, hull methods can predict species occurrence in grid cells where a species may not occur, leading to overestimated richness (Graham & Hijmans 2006; Raedig & Kreft 2011). On the other hand, lower rarefied richness estimated from local inventories may be related to the species-area effect, given that the sample area of each local inventory comprised less than 0.001% of the area of one grid cell. Species richness increases with the size of the area sampled because the number of occurrence records also increases as does the likelihood of finding new species (Scheiner 2003).

Variations in responses of different richness estimates to AET and to the quadratic trend surface are likely to be related to scale (Whittaker et al. 2001; Field et al. 2009). The richness estimates derived from hull methods were carried out on a coarse geographic scale that covered the whole occurrence area of tribe Bignonieae. On the other hand, rarefied richness patterns were estimated at a finer scale. More specifically, we only used 14 of the overall grid cells to estimate richness from museum occurrence records and only 25 inventories, with 0.1 ha of sampled area each, to estimate richness from local inventories. At large geographical scales, richness is generally

strongly correlated with climatic variables (Whittaker et al. 2001; Field et al. 2009; Belmaker & Jetz 2011), as is the relationship between the richness generated by hull methods and AET. At finer scales, disturbance, stochastic processes and biotic interactions reduce the strength of the richness-climate relationship (Whittaker et al. 2001; Field et al. 2009), which can help explain the weak correlation between the rarefied richness and AET. Regarding the quadratic trend surface, the richness pattern for Bignonieae was well described by spatial variables when all grid cells of the occurrence area were considered. However, when a reduced number of grid cells were considered to estimate rarefied richness, the spatial variables could no longer recover the richness pattern.

Wallacean shortfall, richness maps and species ranges

Our results indicate that the largest differences in richness estimates generated by the hull methods tend to be concentrated on grid cells with low collection effort. The Amazon rainforest, which showed the greatest differences in richness estimates, also showed a large number of grid cells with low or no collection effort. Apart from the restricted sampling coverage, collection effort found in the Amazon rainforest also seems to be clumped near large cities or routes of access, corroborating earlier findings (Hopkins 2007; Schulman et al. 2007). The restricted sampling coverage and collection clumping led some Amazonian locations to be used more frequently in the hull delimitation of different species. With the same set of locations, alpha hull may have generated more jagged ranges than convex hull because the former allows hulls with concave and convex inner angles while the last method allows only convex angles (Burgman & Fox 2003); this pattern became even more evident after stacking the ranges produced by each method. Grid cells located on the edges of the continent also showed relevant differences in richness estimates, which is likely to be related to the hull drawing criteria of each method and the arrangement of occurrence records on the continent edges.

Apart from the large sampling gap in the central portion of South America, the collections of Bignonieae show a clumped distribution pattern and higher number of collections in the Atlantic rainforest, a pattern that is also common among other taxonomic groups (Oliveira et al. 2016). Differently from other studies (e.g., Ballesteros-Mejia et al. 2013; Oliveira et al. 2016), the bias in the tribe collections does not seem to have impacted the richness estimates of Bignonieae (Fig. S1.2). In fact, even though the Amazon rainforest showed the largest sampling shortfall, Bignonieae richness was higher in this region. Improved sampling within Amazon rainforest would likely lead to the discovery of new species, the collection of taxa in new areas of occurrence, the expansion of the ranges of various species and a reduction of uncertainty in richness estimates.

In addition to the unequal sampling effort across the area of occurrence of the whole tribe Bignonieae, the level of knowledge of species occurrences also varied among species. The number of occurrence records per species varied considerably (Table S1.1), as well as the date of description of each species (Fig. 3d). Species with higher knowledge about their occurrence area were expected to show lower variation in their range estimates generated by both hull methods (i.e., their occurrence records were thought to better describe their ranges). Contrary to our expectations, differences in range estimates were not related to the knowledge of species occurrences (here measured as the date of description of each species and the CV of pseudo-values of ranges generated by jack-knife). Although there is shortfall in distribution of sample effort across the geographic space of tribe Bignonieae and among species, this shortfall seems to have affected range estimates generated by both hull methods evenly. Indeed, differences in range estimates are likely to be only related to the hull drawing criteria of each hull method.

Conclusions

In this study, we showed that the convex hull and alpha hull methods could be used in equivalence

to generate species richness maps of the tribe Bignonieae. However, the convex hull may not be the best method to estimate species ranges because it overestimates species ranges, whereas the alpha hull is a more conservative approach that reduces the chance of range overestimation. These findings provide additional support for the recommendation by IUCN to use alpha hulls to delimit species ranges (IUCN 2014).

Another alternative is to use the alpha hull method and build multiple hulls for each species by varying the alpha value, so that the uncertainty in species range delimitation is estimated and can be considered in further analyses. One potential problem associated with hull methods is the assumption that species occur throughout their entire hulls, which is not always true as species may be absent in some areas due to unsuitable environmental condition or dispersal limitation (Graham & Hijmans 2006; Bombi et al. 2011; Raedig & Kreft 2011). This can lead to commission errors in range and richness estimates, which are especially important in finer geographic scales, but tend to be diluted at coarser scales (Raedig & Kreft 2011), such as the scale used in the present study. Apart from the problems associated with commission errors, hull methods are easily implemented and extremely interesting for broad-scale studies that aim to evaluate the correlation between environmental variables and species ranges or richness maps.

Further studies are necessary to investigate and propose sampling strategies that aim to solve or reduce sampling gaps across space and among different taxa. However, increasing sampling efforts demand financial resources, which is not always feasible. Another possibility would be to develop analytical frameworks that take the Wallacean shortfall into account. Specifically, in the case of tribe Bignonieae, it would be interesting to investigate the ecological and evolutionary processes that have generated current richness patterns.

Acknowledgements

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Capítulo 2

O papel de processos em nível de espécie sobre padrões de riqueza no maior clado de lianas neotropicais (Bignonieae, Bignoniaceae)

The role of species-level processes on richness patterns in the largest clade of Neotropical lianas (Bignonieae, Bignoniaceae)

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Abstract

Aims: Species richness can be defined as an aggregate variable when recovered by stacking the geographic range of different species. Therefore, processes constraining species range limits could be the main drivers of geographic patterns of species richness. We evaluate the influence of species-level processes in structuring richness patterns in the tribe Bignonieae.

Methods: We test the congruence of species ranges and richness responses to predictors using the extreme deconstruction principle. We also evaluate if such congruence varies according to species subsets with distinct ecological, geographical and evolutionary attributes using the richness deconstruction approach. We modeled and partitioned the variance of the richness pattern of the whole tribe, as well as the richness of each species subset with different attributes and species ranges using three sets of predictors: climatic, edaphic, and spatial components. We correlated components of variation partitioning of species ranges and richness to evaluate how they respond to predictors.

Results: We found that species ranges and the overall Bignonieae richness pattern respond similarly to the predictors (r = 0.96). The same pattern was observed when the correlations using the richness of species subsets defined by different attributes were replicated.

Conclusions: Although some species attributes (e.g., lack of herbivory protection, small to medium range sizes, late-diverging species) reduced the congruence between ranges and richness responses, species-level processes acting on species ranges appear to be the main drivers of Bignonieae richness patterns. The distribution of overall tribe richness is associated with the current distribution of forest and savanna habitats in the Neotropics.

Keywords: diversity patterns, extreme deconstruction principle, macroecological modeling, species richness deconstruction, species traits, stacked species distribution modeling.

Introduction

Understanding geographical patterns of species richness and their underlying processes is one of the major goals of biogeography and macroecology (Field et al. 2009; Fine 2015). Two main approaches have been used to model species richness patterns (Guisan & Rahbek 2011): macroecological modeling and stacked species distribution modeling (i.e., top-down and bottom-up approaches according to Diniz-Filho et al. 2012; Boucher-Lalonde et al. 2014), which focus on processes acting at the assemblage and species levels, respectively. Both approaches use environmental factors (typically climate variables) to predict richness patterns, even though the underlying processes behind the rationale of these two families of models are different (Guisan & Rahbek 2011; Boucher-Lalonde et al. 2014). The macroecological modeling assumes that overall richness is directly established by environmental variables, limiting the number of individuals and species in a given area and time (Guisan & Rahbek 2011). In contrast, stacked species distribution modeling uses environmental variables to model individual species ranges, reconstructing the overall pattern of species richness from their collective overlap (Terribile et al. 2009; Guisan & Rahbek 2011).

The extreme deconstruction principle, originally proposed by Terribile et al. (2009) following the rationale of Marquet et al. (2004), is a useful approach to assess whether species-level processes are structuring the richness pattern of particular taxa. Additional conceptually and methodologically related models have been subsequently proposed, such as the SESAM (Spatially Explicit Species Assemblage Modeling; Guisan & Rahbek 2011). In the extreme deconstruction principle, ecologically relevant environmental variables are correlated to individual species ranges and to the overall richness of the taxon to provide the predictive power of these variables over species ranges and richness patterns (Terribile et al. 2009). A high congruence in the predictive power of these variables could indicate that species-level

processes are acting to determine the overall richness pattern, while a low congruence points to the effect of other processes not considered in the analysis. For example, environmental variables can explain well richness patterns but represent poor predictors of species ranges and their limits, suggesting that macroecological processes may be acting directly over species richness, but not on the species' individual responses.

Processes structuring species ranges and richness are intrinsically correlated, explaining why environmental variables limiting individual species ranges tend to be the main predictors of the taxon richness (see Terribile et al. 2009; Guisan & Rahbek 2011). However, the predictive power of environmental variables over these two levels of organization may vary according to some species attributes (e.g., Terribile et al. 2009; Diniz-Filho et al. 2012). The heterogeneity among species may reflect the distinct ecological and evolutionary histories of taxa (Marquet et al. 2004). Furthermore, distinct histories may have impacted the properties of species ranges (e.g., range size and position), which in turn are the main determinants of species richness patterns (Marquet et al. 2004; Arita et al. 2008). The richness deconstruction approach was proposed by Marquet et al. (2004) to investigate species richness patterns while taking the heterogeneity among species into account. Under this approach, species are grouped into subsets defined based on their ecological and/or evolutionary attributes. The richness pattern derived from each of these subsets is then correlated to environmental variables (Marquet et al. 2004). Ultimately, this approach allows us to assess the different responses of each subset of species to environmental factors, as well as to establish how they contribute to the overall richness pattern (Marquet et al. 2004; see Hawkins et al. 2005; Hawkins, Diniz-Filho et al. 2007; Terribile et al. 2009). Indeed, studies deconstructing richness found that both richness patterns and joint species responses to environmental variables vary according to

species attributes in both animals (Jetz & Rahbek 2002; Diniz-Filho et al. 2012; Pinto-Ledezma et al. 2017), and plants (Kreft et al. 2006; Lennon et al. 2011).

Lianas are plants that use trees and shrubs as physical support (van der Heijden & Phillips 2009). They play a major role in structuring tropical ecosystems, comprising up to 35% of species and 25% of the overall density of woody plants in tropical forests (Schnitzer et al. 2012). Despite their importance, the distribution of liana species richness still needs to be further investigated as studies conducted so far mainly focused at local scales (e.g., Dewalt et al. 2000; Macía et al. 2007; Schnitzer et al. 2012; but see van der Heijden & Phillips 2009; Couvreur et al. 2015). In the Neotropics, the tribe Bignonieae (Bignoniaceae) represents the largest clade of lianas, including almost 400 species (Lohmann & Taylor 2014). Despite the high diversity and ecological importance of this tribe in Neotropical ecosystems (Lohmann 2006), a single study on its species richness patterns has been conducted to date (Meyer et al. 2018).

Bignonieae represents an excellent model group for studies of this nature because it includes species whose taxonomy, phylogenetic history, and morphology have been well studied (e.g., Lohmann 2006; Lohmann & Taylor 2014). Besides, this tribe encompasses species with varied range sizes that are distributed throughout a variety of habitats, ranging from wet forests to dry savannas (Lohmann et al. 2013). Most Bignonieae species have wind-dispersed seeds (Gentry 1974; Lohmann 2006), suggesting that they have high dispersal potential, thus increasing opportunities to reach different areas with suitable environmental conditions (Gentry 1974). Thereby, environmental variables should predict well both species ranges and richness patterns within this tribe. Investigating how richness–environment and species range–environment relationships vary according to species attributes would improve our understanding of the ecological and evolutionary attributes that may limit species

distributions and coexistence. In addition, deconstructing richness patterns would also allow us to identify different subsets of species adapted to distinct habitats (e.g., forests or savannas), complementing our current understanding of Bignonieae species richness patterns.

In this study, we evaluate whether species-level processes operating on species ranges are structuring richness patterns within Bignonieae. We also evaluate if richness–environment and species range–environment relationships vary according to species attributes. For that, we first defined the set of climatic, edaphic, and spatial variables that predict the overall tribe richness. We then evaluate the congruence of the predictive power of these variables between species ranges and the overall richness by using the extreme deconstruction principle of Terribile et al. (2009). To evaluate if incongruences in predictive power are related to species attributes, we followed Marquet et al. (2004) and deconstructed tribe richness using several ecological, geographical, and evolutionary attributes (see Table S2.1).

Methods

Species occurrence records

We mapped the distribution of Bignonieae species richness and built individual species ranges using data from a georeferenced database of species occurrence records of the tribe compiled by LG Lohmann (unpublished data) from her own samples and from herbarium records, especially those deposited at the Missouri Botanical Garden herbarium (www.tropicos.org), the largest Bignoniaceae collection in the world. To verify the database, we plotted occurrence records of each species and checked the distribution records using available taxonomic reviews and expert knowledge (LG Lohmann reviewed all genera, with *Adenocalymma* Mart. ex Meisn. being reviewed simultaneously by LG Lohmann and LHM Fonseca). We excluded from the database all unusual occurrence records in relation to known species distributions. For species with less than

10 occurrence records, we searched for additional records in the monographs available for *Adenocalymma* (Fonseca 2017), *Amphilophium* Kunth (Pool 2007a, 2007b, 2008, 2009), *Bignonia* L. (Zuntini 2015), *Dolichandra* Cham. (Fonseca et al. 2017), *Lundia* DC. (Kaehler 2011), *Mansoa* DC. (Silva-Castro 2010), *Pleonotoma* Miers (Gomes 2006), and *Tynanthus* Miers (Medeiros & Lohmann 2015). All new records found for species with less than 10 occurrence records were included in our database. For species with 10 records or more, a preliminary assessment showed that the record distribution represented well the documented species range and thereby no more records were searched. Species taxonomic delimitation followed Lohmann & Taylor (2014), except *Adenocalymma* for which a newer synopsis is available (Fonseca 2017), and some taxa for which taxonomic updates were published recently (e.g., Zuntini et al. 2015a, 2015b; Fonseca et al. 2016). Our final database has 28,763 occurrence records and includes 386 species belonging to all 20 recognized genera of Bignonieae. All species occur in the Neotropics except *Bignonia capreolata* L., which is restricted to southern United States (Lohmann & Taylor 2014).

For species with three occurrence records or more (i.e., 356 out of the 386 species), we built species ranges according to the alpha hull method (see Burgman & Fox 2003) using the 'ashape' function of the 'alphahull' package (Pateiro-López & Rodríguez-Casal 2016; for more details, see Meyer et al. 2018) implemented in R (R Core Team 2017). We mapped the richness distribution of Bignonieae by overlapping: (i) the resulting 356 species ranges on a grid of cells of 0.5° (~ 55 km) width that covered the entire occurrence area of the tribe, and (ii) all occurrence records from the remaining 30 species with less than three records. We projected all geographic data using the Behrmann equal-area projection.

Species ecological, geographical and evolutionary attributes

To perform a Bignonieae richness deconstruction following Marquet et al. (2004), we gathered five ecological, one geographical, and two evolutionary species attributes (see Table S2.1-4). We chose attributes that have been used in other deconstruction analyses (e.g., range size, taxon distance from the phylogeny root, and higher-level clades recognized in taxonomic classifications), as well as others that represent relevant ecological characteristics of the tribe (e.g., life-form, pollination strategy, and seed dispersal mechanism).

For the ecological attributes, we used species descriptions available in taxonomic reviews and expert knowledge (LG Lohmann), as well as examined herbarium specimens to classify all species of the tribe according to five attributes and their respective character-states described by Lohmann (2003): (i) plant life-form: liana or shrub, (ii) tendrils: present or absent, (iii) herbivory protection: absent, present through extrafloral nectaries located in the interpetiolar region of stems, or present through glands located in the prophylls of the axillary buds, (iv) pollination syndrome: bees, butterflies, hawk moths, or hummingbirds, and (v) seed dispersal: water-dispersed seeds, wind-dispersed seeds with linear wings, or wind-dispersed seeds with ellipsoid wings (see Table S2.2-3). For the geographical attribute, we used species range size categories. For that, we first counted the number of grid cells in which each species occurs, and then defined the categories as the quartiles of the range size frequency distribution, following the approach used by Terribile et al. (2009) (see Table S2.3).

For the evolutionary attributes, we used the most recent phylogeny available for the tribe Bignonieae as a whole (Lohmann et al. 2013). This phylogeny was built based on the analysis of a combined dataset composed of sequences of the chloroplast ndhF and the nuclear PepC for 104 species, representing one-fourth of all currently recognized species (Lohmann et al. 2013; Lohmann & Taylor 2014). To gather the first evolutionary attribute, we considered the distance

between each taxon and the phylogeny root and classified individual species as early-diverging (1-6 nodes of distance) and late-diverging (9-10 nodes), following the protocol proposed by Hawkins et al. (2005, 2007). To define the root distance, we counted the number of nodes between each genus of the tribe and the root of the phylogenetic tree, and assigned the number of nodes to all species belonging to each genus. Under the assumption of random speciation and extinction, this approach represents an estimate of relative diversification rate (Freckleton et al. 2008). For the second evolutionary attribute, we used the genus-level classification proposed by Lohmann & Taylor (2014) and considered the five genera of the tribe that encompass 30 species or more as categories of this attribute (see Table S2.4).

Environmental variables

We considered two sets of environmental variables in our analyses: climatic and edaphic variables (see Table S2.5). As climatic variables, we used 19 bioclimatic variables from the ecoClimate database (Lima-Ribeiro et al. 2015), which were generated according to the Community Climate System Model (CCSM4), in a modern baseline (1950-1999) and at 0.5° of resolution. Most of our species occurrence records were collected between 1950 and 1999 (Meyer et al. 2018), therefore we chose bioclimatic variables estimated in a modern baseline. Variables derived from altitude are associated with climatic variation (McCain & Grytnes 2010). Thereby, we included mean altitude and altitude range within the set of climatic variables. We used the SRTM digital elevation map (Jarvis et al. 2008) at 1 km of resolution to calculate the mean altitude and altitude range (i.e., the difference between maximum and minimum elevation) within each grid cell. We ended up with 21 climatic variables.

We used the Harmonized World Soil Database (HWSD; FAO 2012) to obtain edaphic variables. The HWSD provides a map of soil codes that covers all land areas in the world at 1 km

of resolution (FAO 2012). Each soil code is associated with a soil attribute table (FAO 2012). For each grid cell, we identified the soil code that covered the greatest proportion of the cell area. Soil codes that represent water bodies, urban areas, and salt flats were disregarded from the analyses. We attributed 14 physicochemical variables of the top-soil layer to each grid cell according to the main soil code of the cell (see Table S2.5). In addition, we considered the number of different soil codes per grid cell as an edaphic variable to represent the heterogeneity in soil data. Overall, we compiled information on 15 edaphic variables.

Modeling species richness distribution of Bignonieae

To avoid collinearity in predictor variables, we selected a subset of the environmental variables to build up the regression model for the overall tribe richness (see Quinn & Keough 2002; Eisenlohr 2014). We performed two principal component analyses (PCA), one for climatic and another for edaphic variables, and chose predictors within each one of these groups considering the correlation with both their first PCA axes and Bignonieae species richness, avoiding highly correlated variables while prioritizing variables known to be ecologically relevant to explain richness patterns (see Eisenlohr 2014). We ended up with five climatic and seven edaphic variables (see Table S2.5), which showed no collinearity among them (variance inflation factor, VIF < 3.5 for all variables; see Quinn & Keough 2002).

The residuals of the ordinary least squares (OLS) regression model for the overall tribe richness and the selected environmental variables were spatially autocorrelated, according to Moran's I correlogram (Legendre 1993; Diniz-Filho et al. 2003). To deal with such spatial autocorrelation we computed Moran's eigenvector maps (MEMs) and included them in the regression model as additional predictor variables (Diniz-Filho & Bini 2005; Dormann et al. 2007; Diniz-Filho et al. 2008). We used the 'dbmem' function of the 'adespatial' package (Dray et al.

2017) implemented in R (R Core Team 2017) to compute MEMs. The MEMs were generated using a pairwise Euclidian distance matrix of centroid coordinates of grid cells (Borcard & Legendre 2002; Dray et al. 2006, 2017). This matrix was truncated by the largest distance in a minimum spanning tree linking all grid cells multiplied by four (Dray et al. 2006, 2017). From all computed MEMs, we calculated their associated Moran's I values and tested their significance using the 'moran.randtest' function of the 'adespatial' R package (Dray et al. 2017) implemented in R (R Core Team 2017), selecting only those that were positive and significant. We used residuals of the OLS model of tribe richness and environmental variables to guide a forward selection of MEMs (Blanchet et al. 2008; but see Bauman et al. 2018). We ended up with 23 selected MEMs, which were used to avid spatial autocorrelation in model residuals following Diniz-Filho et al. (2008).

Variation partitioning analysis

We used variation partitioning analysis to carry out the extreme deconstruction and richness deconstruction (Fig. 1). This analysis allowed us to assess and compare how the variance in species ranges and richness is shared among different components (see Legendre & Legendre 2012). First, we partitioned the variance in overall Bignonieae richness using selected predictors variables grouped in three components: (i) climate represented by five climatic variables (Table S2.5), (ii) edaphic including seven soil variables, and (iii) spatial component represented by 23 Moran's eigenvector map. Subsequently, we performed variation partitioning for individual species ranges and for the richness pattern of each species subset determined by ecological, geographical, and evolutionary attributes. In all variation partitioning analyses, we used the same predictor variables of the overall tribe richness pattern grouped in three components. Our main interest was to look at the distribution of variance among components of variation partitioning for species ranges and richness patterns, rather than to interpret the ecological meaning of each component per se. All

variation partitioning analyses were performed using the 'varpart' function of the 'vegan' package (Oksanen et al. 2007) implemented in R (R Core Team 2017).

Extreme deconstruction – To perform the extreme deconstruction, we first identified a balanced number of grid cells with species presence and absence. For species with small range size (i.e., range covering less than half grid cells), we used all grid cells occupied by the species as presences, while we randomly selected the same number of absences from the grid cells unoccupied by the species range. For species with large ranges (i.e., ranges covering more than half of all grid cells), we considered all unoccupied grid cells as absences and randomly selected the same number of cells covered by species ranges to represent presences. We then fitted seven generalized linear models (GLM) for each species range, using a binomial family with logit link. The response variable in GLMs was always the species presence and absence, while the predictor variables were each one of the possible combinations among the three sets of variables (i.e., climate, soil, and spatial variables). We estimated the adjusted amount of deviance accounted for each GLM (adjusted D-squared) using the 'Dsquared' function of the 'modEvA' package (Barbosa et al. 2016) implemented in R (R Core Team 2017), which is equivalent to the adjusted R-squared of OLS models (Guisan & Zimmermann 2000). We used the adjusted D-squared of GLMs to partition the variance in species ranges according to the climate, soil, and spatial components (see Araújo et al. 2014; Barbosa et al. 2016). We performed 1000 partitions for each species range, each one considering a new random selection of species absences or presences. To assess the final partition for each species range, we calculated a median of 1000 variance values for each component of the partitions. We only performed variation partitioning for species that occur in more than 50 grid cells (276 out of 386 species) to avoid uncertainties in GLM parameter estimates due to small sample size.
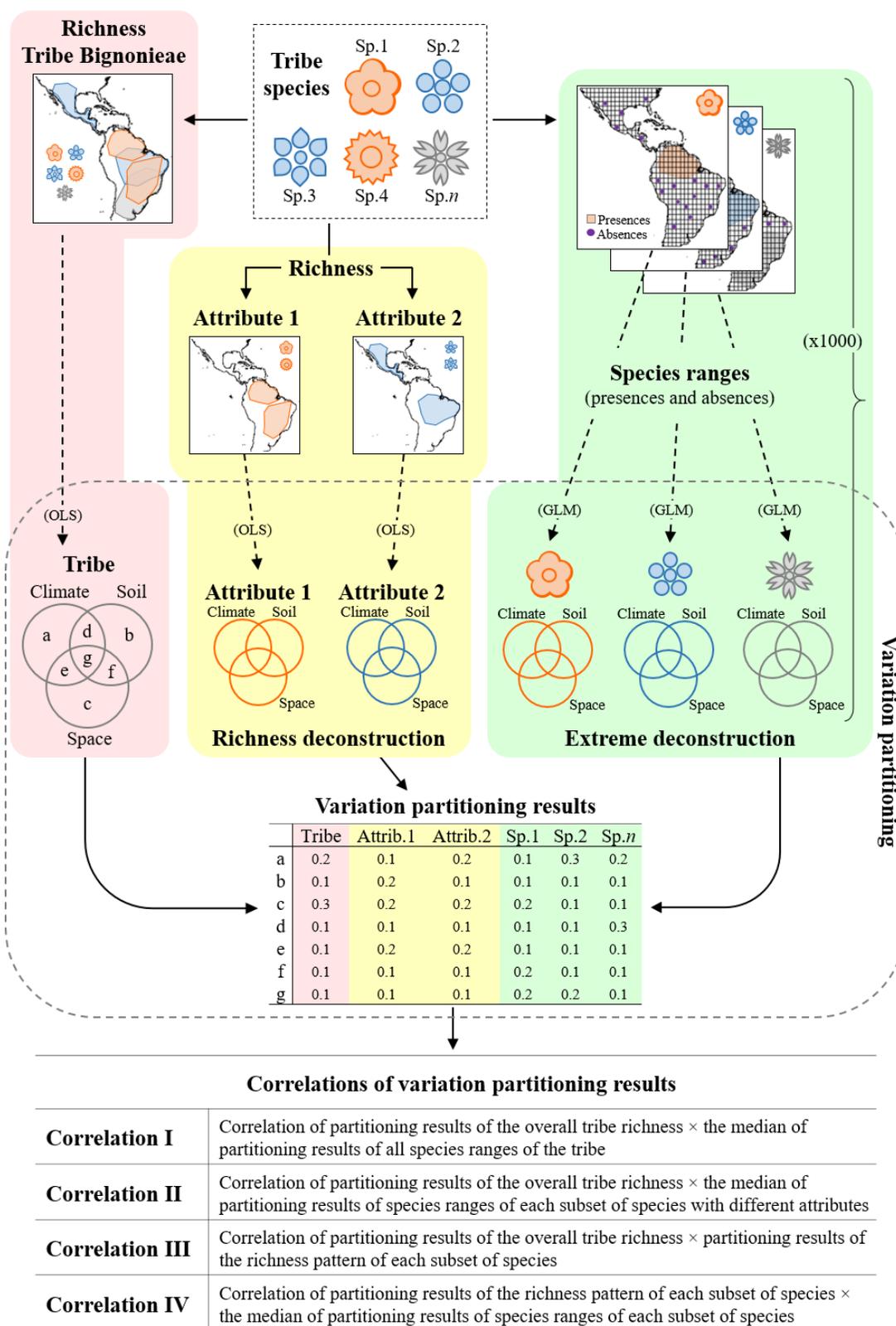
Figure 1. Representation of the extreme deconstruction and richness deconstruction performed using variation partitioning analyses, as well as subsequent correlations among variation partitioning results.

Richness deconstruction – To perform the richness deconstruction, we identified which species belong to each subset of species according to the ecological, geographical, and evolutionary attributes (see Table S2.1). We stacked species ranges of each subset to obtain their respective richness pattern. We then calculated a variation partitioning for each richness pattern using the same predictor variables used to estimate the overall tribe richness.

Correlations among variation partitioning components

We calculated four different Pearson correlations to evaluate similarity and congruence of deconstruction patterns among subsets of species (see Fig. 1):

– *Correlation I:* measures the congruence of predictor variables in predicting both species ranges and the overall tribe richness. For this correlation, we first calculated a median value for each component of variation partitioning considering all partitions of species ranges of the tribe. We then correlated the variation partitioning of overall tribe richness with the median of the partitions of all species ranges.

– *Correlation II:* evaluates whether the congruence of the predictors of species ranges and richness varies according to species attributes. For this correlation, we first calculated the median values of the partitions of all species ranges pertaining to each subset of species determined by ecological, geographical, and evolutionary attributes. We then correlated the variation partitioning of the overall tribe richness with the median partition of species ranges of each subset.

– *Correlation III:* measures the congruence between richness patterns of subsets of species with different attributes and the overall tribe richness pattern. We correlated the variation

partitioning of the overall tribe richness with the partition of the richness pattern of each subset of species.

- – *Correlation IV:* also evaluates whether the congruence of predictors in predicting species ranges and richness varies according to species attributes. We correlated the partition of richness pattern of each subset with their respective median partition of species ranges.

Frequency distribution of correlations

Correlations among variation partitioning components are strongly affected by the number of species in each partition (Fig. S2.1). To avoid making an ecological interpretation of correlation coefficients that are statistical artifacts, we determined the expected frequency distribution of correlations using a Monte Carlo approach. We first generated random values of variation partitioning for both species ranges and richness pattern for each species subset. From all original partitions of species ranges of the tribe calculated before, we randomly resampled, with replacement, partitions in the same number of species belonging to each species subset, using a bootstrap procedure (see Quinn & Keough 2002). We then calculated median values of components of all resampled partitions per species subset, which represented the random partitions of species ranges for each subset. For random richness patterns, we resampled with replacement species from the tribe using the same number of species found in each subset. We built random richness patterns for each subset by stacking ranges of resampled species and calculating the variation partitioning for these random richness patterns. We conducted 5000 bootstrap replicates for the species ranges and richness patterns of each species subset.

To generate the frequency distribution of Correlation II, we correlated the variation partitioning of the overall tribe richness with the random partitions of species ranges for each species subset. To obtain the frequency distribution of Correlation III, we correlated the variation

partitioning of the overall tribe richness with random partitions of richness for each subset. Finally, to generate the frequency distribution of Correlation IV, we correlated random partitions of species richness patterns for each subset with their respective random species ranges. For each correlation frequency distribution, we built a confidence interval by keeping 95% of the greatest correlation values (see Quinn & Keough 2002).

Results

Many species of the tribe Bignonieae occur in rainforests, such as the Amazon and the Atlantic rainforests (Fig. 2). Savanna habitats from Central South America, such as the Cerrado and Caatinga, hold fewer species. Species richness also reduces towards subtropical regions. A large amount of the variance of overall tribe richness (88%) can be explained by climate, soil, and spatial variables. However, the portion of richness variance explained independently by climate and soil variables was low, only 5% and 1%, respectively (Fig. 3; Table S2.6). Larger proportions of richness variance were explained by spatial variables independently (27%), and by the overlap between environmental variables and space (from 10% to 24%).
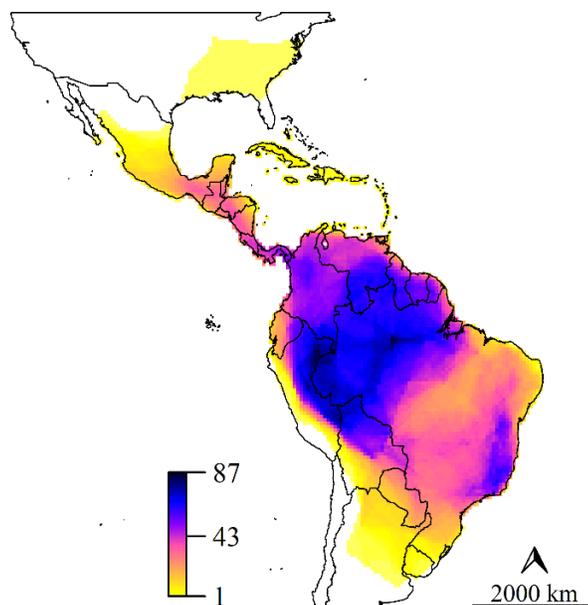
Figure 2. Overall species richness pattern of the tribe Bignonieae (Bignoniaceae). The map was built by stacking 386 species ranges on a grid at 0.5° (~ 55 km) of resolution.
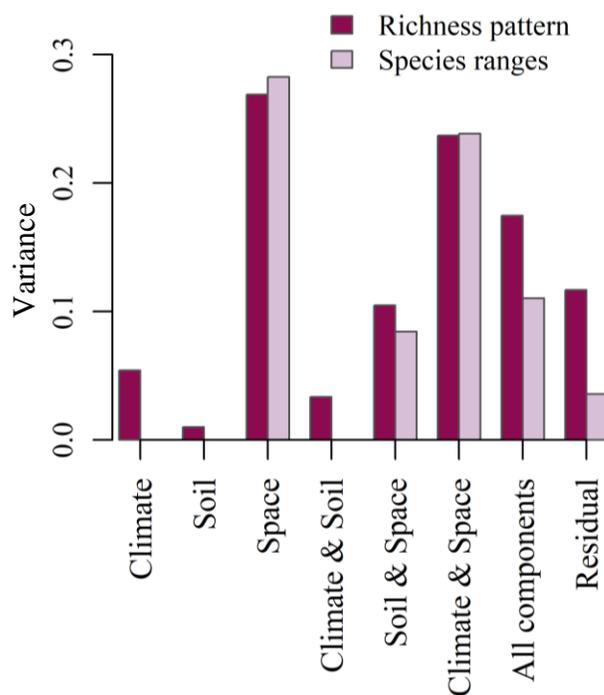
Figure 3. Median variance of all species ranges of tribe Bignonieae and variance of the overall richness pattern of the tribe accounted by components of variation partitioning considering the set of climate, soil, and spatial variables.

The variance in overall Bignonieae richness explained by each component of the variation partitioning was similar to the median values of components of partition of species ranges (Fig. 3). A high correlation of variation partitioning was observed for the overall tribe richness and species ranges (r = 0.96; see Correlation I in Table S2.6). The correlation of partitions remained high even when species subsets determined by different ecological, geographical, and evolutionary attributes were considered (see Correlation II and III in Fig. 4; Table S2.6). These results suggest that climate, soil, and spatial variables are contributing similarly to structuring species ranges and the overall richness pattern of the tribe Bignonieae.
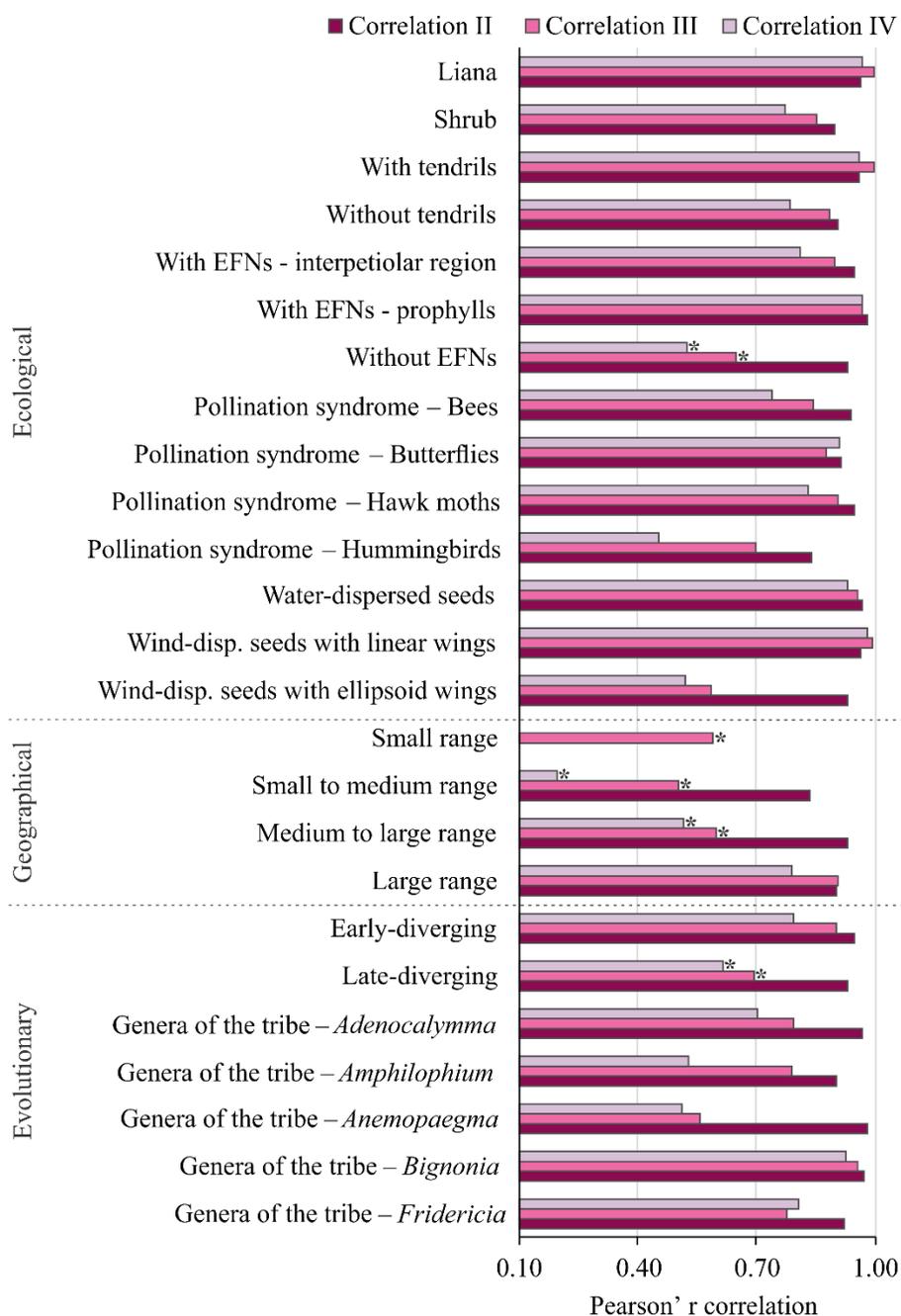
Figure 4. Pearson's r correlation values for subsets of species with different attributes of the tribe Bignonieae (Bignoniaceae). Correlation II is the correlation of variation partitioning of the overall tribe richness and species ranges of each subset of species with different attributes; Correlation III is the correlation of variation partitioning of the overall tribe richness and the richness pattern of each subset of species; and Correlation IV is the correlation of variation partitioning of richness pattern and species ranges of each subset of species. Asterisks indicate r correlation values not expected (i.e., significant) if species would be randomly selected for variation partitioning.

Differences between richness patterns of subsets of species with different attributes and the overall tribe richness were only detected for species with the following attributes: (i) lack of herbivory protection, (ii) small ranges, (iii) small to medium ranges, (iv) medium to large ranges, and (v) late-diverging species (Fig. 5, 6 and 7). For species with these attributes, correlations of variation partitioning results were low and significant both between overall tribe richness and the richness of subsets of species (from 0.51 to 0.70; Correlation III) and between the richness pattern of subsets of species and their species ranges (from 0.20 to 0.62; Correlation IV) (see Fig. 4; Table S2.6).
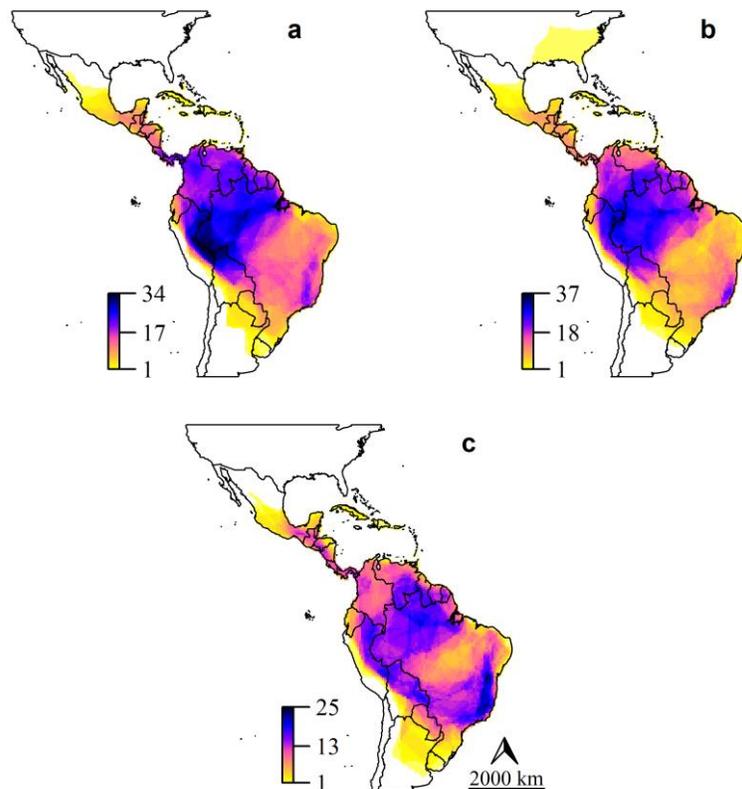
Figure 5. Richness deconstruction of tribe Bignonieae according to the presence of herbivory protection represented by the presence of extrafloral nectaries. (a) Richness pattern of species with extrafloral nectaries in the interpetiolar region; (b) with extrafloral nectaries in prophylls; and (c) without extrafloral nectaries.
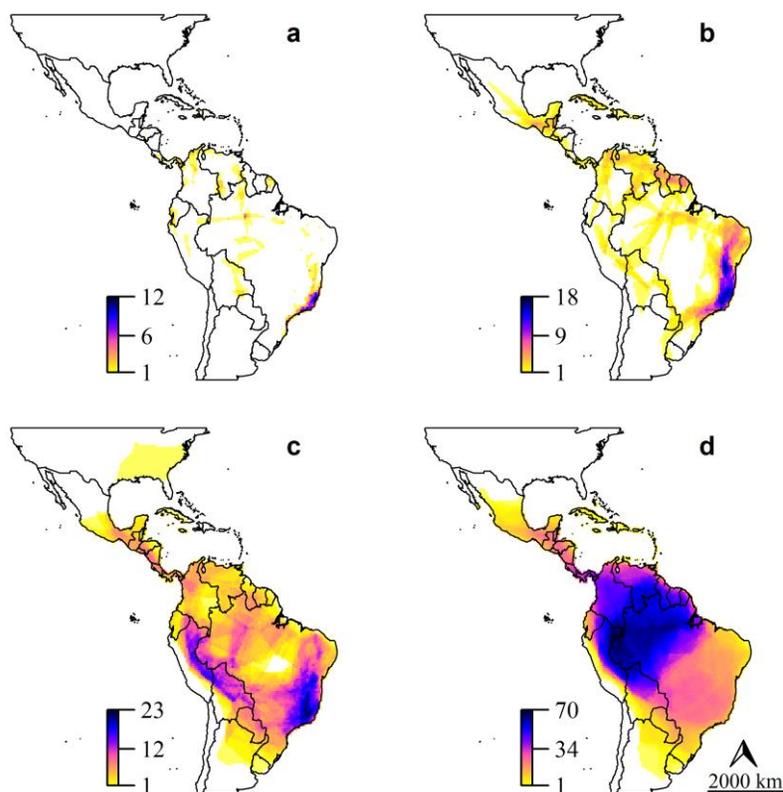
Figure 6. Richness deconstruction of tribe Bignonieae according to species range size. (a) Richness pattern of species with small ranges; (b) small to medium ranges; (c) medium to large ranges; and (d) large ranges.
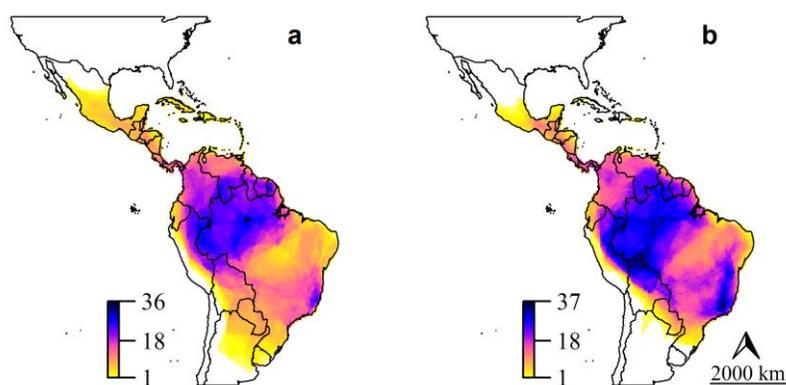
Figure 7. Richness deconstruction of tribe Bignonieae according to the root distance of each species within the Bignonieae phylogenetic tree. (a) Richness pattern of early-diverging species; and (b) late-diverging species.

Richness patterns of species with smaller ranges differ substantially from the overall tribe richness pattern. Most species with small and intermediate ranges concentrate their distributions in the Atlantic rainforest, while species with large ranges contribute strongly to the high richness in the Amazon region (Fig. 6 and S2.2). Although no clear visual difference was observed between the overall tribe richness and the richness of species lacking herbivory protection or the richness of late-diverging species, species with these attributes contribute substantially to the richness of savanna habitats from Central South America (Fig. 5 and 7). Despite not showing significant differences from the overall tribe richness, species without tendrils, or with wind-dispersed seeds with ellipsoid wings, or shrubs show higher richness in the savanna habitats in Central South America (Fig. S2.2-5). In contrast, species with water-dispersed seeds concentrated their distribution in wet forests, such as the Amazon and the Atlantic rainforests (Fig. S2.5).

Discussion

The extreme deconstruction and richness deconstruction represent complementary approaches that allow us to investigate whether the processes shaping species ranges (species-level processes) are also driving species richness patterns. Using the extreme deconstruction approach, we found that species ranges and overall species richness of Bignonieae respond in a similar way to environmental and spatial variables. These findings suggest that species-level processes are structuring the richness patterns of the tribe at macroecological scales. Despite that, the richness deconstruction approach indicates that some species attributes reduce the congruence between the responses of ranges and richness to predictor variables. Overall, our results show that the distribution of species with distinct attributes tends to reflect an association between attributes and environmental conditions. In addition, the overall richness pattern of the tribe is associated with

the distribution of forest and savanna habitats, as well as with the biogeographical areas *sensu* Gentry (1979) throughout the Neotropics.

Deconstruction of Bignonieae richness pattern

Responses of species ranges and overall tribe richness to environmental and spatial variables are strongly correlated in Bignonieae. The same pattern was observed when correlations were replicated using subsets of species with different ecological, geographical, and evolutionary attributes. This congruence among species ranges and richness responses to predictor variables supports the hypothesis that species-level processes are operating to establish Bignonieae richness patterns. Even though different processes are known to act in a complex way to determine individual species ranges (Gaston 2003; Sexton et al. 2009), abiotic conditions and biogeographical factors represent the main drivers of species distribution at large scales (Soberón & Nakamura 2009; Hortal et al. 2010). Biotic conditions and metapopulation dynamics gain strength only when abundance (i.e., a within-range perspective) is considered (Gaston 2003; Soberón & Nakamura 2009; Hortal et al. 2010). In general, species-level information (e.g., presence or absence of a particular species) is the main requirement to recover richness patterns. Overall, the richness distribution through the geographic space is not weighted considering species abundances. Indeed, species richness are strongly correlated with environmental variables, especially climatic ones (Field et al. 2009; Fine 2015). As such, richness patterns are expected to be strongly correlated, as well as to be driven by the same processes that act on the individual species ranges (see Terribile et al. 2009), as observed for the tribe Bignonieae.

Species richness is a complex aggregated variable, where all the individual species are considered as equivalent, even though they actually represent distinct units (Marquet et al. 2004). Thus, overall richness patterns may hide particularities that are associated to the diversity of

ecological and evolutionary histories of the individual species (Marquet et al. 2004; e.g., Terribile et al. 2009; Pinto-Ledezma et al. 2017). Despite the high congruence among species ranges and richness responses in Bignonieae, some subsets of species with specific attributes (e.g., lack of herbivory protection, small to medium range size, late-diverging species) showed richness patterns that differed from the overall tribe richness. For these subsets of species, the richness distribution deviated from the classic gradient of decreasing richness from forest to savanna habitats observed for the whole tribe. Strikingly, most of the richness variance of these subsets was accounted in the pure spatial component of variation partitioning. In contrast, species ranges of these subsets had similar variation partitioning results to those found for the overall tribe richness, with variance being concentered in environmental spatially structured and pure spatial components. These findings suggest that while the shape and size of species ranges may be established by environmental and biogeographical factors (Soberón & Nakamura 2009; Hortal et al. 2010), the position of these ranges may be constrained to specific regions of the geographic space according to species attributes (e.g., species with small ranges are mostly restricted to the Atlantic rainforest), which in turn generates distinct richness patterns for these subsets of species.

In macroecological scales, such as overall species ranges or species richness, biotic interactions are thought to be of lesser importance (Soberón & Nakamura 2009; Hortal et al. 2010). However, the importance of biotic interactions in setting species ranges is often overlooked (e.g., Meier et al. 2010; Araújo et al. 2014). In Bignonieae, the distinct richness pattern observed for species lacking herbivory protection suggests that biotic interactions should be taken into account to understand the geographic distributions of both species ranges and richness. Here, the lack of extrafloral nectaries (EFNs) was considered as a proxy for a lack of herbivory protection. EFNs are structures that promote ant-plant interactions where ants consume the nectar produced by the EFNs while protecting the plant from herbivores (Nogueira et al. 2012; Nogueira et al. 2015).

Nogueira et al. (2012) found that the abundance of EFNs in Bignonieae species is related to environmental conditions, with savanna species having fewer EFNs than forest species, which may be associated with the fact that EFNs increase water loss in dry habitats. The putative higher cost of EFNs for species from savannas may explain the accumulation of species lacking herbivory protection in savanna habitats. Nonetheless, the cost-benefit balance of EFNs is not only determined by environmental conditions but may also vary within individual species, with abundance of EFNs varying substantially across the species geographic range, as observed for *Anemopaegma album* Mart. ex DC. (Nogueira et al. 2015). In contrast, the strength of the influence of plant-pollinator interactions over richness patterns seems to be smaller at macroecological scales (Fig. S2.6), although acting as an 'environmental filter' at local scales, influencing which Bignonieae species co-occur in an assemblage (Alcantara et al. 2014).

Overview of Bignonieae richness patterns

The distributions of both individual species ranges and overall Bignonieae richness are strongly associated with the distribution of forest and savanna habitats throughout the Neotropics, with most species being found in forest habitats. Indeed, most Bignonieae species have ecological attributes associated with the occurrence in forest habitats (e.g., species that are tendrillate lianas, with herbivory protection, or with wind-dispersed seeds with linear wings; Lohmann 2003). This richness gradient between forest and savanna habitats is not surprising for Bignonieae considering that most species are lianas and require other trees to climb (Schnitzer & Bongers 2002). Neotropical forests hold a large tree diversity and a broad range of support for lianas (Fine & Ree 2006). Although the importance of tree species for Bignonieae richness has never been evaluated, Couvreur et al. (2015) found a positive correlation between tree canopy height and richness of climbing palms. The preference of forest habitats by Bignonieae species may also represent

phylogenetic inertia given that the tribe originated in forested habitats in Eastern South America during the Eocene (~50 Mya; Lohmann et al. 2013). However, species with forest-related attributes are not restricted to Neotropical rainforests. Some of the species bearing those attributes also occur in savanna habitats (e.g., the diagonal of open formations in Central South America). This may be due to the fact that savanna habitats are composed by a mosaic that include wet habitats with woodier vegetation (e.g., areas nearby to river channels) within a savanna matrix (Oliveira-Filho & Ratter 2005).

Although most Bignonieae species are distributed in forest habitats and/or present attributes associated with forest occurrence, this tribe occupies a broad range of habitats (Lohmann et al. 2013; Lohmann & Taylor 2014). The ancestors of almost all genera occurred in forest habitats, with multiple independent colonization to savanna habitats occurring subsequently (Lohmann et al. 2013). These transitions are also observed within broadly distributed species, whose distribution extends from the Atlantic rainforest to the Amazon region, including savanna habitats in Central South America (Lohmann 2003; Lohmann et al. 2013). The most recent common ancestor (i.e., MRCA) of a single clade (i.e., *Fridericia*-*Xylophragma* clade), was restricted to savanna habitats at ~30 Mya (Lohmann et al. 2013). Even though habitat shifts between forest and savanna habitats represent an important adaptive barrier (Pennington et al. 2009), they may not have been such a big challenge for Bignonieae in the past considering that many shifts occurred during the evolutionary history of this tribe (Lohmann 2003; Lohmann et al. 2013). In addition, transitions to savanna habitats were associated with the evolution of various ecological attributes (e.g., species with shrubby habit, lacking tendrils, or bearing wind-dispersed seeds with ellipsoid wings), most of that evolving simultaneously or soon after the colonization of savannas (Lohmann 2003).

The richness deconstruction using early-diverging and late-diverging species usually shows distinct richness distribution patterns, with early-diverging species occupying areas with similar

environmental conditions as those occupied by their MRCA, while late-diverging species are thought to be more dispersed throughout the overall distribution area of the focal group (e.g., Hawkins et al. 2005, 2007; Pinto-Ledezma et al. 2017). Such pattern is expected under climatic niche conservatism over time (Hawkins et al. 2005, 2007). Strikingly, the richness patterns of early-diverging and late-diverging Bignonieae species were very similar, with both subsets showing the same gradient of richness between forest and savanna habitats observed for the tribe as a whole, despite a statistically significant difference between late-diverging species richness and overall tribe richness. The many events of habitat shift that occurred during the history of diversification of Bignonieae may explain the weak differences encountered between richness patterns of early-diverging and late-diverging species in this clade.

The richness deconstruction using the five most specious genera of the tribe revealed similar results observed for early-diverging and late-diverging species. All genera showed the classic gradient of richness distribution between forests and savannas and contributed in similar ways to the overall tribe richness pattern (Fig. S2.7). In other words, even though differences among genera would be expected given that the MRCA of several genera were distributed in either forest (e.g., *Adenocalymma* and *Amphilophium*) or savanna habitats (e.g., *Fridericia* Mart.), no deviations from the richness gradient between these two types of habitats were observed. Alcantara et al. (2014) found that similar abiotic requirements have evolved multiple times in Bignonieae, with closely related species tending to show distinct abiotic preferences. In this sense, richness patterns of species with different evolutionary attributes (e.g., different genera or early-diverging vs. late-diverging species) can be similar to each other and to the overall tribe richness because species of each subset can occur over a wide range of environmental conditions.

The distribution of species with different range sizes seems to be associated with the distribution and size of the broad biogeographical areas proposed by Gentry (1979). Species with

large ranges are concentrated in the Amazon region and, in a lower proportion, in the diagonal of open formations of Central South America. Apart from their dynamic distribution over time, these biomes currently cover large extensions, thus allowing species to thrive over broad extents of territory and build up large range sizes (Jetz & Rahbek 2002; Gaston 2003; Morueta-Holme et al. 2013). In turn, species with small and intermediate range sizes are mainly distributed through the Atlantic rainforest, a biome that covers a small extension of territory that may have limited the expansion of individual species ranges. Indeed, range size distribution of Neotropical vascular plants can be partially explained by differences in the extent of the Amazon and the Atlantic rainforests (Morueta-Holme et al. 2013).

To summarize, the high congruence in the responses of both species ranges and richness to environmental and spatial predictors allows us to conclude that species-level processes may be driving overall species richness patterns in Bignonieae. Both the overall tribe richness and the distribution of species with different ecological attributes reflect the current distribution of forests and savanna habitats (or biogeographical areas *sensu* Gentry 1979) in the Neotropics. Comparisons of diversification rates between forest and savanna habitats using comparative phylogenetic approaches (e.g., Pinto-Ledezma et al. 2017) would provide additional insights towards an improved understanding of the geographic patterns of Bignonieae diversity. Such comparative analyses lead to more robust results when applied to densely sampled phylogenies and will be feasible once a species-level phylogeny of the whole tribe including all ca. 400 species currently recognized becomes available (Lohmann et al. *in prep.*). Such analyses would also strongly benefit from the incorporation of a higher number of species attributes, those of which could contribute to a finer scale understanding of species co-occurrence patterns and their associated processes (e.g., environmental filtering and biotic interactions) through the geographic space.

Acknowledgements

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Capítulo 3

A altura de dossel explica padrões de riqueza de espécies no maior clado de lianas Neotropicais

Canopy height explains species richness patterns in the largest clade of Neotropical lianas

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Abstract

Aims: Tall and structurally complex forests can provide ample habitat and niche space for climbing plants, hence supporting high liana species richness. We test to what extent canopy height (as proxy of 3D habitat structure), climate and soil interact to determine liana species richness of the tribe Bignonieae (Bignonieaceae). We expect that the effect of canopy height on species richness is higher for lianas from closed tropical rainforests compared to riparian and savanna habitats.

Methods: We used structural equation models to evaluate direct and indirect effects of canopy height, climate and soil on overall Bignonieae species richness (339 species), as well as on species richness of lianas from forest, riparian and savanna habitats, respectively. We further performed multiple regression models with Moran's eigenvector maps to account for spatial autocorrelation.

Results: Canopy height was a key driver of liana species richness, in addition to climate and soil. Both, overall species richness and forest liana richness showed a strong positive relationship with canopy height whereas the relationship was less pronounced for riparian species. Species richness of savanna species even decreased with increasing canopy height. Climate also explained a substantial proportion of variation in liana species richness whereas soil variables showed little explanatory power.

Conclusions: The relationship between canopy height and liana species richness differs among habitats. While forest and riparian lianas probably benefit from physical support to reach the forest canopy to escape low light availability in the understory, a high light availability in open habitats and an increased risk of embolism of conductive vessels for lianas with long stems living in sites with severe seasonality might explain the inverse relationship between species richness and canopy height in savannas.

Keywords: Bignoniaceae, Bignonieae, climbing plants, diversity, liana-tree interaction.

Introduction

A key challenge in ecology and biogeography is to understand the mechanisms behind broad-scale patterns of species richness (e.g., the latitudinal and altitudinal diversity gradients) (Brown 2014; Fine 2015). Richness patterns emerge from a complex interaction of historical (e.g., evolution and biogeography) and ecological (e.g., climate and environmental variables) factors (Fine 2015; Rangel et al. 2018). Climate is seen as a main determinant of species richness (Fine 2015), e.g. because (i) high water and energy availability can provide many resources for a large number of species (Gillman et al. 2015), (ii) high temperatures might speed up metabolic and evolutionary rates (Brown 2014), and (iii) the persistence and stability of warm and wet climates over geological time scales has reduced extinctions and increased the accumulation of species adapted to tropical climates (Wiens & Donoghue 2004). In addition, biotic interactions (such as competition or facilitation) may influence species richness by increasing habitat specialization or reducing extinction due to species coexistence (Gotelli et al. 2010). Finally, environmental heterogeneity (e.g., topographic, edaphic and 3D ecosystem heterogeneity) also contributes to diversification, species specialization and coexistence and ultimately increases species richness (Stein et al. 2014; Oliveira & Scheffers 2019). Apart from the individual effect of each factor, they interact and influence species richness in a complex way (Rangel et al. 2018), which makes it difficult to formulate a unique explanation of richness patterns.

Regarding environmental heterogeneity, 3D vegetation structure has been highlighted as a key determinant of species richness in several groups of organisms (e.g., amphibians: Oliveira & Scheffers 2019; birds: Zhang et al. 2013; non-human primates: Gouveia et al. 2014; epiphytic lichens: Marini et al. 2011; vascular epiphytes: Hirata et al. 2009; and lianas: Couvreur et al. 2015). Forests, especially tropical rainforests, are composed of multiple layers that provide habitat resources and thereby increase niche space (e.g., Gouveia et al. 2014; Oliveira & Scheffers 2019).

Many organisms prefer particular forest strata (Krömer et al. 2007) and a diverse sub-canopy structure provides substrate for epiphytic lichens and plants (Hirata et al. 2009; Marini et al. 2011) as well as physical support for lianas (Couvreur et al. 2015). Despite recognizing the role of vegetation heterogeneity in promoting species richness, it is far from trivial to quantify 3D vegetation structure across large spatial scales (Lefsky 2010). One possibility is to use proxies of vegetation structure such as canopy height which can be derived from spaceborne light detection and ranging (LiDAR) (Lefsky 2010; Simard et al. 2011). Such canopy height estimates can then be used to test hypotheses on the relationship between 3D habitat structure and the distribution and diversity of organisms (Gouveia et al. 2014; Couvreur et al. 2015).

Lianas are climbing plants which depend on physical support (e.g., tree trunks) for their growth and development (Schnitzer & Bongers 2002). The climbing life-form allows lianas to reach many forest layers and to access different light conditions, pollinators and seed dispersal agents (Gianoli 2004; Phillips et al. 2005). Moreover, the climbing life-form enables lianas to reach the forest canopy to escape the light shortage in the understory (Phillips et al. 2005; Ichihashi & Tateno 2011). Hence, canopy height as a proxy of vertical vegetation heterogeneity could be a main determinant of liana species richness. For instance, at a global scale the species richness of climbing palms (Arecaceae) increases with canopy height of forests (Couvreur et al. 2015). Nonetheless, the relationship of liana richness and canopy height could result from an indirect effect of climate and soil variables, as these variables also determine liana species richness (van der Heijden & Phillips 2008; DeWalt et al. 2015; Powers 2015) as well as the spatial and vertical structure of vegetation (Simard et al. 2011). Moreover, an increase of liana species richness with taller canopies can be expected in closed forest habitats where competition for light is pronounced, but such a relationship may be less pronounced for lianas from habitats with lower canopies (e.g., riparian and savanna habitats) where vertical vegetation structure is less complex (reducing the amount of physical

support and niche space) and light availability in the understory is higher (resulting in less competition for light) (Schnitzer 2005). Hence, the relationship of liana species richness and canopy height needs to be tested in different habitat types where lianas occur.

Here, we use a comprehensive dataset on the Neotropical distributions of 339 liana species of the tribe Bignonieae (Bignoniaceae) to test to what extent forest canopy height, climate and soil can explain variation in species richness at a macroecological scale. Bignonieae represents the largest clade of Neotropical lianas (Lohmann & Taylor 2014), is among one of the most well-known plant groups in the Neotropics (e.g., Lohmann 2006; Lohmann et al. 2013), and contains species that occur in forest, riparian and savanna habitats (Lohmann & Taylor 2014). More specifically, we test whether (i) forest canopy height, in addition to climate and soil variables, shows a positive relationship with liana species richness (i.e., more species in taller forests) because tall forests may provide ample opportunities for physical support and increase the amount of available habitat and niche space (Couvreur et al. 2015), and (ii) species richness of lianas in riparian and savanna habitats is less strongly related to canopy height than lianas from closed forest habitats because these open habitats have a higher light availability than closed forest habitats. We use structural equation models (SEMs) to evaluate direct and indirect effects of predictor variables and account for spatial autocorrelation using Moran's eigenvector maps. With these analyses, we shed light on the role of 3D vegetation structure in shaping broad-scale patterns of species richness in tropical ecosystems.

Methods

Tribe Bignonieae

The tribe Bignonieae (Bignoniaceae) includes 386 species from which 339 (88%) are lianas and 47 (12%) are shrubs (Lohmann & Taylor 2014). All liana species are exclusively distributed in the

New World from southern United States to northern Chile and Argentina (Lohmann et al. 2013). Liana species occur in a variety of habitats with some species being restricted to forest, riparian or savanna habitats, while others are widely distributed (Lohmann et al. 2013; Lohmann & Taylor 2014). Bignonieae is a well-known plant group in the Neotropics with several studies on their taxonomy, phylogenetic history, evolution and biogeography (e.g., Lohmann 2006; Lohmann et al. 2013; Lohmann & Taylor 2014). Given its high species diversity, broad distribution and comprehensive level of knowledge, this tribe represents a good model group to understand the distribution of liana species richness at macroecological scales.

Species occurrence records

We focus solely on the liana species of the tribe Bignonieae (339 out of 386 species). Species occurrence records were derived from a georeferenced database compiled by LG Lohmann (unpublished data) based on her own field collections and from herbarium records, especially the Missouri Botanical Garden (www.tropicos.org), which represents the largest herbarium collection of Bignonieae. Geographic coordinates were directly extracted from herbarium specimens or assigned according to the locality description on the label of herbarium specimen. We compared the geographic distribution of occurrence records with species distribution information as available from taxonomic reviews and expert knowledge (all species were checked by LG Lohmann, except *Adenocalymma* Mart. ex Meisn. which was checked simultaneously by LG Lohmann and LHM Fonseca). We discarded all occurrence records falling outside the known extent of occurrence of a species (based on the species geographic range as described in taxonomic reviews). For species with less than 10 occurrence records, we searched for additional records in monographs on *Adenocalymma* (Fonseca 2017), *Amphilophium* Kunth (Pool 2007a, 2007b, 2008, 2009), *Bignonia* L. (Zuntini 2015), *Dolichandra* Cham. (Fonseca et al. 2017), *Lundia* DC. (Kaehler 2011), *Mansoa*

DC. (Silva-Castro 2010), *Pleonotoma* Miers (Gomes 2006), and *Tynanthus* Miers (Medeiros & Lohmann 2015). By plotting occurrence records on a map and comparing their spatial distribution with the known species geographic range, we could confirm that species with ≥ 10 records were spatially well represented. The taxonomic nomenclature followed Lohmann & Taylor (2014), except for *Adenocalymma* for which a new synopsis is available (Fonseca 2017) and for some taxa that recently received taxonomic updates. Our final database encompasses 26,373 occurrence records of the 339 liana species.

For all species with ≥ 3 records (322 out of the 339 species), we used the 'ashape' function of the 'alphahull' package (Pateiro-López & Rodríguez-Casal 2016) implemented in R (R Core Team 2018) to represent species ranges according to the alpha hull method (for more details see Meyer et al. 2018). To map liana species richness, we overlapped the 322 species ranges on a grid with 0.5° resolution (~ 55 km), covering the entire occurrence area of the tribe. We added to the grid the occurrence records of the species with < 3 records. We used the Behrmann equal-area projection to project all geographic data.

Species habitat classification

We defined three broad habitat categories (forest, riparian and savanna habitats) in which liana species can occur in. This habitat classification aims to represent key differences in light availability, vegetation structure and canopy height among those habitats (e.g., forests tend to be taller and have less light available than riparian and savanna habitats). These factors are important in shaping the ecology and evolution of Bignonieae liana species (Lohmann 2003). Forest habitats are semi-deciduous to evergreen wet forests in South and Central America, including the Amazon and the Atlantic rainforests. Riparian habitats included river channels, in gallery or swamp forests and mangrove vegetation. Savanna habitats are dry forests and savanna ecosystems in South and

Central America, including the Cerrado, Caatinga and Chaco. To obtain information on habitats, we first searched for species' habitat descriptions in Lohmann & Taylor (2014) and in the available monographs mentioned above. We further checked habitat descriptions by overlaying the occurrence records of each species with the global biomes from the Terrestrial Ecoregions of the World (Olson et al. 2001) and with the Brazilian biomes (IBGE 2004). This procedure allowed us to classify species into forest, riparian and savanna species. The habitat classification for each species was finally revised by an expert (LG Lohmann). The final habitat classification resulted in 243 liana species from forest habitats, 25 species from riparian habitats, and 54 species from savanna habitats (Table S3.1). We disregarded 17 liana species that occur in more than one of our three habitat categories.

Environmental variables

We used canopy height, climate and soil variables as predictors of liana species richness (Fig. S3.1-4). Canopy height as derived from spaceborne LIDAR represents variation in tree stem height of the upper canopy as a proxy of forest height (Lefsky 2010; Simard et al. 2011). We used the 1 km resolution canopy height map from Simard et al. (2011) and calculated the mean canopy height within each grid cell. The canopy height map is derived from LiDAR data from the Geoscience Laser Altimeter System (GLAS) which was acquired globally between 2003 and 2009, in combination with ancillary variables (e.g., climate, topography and vegetation cover) (Simard et al. 2011).

To quantify climate, we used the 19 bioclimatic variables of the ecoClimate database (Lima-Ribeiro et al. 2015). These climate data are based on the community climate system model (CCSM4) atmosphere-ocean general circulation model (AOGCM) with a modern baseline (1950-1999) and an original resolution of 0.5°. We selected the modern baseline because most of the

species occurrence records were collected between 1950 and 1999 (Meyer et al. 2018). We performed a principal component analysis (PCA) including all bioclimatic variables to reduce the number of variables and to avoid multi-collinearity. We selected the first three axes of the PCA which accounted for 75% of the variance in all bioclimatic variables. PCA axis 1 synthetized bioclimatic variables mainly related to mean annual temperature, PCA axis 2 mostly reflected annual precipitation, and PCA axis 3 captured especially precipitation seasonality (Table S3.2).

We selected two soil variables as predictors: (i) cation exchange capacity (CEC) as a proxy for soil nutrients (FAO 2012), and (ii) the number of soil types per grid cell representing soil heterogeneity (Stein et al. 2014). We used the Harmonized World Soil Database (HWSD; FAO 2012) which provides soil information at 1 km resolution. We first identified which soil codes are represented in each grid cell, then extracted the CEC of the top-soil layer using the available soil codes, and finally calculated the mean CEC per grid cell. We obtained the number of soil types by counting the number of different soil codes per grid cell.

Analyses

We used structural equation models (SEMs) to evaluate the direct effect of canopy height on liana species richness and the direct and indirect effects of climate and soil variables. SEMs are useful to test hypothetical complex causal relationships among variables in which some variables can simultaneously act as response and predictor variables (Grace 2006). In addition, SEMs allow the partitioning of the total effect of the relationship between variables into direct and indirect effects (Grace 2006). Direct effects are relationships that are not explained through another variable in the model, while indirect effects represent relationships mediated through another variable (Grace 2006). We built a theoretical SEM (Fig. 1a) based on hypothesized and established relationships between environmental variables and species richness of lianas and plants in general (see Table 1).

Table 1. Hypothesized relationships between environmental variables and liana species richness of the tribe Bignonieae as used for implementing the theoretical structural equation model (Fig. 1).

Variable	Hypothesis	Findings from liana studies	Expectations
Canopy height	Liana species richness increases with canopy height because taller forests provide more physical support and niche space for lianas (Phillips et al. 2005; Couvreur et al. 2015).	Species richness of climbing palms across the world correlates with forest canopy height (Couvreur et al. 2015).	A direct and positive effect of canopy height on liana species richness.
Temperature (TEMP)	TEMP represents energy availability and increases species richness through supporting a high number of individuals, high speciation rates, and low extinction rates (Gillman et al. 2015).	TEMP was not related to liana species richness in lowland and montane Neotropical forests (van der Heijden & Phillips 2009), but globally showed a positive relationship with species richness of climbing palms (Couvreur et al. 2015).	TEMP may correlate directly and positively with liana species richness.
Precipitation (PREC)	PREC represents water availability which leads to a high biomass accumulation and high number of individuals which ultimately promotes diversification (Gillman et al. 2015).	PREC showed a positive relationship with liana species richness in lowland and montane Neotropical forests (van der Heijden & Phillips 2009). Liana richness from plots of the Global Liana Database tends to be highest at intermediate levels of rainfall (DeWalt et al. 2015). PREC was not relevant to explain species richness of climbing palms globally (Couvreur et al. 2015).	PREC may correlate directly and positively with liana species richness.

Variable	Hypothesis	Findings from liana studies	Expectations
Precipitation seasonality (PRE SEAS)	PREC SEAS reduces the water availability and increases drought stress, thus potentially reducing the accumulation of species (Gillman et al. 2015).	PREC SEAS showed a negative relationship with liana species richness in lowland and montane Neotropical forests (van der Heijden & Phillips 2009) and with species richness of climbing palms (Couvreur et al. 2015). Liana richness from plots of the Global Liana Database showed no relationship with PREC SEAS (DeWalt et al. 2015).	PREC SEAS may correlate directly and negatively with liana species richness.
Cation exchange capacity (CEC)	CEC affects soil chemistry and soil fertility and therefore increases production and accumulation of plant biomass which ultimately increases species richness (Pausas & Austin 2001; Gillman et al. 2015).	Soil nutrients showed a weak negative relationship with liana species richness in lowland and montane Neotropical forests (van der Heijden & Phillips 2009). A review suggests that the relationship between soil nutrients and liana species richness is weak at macroecological scales (Powers 2015).	CEC may only show a weak relationship with liana species richness.
Soil types	Environmental heterogeneity (e.g., number of different soil types) increases species richness by promoting niche diversity and allowing species coexistence (Pausas & Austin 2001).	No clear empirical evidence for a relationship between liana species richness and soil heterogeneity (Powers 2015).	Soil type diversity may be positively related to liana species richness.

We evaluated model fit of the theoretical SEM and considered it satisfactory when: (i) the p-value of the chi-square test was > 0.05, (ii) the lower 90% confidence interval of the root mean square error of approximation was < 0.05, and (iii) the comparative fit index was > 0.90 (see Grace 2006; van der Heijden & Phillips 2009; Zhang et al. 2013). To improve model fit, we included a correlative path between CEC and soil type, as suggested by high values of the modification index and the residual correlation (Grace 2006). We used the same theoretical SEM and model fit evaluation approach to implement a SEM for total liana species richness and to evaluate how differences in light availability and canopy height affect the liana species richness from forests, riparian and savanna habitats. We ran SEM analyses using the 'lavaan' package (Rosseel 2012).

Results of non-spatial models (e.g., SEMs) fitted with spatially structured data may be affected by spatial autocorrelation (SAC). To assess SAC, we first built ordinary least squares (OLS) models for species richness of each set of lianas and quantified the presence of SAC in model residuals using Moran's I correlograms (Legendre 1993). To account for residual SAC, we computed Moran's eigenvector maps (MEMs) and included them in the OLS models as additional predictors (Diniz-Filho & Bini 2005).

Because the final set of MEMs may depend on the spatial weighting matrix (W-matrix) as well as the method of MEM selection (Bauman et al. 2018a, 2018b), we computed several W-matrices (58 matrices in total) to represent the spatial structure in different ways (following Bauman et al. 2018a). We generated W-matrices using the 'listw.candidates' function of the 'adespatial' package (Dray et al. 2017) implemented in R (R Core Team 2018) by combining: (i) seven connectivity matrices (i.e., Delaunay triangulation, Gabriel's graph, relative neighborhood graph, minimum spanning tree, distance-based matrix connecting all site at a distance equals to once, once and a half and twice of the largest edge of the minimum spanning tree), (ii) four weight matrices (i.e., without weight between connections, linear, concave-down and concave-up

weighting functions), and (iii) two connective styles (i.e., "B" and "W"), in addition to two principal coordinates of neighbor matrices (PCNM) in "B" and "W" styles (see the manual of the "adespatial" R package for more details; Dray et al. 2017). For the selection of MEMs, we followed Bauman et al. (2018b) and used the approach that minimizes residual autocorrelation (MIR approach). The MIR approach ensures the reduction of SAC and the maintenance of a high explanatory power for environmental predictors by selecting as few MEMs as possible (Bauman et al. 2018b). We selected MEMs using the MIR approach until the global Moran's I of model residuals was < 0.05 (i.e., the default threshold for MEM selection using the MIR approach in SAM software; Rangel et al. 2010) or until at least 200 MEMs were selected. We used the later criterion to ensure that the number of MEMs did not grow endlessly.

We performed a variation partitioning analysis for the selected MEMs of each W-matrix using the 'varpart' function of the 'vegan' package (Oksanen et al. 2007) implemented in R (R Core Team 2018). We grouped environmental variables (i.e., canopy height, climate and soil) and the selected MEMs separately and then partitioned the variance in liana species richness among: (i) the pure environmental component which is the variance accounted exclusively by environmental variables, (ii) the spatially structured environmental component which is the variance explained by environmental variables and MEMs together, (iii) the pure spatial component that is the variance explained solely by the selected MEMs, and (iv) the unexplained residual variance. As additional predictors in OLS model we only included the selected MEMs from the W-matrix that showed a higher variance accounted in the pure environmental component in comparison to the environmental spatially structured component. We adopted this criterion to choose the set of MEMs that is least redundant to the included environmental variables. We built the 58 W-matrices and performed the MEM selection procedure for each set of liana species richness separately (i.e., total, forest, riparian and savanna liana species).

Results

Spatial distribution of liana species richness

Liana species from the tribe Bignonieae are found in various habitats, but most occur in forest habitats (e.g., the Amazon and the Atlantic rainforests), where up to 84 species can be found in a single grid cell (Fig. 2a). Indeed, lianas species richness decreases towards savanna and subtropical ecosystems. Consequently, the diversity of liana species that occur only in forest habitats shows a similar distribution to that of all lianas, reaching up to 67 species in the Amazon rainforest (Fig. 2b). Similar to forest species, riparian liana species richness also peaks in the Amazon rainforest and decreases strongly outside this region (Fig. 2c). In contrast, savanna species show highest species richness outside the Amazon basin, e.g. in Central South America within the Cerrado and Caatinga regions (Fig. 2d). Riparian and savanna species are less diverse than lianas in forest habitats, with a maximum species richness of 12 and 21 species per grid cell, respectively.

Determinants of total liana species richness

SEM results showed that canopy height has a strong positive effect on total liana species richness, i.e. the number of species increases with canopy height (Fig. 1b; Table S3.3). Temperature and precipitation also showed large direct positive effects on liana species richness, while precipitation seasonality and soil variables were less important. A substantial part of the effects of precipitation, precipitation seasonality and CEC on species richness were indirect, via their effect on canopy height (Table S3.3). In addition, precipitation seasonality showed the highest standardized coefficient for predicting canopy height, followed by precipitation, CEC and temperature (Fig. 1b; Table S3.4).
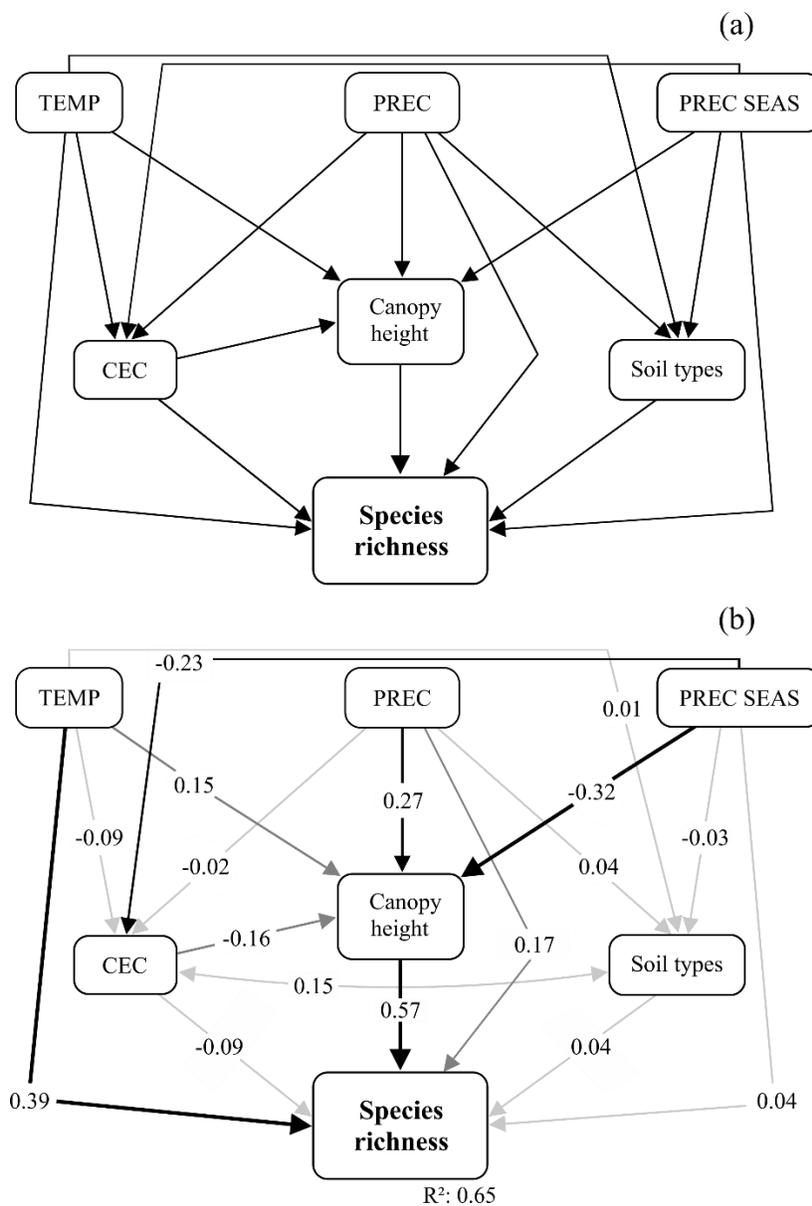
Figure 1. Structural equation models (SEMs) explaining liana species richness of the tribe Bignonieae (Bignoniaceae). (a) *A priori* theoretical SEM including all variables and relationships among them; and (b) final SEM of the direct and indirect effects (standardized coefficients) of variables to explain total liana species richness. TEMP: temperature; PREC: precipitation; PREC SEAS: precipitation seasonality; and CEC: cation exchange capacity. Black and thick arrows represent strong relationships while grey and thin arrows represent weak relationships.
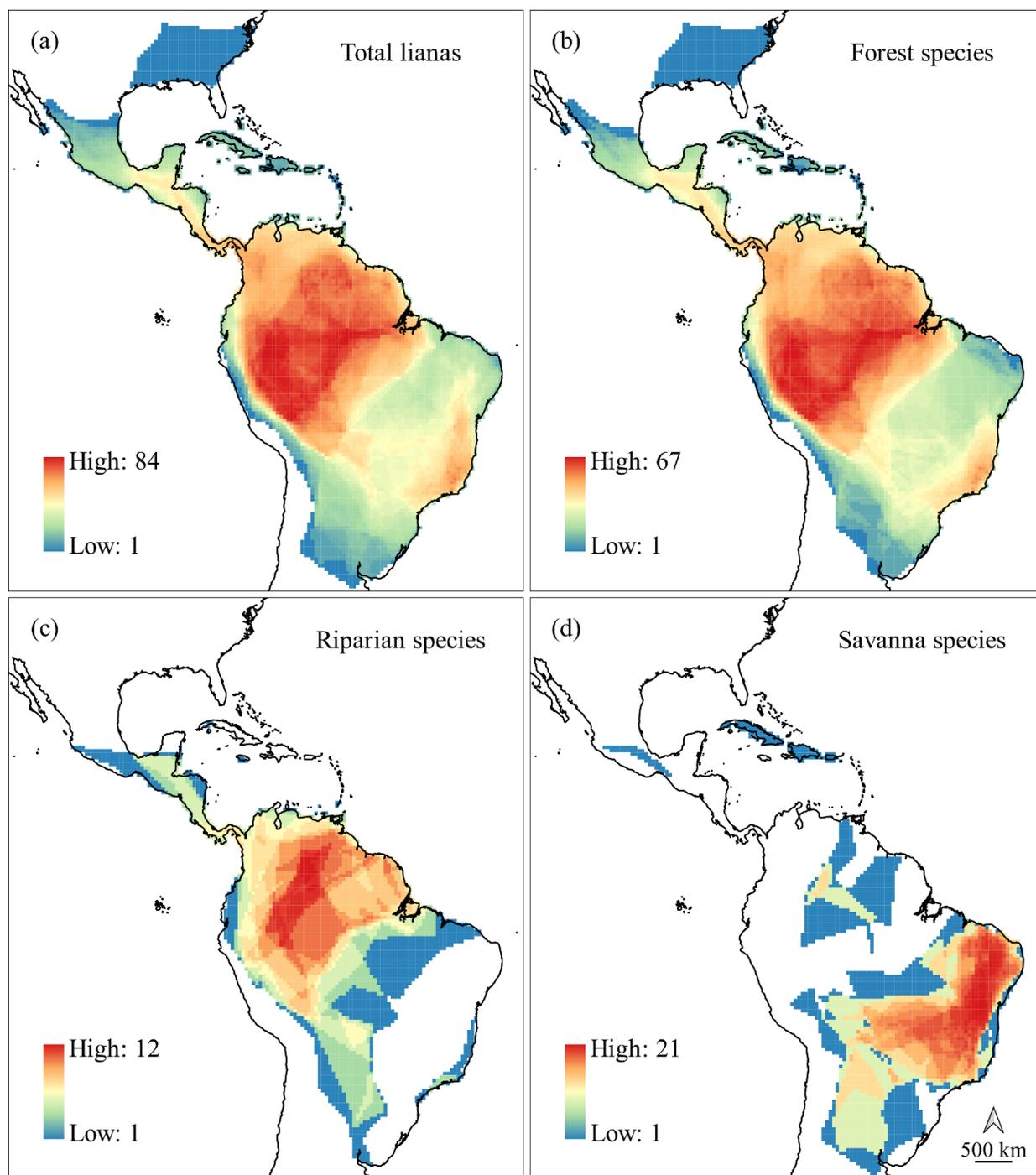
Figure 2. Spatial distribution of liana species richness of the tribe Bignonieae (Bignoniaceae) across the Neotropics. (a) Total species richness; and (b-d) subsets of lianas from different habitats (forest, riparian and savanna).

Determinants of liana species richness from different habitats

Canopy height was an important determinant of liana species richness from all habitats, but the strength and direction (positive or negative) of their relationship varied according to the habitat of the species (Fig. 3a; Table S3.3). Forest liana species richness showed a strong (positive) relationship with canopy height whereas the strength of the relationship was weaker for riparian and savanna lianas. Strikingly, this relationship was even negative for savanna species, pointing to lower diversity in habitats with tall canopies. Temperature also had a strong direct and positive effect on the species richness of lianas from the three habitat types (Fig. 3b). Precipitation was less important for explaining species richness of riparian and savanna lianas compared to forest lianas (Fig. 3c). The relationship with precipitation was positive for forest and riparian species and negative for savanna species. Precipitation seasonality showed a direct and negative relationship with riparian liana richness whereas it mostly affected the species richness of forest and savanna lianas indirectly, i.e. via the effect of canopy height (Fig. 3d; Table S3.3). CEC was an important predictor of savanna liana richness showing a direct and negative effect, but was a weak predictor of forest and riparian liana richness, acting mostly indirectly via canopy height (Fig. 3e; Table S3.3). Number of soil types showed a weak relationship with species richness of lianas in all three habitat types (Fig. 3f).
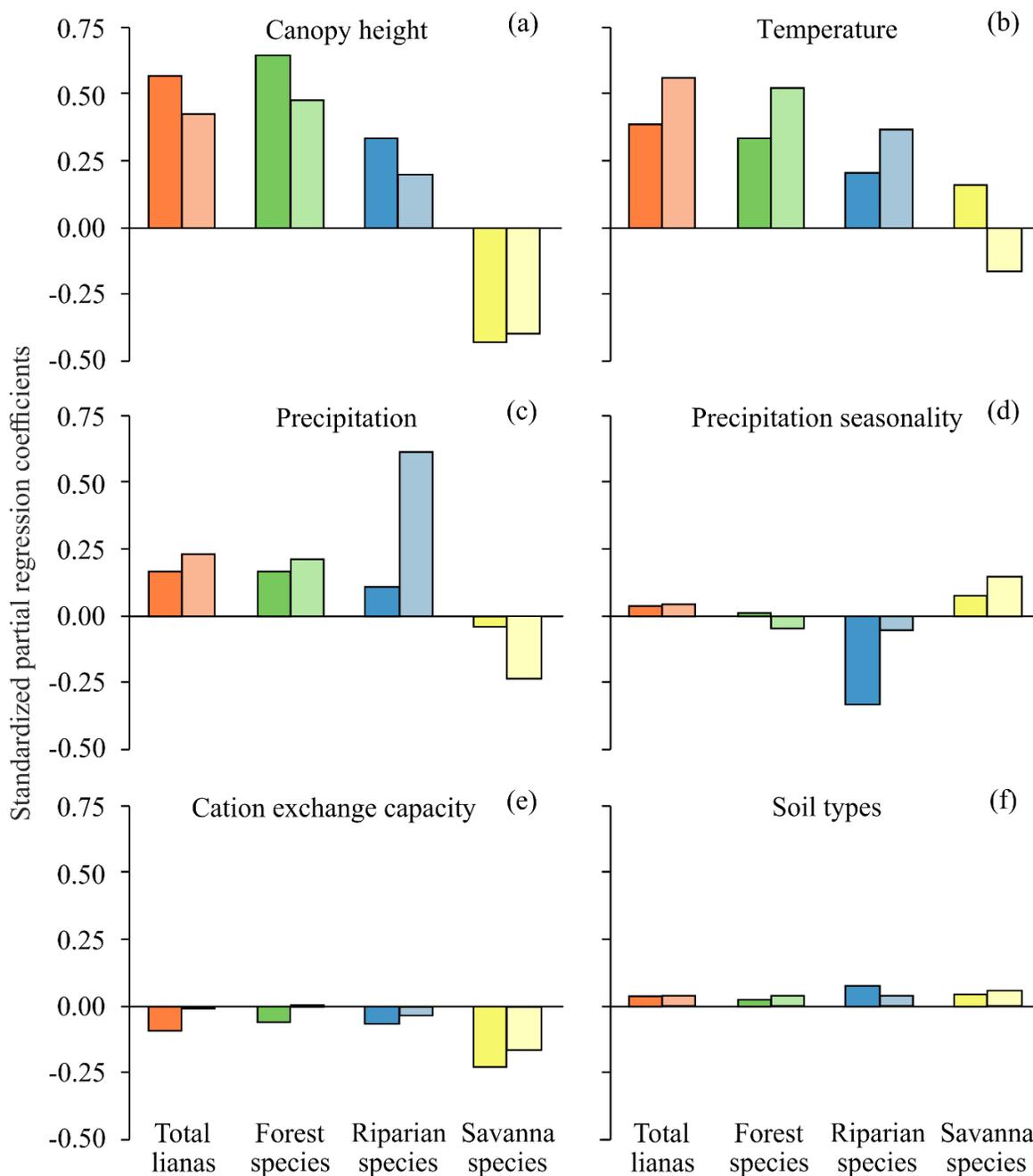
Figure 3. Direct effects of environmental variables on liana species richness of the tribe Bignonieae (Bignoniaceae) as derived from structural equation models (SEMs). Different colors of bars represent different subsets of lianas (orange: all species; green: forest species; blue: riparian species; and yellow: savanna species). Bars in dark colors represent standardized coefficients from structural equation models similar to Fig. 1, while light colors represent standardized coefficients from ordinary least squares models with inclusion of Moran's eigenvector maps to account for spatial autocorrelation.

Effects of spatial autocorrelation

The residuals of all species richness models (i.e., total lianas, forest, riparian and savanna species) were spatially autocorrelated (Fig. S3.5; Table S3.5). After accounting for spatial autocorrelation in OLS + MEMs models, environmental variables showed similar effects on liana species richness, i.e. canopy height, temperature and precipitation accounted for the largest variation in species richness whereas precipitation seasonality, CEC and soil types were less relevant (Fig. 3; Table S3.5). Some changes in standardized coefficients values happened (Fig. 3), which is expected due to some collinearity between environmental variables and selected MEMs, but the main results were robust.

The variation partitioning analysis showed that the pure environmental component (i.e., canopy height, climate and soil variables) accounted for the largest proportion of the variance (around 55%) in species richness of total lianas and forest lianas, as well as an important proportion of variance in liana richness of riparian (45%) and savanna (34%) habitats (Fig. 4). The pure spatial component explained a small proportion (< 25%) of variance in total lianas, forest and savanna species, but accounted for 45% of the variance in riparian lianas. The spatially structured environmental component explained little variance in all sets of lianas. For savanna species, the explained variance of both environmental and spatial variables was low, leaving a high proportion of the variance (58%) unexplained.
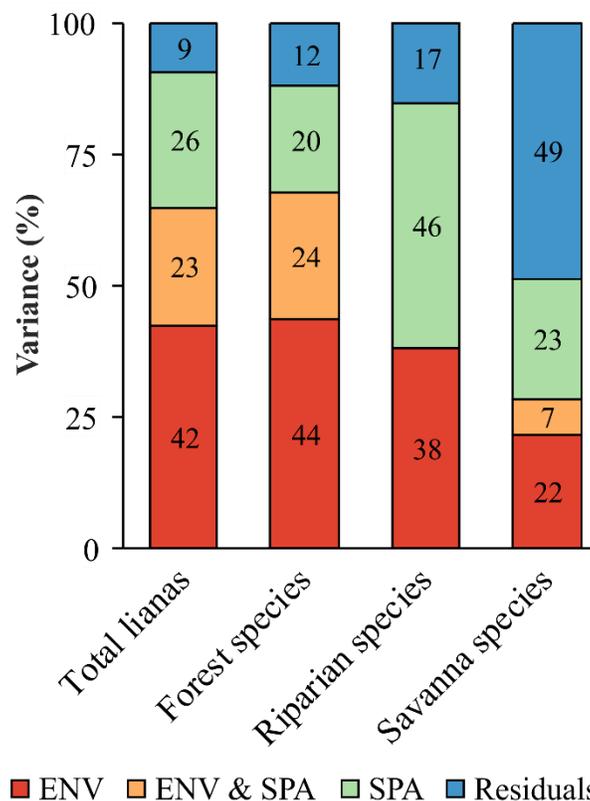
Figure 4. Variance partitioning of liana species richness of the tribe Bignonieae (Bignoniaceae), separately for different subsets of lianas (total, forest, riparian, and savanna species). Variance is explained by either the pure environmental component (ENV), by the spatially structured environmental component (ENV & SPA), by a pure spatial component (SPA), or unexplained residual variance.

Discussion

Our results show that total liana species richness increases with larger canopy heights, suggesting that vertical vegetation structure could be an important driver of liana diversity of the tribe Bignonieae (Bignoniaceae) across the Neotropics. When species were grouped according to their main habitat preferences, canopy height remained an important predictor, but the strength and direction of the relationship changed. Lianas from forest habitats showed a strong positive relationship with canopy height, while the relationship for riparian species was positive but weaker.

In contrast, species richness of savanna lianas decreased with canopy height. These results suggest that the relationship between species richness and canopy height can be shaped by 3D forest structure, light availability below the canopy and species ecological response to environmental conditions.

A high liana richness in habitats with taller canopies can be associated to liana dependence on the availability of physical support (e.g., host trees) as this allows them to reach the forest canopy, thus avoiding light competition in the understory (Phillips et al. 2005; van der Heijde & Phillips 2008; Ichihashi & Tateno 2011). In addition, taller canopy habitats show a more complex 3D structure with many vertical layers and large variation in the diameter of tree stems which increase the availability of thinner stems that are the suitable support for tendril-climbers (DeWalt et al. 2000), as the case of all liana species of Bignonieae (Lohmann & Taylor 2014). Nonetheless, the increase of liana richness with canopy height might be penalized by a large demand for growth investment to reach canopy and escape light storage in the understory (DeWalt et al. 2000).

At a broader scale, the geographic distribution of canopy height corresponds to biome differences between forest and savanna habitats (Simard et al. 2011). The positive relationship between liana species richness of Bignonieae and canopy height can be explained by the Neotropical distribution of biomes, with the Amazon and the Atlantic rainforests being taller and more diverse in liana species than the savanna habitats (i.e., Caatinga, Cerrado and Chaco) in Central South America (see Fig. 2a; Lohmann et al. 2013). Such biogeographic differences in forest canopy height have also been shown to influence the global distribution of species richness of climbing palms, with species diversity being highest in the rainforests of Southeast Asia where dipterocarp trees grow very tall and form a large proportion of the emergent and canopy layer (Couvreur et al. 2015).

Different responses of liana richness to canopy height according to their habitat may be partly related to the evolutionary history of Bignonieae and shifts in functional and morphological adaptations of these species (Lohmann 2003; Angyalossy et al. 2012). Almost all ancestors of the currently recognized genera of the tribe were from forest habitats (Lohmann et al. 2013). Forest history may thus have intensified an association between liana ecology and 3D forest structure, e.g. by promoting specific anchoring mechanisms (e.g., tendrils) that could have increased diversification of Bignonieae in closed forest and riparian habitats (Lohmann 2003). Multiple independent events of colonization of savanna habitats have occurred in all clades of the tribe throughout their evolution (Lohmann et al. 2013). These habitat shifts may have resulted in divergent selection and the evolution of traits towards optima distinctly different from those in closed forests. In Bignonieae, this is most obvious through the loss of tendrils in those species that occur in savanna habitats (Lohmann 2003).

In savanna habitats, our results show that Bignonieae liana species richness decreased with canopy height. In these sunny habitats with an open canopy, plenty of light is available (Oliveira-Filho & Ratter 2002) and lianas may no longer need to climb to the canopy to avoid light competition. The high light availability in the understory of savanna habitats may thus partly explain the low diversity of lianas in tall canopies. At same time, savanna habitats are composed by a mosaic of vegetation ranging from grasslands to dry forests (Oliveira-Filho & Ratter 2002) providing shrubs and trees used as physical support by lianas. However, long stems to grow on tall trees may be disadvantaged in dry habitats as the chance of embolism of xylem vessels increases with the distance between roots and leaves. Lianas have wide and long vessels that provide an efficient transport of water and nutrients through the long stems, but it increases risks of embolism and loss of large areas when the vessels become embolized (Schnitzer 2005; Angyalossy et al. 2012). Lianas developed strategies to reduce embolism (e.g., deep root system) (Schnitzer 2005),

that may be less efficient for lianas with long stems living in sites with long dry seasons (Angyalossy et al. 2012), thus partly explaining the negative relationship between liana richness and canopy height in savanna habitats. Moreover, vegetation structure of savanna habitats is strongly related to fire dynamics which is a constant source of disturbance that prevents the succession of grassland in forest (Oliveira-Filho & Ratter 2002). It is known that disturbances play a substantial role on maintaining diversity and density of lianas in forest habitats (Schnitzer & Bongers 2002; van der Heijden & Phillips 2008, 2009). In this sense, fire disturbances could be acting as a positive factor on liana richness and reducing the canopy height at the same time, but such relationship still needs to be investigated as nothing is known about the fire influence on liana richness.

Our results support a strong role of climate in shaping Bignonieae diversity at macroecological scales. This is broadly in line with studies on several organism groups (Field et al. 2009), including lianas (van der Heijden & Phillips 2009; Couvreur et al. 2015; DeWalt et al. 2015). Specifically, we found a strong positive relationship of liana richness with temperature and precipitation, and a mostly indirect relationship with precipitation seasonality via an effect of canopy height. A previous study that did not include canopy height as predictor showed that liana richness from lowland and montane Neotropical forests is mainly negatively related to dry season length (i.e., a measure of precipitation seasonality) (van der Heijden & Phillips 2009), whereas a study including tropical forests outside the Neotropics showed that liana richness peaks at intermediate levels of rainfall but was not related to dry season length (DeWalt et al. 2015). The relationship of liana richness and climate seems to vary according to (i) the geographic extend of the study as different biogeographical regions and climate conditions are included (van der Heijden & Phillips 2009; DeWalt et al. 2015), and (ii) the environmental variables considered as different interaction among them can be investigated. For Bignonieae, processes related to productivity (i.e.,

water-energy availability) seems to play a role in shaping species richness taking into account direct effects of climate on liana richness, but indirect effects via canopy height, especially for precipitation seasonality reinforce the key importance of 3D forest structure in determining liana species richness. For liana richness from forest habitats, precipitation seasonality acts mostly indirectly reducing canopy height and simplifying vegetation structure limiting the availability of physical supports for lianas. Small trees where seasonality is strong may be advantageous for lianas from savanna habitats by preventing them to grow and have long stem which increases risks of embolism of xylem vessels, explaining an indirect positive effect of precipitation seasonality on liana richness via canopy height. In contrast, lianas from riparian habitats seems to respond more directly to seasonality likely due the water dependence of many species with seed dispersal by water (Lohmann 2003).

At the macroecological scale of our analysis, soil variables only showed a weak effect, which is consistent with soil properties usually becoming more important at fine spatial resolutions (van der Heijden & Phillips 2009; Powers 2015). We found cation exchange capacity to be more important in explaining liana species richness than the number of soil types, especially in savanna habitats. Liana species richness generally decreased with soil fertility (i.e., with increasing cation exchange capacity), in contrast to our initial expectation that higher nutrient availability should increase species richness (Pausas & Austin 2001; Gillman et al. 2015). The weak soil effects, especially in forest and riparian habitats, are consistent with the hypothesis that plants in mature tropical forests may obtain mineral nutrients directly from litterfall before they enter into the soil (Clinebell et al. 1995). The negative relationship between liana species richness and soil fertility in savannas could be explained by competitors being able to outcompete Bignonieae species on fertile soils, which usually show a high tree species diversity in savannas (Vourlitis et al. 2013).

The high importance of canopy height in predicting Bignonieae liana richness emphasizes the need to include variables summarizing key species resources (e.g., habitat availability, habitat complexity) in richness modeling to better predict richness patterns, rather than exclusively considering climate or edaphic variables. Moreover, the unexplained variance, coupled with a strong spatial pattern in the residuals of regression models using only the environmental variables, indicate that other factors should also be investigated. Interestingly, the spatial pattern of residuals was quite similar to the distribution of biomes. It follows that the large-scale ecological structure depicted by these biomes also determines liana richness, perhaps as a result of the long-term eco-evolutionary history of the different regional communities of the Neotropics (see Couvreur et al. 2015; Ricklefs 2015). Further studies are needed to understand how canopy height, climate and soil conditions interact with the different traits of the lianas present in the regional pool of each biome to determine liana species richness at the finer scale of local assemblages. In this sense, spaceborne LiDAR data that quantify 3D vegetation structure in finer scales across the world could be of key importance to investigate local process questions across broad landscapes. Such studies will benefit even more when new spaceborne LiDAR data will become available from the forthcoming Global Ecosystem Dynamics Investigation (GEDI) mission by installing instruments on the International Space Station, which will provide new estimates of height metrics, canopy metrics and aboveground biomass (Stavros et al. 2017). In addition to refined environmental data, a deeper explanation of species richness patterns still needs a better understanding of physiological and anatomical traits related to the climbing life-form (e.g., morphology of tendril or conductive and storage tissues) and how they vary according to environmental conditions (see Angyalossy et al. 2012) and how their evolutionary history was.

Acknowledgments

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Conclusões

Nesta tese mapeamos a distribuição geográfica da riqueza de espécies da tribo Bignonieae (Bignoniaceae). Também estudamos a atuação de diferentes fatores (e.g., clima, solo, altura de dossel) na determinação dos padrões de riqueza de Bignonieae em ampla escala geográfica. Além disso, contribuímos com aspectos metodológicos do estudo de padrões de riqueza ao comparar dois métodos de polígonos comumente usados para representar a área de distribuição das espécies.

Com o primeiro capítulo, encontramos que os métodos de polígonos (i.e., o mínimo polígono convexo e o *alpha hull*) podem ser usados em equivalência para construir mapas de distribuição da riqueza de espécies para a tribo Bignonieae, uma vez que os mapas gerados são muito semelhantes entre si. No entanto, o mínimo polígono convexo deve ser usado com cautela para estimar a área de distribuição geográfica das espécies, visto que este método tende a superestimar a área de distribuição. O método *alpha hull* é uma estratégia mais conservadora que tende a reduzir a superestimação da área de distribuição das espécies. Além disso, observamos que estimativas da área de distribuição das espécies são afetadas igualmente pela lacuna de conhecimento Wallaceana, independentemente do método de polígono utilizado, uma vez que incongruências nas estimativas não estão relacionadas ao grau de conhecimento sobre a distribuição geográfica das espécies.

Com o uso da abordagem de extrema desconstrução da riqueza, no segundo capítulo, observamos que tanto a área de distribuição geográfica das espécies de Bignonieae quanto a riqueza total da tribo respondem de maneira similar às variáveis ambientais e espaciais. Esse resultado sugere que processos que atuam para definir a área de distribuição das espécies também estão agindo para determinar o padrão geral de distribuição de riqueza de Bignonieae em escala macroecológica. No entanto, com a abordagem de desconstrução da riqueza, notamos que alguns

atributos das espécies diminuem a congruência na resposta da área de distribuição das espécies e da riqueza em relação às variáveis preditoras. Tais atributos são: (i) ausência de nectários extraflorais na região interpeciolar e nos profilos, (ii) área de distribuição geográfica pequena a intermediária, e (iii) tempo de divergência recente.

Com o terceiro capítulo, observamos que a altura do dossel é um preditor importante da riqueza de espécies de lianas da tribo Bignonieae, além do papel de variáveis climáticas e edáficas. A riqueza de lianas tende a ser maior em florestas com dossel mais alto, o que pode ser resultado da maior disponibilidade de habitat e suporte físico nestes ambientes. No entanto, a relação entre riqueza de lianas e altura de dossel depende do ambiente em que as lianas ocorrem. Enquanto a riqueza de lianas de floresta tem uma forte relação positiva com a altura de dossel, a relação perde força para as lianas de ambientes ripários e savânicos. No caso das lianas de savana, a relação passa a ser negativa (i.e., a riqueza de lianas tende a aumentar em ambientes com vegetação mais baixa). A forte relação entre altura de dossel e riqueza de lianas é um indicativo de que variáveis que representam recursos chave para o grupo de estudo devem ser incluídos na modelagem de padrões de riqueza. Além da altura de dossel, o clima (i.e., temperatura e precipitação) também tem papel importante para explicar a variação na riqueza de lianas, enquanto variáveis de solo têm menor influência.

Ao longo dos três capítulos da tese, notamos que a distribuição da riqueza de espécies da tribo em escala macroecológica está fortemente associada à distribuição de ambientes florestais e savânicos pela região Neotropical. O maior número de espécies de Bignonieae se concentra na Amazônia e na Mata Atlântica, enquanto a riqueza reduz drasticamente em ambientes savânicos (e.g., Cerrado, Caatinga, Chaco) e em direção à região subtropical.

Com esta tese avançamos em relação ao conhecimento dos padrões de distribuição de riqueza da tribo Bignonieae. No entanto, muita coisa ainda está por ser estudada! Ainda precisamos

entender a influência de fatores históricos e processos evolutivos na distribuição da diversidade da tribo. Considerando a marcada diferença de riqueza entre ambientes florestais e savânicos, seria interessante comparar as taxas de diversificação e entender os processos de especiação e extinção entre esses ambientes. Também seria interessante estudar padrões de coocorrência entre espécies ao longo do espaço e como fatores ambientais e atributos das espécies influenciam tais padrões. Além de entender processos subjacentes aos padrões de diversidade, também é importante investigar como e quanto as lacunas de conhecimentos (e.g., Linneana, Wallacena) influenciam as interpretações dos padrões e processos.

"O que sabemos é uma gota; o que ignoramos é um oceano. "

Isaac Newton

Material suplementar – Capítulo 1

Table S1.1. List of the 386 species of the tribe Bignonieae considered in this study, followed by the number of occurrence records used to build the hull of each species, the alpha value used to generate the alpha hull, the species range size estimated by each hull method (i.e., species range size corresponds to the hull size in km^2), and the year of description of each species. Asterisks (*) indicate species with disjoint geographic distributions.

Species	Number of occurrence records	Alpha value	Range area Convex hull	Range area Alpha hull	Description year
Adenocalymma ackermannii	4	2	1032	935	1896
Adenocalymma adenophorum	9	3	117922	44054	1958
*Adenocalymma albiflorum**	29	7	256494	250722	1976
Adenocalymma alboaurantiacum	9	6	728239	723404	2016
Adenocalymma album	6	2	27787	27787	1775
Adenocalymma allamandiflorum	15	3	495082	462606	1894
Adenocalymma apetiolatum	1	-	-	-	2016
Adenocalymma apparicianum	11	3	70599	70537	1949
Adenocalymma apurense	201	7	8111227	6899415	1938
Adenocalymma arthropetiolatum	12	1	23529	19113	1973
Adenocalymma aspericarpum	6	3	181867	181867	1976
Adenocalymma aurantiacum	19	2	89895	79984	2013
Adenocalymma biternatum	37	5	3664592	1539637	1940
Adenocalymma bracteatum	204	4	2242512	1644682	1845
Adenocalymma bracteolatum	74	8	5291107	4900500	1845
Adenocalymma bracteosum	39	8	5056286	4321697	1845
Adenocalymma bullatum	4	2	1702	1702	1894
Adenocalymma calcareum	5	4	48104	48104	2009
Adenocalymma candolleanum	40	3	623206	585410	1897
Adenocalymma chocoense	3	2	2095	2095	1985

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Adenocalymma cidii	1	-	-	-	1999
Adenocalymma cinereum	11	2	30989	30989	2013
Adenocalymma cladotrichum	157	4	2646760	2236724	1953
Adenocalymma contractum	12	8	1098757	1098757	1999
Adenocalymma coriaceum	54	11	477539	459004	1845
Adenocalymma cristicalyx	9	18	115216	109963	1977
Adenocalymma cymbalum	51	4	394401	282845	1896
Adenocalymma dichilum	17	2	113434	106360	1993
Adenocalymma divaricatum	43	3	822078	432308	1861
Adenocalymma dugandii	3	1	556	556	1953
Adenocalymma dusenii	28	2	38234	26307	1921
Adenocalymma flaviflorum*	51	6	4257283	4035911	1850
Adenocalymma flavum	1	-	-	-	1845
Adenocalymma gibbosum	2	-	-	-	2013
Adenocalymma gracielzae	6	3	115996	115996	1993
Adenocalymma grandifolium	36	2	47932	32359	1845
Adenocalymma hatschbachii	33	1	25479	21709	1993
Adenocalymma hirtum	2	-	-	-	1896
Adenocalymma hypostictum	23	2	60239	59423	1896
Adenocalymma impressum	90	5	5338308	4102062	1937
Adenocalymma juliae	4	7	59814	59814	1981
Adenocalymma lineare	2	-	-	-	2016
Adenocalymma longilineum	14	5	578554	496943	1936
Adenocalymma macrophyllum	30	2	46943	46166	1845
Adenocalymma magdalenense	8	2	25639	24838	1946
Adenocalymma magnificum	38	3	696343	617514	1845
Adenocalymma marginatum	235	3	2128342	1019974	1845
Adenocalymma mirabile	7	3	177844	122673	1954

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Adenocalymma molle	3	1	1219	1219	1980
Adenocalymma moringifolium	15	7	259612	250000	1845
Adenocalymma nervosum	1	-	-	-	1896
Adenocalymma nodosum	66	2	995383	798650	1836
Adenocalymma patulum	53	12	1453993	871303	1864
Adenocalymma paulistarum	68	2	317376	270432	1894
Adenocalymma pedunculatum	142	3	1472063	932040	1825
Adenocalymma peregrinum	133	5	2864523	2373307	1863
Adenocalymma pubescens	48	2	970380	573122	1825
Adenocalymma salmoneum	29	1	31068	30394	1951
Adenocalymma sastrei	1	-	-	-	1999
Adenocalymma saulense	2	-	-	-	1993
Adenocalymma scabriusculum	14	4	1034277	713740	1845
Adenocalymma schomburgkii	112	5	3560711	3179923	1845
Adenocalymma sessile	11	2	55681	48391	2013
Adenocalymma subincanum	20	8	2225901	2152495	1914
Adenocalymma subsessilifolium	18	2	41426	29286	1845
Adenocalymma subspicatum	2	-	-	-	1993
Adenocalymma tanaeciicarpum	13	5	1410015	1178882	1976
Adenocalymma trifoliatum	104	1	46443	32772	1973
Adenocalymma ubatubense	1	-	-	-	1999
Adenocalymma uleanum	29	3	738640	354936	1915
Adenocalymma validum	149	8	7240480	4908939	1894
Adenocalymma velutinum	5	3	15657	15657	1999
Amphilophium arenarium	9	4	139946	117965	1978
Amphilophium aschersonii	47	5	3565285	2976858	1904
Amphilophium bauhinioides	13	4	165710	161657	1888
Amphilophium blanchetii	6	3	20876	14734	1896

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Amphilophium bracteatum	8	7	46820	46820	1832
Amphilophium buccinatorium	9	8	122630	57564	1845
Amphilophium campinae	8	10	1327368	1217723	1935
Amphilophium carolinae	100	2	1115454	1011397	1842
Amphilophium chocoense	7	1	13865	13865	1980
Amphilophium cremersii	8	4	88783	88783	1980
Amphilophium crucigerum	644	5	16358758	9253223	1753
Amphilophium cuneifolium	13	5	78351	78351	1845
Amphilophium dasytrichum	9	13	1349532	912700	1953
Amphilophium dolichoides	16	9	124233	101397	1832
Amphilophium dusenianum	9	5	170129	161685	1921
Amphilophium ecuadorense	14	2	72018	46426	1977
Amphilophium elongatum	7	7	187385	108386	1798
Amphilophium falcatum	5	11	1590981	1590981	1825
Amphilophium frutescens	9	2	39193	28372	1845
Amphilophium gnaphalanthum	12	3	57070	45218	1850
Amphilophium granulosum	45	6	3937338	3019381	1848
Amphilophium lactiflorum	58	14	161596	146229	1794
Amphilophium laeve	9	5	104709	52406	1957
Amphilophium laxiflorum	21	15	368246	290515	1845
Amphilophium lohmanniae	6	4	65741	53563	2009
Amphilophium magnoliifolium	12	8	290986	241806	1818
Amphilophium mansoanum	170	6	5465250	3714662	1845
Amphilophium monophyllum	29	2	46956	41504	1957
Amphilophium nunezii	7	8	134345	134345	1992
Amphilophium obovatum	8	1	22689	22632	1957
Amphilophium occidentale	19	11	1643573	1350046	1992
Amphilophium paniculatum	742	6	15475256	12368136	1818

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Amphilophium pannosum	38	15	3191431	2133096	1896
Amphilophium parkeri	14	3	232740	154670	1845
Amphilophium pauciflorum	1	-	-	-	1974
Amphilophium perbracteatum	1	-	-	-	1985
Amphilophium pilosum	3	1	159	159	1938
Amphilophium porphyrotrichum	7	6	120790	96450	1963
Amphilophium pulverulentum	28	5	2477490	2018017	1938
Amphilophium racemosum	183	5	5910786	5238049	1896
Amphilophium reticulatum	1	-	-	-	1978
Amphilophium rodriguesii	16	13	4944948	4547503	1976
Amphilophium sandwithii	12	5	205479	197456	1964
Amphilophium scabriusculum	6	9	344159	341814	1845
Amphilophium stamineum	3	62	115	115	1785
Amphilophium steyermarkii	16	5	139027	107307	1974
Anemopaegma acutifolium	19	6	1510083	1354387	1845
Anemopaegma alatum	15	5	314848	233418	1976
Anemopaegma album	11	4	173920	142017	1945
Anemopaegma arvense	79	3	2263374	1825451	1945
Anemopaegma brevipes	4	13	2870095	2870095	1895
Anemopaegma chamberlaynii	76	9	2378989	1342056	1896
Anemopaegma chrysanthum	85	3	847852	568926	1947
Anemopaegma chrysoleucum	179	5	3927852	2880080	1938
Anemopaegma citrinum	17	3	348336	302869	1845
Anemopaegma colombianum	5	6	239632	62725	1976
Anemopaegma flavum	33	8	1364829	1054205	1892
*Anemopaegma floridum**	57	5	5145268	3192996	1845
Anemopaegma foetidum	11	6	1355677	1075595	1896
Anemopaegma glaucum	43	5	2244390	1764967	1845

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Anemopaegma goyazense	7	7	348275	298228	1896
Anemopaegma gracile	11	6	1250565	602718	1896
Anemopaegma grandifolium	5	9	183691	183078	1947
Anemopaegma granvillei	2	-	-	-	1977
Anemopaegma heringeri	1	-	-	-	1953
Anemopaegma hilarianum	8	3	160557	160413	1896
Anemopaegma insculptum	23	5	1789947	1632660	1976
Anemopaegma ionanthum	7	7	688901	603836	1985
Anemopaegma jucundum	4	4	45661	45661	1896
Anemopaegma karstenii	93	4	1516855	1232048	1896
Anemopaegma laeve	35	4	871405	601332	1845
Anemopaegma longidens	9	7	1955655	1733790	1845
Anemopaegma longipetiolatum	12	3	267461	213820	1905
Anemopaegma mirabile	2	-	-	-	1976
Anemopaegma nebulosum	3	1	18	18	2015
Anemopaegma oligoneuron	24	6	3461917	2674761	1976
Anemopaegma orbiculatum	78	10	520962	510305	1845
Anemopaegma pabstii	12	8	743970	607470	1980
Anemopaegma pachyphyllum	1	-	-	-	1896
Anemopaegma paraense	65	6	5353325	4372445	1896
Anemopaegma parkeri	22	7	4097678	2952037	1906
Anemopaegma patelliforme	7	11	3279818	2539422	1976
Anemopaegma prostratum	27	11	1448025	1198884	1845
Anemopaegma puberulum	42	7	814132	612734	1953
Anemopaegma robustum	10	5	1039388	1019219	1896
Anemopaegma rugosum	11	1	2538	2382	1931
Anemopaegma salicifolium	3	3	8421	8421	1938
Anemopaegma santaritense	18	4	231956	212639	1971

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Anemopaegma scabriusculum	19	3	644534	428917	1845
Anemopaegma setilobum	10	2	17693	17459	1980
Anemopaegma velutinum	21	4	256867	196029	1845
Anemopaegma villosum	1	-	-	-	1976
Bignonia aequinoctialis	738	4	9979724	8566955	1753
Bignonia binata	44	3	876276	701482	1821
Bignonia bracteomana	69	3	970824	653326	1908
Bignonia callistegioides	32	5	1135399	676355	1832
*Bignonia campanulata**	13	4	177605	130434	1832
Bignonia capreolata	109	4	1274582	1173400	1753
Bignonia cararensis	1	-	-	-	2015
Bignonia corymbosa	389	5	10047777	8496483	1807
Bignonia costata	5	1	3616	3596	1896
Bignonia cuneata	5	31	16605	16605	1945
*Bignonia decora**	48	5	989796	657344	1895
Bignonia diversifolia	316	6	1903796	1437974	1818
Bignonia hyacinthina	103	5	5027934	3388093	1935
Bignonia lilacina	67	5	7143555	6134201	1978
Bignonia longiflora	29	1	36633	28747	1801
Bignonia magnifica	21	27	285780	252591	1879
Bignonia microcalyx	15	4	466456	370442	1818
Bignonia neoheterophylla	145	3	759447	445567	1940
Bignonia neouliginosa	15	1	60102	54929	1946
Bignonia nocturna	107	6	6260484	4764332	1891
Bignonia noterophila	299	6	9080918	7949612	1845
Bignonia phellosperma	24	3	77838	40204	1882
Bignonia potosina	89	10	788326	722351	1895
*Bignonia prieurii**	69	6	4944778	3907057	1845

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Bignonia pterocalyx	19	2	147797	105329	1916
Bignonia ramentacea	18	9	2001074	852022	1845
Bignonia sanctae-crucis	10	5	200067	73969	2015
Bignonia sciuripabulum	137	9	12100033	11097064	1894
Bignonia sordida	30	7	2751611	2276015	1896
Bignonia uleana	47	4	1450632	1200057	1915
Callichlamys latifolia	357	5	11921428	11247309	1894
Cuspidaria argentea	15	2	338794	320864	1954
Cuspidaria bracteata	6	15	1069492	1069492	1896
Cuspidaria bracteolata	61	5	699987	519751	1845
Cuspidaria cinerea	6	4	8255	6397	1894
Cuspidaria convoluta	77	5	1668564	825281	1975
Cuspidaria cratensis	10	3	335078	335078	1949
Cuspidaria emmonsii	8	7	851963	758458	1992
Cuspidaria floribunda	82	5	3981309	2497594	1973
Cuspidaria inaequalis	91	5	5975688	4882796	1842
Cuspidaria lachnaea	13	14	1325671	868066	1893
Cuspidaria lasiantha	17	3	502023	375136	1896
Cuspidaria lateriflora	77	6	7183422	6442351	1845
Cuspidaria monophylla	6	3	19991	19991	1978
Cuspidaria multiflora	19	3	361717	317251	1845
Cuspidaria octoptera	9	5	212822	210742	1977
Cuspidaria pulchella	21	4	421148	372705	1894
Cuspidaria pulchra	39	6	2350127	1447204	1832
Cuspidaria sceptrum	96	5	2252011	1581485	1832
Cuspidaria simplicifolia	20	15	2210181	1576295	1838
Cuspidaria subincana	14	4	688571	617932	1976
Cuspidaria weberbaueri	10	4	17409	13347	1973

Species	Number of occurrence records	Alpha value	Range area		Description year
			Convex hull	Alpha hull	
Dolichandra chodatii	25	4	1833991	783423	1907
Dolichandra cynanchoides	77	5	1961456	1774401	1832
Dolichandra dentata	24	3	437279	268758	1894
Dolichandra hispida	18	8	1880313	1778946	2015
Dolichandra quadrivalvis	245	7	15394939	12279650	1800
Dolichandra steyermarkii	29	12	5002167	4997681	1966
Dolichandra uncata	250	5	10595331	5039486	1808
Dolichandra unguiculata	14	7	270594	79344	1825
Dolichandra unguis-cati	763	4	16811048	14534540	1753
Fridericia arthrerion	26	4	1657332	828402	1841
Fridericia bahiensis	16	4	539421	470851	1847
Fridericia candicans	237	5	8185015	7080135	1792
Fridericia carichanensis	24	3	146109	86869	1818
Fridericia caudigera	84	4	688913	606711	1895
Fridericia chica	312	5	13758903	12905019	1807
*Fridericia cinerea**	24	3	392818	324448	1894
Fridericia cinnamomea	67	5	6485651	5499302	1845
Fridericia conjugata	96	8	11619421	8167901	1825
Fridericia costaricensis	45	6	185042	172871	1921
Fridericia crassa	3	8	3085	3085	1896
Fridericia craterophora	37	10	1788020	1761098	1845
Fridericia cuneifolia	15	4	255841	216087	1845
Fridericia dispar	14	6	787299	699554	1894
Fridericia egensis	13	12	2767131	2360443	1896
Fridericia elegans	4	7	335	335	1825
Fridericia erubescens	40	7	883723	714588	1845
Fridericia fagoides	13	4	178627	115686	1832
Fridericia fanshawei	39	5	5452608	4661891	1948

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Fridericia floribunda	70	3	408776	291574	1818
Fridericia florida	331	6	10625366	9497302	1845
Fridericia formosa	14	4	94840	82031	1868
Fridericia grosourdyana	11	3	54333	39438	1888
Fridericia japurensis	81	9	6610337	6003375	1845
Fridericia lauta	8	7	435545	348335	1896
Fridericia leucopogon	20	2	58185	53260	1832
Fridericia limae	18	3	452163	370207	1980
Fridericia mollis	20	4	742719	512962	1798
Fridericia mollissima	154	5	1622762	974166	1818
Fridericia mutabilis	38	4	382605	345175	1896
Fridericia nicotianiflora	16	7	1124190	960974	1915
Fridericia nigrescens	48	5	3333558	2964134	1939
Fridericia oligantha	13	2	98592	77740	1896
Fridericia oxycarpa	42	4	1060796	993957	1916
Fridericia patellifera	385	4	8691528	7851355	1833
Fridericia pearcei	47	4	1513282	887906	1906
*Fridericia platyphylla**	313	3	8501621	5672575	1832
Fridericia pliciflora	2	-	-	-	1845
Fridericia podopogon	31	4	100956	84519	1845
Fridericia poeppigii	33	3	708024	385595	1845
Fridericia prancei	17	10	2163087	2037760	1976
Fridericia pubescens	241	5	12646755	10564891	1763
Fridericia rego	20	4	206448	55247	1825
Fridericia samydoides	47	3	856963	602917	1832
Fridericia schumanniana	180	4	4193283	2578224	1896
Fridericia simplex	9	4	362665	324609	1980
Fridericia speciosa	66	2	805670	514862	1827

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Fridericia spicata	65	8	4305366	3402708	1896
Fridericia subexserta	1	-	-	-	1896
Fridericia subincana	18	4	59381	41836	1841
Fridericia subverticillata	1	-	-	-	1896
Fridericia trachyphylla	4	6	76878	75772	1896
Fridericia trailii	43	5	3245938	1979519	1906
Fridericia triplinervia	80	6	6813021	3581023	1845
Fridericia truncata	44	4	721634	570928	1905
Fridericia tuberculata	56	4	5484832	4444259	1845
Fridericia tynanthoides	6	8	51068	40479	1980
Fridericia viscida	18	6	661400	542779	1895
Fridericia whitei	4	4	54871	54871	1927
*Lundia corymbifera**	176	5	6688664	2611664	1937
Lundia damazioi	11	2	78549	57678	1905
Lundia densiflora	88	5	6038011	4343836	1845
Lundia erionema	38	6	4235905	3761099	1845
Lundia gardneri	15	3	211726	211724	1954
Lundia helicocalyx	11	2	118247	104801	1980
Lundia laevis	12	9	1305136	584499	2011
Lundia longa	52	3	1249395	668703	1845
Lundia nitidula	31	4	906258	444062	1845
Lundia obliqua	13	2	171833	131650	1849
Lundia puberula	99	6	7108962	6485100	1917
Lundia spruceana	66	3	1311883	515114	1868
Lundia virginalis	21	4	523630	469509	1845
*Manaosella cordifolia**	42	4	3140069	1895002	1978
Mansoa alliacea	70	9	6901242	5667054	1979
Mansoa angustidens	11	6	467019	296061	1896

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Mansoa difficilis	106	5	3199976	1826552	1896
Mansoa gentryi	6	3	103158	102177	2016
Mansoa glaziovii	21	5	627993	274111	1896
Mansoa hirsuta	13	3	144385	103904	1845
Mansoa hymenaea	15	3	97113	45562	1979
Mansoa ivanii	3	2	409	409	2016
Mansoa lanceolata	18	8	163969	162191	1979
Mansoa longicalyx	1	-	-	-	2016
Mansoa minensis	6	2	7738	7738	2016
Mansoa onohualcoides*	16	4	152918	65558	1976
Mansoa paganuccii	12	5	385191	276860	2016
Mansoa parvifolia	56	9	2340232	1503029	1979
Mansoa sagotii	33	9	2336371	1986950	1896
Mansoa standleyi	88	8	5840485	3333700	1979
Mansoa verrucifera	181	7	6830162	5663102	1976
Martinella insignis	6	2	12604	12604	2014
Martinella iquitoensis	24	6	1578130	1557449	1935
Martinella obovata	288	5	8192718	7288861	1896
Pachyptera aromatica	11	18	73881	71884	1891
Pachyptera erythraea	7	2	7517	7504	1977
Pachyptera kerere	187	4	7269004	5942144	1937
Pachyptera ventricosa	1	-	-	-	1979
Perianthomega vellozoi	23	13	1055418	925237	1893
Pleonotoma bracteata	13	4	180760	177609	1980
Pleonotoma castelnaei	14	6	400023	390514	1958
Pleonotoma clematis	65	6	2861627	2583425	1863
Pleonotoma dendrotricha	1	-	-	-	1958
Pleonotoma echitidea	10	4	117196	111002	1934

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Pleonotoma exserta	20	2	42523	40449	1978
Pleonotoma fissicalyx	1	-	-	-	2010
Pleonotoma fluminensis	2	-	-	-	1975
Pleonotoma jasminifolia	47	4	1980304	1441794	1863
Pleonotoma longiflora	4	4	19304	19304	2010
Pleonotoma melioides	93	7	5778461	4860894	1976
Pleonotoma orientalis	10	6	649630	601495	1938
Pleonotoma pavettiflora	12	5	708002	620206	1934
Pleonotoma stichadenia	9	5	432956	432789	1894
Pleonotoma tetraquetra	27	4	668153	656554	1868
Pleonotoma variabilis	180	7	6807661	6362081	1863
Pyrostegia millingtonioides	3	6	105592	105592	1962
Pyrostegia venusta	323	7	12694087	11400629	1863
Stizophyllum inaequilaterum	76	7	5530590	2892545	1896
Stizophyllum perforatum	46	15	1536579	1409723	1863
Stizophyllum riparium	276	6	8789501	7599467	1938
Tanaecium affine	24	5	994828	906699	1992
Tanaecium apiculatum	1	-	-	-	1976
Tanaecium bilabiatum	90	5	5030784	3752570	1906
Tanaecium caudiculatum	14	8	112502	99947	1932
Tanaecium crucigerum	16	5	427115	340978	1856
Tanaecium cyrtanthum	9	7	200111	171983	1896
Tanaecium dichotomum	303	6	15019896	12814135	1760
Tanaecium duckei	9	9	2531474	1681625	1935
Tanaecium exitiosum	5	1	6029	6029	1942
Tanaecium jaroba	80	6	6767390	4380356	1788
Tanaecium neobrasiliense	6	4	91348	78464	1888
Tanaecium ornithophilum	13	12	1085936	999558	1977

| Species | Number of occurrence records | Alpha value | Range area | | Description year |
			Convex hull	Alpha hull	
Tanaecium paradoxum	3	4	61314	61314	1954
Tanaecium parviflorum	15	4	409751	294186	1845
Tanaecium pyramidatum	675	6	14248150	13187495	1792
Tanaecium revillae	11	39	364831	290806	1978
Tanaecium selloi	109	5	3829998	1509162	1825
Tanaecium tetragonolobum	182	6	6268409	3532089	1809
Tanaecium tetramerum	4	3	37190	37190	1990
Tanaecium truncatum	17	6	1418562	432479	1936
Tanaecium xanthophyllum	80	3	1762221	917471	1845
Tynanthus cognatus	28	13	723410	717167	1863
Tynanthus croatianus	15	1	11977	9028	1971
Tynanthus densiflorus	4	1	2068	2007	2014
Tynanthus espiritosantensis	2	-	-	-	2014
Tynanthus fasciculatus	13	2	99310	76966	1863
Tynanthus guatemalensis	48	2	142020	122638	1893
Tynanthus labiatus	11	4	313520	312379	1863
Tynanthus macranthus	4	3	4440	4440	1967
Tynanthus micranthus	43	2	209628	146663	1894
Tynanthus panurensis	25	3	666098	561816	1953
Tynanthus polyanthus	110	4	5662036	4579597	1953
Tynanthus pubescens	11	9	4457982	3295497	1978
Tynanthus sastrei	7	1	4911	3226	1980
Tynanthus schumannianus	68	6	4269424	3431859	1974
Xylophragma corchoroides	9	4	274299	248662	1832
Xylophragma harleyi	14	3	346271	267678	2001
Xylophragma heterocalyx	3	6	150969	150969	1979
Xylophragma myrianthum	17	8	334207	323512	1905
Xylophragma platyphyllum	44	7	1534633	1465874	1845

Species	Number of occurrence records	Alpha value	Range area		Description year
			Convex hull	Alpha hull	
Xylophragma pratense	57	5	5775579	3852214	1903
Xylophragma seemannianum	220	5	2731312	2317608	1953
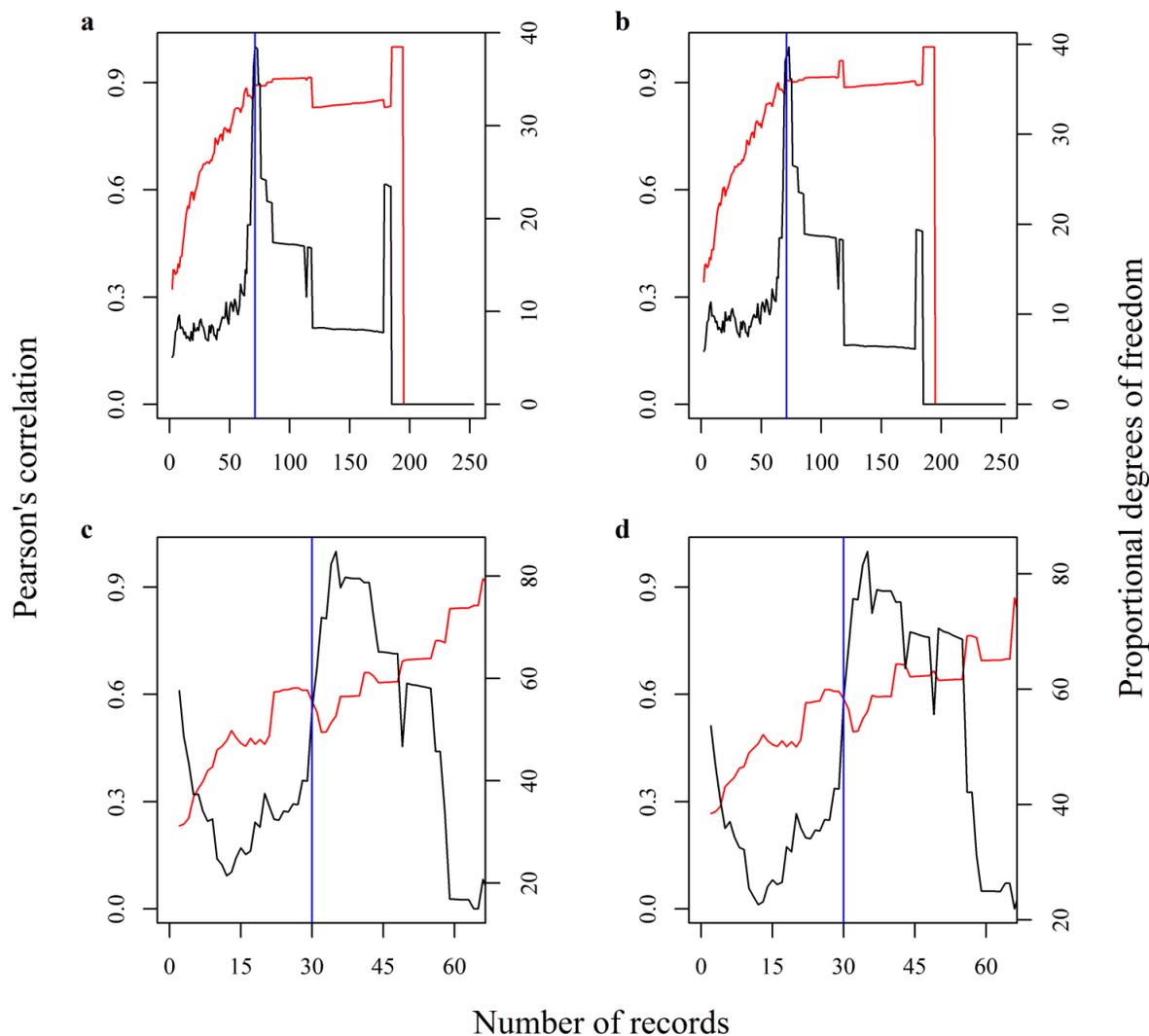
Figure S1.1. Scatterplot of Pearson's correlation (from correlation between the richness of the tribe Bignonieae estimated by hull methods and rarefied richness), the number of occurrence records, and the proportion of degrees of freedom (after using Dutilleul's method to deal with spatial autocorrelation) in relation to the total sample unit in each step of the rarefaction. Red lines indicate the correlation between richness as the number of occurrence records increase. Black lines indicate the variation in proportional degrees of freedom as the number of occurrence records increase. Blue lines indicate the balance between the richness correlation and the proportional degrees of freedom. Blue lines also represent the truncation threshold of the number of occurrence records per sample unit used to estimate rarefied richness. (a) Comparison between the convex hull richness and the rarefied richness from museum occurrence records; (b) Alpha hull richness and rarefied richness from museum occurrence records; (c) Convex hull richness and rarefied richness from local inventories; and (d) Alpha hull richness and rarefied richness from local inventories.
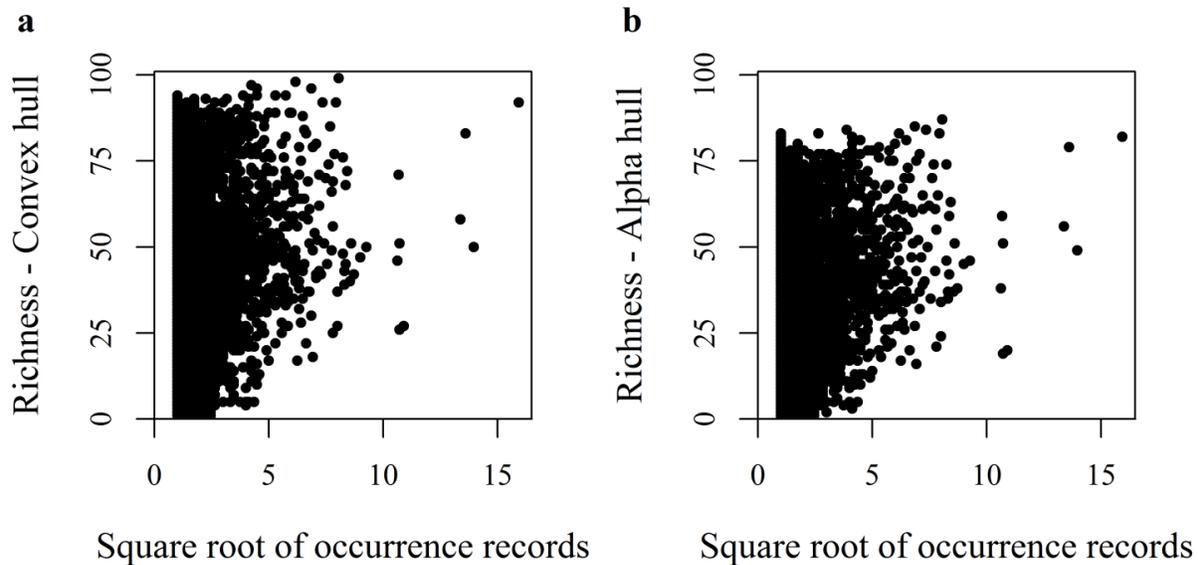
Figure S1.2. Correlation between the number of occurrence records per grid cell and the richness of the tribe Bignonieae estimated by the: (a) Convex hull method ($r_s = 0.13$, $t = 1.38$, $v^* = 107.70$, $p = 0.17$); and (b) Alpha hull method ($r_s = 0.18$, $t = 1.96$, $v^* = 112.11$, $p = 0.05$).

Material suplementar – Capítulo 2

Table S2.1. Ecological, geographical, and evolutionary attributes of species of the tribe Bignonieae (Bignoniaceae) used in richness deconstruction.

Attribute	Categories	Expectations
Ecological attributes		
Plant life-form	(i) Liana (ii) Shrub	Most Bignonieae species are lianas, but the tribe also includes some shrubs (Lohmann 2006; Lohmann & Taylor 2014). The distribution of lianas is related to the distribution of other trees that are used as support by lianas (Schnitzer & Bongers 2002), while the occurrence of shrubs has no such limitation. In addition, it is known that Bignonieae shrub species occur frequently in savanna habitats (Lohmann & Taylor 2014). Indeed, events of habitat shift between forest and savanna are correlated to changes in plant life-form throughout the history of the tribe (Lohmann 2003). A richness deconstruction using these two categories may reveal distinct patterns, with lianas being more closely associated with forest and shrubs with savanna habitats.
Tendrils	(i) Present (ii) Absent	Tendrils are threadlike modified organs with the ability to twine over other structures providing support to lianas (Darwin 1875). The presence of tendrils is related to plant life-form, with Bignonieae shrub species lacking tendrils. Tendril are quite variable among the liana species of the tribe, varying from simple or bifid to trifid or multifid (Sousa-Baena et al. 2014; Lohmann & Taylor 2014). Some

		liana species can lack tendrils. Tendril diversity is thought to be higher in species growing on forest habitats due the large amount and diversity of supports in these areas (e.g., high tree species richness) when compared to savanna habitats. Indeed, habitat shifts between forest and savanna habitats during the evolutionary history of the tribe are correlated to multiple losses and diversification of tendrils (Lohmann 2003). This richness deconstruction may show different patterns, with species bearing tendrils being more common in forest habitats and species without tendrils in savanna habitats.
Herbivory protection	(i) Presence of extrafloral nectaries in the interpetiolar region (ii) Presence of extrafloral nectaries in prophylls of the axillary buds (iii) Absence of extrafloral nectaries	We considered extrafloral nectaries (EFNs) in the interpetiolar region and in prophylls of the axillary buds as proxies of herbivory protection (Nogueira et al. 2012a, 2012b, 2015; Lohmann & Taylor 2014). Extrafloral nectaries are important in ant-plant interactions, where ants consume nectar secreted by EFNs while protecting the plant of herbivores (e.g., Oliveira & Freitas 2004; Nogueira et al. 2012a, 2015). The abundance of EFNs in the prophylls of the axillary buds of Bignonieae species seems to be associated with environment conditions, with savanna species having less EFNs than forest species, likely due to the increased water loss caused by these EFNs (Nogueira et al. 2012a). On the other hand, no variation in abundance pattern of EFNs was observed in the EFNs located in the interpetiolar region (Nogueira et al. 2012a). Moreover, abundance of EFNs may be plastic within individual species, so that abundance of EFNs can vary substantially across the geographic range of plant species (Nogueira et al. 2015). Although we can expect more species lacking herbivory protection (i.e., lacking EFNs) in dry

		areas, as EFNs may increase water loss in these areas, different factors seem to act in a complex way to determine the presence and abundance of EFNs in Bignonieae species. Thereby, exploratory richness deconstruction considering presence of herbivore protection may reveal distinct richness patterns.
Pollination syndrome	(i) Bees (ii) Butterflies (iii) Hawk moths (iv) Hummingbirds	Species of Bignonieae show great diversity in floral morphology (Lohmann & Taylor 2014). The various flower morphologies can be grouped in seven floral types, each of which is associated with a different pollination syndrome (Gentry 1974; Alcantara et al. 2014). Pollinator availability is crucial for the successful reproduction of Bignonieae species and may limit species distribution, as species tend to be self-incompatible and obligatorily outcrossing (Gentry 1974, 1990). At local scales, pollinators act as 'environmental filters', influencing which species of Bignonieae can co-occur in an assemblage (Alcantara et al. 2014). Thereby, exploratory richness deconstruction considering pollination syndromes may reveal distinct richness patterns at different macroecological scales.
Type of seed dispersion	(i) Water-dispersed seeds (ii) Wind-dispersed seeds with linear wings (iii) Wind-dispersed seeds with ellipsoid wings	Species of Bignonieae have water- or wind-dispersed seeds (Gentry 1983; Lohmann & Taylor 2014). The distribution of water-dispersed species is thought to be associated with water sources (e.g., rivers in the Amazon region), while wind-dispersed species have no such association. Wind-dispersed species have seeds with different wing morphologies, some of which are linear while others are ellipsoid, which may be associated to the distribution of species in different habitats (Lohmann 2003; Rochelle 2013; Lohmann & Taylor 2014). The area of the ellipsoid wings is larger than that of the linear wings (Rochelle 2013), which can

increase the weight of ellipsoid wings in forest habitats due to moisture retention. Thereby, wind-dispersed species with ellipsoid wings are thought to occur more commonly in savanna (e.g., the diagonal of open formations in Central South America) than in forest habitats, while wind-dispersed species with linear wings would not have this distribution limitation. Indeed, habitat shifts between forest and savanna habitats that occurred during the evolutionary history of the tribe are correlated to changes in seed wing morphology, with ellipsoid wings being associated with the colonization of savannas (Lohmann 2003). Richness deconstruction considering differences in seed dispersion may reveal distinct patterns, with water-dispersed species and wind-dispersed species with linear wings being more frequently associated with forest habitats and wind-dispersed species with ellipsoid wings being more common in savanna habitats.

Geographic attributes

Species range size	(i) Small (ii) Small to medium (iii) Medium to large (iv) Large	Richness deconstruction considering species range sizes has been evaluated by some studies that investigated richness patterns (e.g., Jetz & Rahbek 2002; Kreft et al. 2006; Terribile et al. 2009). This deconstruction usually reveals different richness patterns according to range size. For instance, species with larger ranges tend to contribute strongly to the overall richness pattern and have their richness distribution well predicted by environmental variables. On the other hand, species with small ranges are frequently randomly distributed throughout the geographic space with their richness pattern tending to be weakly correlated to environmental variables (Terribile et al. 2009). Thereby, exploratory deconstruction of Bignonieae

richness using range sizes may reveal distinct richness patterns for each subset of species.

Evolutionary attributes

Root distance	(i) Early-diverging (ii) Late-diverging	Some studies deconstructing richness using root distance found distinct richness patterns for early-diverging and late-diverging species (also called as 'basal' and 'derived' species in other studies; see Hawkins et al. 2005, 2007; Terribile et al. 2009). In general, richness patterns of early-diverging species are similar to the overall richness map and well predicted by environmental variables, while richness of late-diverging species tends to be weakly correlated to these variables. These results for early-diverging and late-diverging species richness have been attributed to niche conservatism processes (Hawkins et al. 2005, 2007; Terribile et al. 2009). For Bignonieae, climate niche conservatism did not explain the restricted distribution patterns of *Tynanthus* (Medeiros et al. 2015). However, niche conservatism is still expected to have some influence in species distribution, although this effect should be weak given that the tribe has a dynamic colonization history among forest and savanna habitats and many species are widely distributed occurring in different environmental conditions (Lohmann et al. 2013). Deconstructing richness pattern using root distance may help to understand richness patterns within the tribe in an evolutionary perspective.
Bignonieae Genera	(i) *Adenocalymma* (ii) *Amphilophium* (iii) *Anemopaegma*	We selected as categories the five most specious genera of the tribe (i.e., > 30 species), which represent lineages that diverged at different times within the history of Bignonieae (e.g., *Adenocalymma*, *Amphilophium* and *Bignonia* started to

(iv) *Bignonia*	diverge at around 30 Mya, while *Anemopaegma* and *Fridericia* started to diverge
(v) *Fridericia*	at around 20 Mya; Lohmann et al. 2013). Richness deconstruction considering
	genera allows for a different evolutionary interpretation of the tribe richness than
	the root distance deconstruction approach. We choose to consider only genera with
	more than 30 species to reduce uncertainties in deconstruction analyses due to the
	low number of species.

Table S2.2. Classification of the species of the tribe Bignonieae (Bignoniaceae) according to the life-form, presence of tendrils, presence of extrafloral nectaries and pollination syndrome. Pres: presence; and Abs: absence.

Species	Life-form		Tendrils		Extrafloral nectaries			Pollination syndrome			
	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Adenocalymma ackermannii	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma adenophorum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma albiflorum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma alboaurantiacum	0	0	1	0	0	0	1	1	0	0	0
Adenocalymma album	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma allamandiflorum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma apetiolatum	0	1	0	1	0	1	0	0	0	0	1
Adenocalymma apparicianum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma apurense	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma arthropetiolatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma aspericarpum	0	1	1	0	0	1	0	1	0	0	0
Adenocalymma aurantiacum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma biternatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma bracteatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma bracteolatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma bracteosum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma bullatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma calcareum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma candolleanum	0	1	1	0	0	0	1	1	0	0	0
Adenocalymma chocoense	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma cidii	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma cinereum	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma cladotrichum	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma contractum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma coriaceum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma cristicalyx	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma cymbalum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma dichilum	1	0	1	0	0	1	0	0	0	0	0
Adenocalymma divaricatum	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma dugandii	1	0	1	0	0	1	0	1	0	0	0

Species	Life-form		Tendrils		Extrafloral nectaries			Pollination syndrome			
	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Adenocalymma dusenii	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma flaviflorum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma flavum	0	1	0	1	0	0	1	1	0	0	0
Adenocalymma gibbosum	1	0	1	0	0	1	0	0	0	0	1
Adenocalymma gracielzae	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma grandifolium	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma hatschbachii	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma hirtum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma hypostictum	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma impressum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma juliae	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma lineare	0	1	0	1	0	1	0	0	0	0	1
Adenocalymma longilineum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma macrophyllum	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma magdalenense	1	0	1	0	0	1	0	0	0	0	1
Adenocalymma magnificum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma marginatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma mirabile	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma molle	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma moringifolium	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma nervosum	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma nodosum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma patulum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma paulistarum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma pedunculatum	0	1	1	0	0	1	0	1	0	0	0
Adenocalymma peregrinum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma pubescens	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma salmoneum	1	0	1	0	0	1	0	0	0	0	1
Adenocalymma sastrei	0	1	0	1	0	0	1	1	0	0	0
Adenocalymma saulense	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma scabriusculum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma schomburgkii	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma sessile	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma subincanum	1	0	1	0	0	1	0	1	0	0	0

Species	Life-form		Tendrils		Extrafloral nectaries			Pollination syndrome			
	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Adenocalymma subsessilifolium	0	1	0	1	0	1	0	1	0	0	0
Adenocalymma subspicatum	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma tanaeciicarpum	1	0	1	0	0	0	1	1	0	0	0
Adenocalymma trifoliatum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma ubatubense	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma uleanum	1	0	1	0	0	1	0	1	0	0	0
Adenocalymma validum	0	1	1	0	0	1	0	1	0	0	0
Adenocalymma velutinum	1	0	1	0	0	1	0	1	0	0	0
Amphilophium arenarium	1	0	1	0	0	1	0	1	0	0	0
Amphilophium aschersonii	1	0	1	0	0	1	0	0	0	0	0
Amphilophium bauhinioides	1	0	1	0	0	1	0	1	0	0	0
Amphilophium blanchetii	1	0	1	0	0	0	1	1	0	0	0
Amphilophium bracteatum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium buccinatorium	1	0	1	0	0	1	0	0	0	0	1
Amphilophium campinae	0	0	1	0	0	0	1	1	0	0	0
Amphilophium carolinae	1	0	1	0	0	0	1	1	0	0	0
Amphilophium chocoense	1	0	1	0	0	0	1	1	0	0	0
Amphilophium cremersii	1	0	1	0	0	0	1	1	0	0	0
Amphilophium crucigerum	1	0	1	0	0	1	0	1	0	0	0
Amphilophium cuneifolium	0	0	1	0	0	1	0	1	0	0	0
Amphilophium dasytrichum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium dolichoides	1	0	1	0	0	0	1	1	0	0	0
Amphilophium dusenianum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium ecuadorense	1	0	1	0	0	1	0	1	0	0	0
Amphilophium elongatum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium falcatum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium frutescens	1	0	1	0	0	0	1	1	0	0	0
Amphilophium gnaphalanthum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium granulosum	1	0	1	0	0	1	0	1	0	0	0
Amphilophium lactiflorum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium laeve	0	1	0	1	0	0	1	1	0	0	0
Amphilophium laxiflorum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium lohmanniae	1	0	1	0	0	0	1	1	0	0	0
Amphilophium magnoliifolium	1	0	1	0	0	0	1	1	0	0	0

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	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Amphilophium mansoanum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium monophyllum	0	1	0	1	0	0	1	1	0	0	0
Amphilophium nunezii	1	0	1	0	0	1	0	1	0	0	0
Amphilophium obovatum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium occidentale	1	0	1	0	0	1	0	1	0	0	0
Amphilophium paniculatum	1	0	1	0	0	1	0	0	0	0	0
Amphilophium pannosum	1	0	1	0	0	1	0	1	0	0	0
Amphilophium parkeri	1	0	1	0	0	0	1	1	0	0	0
Amphilophium pauciflorum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium perbracteatum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium pilosum	1	0	1	0	NA	NA	NA	1	0	0	0
Amphilophium porphyrotrichum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium pulverulentum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium racemosum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium reticulatum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium rodriguesii	1	0	1	0	0	1	0	1	0	0	0
Amphilophium sandwithii	1	0	1	0	0	0	1	1	0	0	0
Amphilophium scabriusculum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium stamineum	1	0	1	0	0	0	1	1	0	0	0
Amphilophium steyermarkii	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma acutifolium	0	1	0	1	0	0	1	1	0	0	0
Anemopaegma alatum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma album	0	1	0	1	0	0	1	1	0	0	0
Anemopaegma arvense	0	1	0	1	0	0	1	1	0	0	0
Anemopaegma brevipes	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma chamberlaynii	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma chrysanthum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma chrysoleucum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma citrinum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma colombianum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma flavum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma floridum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma foetidum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma glaucum	0	1	0	1	0	0	1	1	0	0	0

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	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Anemopaegma goyazense	0	1	0	1	0	1	0	1	0	0	0
Anemopaegma gracile	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma grandifolium	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma granvillei	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma heringeri	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma hilarianum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma insculptum	1	0	1	0	1	0	0	1	0	0	0
Anemopaegma ionanthum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma jucundum	1	0	1	0	NA	NA	NA	1	0	0	0
Anemopaegma karstenii	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma laeve	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma longidens	1	0	1	0	1	0	0	1	0	0	0
Anemopaegma longipetiolatum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma mirabile	1	0	NA	NA	1	0	0	1	0	0	0
Anemopaegma nebulosum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma oligoneuron	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma orbiculatum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma pabstii	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma pachyphyllum	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma paraense	1	0	1	0	0	1	0	1	0	0	0
Anemopaegma parkeri	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma patelliforme	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma prostratum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma puberulum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma robustum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma rugosum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma salicifolium	0	1	1	0	0	0	1	1	0	0	0
Anemopaegma santaritense	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma scabriusculum	0	1	0	1	0	0	1	1	0	0	0
Anemopaegma setilobum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma velutinum	1	0	1	0	0	0	1	1	0	0	0
Anemopaegma villosum	1	0	1	0	0	1	0	1	0	0	0
Bignonia aequinoctialis	1	0	1	0	0	1	0	1	0	0	0
Bignonia binata	1	0	1	0	0	1	0	1	0	0	0

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	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Bignonia bracteomana	1	0	1	0	0	1	0	1	0	0	0
Bignonia callistegioides	1	0	1	0	0	0	1	1	0	0	0
Bignonia campanulata	1	0	1	0	0	0	1	1	0	0	0
Bignonia capreolata	1	0	1	0	0	1	0	0	0	0	1
Bignonia cararensis	1	0	1	0	0	0	1	1	0	0	0
Bignonia corymbosa	1	0	1	0	0	1	0	1	0	0	0
Bignonia costata	1	0	1	0	0	0	1	1	0	0	0
Bignonia cuneata	1	0	1	0	0	1	0	1	0	0	0
Bignonia decora	1	0	1	0	0	1	0	1	0	0	0
Bignonia diversifolia	1	0	1	0	0	1	0	1	0	0	0
Bignonia hyacinthina	1	0	1	0	0	1	0	0	1	0	0
Bignonia lilacina	1	0	1	0	0	1	0	1	0	0	0
Bignonia longiflora	0	0	1	0	0	1	0	0	0	0	1
Bignonia magnifica	1	0	1	0	0	1	0	1	0	0	0
Bignonia microcalyx	1	0	1	0	NA	NA	NA	1	0	0	0
Bignonia neoheterophylla	1	0	1	0	0	0	1	1	0	0	0
Bignonia neouliginosa	1	0	1	0	0	1	0	1	0	0	0
Bignonia nocturna	1	0	1	0	0	0	1	0	0	1	0
Bignonia noterophila	1	0	1	0	0	1	0	1	0	0	0
Bignonia phellosperma	1	0	1	0	0	1	0	1	0	0	0
Bignonia potosina	1	0	1	0	0	1	0	1	0	0	0
Bignonia prieurii	1	0	1	0	0	1	0	0	1	0	0
Bignonia pterocalyx	1	0	1	0	0	0	1	1	0	0	0
Bignonia ramentacea	1	0	1	0	0	0	1	1	0	0	0
Bignonia sanctae-crucis	1	0	1	0	0	1	0	1	0	0	0
Bignonia sciuripabulum	1	0	1	0	0	1	0	1	0	0	0
Bignonia sordida	1	0	1	0	0	1	0	1	0	0	0
Bignonia uleana	1	0	1	0	0	1	0	1	0	0	0
Callichlamys latifolia	1	0	1	0	0	0	1	1	0	0	0
Cuspidaria argentea	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria bracteata	1	0	1	0	0	1	0	1	0	0	0
Cuspidaria bracteolata	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria cinerea	1	0	1	0	1	0	0	0	0	0	1
Cuspidaria convoluta	1	0	1	0	1	0	0	1	0	0	0

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	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Cuspidaria cratensis	0	1	1	0	0	0	1	1	0	0	0
Cuspidaria emmonsii	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria floribunda	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria inaequalis	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria lachnaea	0	1	1	0	0	0	1	1	0	0	0
Cuspidaria lasiantha	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria lateriflora	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria monophylla	0	1	0	1	1	0	0	1	0	0	0
Cuspidaria multiflora	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria octoptera	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria pulchella	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria pulchra	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria sceptrum	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria simplicifolia	1	0	1	0	0	0	1	1	0	0	0
Cuspidaria subincana	1	0	1	0	1	0	0	1	0	0	0
Cuspidaria weberbaueri	1	0	1	0	1	0	0	1	0	0	0
Dolichandra chodatii	1	0	1	0	0	0	1	0	0	0	1
Dolichandra cynanchoides	1	0	1	0	0	0	1	0	0	0	1
Dolichandra dentata	1	0	1	0	1	0	0	1	0	0	0
Dolichandra hispida	1	0	1	0	1	0	0	1	0	0	0
Dolichandra quadrivalvis	1	0	1	0	1	0	0	1	0	0	0
Dolichandra steyermarkii	1	0	1	0	1	0	0	1	0	0	0
Dolichandra uncata	1	0	1	0	1	0	0	1	0	0	0
Dolichandra unguiculata	1	0	1	0	1	0	0	1	0	0	0
Dolichandra unguis-cati	1	0	1	0	1	0	0	1	0	0	0
Fridericia arthrerion	1	0	1	0	0	0	1	1	0	0	0
Fridericia bahiensis	0	1	0	1	0	0	1	1	0	0	0
Fridericia candicans	1	0	1	0	1	0	0	1	0	0	0
Fridericia carichanensis	0	0	1	0	0	0	1	1	0	0	0
Fridericia caudigera	1	0	1	0	0	0	1	1	0	0	0
Fridericia chica	1	0	1	0	1	0	0	1	0	0	0
Fridericia cinerea	1	0	1	0	1	0	0	1	0	0	0
Fridericia cinnamomea	1	0	1	0	1	0	0	1	0	0	0
Fridericia conjugata	1	0	1	0	1	0	0	1	0	0	0

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	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Fridericia costaricensis	0	1	0	1	0	0	1	1	0	0	0
Fridericia crassa	1	0	1	0	1	0	0	1	0	0	0
Fridericia craterophora	1	0	1	0	1	0	0	1	0	0	0
Fridericia cuneifolia	1	0	1	0	0	0	1	1	0	0	0
Fridericia dispar	0	1	1	0	1	0	0	1	0	0	0
Fridericia egensis	1	0	1	0	1	0	0	1	0	0	0
Fridericia elegans	1	0	1	0	1	0	0	1	0	0	0
Fridericia erubescens	0	1	1	0	1	0	0	0	0	0	1
Fridericia fagoides	1	0	1	0	1	0	0	1	0	0	0
Fridericia fanshawei	1	0	1	0	1	0	0	1	0	0	0
Fridericia floribunda	1	0	1	0	0	0	1	1	0	0	0
Fridericia florida	1	0	1	0	0	0	1	0	0	0	0
Fridericia formosa	1	0	1	0	0	0	1	1	0	0	0
Fridericia grosourdyana	1	0	1	0	0	0	1	0	0	0	1
Fridericia japurensis	1	0	1	0	1	0	0	0	0	0	0
Fridericia lauta	1	0	1	0	1	0	0	1	0	0	0
Fridericia leucopogon	1	0	1	0	0	0	1	0	0	0	0
Fridericia limae	1	0	1	0	1	0	0	0	0	0	0
Fridericia mollis	1	0	1	0	1	0	0	1	0	0	0
Fridericia mollissima	1	0	1	0	1	0	0	1	0	0	0
Fridericia mutabilis	1	0	1	0	0	0	1	1	0	0	0
Fridericia nicotianiflora	1	0	1	0	0	0	1	0	0	0	0
Fridericia nigrescens	1	0	1	0	0	0	1	1	0	0	0
Fridericia oligantha	1	0	1	0	1	0	0	0	0	1	0
Fridericia oxycarpa	1	0	1	0	0	0	1	1	0	0	0
Fridericia patellifera	1	0	1	0	0	0	1	0	0	0	0
Fridericia pearcei	1	0	1	0	0	0	1	0	0	1	0
Fridericia platyphylla	0	1	1	0	0	0	1	0	0	0	0
Fridericia pliciflora	0	1	1	0	1	0	0	1	0	0	0
Fridericia podopogon	1	0	1	0	0	0	1	1	0	0	0
Fridericia poeppigii	1	0	1	0	0	0	1	1	0	0	0
Fridericia prancei	1	0	1	0	1	0	0	0	0	1	0
Fridericia pubescens	1	0	1	0	1	0	0	1	0	0	0
Fridericia rego	1	0	1	0	1	0	0	0	1	0	0

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	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Fridericia samydoides	1	0	1	0	0	0	1	1	0	0	0
Fridericia schumanniana	1	0	1	0	1	0	0	0	0	0	1
Fridericia simplex	0	1	0	1	0	0	1	1	0	0	0
Fridericia speciosa	1	0	1	0	0	0	1	0	0	0	1
Fridericia spicata	1	0	1	0	1	0	0	1	0	0	0
Fridericia subexserta	1	0	1	0	0	0	1	0	1	0	0
Fridericia subincana	1	0	1	0	1	0	0	0	1	0	0
Fridericia subverticillata	1	0	1	0	0	0	1	1	0	0	0
Fridericia trachyphylla	1	0	1	0	0	0	1	1	0	0	0
Fridericia trailii	1	0	1	0	1	0	0	0	1	0	0
Fridericia triplinervia	1	0	1	0	0	0	1	0	0	1	0
Fridericia truncata	1	0	1	0	0	0	1	0	0	1	0
Fridericia tuberculata	1	0	1	0	1	0	0	1	0	0	0
Fridericia tynanthoides	0	1	1	0	0	0	1	0	0	0	1
Fridericia viscida	1	0	1	0	0	0	1	1	0	0	0
Fridericia whitei	1	0	1	0	0	0	1	0	0	0	0
Lundia corymbifera	1	0	1	0	1	0	0	1	0	0	0
Lundia damazioi	1	0	1	0	1	0	0	1	0	0	0
Lundia densiflora	1	0	1	0	1	0	0	1	0	0	0
Lundia erionema	1	0	1	0	1	0	0	1	0	0	0
Lundia gardneri	1	0	1	0	1	0	0	1	0	0	0
Lundia helicocalyx	1	0	1	0	1	0	0	1	0	0	0
Lundia laevis	1	0	1	0	1	0	0	1	0	0	0
Lundia longa	1	0	1	0	1	0	0	0	0	0	1
Lundia nitidula	1	0	1	0	1	0	0	1	0	0	0
Lundia obliqua	1	0	1	0	1	0	0	1	0	0	0
Lundia puberula	1	0	1	0	1	0	0	1	0	0	0
Lundia spruceana	1	0	1	0	1	0	0	1	0	0	0
Lundia virginalis	1	0	1	0	1	0	0	1	0	0	0
Manaosella cordifolia	1	0	1	0	0	1	0	1	0	0	0
Mansoa alliacea	1	0	1	0	1	0	0	1	0	0	0
Mansoa angustidens	1	0	1	0	0	0	1	1	0	0	0
Mansoa difficilis	1	0	1	0	0	0	1	1	0	0	0
Mansoa gentryi	1	0	1	0	1	0	0	1	0	0	0

Species	Life-form		Tendrils		Extrafloral nectaries			Pollination syndrome			
	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Mansoa glaziovii	1	0	1	0	0	0	1	1	0	0	0
Mansoa hirsuta	1	0	1	0	0	0	1	1	0	0	0
Mansoa hymenaea	1	0	1	0	1	0	0	1	0	0	0
Mansoa ivanii	1	0	1	0	1	0	0	1	0	0	0
Mansoa lanceolata	1	0	1	0	0	0	1	1	0	0	0
Mansoa longicalyx	1	0	1	0	0	0	1	1	0	0	0
Mansoa minensis	1	0	1	0	0	0	1	1	0	0	0
Mansoa onohualcoides	1	0	1	0	0	0	1	1	0	0	0
Mansoa paganuccii	1	0	1	0	0	0	1	1	0	0	0
Mansoa parvifolia	1	0	1	0	0	0	1	1	0	0	0
Mansoa sagotii	1	0	1	0	1	0	0	1	0	0	0
Mansoa standleyi	1	0	1	0	1	0	0	0	0	0	1
Mansoa verrucifera	1	0	1	0	0	0	1	1	0	0	0
Martinella insignis	1	0	1	0	0	1	0	1	0	0	0
Martinella iquitoensis	1	0	1	0	0	0	1	0	0	0	1
Martinella obovata	1	0	1	0	0	0	1	0	0	0	1
Pachyptera aromatica	1	0	1	0	1	0	0	0	0	1	0
Pachyptera erythraea	1	0	1	0	1	0	0	0	0	0	1
Pachyptera kerere	1	0	1	0	1	0	0	0	0	1	0
Pachyptera ventricosa	1	0	1	0	1	0	0	0	0	0	1
Perianthomega vellozoi	1	0	1	0	0	0	1	1	0	0	0
Pleonotoma bracteata	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma castelnaei	1	0	1	0	0	1	0	0	0	1	0
Pleonotoma clematis	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma dendrotricha	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma echitidea	1	0	1	0	0	1	0	0	0	1	0
Pleonotoma exserta	1	0	1	0	0	1	0	0	0	1	0
Pleonotoma fissicalyx	1	0	1	0	0	1	0	0	0	1	0
Pleonotoma fluminensis	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma jasminifolia	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma longiflora	1	0	1	0	0	1	0	0	0	1	0
Pleonotoma melioides	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma orientalis	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma pavettiflora	1	0	1	0	0	1	0	0	0	1	0

Species	Life-form		Tendrils		Extrafloral nectaries			Pollination syndrome			
	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Pleonotoma stichadenia	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma tetraquetra	1	0	1	0	0	1	0	1	0	0	0
Pleonotoma variabilis	1	0	1	0	0	1	0	1	0	0	0
Pyrostegia millingtonioides	1	0	1	0	0	0	1	0	0	1	0
Pyrostegia venusta	1	0	1	0	0	0	1	0	0	0	1
Stizophyllum inaequilaterum	1	0	1	0	0	1	0	1	0	0	0
Stizophyllum perforatum	1	0	1	0	0	1	0	1	0	0	0
Stizophyllum riparium	1	0	1	0	0	1	0	1	0	0	0
Tanaecium affine	1	0	1	0	1	0	0	1	0	0	0
Tanaecium apiculatum	1	0	1	0	0	0	1	0	0	1	0
Tanaecium bilabiatum	1	0	1	0	0	0	1	1	0	0	0
Tanaecium caudiculatum	1	0	1	0	0	0	1	1	0	0	0
Tanaecium crucigerum	1	0	1	0	1	0	0	0	0	1	0
Tanaecium cyrtanthum	1	0	1	0	0	0	1	0	0	1	0
Tanaecium dichotomum	1	0	1	0	1	0	0	1	0	0	0
Tanaecium duckei	1	0	1	0	0	0	1	0	0	1	0
Tanaecium exitiosum	1	0	1	0	0	0	1	0	0	1	0
Tanaecium jaroba	1	0	1	0	1	0	0	0	0	1	0
Tanaecium neobrasiliense	1	0	1	0	0	0	1	0	0	1	0
Tanaecium ornithophilum	1	0	1	0	1	0	0	0	0	0	1
Tanaecium paradoxum	1	0	1	0	0	0	1	1	0	0	0
Tanaecium parviflorum	1	0	1	0	0	0	1	1	0	0	0
Tanaecium pyramidatum	1	0	1	0	1	0	0	1	0	0	0
Tanaecium revillae	1	0	1	0	0	0	1	1	0	0	0
Tanaecium selloi	1	0	1	0	0	1	0	1	0	0	0
Tanaecium tetragonolobum	1	0	1	0	1	0	0	1	0	0	0
Tanaecium tetramerum	0	1	0	1	0	0	1	0	0	1	0
Tanaecium truncatum	1	0	1	0	1	0	0	1	0	0	0
Tanaecium xanthophyllum	1	0	1	0	0	0	1	1	0	0	0
Tynanthus cognatus	1	0	1	0	0	1	0	0	1	0	0
Tynanthus croatianus	1	0	1	0	0	0	1	0	0	0	0
Tynanthus densiflorus	1	0	1	0	1	0	0	0	0	0	0
Tynanthus espiritosantensis	1	0	1	0	0	0	1	0	0	0	0
Tynanthus fasciculatus	1	0	1	0	0	0	1	0	0	0	0

Species	Life-form		Tendrils		Extrafloral nectaries			Pollination syndrome			
	Liana	Shrub	Pres	Abs	Interpetiolar region	Prophylls	Abs	Bees	Butterflies	Hawk moths	Hummingbirds
Tynanthus guatemalensis	1	0	1	0	0	1	0	0	0	0	0
Tynanthus labiatus	1	0	1	0	0	0	1	0	0	0	0
Tynanthus macranthus	1	0	1	0	1	0	0	0	0	0	0
Tynanthus micranthus	1	0	1	0	0	1	0	0	0	0	0
Tynanthus panurensis	1	0	1	0	0	1	0	0	1	0	0
Tynanthus polyanthus	1	0	1	0	0	1	0	0	1	0	0
Tynanthus pubescens	1	0	1	0	1	0	0	0	0	0	0
Tynanthus sastrei	1	0	1	0	0	1	0	0	0	0	0
Tynanthus schumannianus	1	0	1	0	0	1	0	0	1	0	0
Xylophragma corchoroides	1	0	1	0	0	0	1	1	0	0	0
Xylophragma harleyi	0	0	1	0	1	0	0	1	0	0	0
Xylophragma heterocalyx	1	0	1	0	1	0	0	1	0	0	0
Xylophragma myrianthum	0	1	1	0	1	0	0	1	0	0	0
Xylophragma platyphyllum	0	1	1	0	1	0	0	1	0	0	0
Xylophragma pratense	0	1	1	0	1	0	0	1	0	0	0
Xylophragma seemannianum	1	0	1	0	1	0	0	1	0	0	0

Table S2.3. Classification of the species of the tribe Bignonieae (Bignoniaceae) according to the seed dispersal and range size.

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Adenocalymma ackermannii	NA	NA	NA	1	0	0	0
Adenocalymma adenophorum	0	1	0	1	0	0	0
Adenocalymma albiflorum	0	1	0	0	1	0	0
Adenocalymma alboaurantiacum	0	1	0	0	0	1	0
Adenocalymma album	1	0	0	1	0	0	0
Adenocalymma allamandiflorum	0	1	0	0	0	1	0
Adenocalymma apetiolatum	1	0	0	1	0	0	0
Adenocalymma apparicianum	0	1	0	0	1	0	0
Adenocalymma apurense	1	0	0	0	0	0	1
Adenocalymma arthropetiolatum	NA	NA	NA	1	0	0	0
Adenocalymma aspericarpum	1	0	0	0	1	0	0
Adenocalymma aurantiacum	1	0	0	0	1	0	0
Adenocalymma biternatum	1	0	0	0	0	1	0
Adenocalymma bracteatum	0	1	0	0	0	0	1
Adenocalymma bracteolatum	0	1	0	0	0	0	1
Adenocalymma bracteosum	1	0	0	0	0	0	1
Adenocalymma bullatum	1	0	0	1	0	0	0
Adenocalymma calcareum	1	0	0	1	0	0	0
Adenocalymma candolleanum	0	0	1	0	0	1	0
Adenocalymma chocoense	NA	NA	NA	1	0	0	0
Adenocalymma cidii	1	0	0	1	0	0	0
Adenocalymma cinereum	1	0	0	1	0	0	0
Adenocalymma cladotrichum	1	0	0	0	0	0	1
Adenocalymma contractum	1	0	0	0	0	1	0
Adenocalymma coriaceum	1	0	0	0	0	1	0
Adenocalymma cristicalyx	0	1	0	0	1	0	0
Adenocalymma cymbalum	0	1	0	0	1	0	0
Adenocalymma dichilum	0	1	0	0	1	0	0
Adenocalymma divaricatum	0	1	0	0	0	1	0
Adenocalymma dugandii	NA	NA	NA	1	0	0	0
Adenocalymma dusenii	1	0	0	1	0	0	0
Adenocalymma flaviflorum	0	1	0	0	0	0	1

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Adenocalymma flavum	0	1	0	1	0	0	0
Adenocalymma gibbosum	1	0	0	1	0	0	0
Adenocalymma gracielzae	1	0	0	0	1	0	0
Adenocalymma grandifolium	1	0	0	1	0	0	0
Adenocalymma hatschbachii	1	0	0	1	0	0	0
Adenocalymma hirtum	NA	NA	NA	1	0	0	0
Adenocalymma hypostictum	0	0	1	1	0	0	0
Adenocalymma impressum	0	1	0	0	0	0	1
Adenocalymma juliae	1	0	0	1	0	0	0
Adenocalymma lineare	1	0	0	1	0	0	0
Adenocalymma longilineum	0	0	1	0	0	1	0
Adenocalymma macrophyllum	1	0	0	1	0	0	0
Adenocalymma magdalenense	NA	NA	NA	1	0	0	0
Adenocalymma magnificum	1	0	0	0	0	1	0
Adenocalymma marginatum	0	1	0	0	0	1	0
Adenocalymma mirabile	0	0	1	0	1	0	0
Adenocalymma molle	0	1	0	1	0	0	0
Adenocalymma moringifolium	0	1	0	0	1	0	0
Adenocalymma nervosum	NA	NA	NA	1	0	0	0
Adenocalymma nodosum	0	0	1	0	0	1	0
Adenocalymma patulum	0	1	0	0	0	1	0
Adenocalymma paulistarum	0	1	0	0	1	0	0
Adenocalymma pedunculatum	0	1	0	0	0	1	0
Adenocalymma peregrinum	0	1	0	0	0	0	1
Adenocalymma pubescens	0	1	0	0	0	1	0
Adenocalymma salmoneum	1	0	0	1	0	0	0
Adenocalymma sastrei	NA	NA	NA	1	0	0	0
Adenocalymma saulense	0	1	0	1	0	0	0
Adenocalymma scabriusculum	1	0	0	0	0	1	0
Adenocalymma schomburgkii	1	0	0	0	0	0	1
Adenocalymma sessile	1	0	0	1	0	0	0
Adenocalymma subincanum	1	0	0	0	0	0	1
Adenocalymma subsessilifolium	1	0	0	1	0	0	0
Adenocalymma subspicatum	NA	NA	NA	1	0	0	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Adenocalymma tanaeciicarpum	1	0	0	0	0	1	0
Adenocalymma trifoliatum	1	0	0	1	0	0	0
Adenocalymma ubatubense	NA	NA	NA	1	0	0	0
Adenocalymma uleanum	0	1	0	0	1	0	0
Adenocalymma validum	0	1	0	0	0	0	1
Adenocalymma velutinum	1	0	0	1	0	0	0
Amphilophium arenarium	0	1	0	0	1	0	0
Amphilophium aschersonii	0	1	0	0	0	0	1
Amphilophium bauhinioides	0	1	0	0	1	0	0
Amphilophium blanchetii	NA	NA	NA	1	0	0	0
Amphilophium bracteatum	0	1	0	1	0	0	0
Amphilophium buccinatorium	0	1	0	0	1	0	0
Amphilophium campinae	1	0	0	0	0	1	0
Amphilophium carolinae	1	0	0	0	0	1	0
Amphilophium chocoense	NA	NA	NA	1	0	0	0
Amphilophium cremersii	1	0	0	0	1	0	0
Amphilophium crucigerum	0	0	1	0	0	0	1
Amphilophium cuneifolium	0	1	0	1	0	0	0
Amphilophium dasytrichum	0	1	0	0	0	1	0
Amphilophium dolichoides	0	0	1	0	1	0	0
Amphilophium dusenianum	NA	NA	NA	0	1	0	0
Amphilophium ecuadorense	NA	NA	NA	1	0	0	0
Amphilophium elongatum	0	1	0	0	1	0	0
Amphilophium falcatum	1	0	0	0	0	1	0
Amphilophium frutescens	0	0	1	1	0	0	0
Amphilophium gnaphalanthum	NA	NA	NA	0	1	0	0
Amphilophium granulosum	0	1	0	0	0	0	1
Amphilophium lactiflorum	0	1	0	0	1	0	0
Amphilophium laeve	0	1	0	1	0	0	0
Amphilophium laxiflorum	0	1	0	0	1	0	0
Amphilophium lohmanniae	0	1	0	0	1	0	0
Amphilophium magnoliifolium	0	1	0	0	1	0	0
Amphilophium mansoanum	0	1	0	0	0	0	1
Amphilophium monophyllum	0	1	0	1	0	0	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Amphilophium nunezii	NA	NA	NA	0	1	0	0
Amphilophium obovatum	0	1	0	1	0	0	0
Amphilophium occidentale	1	0	0	0	0	1	0
Amphilophium paniculatum	0	1	0	0	0	0	1
Amphilophium pannosum	0	1	0	0	0	0	1
Amphilophium parkeri	0	1	0	0	1	0	0
Amphilophium pauciflorum	NA	NA	NA	1	0	0	0
Amphilophium perbracteatum	NA	NA	NA	1	0	0	0
Amphilophium pilosum	NA	NA	NA	1	0	0	0
Amphilophium porphyrotrichum	0	1	0	0	1	0	0
Amphilophium pulverulentum	0	1	0	0	0	0	1
Amphilophium racemosum	0	1	0	0	0	0	1
Amphilophium reticulatum	0	1	0	1	0	0	0
Amphilophium rodriguesii	0	1	0	0	0	0	1
Amphilophium sandwithii	0	0	1	0	1	0	0
Amphilophium scabriusculum	0	1	0	0	1	0	0
Amphilophium stamineum	NA	NA	NA	1	0	0	0
Amphilophium steyermarkii	0	1	0	0	1	0	0
Anemopaegma acutifolium	0	0	1	0	0	1	0
Anemopaegma alatum	0	0	1	0	1	0	0
Anemopaegma album	0	0	1	0	1	0	0
Anemopaegma arvense	0	0	1	0	0	0	1
Anemopaegma brevipes	NA	NA	NA	0	0	0	1
Anemopaegma chamberlaynii	0	0	1	0	0	1	0
Anemopaegma chrysanthum	0	0	1	0	0	1	0
Anemopaegma chrysoleucum	1	0	0	0	0	0	1
Anemopaegma citrinum	0	0	1	0	1	0	0
Anemopaegma colombianum	NA	NA	NA	0	1	0	0
Anemopaegma flavum	1	0	0	0	0	1	0
Anemopaegma floridum	0	0	1	0	0	0	1
Anemopaegma foetidum	0	0	1	0	0	1	0
Anemopaegma glaucum	0	0	1	0	0	0	1
Anemopaegma goyazense	0	0	1	0	1	0	0
Anemopaegma gracile	0	0	1	0	0	1	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Anemopaegma grandifolium	0	0	1	0	1	0	0
Anemopaegma granvillei	0	0	1	1	0	0	0
Anemopaegma heringeri	NA	NA	NA	1	0	0	0
Anemopaegma hilarianum	0	0	1	0	1	0	0
Anemopaegma insculptum	NA	NA	NA	0	0	1	0
Anemopaegma ionanthum	NA	NA	NA	0	0	1	0
Anemopaegma jucundum	NA	NA	NA	1	0	0	0
Anemopaegma karstenii	0	0	1	0	0	1	0
Anemopaegma laeve	0	0	1	0	0	1	0
Anemopaegma longidens	0	0	1	0	0	0	1
Anemopaegma longipetiolatum	0	0	1	0	1	0	0
Anemopaegma mirabile	NA	NA	NA	1	0	0	0
Anemopaegma nebulosum	0	0	1	1	0	0	0
Anemopaegma oligoneuron	0	0	1	0	0	0	1
Anemopaegma orbiculatum	NA	NA	NA	0	0	1	0
Anemopaegma pabstii	0	0	1	0	0	1	0
Anemopaegma pachyphyllum	NA	NA	NA	1	0	0	0
Anemopaegma paraense	1	0	0	0	0	0	1
Anemopaegma parkeri	0	0	1	0	0	0	1
Anemopaegma patelliforme	NA	NA	NA	0	0	0	1
Anemopaegma prostratum	0	0	1	0	0	1	0
Anemopaegma puberulum	NA	NA	NA	0	0	1	0
Anemopaegma robustum	1	0	0	0	0	1	0
Anemopaegma rugosum	NA	NA	NA	1	0	0	0
Anemopaegma salicifolium	NA	NA	NA	1	0	0	0
Anemopaegma santaritense	0	0	1	0	1	0	0
Anemopaegma scabriusculum	0	0	1	0	0	1	0
Anemopaegma setilobum	0	0	1	1	0	0	0
Anemopaegma velutinum	0	0	1	0	1	0	0
Anemopaegma villosum	NA	NA	NA	1	0	0	0
Bignonia aequinoctialis	0	1	0	0	0	0	1
Bignonia binata	1	0	0	0	0	1	0
Bignonia bracteomana	0	1	0	0	0	1	0
Bignonia callistegioides	1	0	0	0	0	1	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Bignonia campanulata	0	1	0	0	1	0	0
Bignonia capreolata	0	1	0	0	0	1	0
Bignonia cararensis	0	1	0	1	0	0	0
Bignonia corymbosa	0	1	0	0	0	0	1
Bignonia costata	0	1	0	1	0	0	0
Bignonia cuneata	0	1	0	1	0	0	0
Bignonia decora	0	1	0	0	0	1	0
Bignonia diversifolia	0	1	0	0	0	1	0
Bignonia hyacinthina	0	1	0	0	0	0	1
Bignonia lilacina	0	1	0	0	0	0	1
Bignonia longiflora	0	1	0	1	0	0	0
Bignonia magnifica	0	1	0	0	1	0	0
Bignonia microcalyx	0	1	0	0	1	0	0
Bignonia neoheterophylla	0	1	0	0	0	1	0
Bignonia neouliginosa	0	0	1	1	0	0	0
Bignonia nocturna	0	1	0	0	0	0	1
Bignonia noterophila	1	0	0	0	0	0	1
Bignonia phellosperma	1	0	0	0	1	0	0
Bignonia potosina	0	1	0	0	0	1	0
Bignonia prieurii	0	1	0	0	0	0	1
Bignonia pterocalyx	0	0	1	0	1	0	0
Bignonia ramentacea	0	0	1	0	0	1	0
Bignonia sanctae-crucis	0	1	0	0	1	0	0
Bignonia sciuripabulum	0	0	1	0	0	0	1
Bignonia sordida	0	1	0	0	0	0	1
Bignonia uleana	0	1	0	0	0	1	0
Callichlamys latifolia	0	1	0	0	0	0	1
Cuspidaria argentea	0	0	1	0	1	0	0
Cuspidaria bracteata	0	1	0	0	0	1	0
Cuspidaria bracteolata	0	1	0	0	0	1	0
Cuspidaria cinerea	0	1	0	1	0	0	0
Cuspidaria convoluta	0	1	0	0	0	1	0
Cuspidaria cratensis	0	1	0	0	1	0	0
Cuspidaria emmonsii	0	1	0	0	0	1	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Cuspidaria floribunda	0	1	0	0	0	0	1
Cuspidaria inaequalis	0	1	0	0	0	0	1
Cuspidaria lachnaea	0	1	0	0	0	1	0
Cuspidaria lasiantha	0	1	0	0	0	1	0
Cuspidaria lateriflora	0	1	0	0	0	0	1
Cuspidaria monophylla	0	1	0	1	0	0	0
Cuspidaria multiflora	NA	NA	NA	0	1	0	0
Cuspidaria octoptera	0	1	0	0	1	0	0
Cuspidaria pulchella	0	1	0	0	1	0	0
Cuspidaria pulchra	0	1	0	0	0	1	0
Cuspidaria sceptrum	0	1	0	0	0	1	0
Cuspidaria simplicifolia	0	1	0	0	0	1	0
Cuspidaria subincana	0	1	0	0	0	1	0
Cuspidaria weberbaueri	0	1	0	1	0	0	0
Dolichandra chodatii	0	1	0	0	0	1	0
Dolichandra cynanchoides	0	0	1	0	0	0	1
Dolichandra dentata	0	1	0	0	1	0	0
Dolichandra hispida	0	0	1	0	0	0	1
Dolichandra quadrivalvis	0	1	0	0	0	0	1
Dolichandra steyermarkii	0	1	0	0	0	0	1
Dolichandra uncata	1	0	0	0	0	0	1
Dolichandra unguiculata	0	1	0	0	1	0	0
Dolichandra unguis-cati	0	1	0	0	0	0	1
Fridericia arthrerion	0	1	0	0	0	1	0
Fridericia bahiensis	0	1	0	0	0	1	0
Fridericia candicans	0	1	0	0	0	0	1
Fridericia carichanensis	1	0	0	0	1	0	0
Fridericia caudigera	0	1	0	0	0	1	0
Fridericia chica	0	1	0	0	0	0	1
Fridericia cinerea	0	0	1	0	1	0	0
Fridericia cinnamomea	0	1	0	0	0	0	1
Fridericia conjugata	0	1	0	0	0	0	1
Fridericia costaricensis	0	1	0	0	1	0	0
Fridericia crassa	0	1	0	1	0	0	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Fridericia craterophora	0	1	0	0	0	0	1
Fridericia cuneifolia	0	1	0	0	1	0	0
Fridericia dispar	0	0	1	0	0	1	0
Fridericia egensis	0	1	0	0	0	0	1
Fridericia elegans	0	1	0	1	0	0	0
Fridericia erubescens	0	1	0	0	0	1	0
Fridericia fagoides	NA	NA	NA	0	1	0	0
Fridericia fanshawei	0	1	0	0	0	0	1
Fridericia floribunda	NA	NA	NA	0	1	0	0
Fridericia florida	0	1	0	0	0	0	1
Fridericia formosa	0	1	0	0	1	0	0
Fridericia grosourdyana	NA	NA	NA	1	0	0	0
Fridericia japurensis	0	1	0	0	0	0	1
Fridericia lauta	0	1	0	0	1	0	0
Fridericia leucopogon	0	1	0	1	0	0	0
Fridericia limae	0	0	1	0	1	0	0
Fridericia mollis	0	1	0	0	0	1	0
Fridericia mollissima	0	1	0	0	0	1	0
Fridericia mutabilis	0	1	0	0	1	0	0
Fridericia nicotianiflora	NA	NA	NA	0	0	1	0
Fridericia nigrescens	0	1	0	0	0	0	1
Fridericia oligantha	0	1	0	0	1	0	0
Fridericia oxycarpa	0	1	0	0	0	1	0
Fridericia patellifera	0	1	0	0	0	0	1
Fridericia pearcei	0	1	0	0	0	1	0
Fridericia platyphylla	0	0	1	0	0	0	1
Fridericia pliciflora	NA	NA	NA	1	0	0	0
Fridericia podopogon	0	1	0	0	1	0	0
Fridericia poeppigii	0	1	0	0	0	1	0
Fridericia prancei	0	1	0	0	0	0	1
Fridericia pubescens	0	0	1	0	0	0	1
Fridericia rego	0	1	0	0	1	0	0
Fridericia samydoides	0	1	0	0	0	1	0
Fridericia schumanniana	0	1	0	0	0	0	1

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Fridericia simplex	0	0	1	0	1	0	0
Fridericia speciosa	0	1	0	0	0	1	0
Fridericia spicata	0	1	0	0	0	0	1
Fridericia subexserta	NA	NA	NA	1	0	0	0
Fridericia subincana	0	1	0	1	0	0	0
Fridericia subverticillata	0	0	1	1	0	0	0
Fridericia trachyphylla	0	1	0	0	1	0	0
Fridericia trailii	0	1	0	0	0	0	1
Fridericia triplinervia	0	1	0	0	0	0	1
Fridericia truncata	NA	NA	NA	0	0	1	0
Fridericia tuberculata	0	1	0	0	0	0	1
Fridericia tynanthoides	0	1	0	1	0	0	0
Fridericia viscida	NA	NA	NA	0	0	1	0
Fridericia whitei	NA	NA	NA	1	0	0	0
Lundia corymbifera	0	1	0	0	0	0	1
Lundia damazioi	0	1	0	1	0	0	0
Lundia densiflora	0	1	0	0	0	0	1
Lundia erionema	0	1	0	0	0	0	1
Lundia gardneri	0	1	0	0	1	0	0
Lundia helicocalyx	0	1	0	0	1	0	0
Lundia laevis	0	1	0	0	0	1	0
Lundia longa	0	1	0	0	0	1	0
Lundia nitidula	0	1	0	0	0	1	0
Lundia obliqua	0	1	0	0	1	0	0
Lundia puberula	0	1	0	0	0	0	1
Lundia spruceana	0	1	0	0	0	1	0
Lundia virginalis	0	1	0	0	0	1	0
Manaosella cordifolia	0	1	0	0	0	0	1
Mansoa alliacea	0	1	0	0	0	0	1
Mansoa angustidens	0	1	0	0	1	0	0
Mansoa difficilis	0	1	0	0	0	0	1
Mansoa gentryi	0	1	0	0	1	0	0
Mansoa glaziovii	0	0	1	0	1	0	0
Mansoa hirsuta	0	0	1	0	1	0	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Mansoa hymenaea	0	1	0	1	0	0	0
Mansoa ivanii	0	1	0	1	0	0	0
Mansoa lanceolata	0	1	0	0	1	0	0
Mansoa longicalyx	0	1	0	1	0	0	0
Mansoa minensis	0	1	0	1	0	0	0
Mansoa onohualcoides	0	1	0	0	1	0	0
Mansoa paganuccii	0	1	0	0	1	0	0
Mansoa parvifolia	0	1	0	0	0	1	0
Mansoa sagotii	0	1	0	0	0	0	1
Mansoa standleyi	0	1	0	0	0	0	1
Mansoa verrucifera	0	1	0	0	0	0	1
Martinella insignis	0	1	0	1	0	0	0
Martinella iquitoensis	0	1	0	0	0	1	0
Martinella obovata	0	1	0	0	0	0	1
Pachyptera aromatica	0	1	0	0	1	0	0
Pachyptera erythraea	0	1	0	1	0	0	0
Pachyptera kerere	1	0	0	0	0	0	1
Pachyptera ventricosa	NA	NA	NA	1	0	0	0
Perianthomega vellozoi	0	1	0	0	0	1	0
Pleonotoma bracteata	0	1	0	0	1	0	0
Pleonotoma castelnaei	NA	NA	NA	0	0	1	0
Pleonotoma clematis	0	1	0	0	0	0	1
Pleonotoma dendrotricha	0	1	0	1	0	0	0
Pleonotoma echitidea	0	1	0	0	1	0	0
Pleonotoma exserta	0	1	0	1	0	0	0
Pleonotoma fissicalyx	NA	NA	NA	1	0	0	0
Pleonotoma fluminensis	NA	NA	NA	1	0	0	0
Pleonotoma jasminifolia	0	1	0	0	0	1	0
Pleonotoma longiflora	NA	NA	NA	1	0	0	0
Pleonotoma melioides	0	1	0	0	0	0	1
Pleonotoma orientalis	0	1	0	0	0	1	0
Pleonotoma pavettiflora	0	1	0	0	0	1	0
Pleonotoma stichadenia	0	1	0	0	0	1	0
Pleonotoma tetraquetra	0	1	0	0	0	1	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Pleonotoma variabilis	0	1	0	0	0	0	1
Pyrostegia millingtonioides	NA	NA	NA	0	1	0	0
Pyrostegia venusta	0	1	0	0	0	0	1
Stizophyllum inaequilaterum	0	1	0	0	0	0	1
Stizophyllum perforatum	0	1	0	0	0	1	0
Stizophyllum riparium	0	1	0	0	0	0	1
Tanaecium affine	0	1	0	0	0	1	0
Tanaecium apiculatum	NA	NA	NA	1	0	0	0
Tanaecium bilabiatum	1	0	0	0	0	0	1
Tanaecium caudiculatum	0	1	0	0	1	0	0
Tanaecium crucigerum	1	0	0	0	1	0	0
Tanaecium cyrtanthum	0	1	0	0	1	0	0
Tanaecium dichotomum	0	1	0	0	0	0	1
Tanaecium duckei	0	1	0	0	0	1	0
Tanaecium exitiosum	NA	NA	NA	1	0	0	0
Tanaecium jaroba	1	0	0	0	0	0	1
Tanaecium neobrasiliense	0	1	0	0	1	0	0
Tanaecium ornithophilum	0	1	0	0	0	1	0
Tanaecium paradoxum	0	0	1	0	1	0	0
Tanaecium parviflorum	0	1	0	0	1	0	0
Tanaecium pyramidatum	0	1	0	0	0	0	1
Tanaecium revillae	1	0	0	0	1	0	0
Tanaecium selloi	0	0	1	0	0	1	0
Tanaecium tetragonolobum	0	1	0	0	0	0	1
Tanaecium tetramerum	0	NA	NA	1	0	0	0
Tanaecium truncatum	0	1	0	0	0	1	0
Tanaecium xanthophyllum	0	1	0	0	0	1	0
Tynanthus cognatus	0	1	0	0	0	1	0
Tynanthus croatianus	0	1	0	1	0	0	0
Tynanthus densiflorus	NA	NA	NA	1	0	0	0
Tynanthus espiritosantensis	NA	NA	NA	1	0	0	0
Tynanthus fasciculatus	0	1	0	0	1	0	0
Tynanthus guatemalensis	0	1	0	0	1	0	0
Tynanthus labiatus	0	1	0	0	1	0	0

Species	Seed dispersal			Range size			
	Water	Wind - linear wings	Wind - ellipsoid wings	Small	Small to medium	Medium to large	Large
Tynanthus macranthus	NA	NA	NA	1	0	0	0
Tynanthus micranthus	0	1	0	0	1	0	0
Tynanthus panurensis	0	1	0	0	0	1	0
Tynanthus polyanthus	0	1	0	0	0	0	1
Tynanthus pubescens	0	1	0	0	0	0	1
Tynanthus sastrei	NA	NA	NA	1	0	0	0
Tynanthus schumannianus	0	1	0	0	0	0	1
Xylophragma corchoroides	0	1	0	0	1	0	0
Xylophragma harleyi	0	1	0	0	1	0	0
Xylophragma heterocalyx	NA	NA	NA	0	1	0	0
Xylophragma myrianthum	0	1	0	0	1	0	0
Xylophragma platyphyllum	0	0	1	0	0	1	0
Xylophragma pratense	0	1	0	0	0	0	1
Xylophragma seemannianum	0	1	0	0	0	0	1

Table S2.4. Classification of the species of the tribe Bignonieae (Bignoniaceae) according to the genera and root distance.

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Adenocalymma ackermannii	1	0	0	0	0	1	0
Adenocalymma adenophorum	1	0	0	0	0	1	0
Adenocalymma albiflorum	1	0	0	0	0	1	0
Adenocalymma alboaurantiacum	1	0	0	0	0	1	0
Adenocalymma album	1	0	0	0	0	1	0
Adenocalymma allamandiflorum	1	0	0	0	0	1	0
Adenocalymma apetiolatum	1	0	0	0	0	1	0
Adenocalymma apparicianum	1	0	0	0	0	1	0
Adenocalymma apurense	1	0	0	0	0	1	0
Adenocalymma arthropetiolatum	1	0	0	0	0	1	0
Adenocalymma aspericarpum	1	0	0	0	0	1	0
Adenocalymma aurantiacum	1	0	0	0	0	1	0
Adenocalymma biternatum	1	0	0	0	0	1	0
Adenocalymma bracteatum	1	0	0	0	0	1	0
Adenocalymma bracteolatum	1	0	0	0	0	1	0
Adenocalymma bracteosum	1	0	0	0	0	1	0
Adenocalymma bullatum	1	0	0	0	0	1	0
Adenocalymma calcareum	1	0	0	0	0	1	0
Adenocalymma candolleanum	1	0	0	0	0	1	0
Adenocalymma chocoense	1	0	0	0	0	1	0
Adenocalymma cidii	1	0	0	0	0	1	0
Adenocalymma cinereum	1	0	0	0	0	1	0
Adenocalymma cladotrichum	1	0	0	0	0	1	0
Adenocalymma contractum	1	0	0	0	0	1	0
Adenocalymma coriaceum	1	0	0	0	0	1	0
Adenocalymma cristicalyx	1	0	0	0	0	1	0
Adenocalymma cymbalum	1	0	0	0	0	1	0
Adenocalymma dichilum	1	0	0	0	0	1	0
Adenocalymma divaricatum	1	0	0	0	0	1	0
Adenocalymma dugandii	1	0	0	0	0	1	0
Adenocalymma dusenii	1	0	0	0	0	1	0
Adenocalymma flaviflorum	1	0	0	0	0	1	0

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Adenocalymma flavum	1	0	0	0	0	1	0
Adenocalymma gibbosum	1	0	0	0	0	1	0
Adenocalymma gracielzae	1	0	0	0	0	1	0
Adenocalymma grandifolium	1	0	0	0	0	1	0
Adenocalymma hatschbachii	1	0	0	0	0	1	0
Adenocalymma hirtum	1	0	0	0	0	1	0
Adenocalymma hypostictum	1	0	0	0	0	1	0
Adenocalymma impressum	1	0	0	0	0	1	0
Adenocalymma juliae	1	0	0	0	0	1	0
Adenocalymma lineare	1	0	0	0	0	1	0
Adenocalymma longilineum	1	0	0	0	0	1	0
Adenocalymma macrophyllum	1	0	0	0	0	1	0
Adenocalymma magdalenense	1	0	0	0	0	1	0
Adenocalymma magnificum	1	0	0	0	0	1	0
Adenocalymma marginatum	1	0	0	0	0	1	0
Adenocalymma mirabile	1	0	0	0	0	1	0
Adenocalymma molle	1	0	0	0	0	1	0
Adenocalymma moringifolium	1	0	0	0	0	1	0
Adenocalymma nervosum	1	0	0	0	0	1	0
Adenocalymma nodosum	1	0	0	0	0	1	0
Adenocalymma patulum	1	0	0	0	0	1	0
Adenocalymma paulistarum	1	0	0	0	0	1	0
Adenocalymma pedunculatum	1	0	0	0	0	1	0
Adenocalymma peregrinum	1	0	0	0	0	1	0
Adenocalymma pubescens	1	0	0	0	0	1	0
Adenocalymma salmoneum	1	0	0	0	0	1	0
Adenocalymma sastrei	1	0	0	0	0	1	0
Adenocalymma saulense	1	0	0	0	0	1	0
Adenocalymma scabriusculum	1	0	0	0	0	1	0
Adenocalymma schomburgkii	1	0	0	0	0	1	0
Adenocalymma sessile	1	0	0	0	0	1	0
Adenocalymma subincanum	1	0	0	0	0	1	0
Adenocalymma subsessilifolium	1	0	0	0	0	1	0
Adenocalymma subspicatum	1	0	0	0	0	1	0

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Adenocalymma tanaeciicarpum	1	0	0	0	0	1	0
Adenocalymma trifoliatum	1	0	0	0	0	1	0
Adenocalymma ubatubense	1	0	0	0	0	1	0
Adenocalymma uleanum	1	0	0	0	0	1	0
Adenocalymma validum	1	0	0	0	0	1	0
Adenocalymma velutinum	1	0	0	0	0	1	0
Amphilophium arenarium	0	1	0	0	0	1	0
Amphilophium aschersonii	0	1	0	0	0	1	0
Amphilophium bauhinioides	0	1	0	0	0	1	0
Amphilophium blanchetii	0	1	0	0	0	1	0
Amphilophium bracteatum	0	1	0	0	0	1	0
Amphilophium buccinatorium	0	1	0	0	0	1	0
Amphilophium campinae	0	1	0	0	0	1	0
Amphilophium carolinae	0	1	0	0	0	1	0
Amphilophium chocoense	0	1	0	0	0	1	0
Amphilophium cremersii	0	1	0	0	0	1	0
Amphilophium crucigerum	0	1	0	0	0	1	0
Amphilophium cuneifolium	0	1	0	0	0	1	0
Amphilophium dasytrichum	0	1	0	0	0	1	0
Amphilophium dolichoides	0	1	0	0	0	1	0
Amphilophium dusenianum	0	1	0	0	0	1	0
Amphilophium ecuadorense	0	1	0	0	0	1	0
Amphilophium elongatum	0	1	0	0	0	1	0
Amphilophium falcatum	0	1	0	0	0	1	0
Amphilophium frutescens	0	1	0	0	0	1	0
Amphilophium gnaphalanthum	0	1	0	0	0	1	0
Amphilophium granulosum	0	1	0	0	0	1	0
Amphilophium lactiflorum	0	1	0	0	0	1	0
Amphilophium laeve	0	1	0	0	0	1	0
Amphilophium laxiflorum	0	1	0	0	0	1	0
Amphilophium lohmanniae	0	1	0	0	0	1	0
Amphilophium magnoliifolium	0	1	0	0	0	1	0
Amphilophium mansoanum	0	1	0	0	0	1	0
Amphilophium monophyllum	0	1	0	0	0	1	0

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Amphilophium nunezii	0	1	0	0	0	1	0
Amphilophium obovatum	0	1	0	0	0	1	0
Amphilophium occidentale	0	1	0	0	0	1	0
Amphilophium paniculatum	0	1	0	0	0	1	0
Amphilophium pannosum	0	1	0	0	0	1	0
Amphilophium parkeri	0	1	0	0	0	1	0
Amphilophium pauciflorum	0	1	0	0	0	1	0
Amphilophium perbracteatum	0	1	0	0	0	1	0
Amphilophium pilosum	0	1	0	0	0	1	0
Amphilophium porphyrotrichum	0	1	0	0	0	1	0
Amphilophium pulverulentum	0	1	0	0	0	1	0
Amphilophium racemosum	0	1	0	0	0	1	0
Amphilophium reticulatum	0	1	0	0	0	1	0
Amphilophium rodriguesii	0	1	0	0	0	1	0
Amphilophium sandwithii	0	1	0	0	0	1	0
Amphilophium scabriusculum	0	1	0	0	0	1	0
Amphilophium stamineum	0	1	0	0	0	1	0
Amphilophium steyermarkii	0	1	0	0	0	1	0
Anemopaegma acutifolium	0	0	1	0	0	0	1
Anemopaegma alatum	0	0	1	0	0	0	1
Anemopaegma album	0	0	1	0	0	0	1
Anemopaegma arvense	0	0	1	0	0	0	1
Anemopaegma brevipes	0	0	1	0	0	0	1
Anemopaegma chamberlaynii	0	0	1	0	0	0	1
Anemopaegma chrysanthum	0	0	1	0	0	0	1
Anemopaegma chrysoleucum	0	0	1	0	0	0	1
Anemopaegma citrinum	0	0	1	0	0	0	1
Anemopaegma colombianum	0	0	1	0	0	0	1
Anemopaegma flavum	0	0	1	0	0	0	1
Anemopaegma floridum	0	0	1	0	0	0	1
Anemopaegma foetidum	0	0	1	0	0	0	1
Anemopaegma glaucum	0	0	1	0	0	0	1
Anemopaegma goyazense	0	0	1	0	0	0	1
Anemopaegma gracile	0	0	1	0	0	0	1

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	**Early-diverging**	**Late-diverging**
Anemopaegma grandifolium	0	0	1	0	0	0	1
Anemopaegma granvillei	0	0	1	0	0	0	1
Anemopaegma heringeri	0	0	1	0	0	0	1
Anemopaegma hilarianum	0	0	1	0	0	0	1
Anemopaegma insculptum	0	0	1	0	0	0	1
Anemopaegma ionanthum	0	0	1	0	0	0	1
Anemopaegma jucundum	0	0	1	0	0	0	1
Anemopaegma karstenii	0	0	1	0	0	0	1
Anemopaegma laeve	0	0	1	0	0	0	1
Anemopaegma longidens	0	0	1	0	0	0	1
Anemopaegma longipetiolatum	0	0	1	0	0	0	1
Anemopaegma mirabile	0	0	1	0	0	0	1
Anemopaegma nebulosum	0	0	1	0	0	0	1
Anemopaegma oligoneuron	0	0	1	0	0	0	1
Anemopaegma orbiculatum	0	0	1	0	0	0	1
Anemopaegma pabstii	0	0	1	0	0	0	1
Anemopaegma pachyphyllum	0	0	1	0	0	0	1
Anemopaegma paraense	0	0	1	0	0	0	1
Anemopaegma parkeri	0	0	1	0	0	0	1
Anemopaegma patelliforme	0	0	1	0	0	0	1
Anemopaegma prostratum	0	0	1	0	0	0	1
Anemopaegma puberulum	0	0	1	0	0	0	1
Anemopaegma robustum	0	0	1	0	0	0	1
Anemopaegma rugosum	0	0	1	0	0	0	1
Anemopaegma salicifolium	0	0	1	0	0	0	1
Anemopaegma santaritense	0	0	1	0	0	0	1
Anemopaegma scabriusculum	0	0	1	0	0	0	1
Anemopaegma setilobum	0	0	1	0	0	0	1
Anemopaegma velutinum	0	0	1	0	0	0	1
Anemopaegma villosum	0	0	1	0	0	0	1
Bignonia aequinoctialis	0	0	0	1	0	0	0
Bignonia binata	0	0	0	1	0	0	0
Bignonia bracteomana	0	0	0	1	0	0	0
Bignonia callistegioides	0	0	0	1	0	0	0

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	**Early-diverging**	**Late-diverging**
Bignonia campanulata	0	0	0	1	0	0	0
Bignonia capreolata	0	0	0	1	0	0	0
Bignonia cararensis	0	0	0	1	0	0	0
Bignonia corymbosa	0	0	0	1	0	0	0
Bignonia costata	0	0	0	1	0	0	0
Bignonia cuneata	0	0	0	1	0	0	0
Bignonia decora	0	0	0	1	0	0	0
Bignonia diversifolia	0	0	0	1	0	0	0
Bignonia hyacinthina	0	0	0	1	0	0	0
Bignonia lilacina	0	0	0	1	0	0	0
Bignonia longiflora	0	0	0	1	0	0	0
Bignonia magnifica	0	0	0	1	0	0	0
Bignonia microcalyx	0	0	0	1	0	0	0
Bignonia neoheterophylla	0	0	0	1	0	0	0
Bignonia neouliginosa	0	0	0	1	0	0	0
Bignonia nocturna	0	0	0	1	0	0	0
Bignonia noterophila	0	0	0	1	0	0	0
Bignonia phellosperma	0	0	0	1	0	0	0
Bignonia potosina	0	0	0	1	0	0	0
Bignonia prieurii	0	0	0	1	0	0	0
Bignonia pterocalyx	0	0	0	1	0	0	0
Bignonia ramentacea	0	0	0	1	0	0	0
Bignonia sanctae-crucis	0	0	0	1	0	0	0
Bignonia sciuripabulum	0	0	0	1	0	0	0
Bignonia sordida	0	0	0	1	0	0	0
Bignonia uleana	0	0	0	1	0	0	0
Callichlamys latifolia	0	0	0	0	0	NA	NA
Cuspidaria argentea	0	0	0	0	0	0	1
Cuspidaria bracteata	0	0	0	0	0	0	1
Cuspidaria bracteolata	0	0	0	0	0	0	1
Cuspidaria cinerea	0	0	0	0	0	0	1
Cuspidaria convoluta	0	0	0	0	0	0	1
Cuspidaria cratensis	0	0	0	0	0	0	1
Cuspidaria emmonsii	0	0	0	0	0	0	1

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Cuspidaria floribunda	0	0	0	0	0	0	1
Cuspidaria inaequalis	0	0	0	0	0	0	1
Cuspidaria lachnaea	0	0	0	0	0	0	1
Cuspidaria lasiantha	0	0	0	0	0	0	1
Cuspidaria lateriflora	0	0	0	0	0	0	1
Cuspidaria monophylla	0	0	0	0	0	0	1
Cuspidaria multiflora	0	0	0	0	0	0	1
Cuspidaria octoptera	0	0	0	0	0	0	1
Cuspidaria pulchella	0	0	0	0	0	0	1
Cuspidaria pulchra	0	0	0	0	0	0	1
Cuspidaria sceptrum	0	0	0	0	0	0	1
Cuspidaria simplicifolia	0	0	0	0	0	0	1
Cuspidaria subincana	0	0	0	0	0	0	1
Cuspidaria weberbaueri	0	0	0	0	0	0	1
Dolichandra chodatii	0	0	0	0	0	1	0
Dolichandra cynanchoides	0	0	0	0	0	1	0
Dolichandra dentata	0	0	0	0	0	1	0
Dolichandra hispida	0	0	0	0	0	1	0
Dolichandra quadrivalvis	0	0	0	0	0	1	0
Dolichandra steyermarkii	0	0	0	0	0	1	0
Dolichandra uncata	0	0	0	0	0	1	0
Dolichandra unguiculata	0	0	0	0	0	1	0
Dolichandra unguis-cati	0	0	0	0	0	1	0
Fridericia arthrerion	0	0	0	0	1	0	1
Fridericia bahiensis	0	0	0	0	1	0	1
Fridericia candicans	0	0	0	0	1	0	1
Fridericia carichanensis	0	0	0	0	1	0	1
Fridericia caudigera	0	0	0	0	1	0	1
Fridericia chica	0	0	0	0	1	0	1
Fridericia cinerea	0	0	0	0	1	0	1
Fridericia cinnamomea	0	0	0	0	1	0	1
Fridericia conjugata	0	0	0	0	1	0	1
Fridericia costaricensis	0	0	0	0	1	0	1
Fridericia crassa	0	0	0	0	1	0	1

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Fridericia craterophora	0	0	0	0	1	0	1
Fridericia cuneifolia	0	0	0	0	1	0	1
Fridericia dispar	0	0	0	0	1	0	1
Fridericia egensis	0	0	0	0	1	0	1
Fridericia elegans	0	0	0	0	1	0	1
Fridericia erubescens	0	0	0	0	1	0	1
Fridericia fagoides	0	0	0	0	1	0	1
Fridericia fanshawei	0	0	0	0	1	0	1
Fridericia floribunda	0	0	0	0	1	0	1
Fridericia florida	0	0	0	0	1	0	1
Fridericia formosa	0	0	0	0	1	0	1
Fridericia grosourdyana	0	0	0	0	1	0	1
Fridericia japurensis	0	0	0	0	1	0	1
Fridericia lauta	0	0	0	0	1	0	1
Fridericia leucopogon	0	0	0	0	1	0	1
Fridericia limae	0	0	0	0	1	0	1
Fridericia mollis	0	0	0	0	1	0	1
Fridericia mollissima	0	0	0	0	1	0	1
Fridericia mutabilis	0	0	0	0	1	0	1
Fridericia nicotianiflora	0	0	0	0	1	0	1
Fridericia nigrescens	0	0	0	0	1	0	1
Fridericia oligantha	0	0	0	0	1	0	1
Fridericia oxycarpa	0	0	0	0	1	0	1
Fridericia patellifera	0	0	0	0	1	0	1
Fridericia pearcei	0	0	0	0	1	0	1
Fridericia platyphylla	0	0	0	0	1	0	1
Fridericia pliciflora	0	0	0	0	1	0	1
Fridericia podopogon	0	0	0	0	1	0	1
Fridericia poeppigii	0	0	0	0	1	0	1
Fridericia prancei	0	0	0	0	1	0	1
Fridericia pubescens	0	0	0	0	1	0	1
Fridericia rego	0	0	0	0	1	0	1
Fridericia samydoides	0	0	0	0	1	0	1
Fridericia schumanniana	0	0	0	0	1	0	1

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	**Early-diverging**	**Late-diverging**
Fridericia simplex	0	0	0	0	1	0	1
Fridericia speciosa	0	0	0	0	1	0	1
Fridericia spicata	0	0	0	0	1	0	1
Fridericia subexserta	0	0	0	0	1	0	1
Fridericia subincana	0	0	0	0	1	0	1
Fridericia subverticillata	0	0	0	0	1	0	1
Fridericia trachyphylla	0	0	0	0	1	0	1
Fridericia trailii	0	0	0	0	1	0	1
Fridericia triplinervia	0	0	0	0	1	0	1
Fridericia truncata	0	0	0	0	1	0	1
Fridericia tuberculata	0	0	0	0	1	0	1
Fridericia tynanthoides	0	0	0	0	1	0	1
Fridericia viscida	0	0	0	0	1	0	1
Fridericia whitei	0	0	0	0	1	0	1
Lundia corymbifera	0	0	0	0	0	0	1
Lundia damazioi	0	0	0	0	0	0	1
Lundia densiflora	0	0	0	0	0	0	1
Lundia erionema	0	0	0	0	0	0	1
Lundia gardneri	0	0	0	0	0	0	1
Lundia helicocalyx	0	0	0	0	0	0	1
Lundia laevis	0	0	0	0	0	0	1
Lundia longa	0	0	0	0	0	0	1
Lundia nitidula	0	0	0	0	0	0	1
Lundia obliqua	0	0	0	0	0	0	1
Lundia puberula	0	0	0	0	0	0	1
Lundia spruceana	0	0	0	0	0	0	1
Lundia virginalis	0	0	0	0	0	0	1
Manaosella cordifolia	0	0	0	0	0	1	0
Mansoa alliacea	0	0	0	0	0	0	0
Mansoa angustidens	0	0	0	0	0	0	0
Mansoa difficilis	0	0	0	0	0	0	0
Mansoa gentryi	0	0	0	0	0	0	0
Mansoa glaziovii	0	0	0	0	0	0	0
Mansoa hirsuta	0	0	0	0	0	0	0

185

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Mansoa hymenaea	0	0	0	0	0	0	0
Mansoa ivanii	0	0	0	0	0	0	0
Mansoa lanceolata	0	0	0	0	0	0	0
Mansoa longicalyx	0	0	0	0	0	0	0
Mansoa minensis	0	0	0	0	0	0	0
Mansoa onohualcoides	0	0	0	0	0	0	0
Mansoa paganuccii	0	0	0	0	0	0	0
Mansoa parvifolia	0	0	0	0	0	0	0
Mansoa sagotii	0	0	0	0	0	0	0
Mansoa standleyi	0	0	0	0	0	0	0
Mansoa verrucifera	0	0	0	0	0	0	0
Martinella insignis	0	0	0	0	0	1	0
Martinella iquitoensis	0	0	0	0	0	1	0
Martinella obovata	0	0	0	0	0	1	0
Pachyptera aromatica	0	0	0	0	0	1	0
Pachyptera erythraea	0	0	0	0	0	1	0
Pachyptera kerere	0	0	0	0	0	1	0
Pachyptera ventricosa	0	0	0	0	0	1	0
Perianthomega vellozoi	0	0	0	0	0	1	0
Pleonotoma bracteata	0	0	0	0	0	1	0
Pleonotoma castelnaei	0	0	0	0	0	1	0
Pleonotoma clematis	0	0	0	0	0	1	0
Pleonotoma dendrotricha	0	0	0	0	0	1	0
Pleonotoma echitidea	0	0	0	0	0	1	0
Pleonotoma exserta	0	0	0	0	0	1	0
Pleonotoma fissicalyx	0	0	0	0	0	1	0
Pleonotoma fluminensis	0	0	0	0	0	1	0
Pleonotoma jasminifolia	0	0	0	0	0	1	0
Pleonotoma longiflora	0	0	0	0	0	1	0
Pleonotoma melioides	0	0	0	0	0	1	0
Pleonotoma orientalis	0	0	0	0	0	1	0
Pleonotoma pavettiflora	0	0	0	0	0	1	0
Pleonotoma stichadenia	0	0	0	0	0	1	0
Pleonotoma tetraquetra	0	0	0	0	0	1	0

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Pleonotoma variabilis	0	0	0	0	0	1	0
Pyrostegia millingtonioides	0	0	0	0	0	0	1
Pyrostegia venusta	0	0	0	0	0	0	1
Stizophyllum inaequilaterum	0	0	0	0	0	1	0
Stizophyllum perforatum	0	0	0	0	0	1	0
Stizophyllum riparium	0	0	0	0	0	1	0
Tanaecium affine	0	0	0	0	0	0	0
Tanaecium apiculatum	0	0	0	0	0	0	0
Tanaecium bilabiatum	0	0	0	0	0	0	0
Tanaecium caudiculatum	0	0	0	0	0	0	0
Tanaecium crucigerum	0	0	0	0	0	0	0
Tanaecium cyrtanthum	0	0	0	0	0	0	0
Tanaecium dichotomum	0	0	0	0	0	0	0
Tanaecium duckei	0	0	0	0	0	0	0
Tanaecium exitiosum	0	0	0	0	0	0	0
Tanaecium jaroba	0	0	0	0	0	0	0
Tanaecium neobrasiliense	0	0	0	0	0	0	0
Tanaecium ornithophilum	0	0	0	0	0	0	0
Tanaecium paradoxum	0	0	0	0	0	0	0
Tanaecium parviflorum	0	0	0	0	0	0	0
Tanaecium pyramidatum	0	0	0	0	0	0	0
Tanaecium revillae	0	0	0	0	0	0	0
Tanaecium selloi	0	0	0	0	0	0	0
Tanaecium tetragonolobum	0	0	0	0	0	0	0
Tanaecium tetramerum	0	0	0	0	0	0	0
Tanaecium truncatum	0	0	0	0	0	0	0
Tanaecium xanthophyllum	0	0	0	0	0	0	0
Tynanthus cognatus	0	0	0	0	0	0	1
Tynanthus croatianus	0	0	0	0	0	0	1
Tynanthus densiflorus	0	0	0	0	0	0	1
Tynanthus espiritosantensis	0	0	0	0	0	0	1
Tynanthus fasciculatus	0	0	0	0	0	0	1
Tynanthus guatemalensis	0	0	0	0	0	0	1
Tynanthus labiatus	0	0	0	0	0	0	1

Species	Genera of the tribe					Root distance	
	Adenocalymma	*Amphilophium*	*Anemopaegma*	*Bignonia*	*Fridericia*	Early-diverging	Late-diverging
Tynanthus macranthus	0	0	0	0	0	0	1
Tynanthus micranthus	0	0	0	0	0	0	1
Tynanthus panurensis	0	0	0	0	0	0	1
Tynanthus polyanthus	0	0	0	0	0	0	1
Tynanthus pubescens	0	0	0	0	0	0	1
Tynanthus sastrei	0	0	0	0	0	0	1
Tynanthus schumannianus	0	0	0	0	0	0	1
Xylophragma corchoroides	0	0	0	0	0	0	1
Xylophragma harleyi	0	0	0	0	0	0	1
Xylophragma heterocalyx	0	0	0	0	0	0	1
Xylophragma myrianthum	0	0	0	0	0	0	1
Xylophragma platyphyllum	0	0	0	0	0	0	1
Xylophragma pratense	0	0	0	0	0	0	1
Xylophragma seemannianum	0	0	0	0	0	0	1

Table S2.5. Environmental variables compiled for the analyses. *: Environmental variables selected as predictors for variation partitioning analyses; 1: Jarvis et al. (2008); 2: Lima-Ribeiro et al. (2015); and 3: FAO (2012).

	Code	Variable	Unit	Source
Climate variables	ALT_MEAN	Mean altitude	m	1
	ALT_RANGE	Range in altitude*	m	1
	Bio1	Annual mean temperature*	°C	2
	Bio2	Mean diurnal range	°C	2
	Bio3	Isothermality	%	2
	Bio4	Temperature seasonality*	%	2
	Bio5	Max temperature of warmest month	°C	2
	Bio6	Min temperature of coldest month	°C	2
	Bio7	Temperature annual range	°C	2
	Bio8	Mean temperature of wettest quarter	°C	2
	Bio9	Mean temperature of driest quarter	°C	2
	Bio10	Mean temperature of warmest quarter	°C	2
	Bio11	Mean temperature of coldest quarter	°C	2
	Bio12	Annual precipitation*	mm/m^2	2
	Bio13	Precipitation of wettest month	mm/m^2	2
	Bio14	Precipitation of driest month	mm/m^2	2
	Bio15	Precipitation seasonality*	%	2
	Bio16	Precipitation of wettest quarter	mm/m^2	2
	Bio17	Precipitation of driest quarter	mm/m^2	2
	Bio18	Precipitation of warmest quarter	mm/m^2	2
	Bio19	Precipitation of coldest quarter	mm/m^2	2
Edaphic variables	Soil_types	Number of soil types*	-	3
	T_GRAVEL	Top-soil gravel content*	%	3
	T_SAND	Top-soil sand fraction	%	3
	T_SILT	Top-soil silt fraction	%	3
	T_CLAY	Top-soil clay fraction*	%	3
	T_BULK_DENSITY	Top-soil bulk density	kg/dm^3	3

	Code	**Variable**	**Unit**	**Source**
Edaphic	T_OC	Top-soil organic carbon	% weight	3
variables	T_PH_H2O	Top-soil pH (H_2O)*	-	3
	T_CEC_SOIL	Top-soil cation exchange capacity of soil	cmol/kg	3
	T_BS	Top-soil base saturation	%	3
	T_TEB	Top-soil total exchangeable bases*	cmol/kg	3
	T_CACO3	Top-soil calcium carbonate	% weight	3
	T_CASO4	Top-soil gypsum*	% weight	3
	T_ESP	Top-soil sodicity	%	3
	T_ECE	Top-soil salinity*	dS/m	3

Table S2.6. Variation partitioning of richness pattern and species ranges of each ecological, geographical, and evolutionary attribute. 'EX.DEC' and 'DEC' are the acronyms of extreme deconstruction and richness deconstruction, respectively. The last three columns represent different Pearson's r correlations: Correlation II or 'cor(DEC.tribe, EX.DEC.attrib)' is the correlation of variation partitioning of the overall tribe richness and species ranges of each subset of species; Correlation III or 'cor(DEC.tribe, DEC.attrib)' is the correlation of variation partitioning of the overall tribe richness and the richness pattern of each subset of species; and Correlation IV or 'cor(DEC.attrib, EX.DEC.attrib)' is the correlation of variation partitioning of richness pattern and species ranges of each subset of species. Confidence intervals correspond to 95% of the greatest correlation values expected if species would be randomly selected for the variation partitioning. Bold values represent correlation lower than expected by chance (i.e., significant correlations). 'N' is the number of species considered to obtain the variation partitioning results.

Species attributes	N	Variation partitioning								Correlation (Confidence interval – 95%)		
		Climate	Soil	Space	Climate & Soil	Soil & Space	Climate & Space	All components	Resi-dual	Correlation II	Correlation III	Correlation IV
Ecological attributes												
Plant life-form – Liana												
DEC.attrib	341	0.04	0.01	0.27	0.03	0.10	0.26	0.18	0.11	0.97	1.00	0.97
EX.DEC.attrib	250	< 0.01	< 0.01	0.28	< 0.01	0.09	0.23	0.11	0.04	(0.93 - 0.99)	(0.82 - 1.00)	(0.71 - 0.99)
Plant life-form – Shrub												
DEC.attrib	39	0.03	0.01	0.31	< 0.01	0.03	0.30	0.09	0.24	0.90	0.85	0.77
EX.DEC.attrib	22	< 0.01	< 0.01	0.27	< 0.01	0.07	0.33	0.09	< 0.01	(0.74 - 0.99)	(0.46 - 0.99)	(0.28 - 1.00)
Presence of tendrils												
DEC.attrib	361	0.05	0.01	0.27	0.03	0.10	0.25	0.18	0.11	0.96	1.00	0.96
EX.DEC.attrib	266	< 0.01	< 0.01	0.29	< 0.01	0.08	0.23	0.11	0.04	(0.93 - 0.99)	(0.82 - 1.00)	(0.72 - 1.00)

Species attributes	N	Variation partitioning								Correlation (Confidence interval – 95%)		
		Climate	Soil	Space	Climate & Soil	Soil & Space	Climate & Space	All components	Resi-dual	Correlation II	Correlation III	Correlation IV
Ecological attributes												
Absence of tendrils												
DEC.attrib	24	0.01	0.01	0.29	< 0.01	0.03	0.30	0.12	0.23	0.91	0.89	0.78
EX.DEC.attrib	10	< 0.01	< 0.01	0.27	< 0.01	0.08	0.35	0.13	< 0.01	(0.05 - 0.99)	(0.39 - 0.99)	(0.12 - 0.99)
Presence of extrafloral nectaries in the interpetiolar region												
DEC.attrib	95	0.03	0.01	0.33	0.02	0.10	0.15	0.24	0.13	0.95	0.90	0.81
EX.DEC.attrib	77	0.01	< 0.01	0.28	< 0.01	0.08	0.23	0.08	0.05	(0.91 - 1.00)	(0.64 - 1.00)	(0.52 - 1.00)
Presence of extrafloral nectaries in prophylls												
DEC.attrib	139	0.03	0.01	0.25	0.02	0.10	0.31	0.18	0.12	0.98	0.97	0.97
EX.DEC.attrib	91	< 0.01	< 0.01	0.27	< 0.01	0.07	0.25	0.13	0.06	(0.91 - 0.99)	(0.71 - 1.00)	(0.61 - 1.00)
Absence of extrafloral nectaries												
DEC.attrib	149	0.03	0.01	0.39	0.02	0.10	0.05	0.13	0.26	0.93	**0.65**	**0.52**
EX.DEC.attrib	107	< 0.01	< 0.01	0.29	< 0.01	0.10	0.23	0.11	< 0.01	(0.91 - 0.99)	**(0.73 - 1.00)**	**(0.62 - 1.00)**
Pollination syndrome – Bees												
DEC.attrib	308	0.02	0.01	0.32	0.02	0.11	0.12	0.26	0.13	0.94	0.84	0.74
EX.DEC.attrib	230	< 0.01	< 0.01	0.27	< 0.01	0.09	0.23	0.11	< 0.01	(0.92 - 0.99)	(0.81 - 1.00)	(0.70 - 1.00)
Pollination syndrome – Butterflies												
DEC.attrib	10	0.01	< 0.01	0.42	< 0.01	0.03	0.21	0.12	0.21	0.91	0.88	0.91
EX.DEC.attrib	7	< 0.01	< 0.01	0.45	< 0.01	0.05	0.25	0.11	0.04	(-0.09 - 0.99)	(0.19 - 0.99)	(-0.12 - 1.00)
Pollination syndrome – Hawk moths												
DEC.attrib	23	0.02	0.01	0.33	< 0.01	0.02	0.23	0.17	0.22	0.95	0.91	0.83
EX.DEC.attrib	14	< 0.01	< 0.01	0.29	< 0.01	0.05	0.26	0.10	0.03	(0.31 - 0.99)	(0.38 - 0.99)	(0.12 - 1.00)

Species attributes	N	Variation partitioning								Correlation (Confidence interval – 95%)		
		Climate	Soil	Space	Climate & Soil	Soil & Space	Climate & Space	All components	Residual	Correlation II	Correlation III	Correlation IV
Ecological attributes												
Pollination syndrome – Hummingbirds												
DEC.attrib	24	0.03	< 0.01	0.21	< 0.01	0.01	0.34	0.09	0.32	0.84	0.70	0.46
EX.DEC.attrib	12	0.06	< 0.01	0.32	< 0.01	0.04	0.10	0.12	0.08	(0.17 - 0.99)	(0.38 - 0.99)	(0.11 - 0.99)
Water-dispersed seeds												
DEC.attrib	52	0.01	< 0.01	0.34	< 0.01	0.03	0.25	0.25	0.12	0.97	0.96	0.93
EX.DEC.attrib	32	< 0.01	< 0.01	0.28	< 0.01	0.08	0.23	0.16	0.03	(0.85 - 1.00)	(0.52 - 1.00)	(0.36 - 1.00)
Wind-dispersed seeds with linear wings												
DEC.attrib	220	0.04	0.01	0.29	0.02	0.11	0.25	0.15	0.12	0.97	0.99	0.98
EX.DEC.attrib	178	< 0.01	< 0.01	0.27	< 0.01	0.08	0.25	0.10	0.05	(0.92 - 0.99)	(0.78 - 1.00)	(0.66 - 1.00)
Wind-dispersed seeds with ellipsoid wings												
DEC.attrib	56	0.07	0.01	0.43	0.03	0.08	0.06	0.04	0.28	0.93	0.59	0.52
EX.DEC.attrib	48	< 0.01	< 0.01	0.29	< 0.01	0.08	0.22	0.11	< 0.01	(0.89 - 0.99)	(0.53 - 1.00)	(0.38 - 1.00)
Geographical attributes												
Small range size												
DEC.attrib	96	0.01	< 0.01	0.39	< 0.01	< 0.01	0.14	0.04	0.41	-	**0.59**	-
EX.DEC.attrib											**(0.65 - 1.00)**	
Small to medium range size												
DEC.attrib	97	0.04	0.01	0.45	< 0.01	0.05	0.07	-0.02	0.40	0.84	**0.51**	**0.20**
EX.DEC.attrib	83	< 0.01	< 0.01	0.27	< 0.01	0.13	0.42	0.08	< 0.01	(0.91 - 0.99)	**(0.64 - 1.00)**	**(0.53 - 1.00)**

Species attributes	N	Variation partitioning								Correlation (Confidence interval – 95%)		
		Climate	Soil	Space	Climate & Soil	Soil & Space	Climate & Space	All components	Resi-dual	Correlation II	Correlation III	Correlation IV
Geographical attributes												
Medium to large range size												
DEC.attrib	97	0.04	0.01	0.48	0.01	0.05	0.08	0.01	0.32	0.93	**0.60**	**0.52**
EX.DEC.attrib	97	0.03	< 0.01	0.24	< 0.01	0.07	0.16	0.11	< 0.01	(0.91 - 0.99)	**(0.64 - 1.00)**	**(0.53 - 0.99)**
Large range size												
DEC.attrib	96	0.02	0.01	0.28	0.02	0.08	0.20	0.30	0.09	0.90	0.91	0.79
EX.DEC.attrib	96	0.02	< 0.01	0.35	< 0.01	0.06	0.18	0.14	0.20	(0.91 - 1.00)	(0.65 - 1.00)	(0.53 - 1.00)
Evolutionary attributes												
Early-diverging species												
DEC.attrib	155	0.02	0.01	0.30	0.02	0.11	0.15	0.25	0.14	0.95	0.90	0.79
EX.DEC.attrib	94	< 0.01	< 0.01	0.29	< 0.01	0.10	0.26	0.13	0.01	(0.91 - 0.99)	(0.73 - 1.00)	(0.62 - 1.00)
Late-diverging species												
DEC.attrib	162	0.04	0.01	0.41	0.02	0.14	0.05	0.13	0.20	0.93	**0.70**	**0.62**
EX.DEC.attrib	128	< 0.01	< 0.01	0.28	< 0.01	0.08	0.24	0.10	< 0.01	(0.92 - 0.99)	**(0.73 - 1.00)**	**(0.63 - 1.00)**
Genera of the tribe – *Adenocalymma*												
DEC.attrib	72	0.01	0.01	0.38	0.01	0.11	0.11	0.15	0.22	0.97	0.79	0.70
EX.DEC.attrib	37	< 0.01	< 0.01	0.24	< 0.01	0.09	0.23	0.13	0.04	(0.87 - 0.99)	(0.57 - 1.00)	(0.45 - 1.00)
Genera of the tribe – *Amphilophium*												
DEC.attrib	46	0.03	< 0.01	0.35	< 0.01	0.06	0.16	0.11	0.27	0.90	0.79	0.53
EX.DEC.attrib	29	< 0.01	< 0.01	0.24	< 0.01	0.15	0.25	0.13	< 0.01	(0.84 - 1.00)	(0.50 - 0.99)	(0.32 - 0.99)

| Species attributes	N	Variation partitioning								Correlation (Confidence interval – 95%)		
		Climate	Soil	Space	Climate & Soil	Soil & Space	Climate & Space	All components	Residual	Correlation II	Correlation III	Correlation IV
Evolutionary attributes												
Genera of the tribe – *Anemopaegma*												
DEC.attrib	46	0.01	0.01	0.49	< 0.01	0.05	0.03	0.05	0.36	0.98	0.56	0.51
EX.DEC.attrib	36	< 0.01	< 0.01	0.25	< 0.01	0.07	0.24	0.13	0.06	(0.87 - 0.99)	(0.50 - 1.00)	(0.33 - 1.00)
Genera of the tribe – *Bignonia*												
DEC.attrib	30	0.01	< 0.01	0.28	< 0.01	0.07	0.32	0.15	0.16	0.97	0.96	0.93
EX.DEC.attrib	24	0.03	< 0.01	0.29	< 0.01	0.06	0.18	0.15	0.11	(0.77 - 1.00)	(0.43 - 0.99)	(0.20 - 0.99)
Genera of the tribe – *Fridericia*												
DEC.attrib	59	0.04	0.01	0.42	0.01	0.10	0.09	0.15	0.19	0.92	0.78	0.81
EX.DEC.attrib	45	0.01	< 0.01	0.35	< 0.01	0.08	0.22	0.08	0.03	(0.89 - 0.99)	(0.54 - 0.99)	(0.41 - 1.00)
Tribe Bignonieae												
DEC.tribe	386	0.05	0.01	0.27	0.03	0.10	0.24	0.17	0.12	0.96 (Correlation I)		
EX.DEC.tribe	276	< 0.01	< 0.01	0.28	< 0.01	0.08	0.24	0.11	0.04			
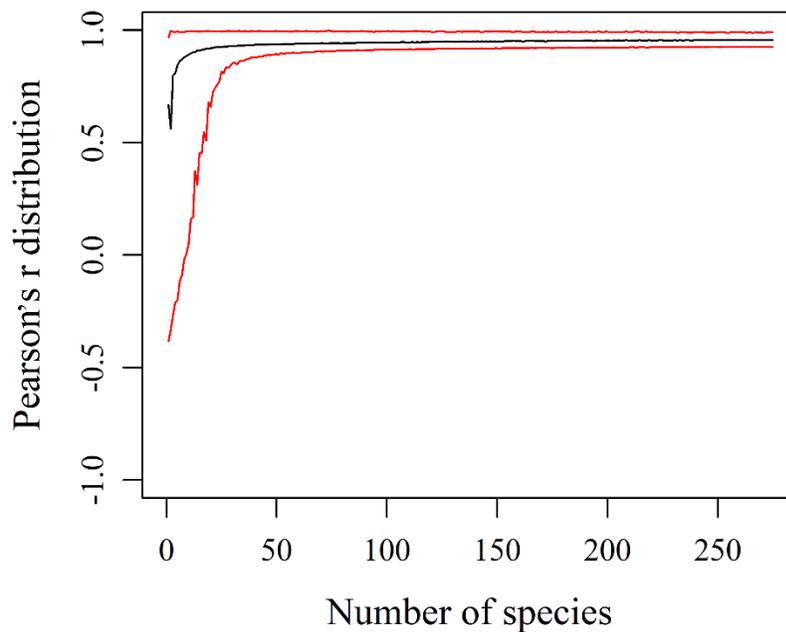
Figure S2.1. Pearson's r distribution of correlations between variation partitioning of the overall Bignonieae richness and random partitions of species ranges. To obtain this correlation distribution, we run 5000 partitions for each number of species. Black line represents median correlation values and red lines represent the confidence intervals of 95% of the greatest correlation values of 5000 runs.
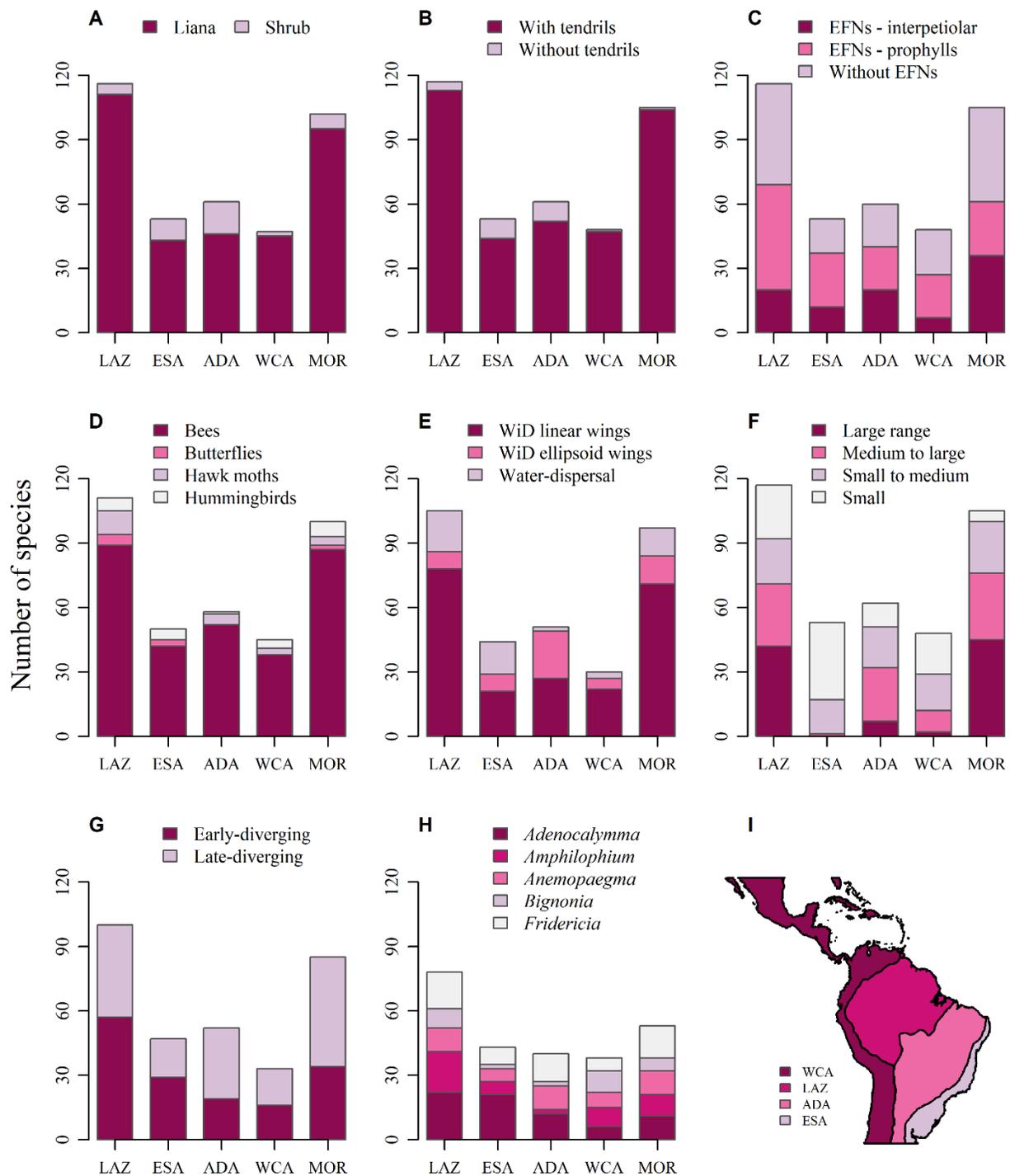
Figure S2.2. Distribution of the species of the tribe Bignonieae with different ecological, geographical, and evolutionary attributes per biogeographical areas *sensu* Gentry (1979): LAZ: lowland Amazonia (equivalent to the Amazon rainforest); ESA: eastern South America (equivalent to the Atlantic rainforest); ADA: South America dry areas (equivalent to savanna habitats such as

the Caatinga, Cerrado and Chaco); WCA: western South America and Central America; and MOR: species that occur in more than one biogeographical area. Ecological, geographical, and evolutionary attributes: (a) plant life-form; (b) presence of tendrils; (c) presence of herbivory protection represented by presence of extrafloral nectaries (NEFs) in the interpetiolar region or in prophylls; (d) pollination syndrome; (e) type of seed dispersion (WiD = wind-dispersed species); (f) species range size; (g) root distance of each species within the Bignonieae phylogenetic tree; (h) genera of the tribe; and (i) geographic representation of the biogeographical areas.
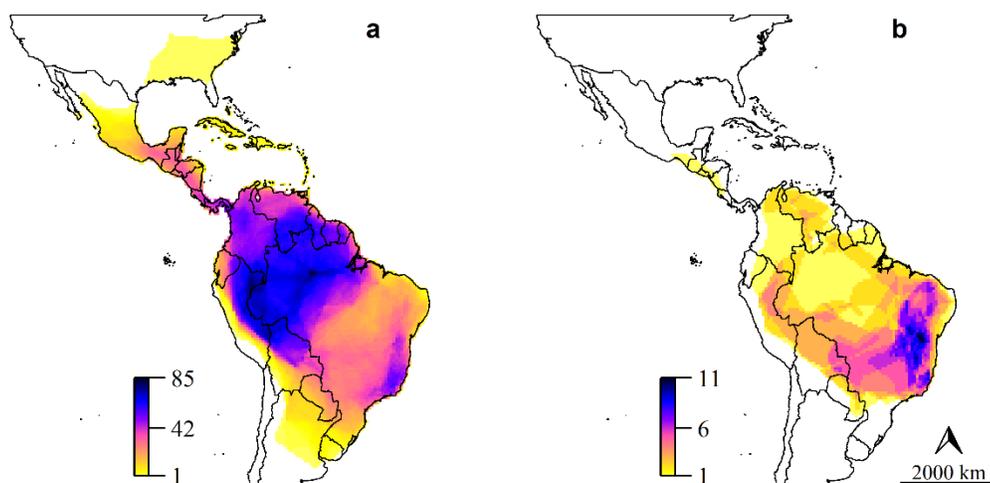
Figure S2.3. Richness deconstruction of the tribe Bignonieae according to plant life-form. (a) Richness pattern of liana species; and (b) shrub species.
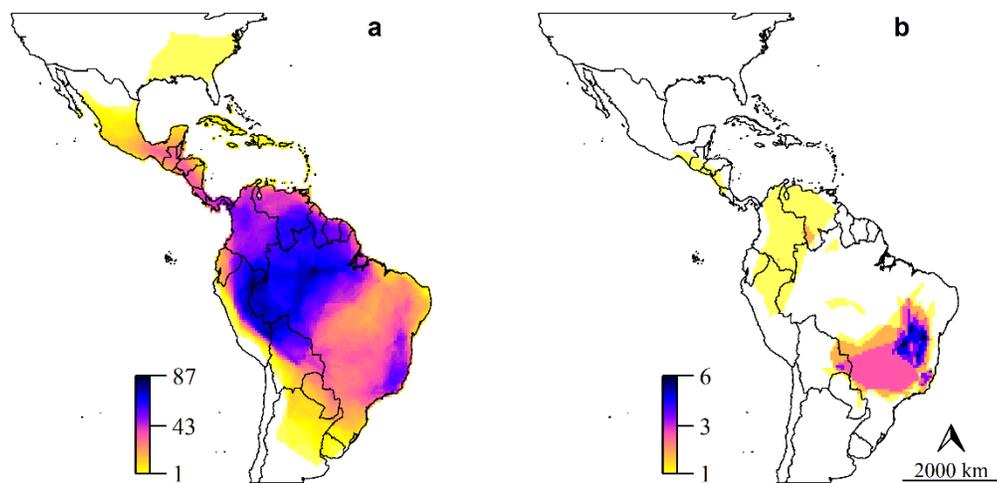
Figure S2.4. Richness deconstruction of the tribe Bignonieae according to the presence of tendrils. (a) Richness pattern of species with tendrils; and (b) without tendrils.
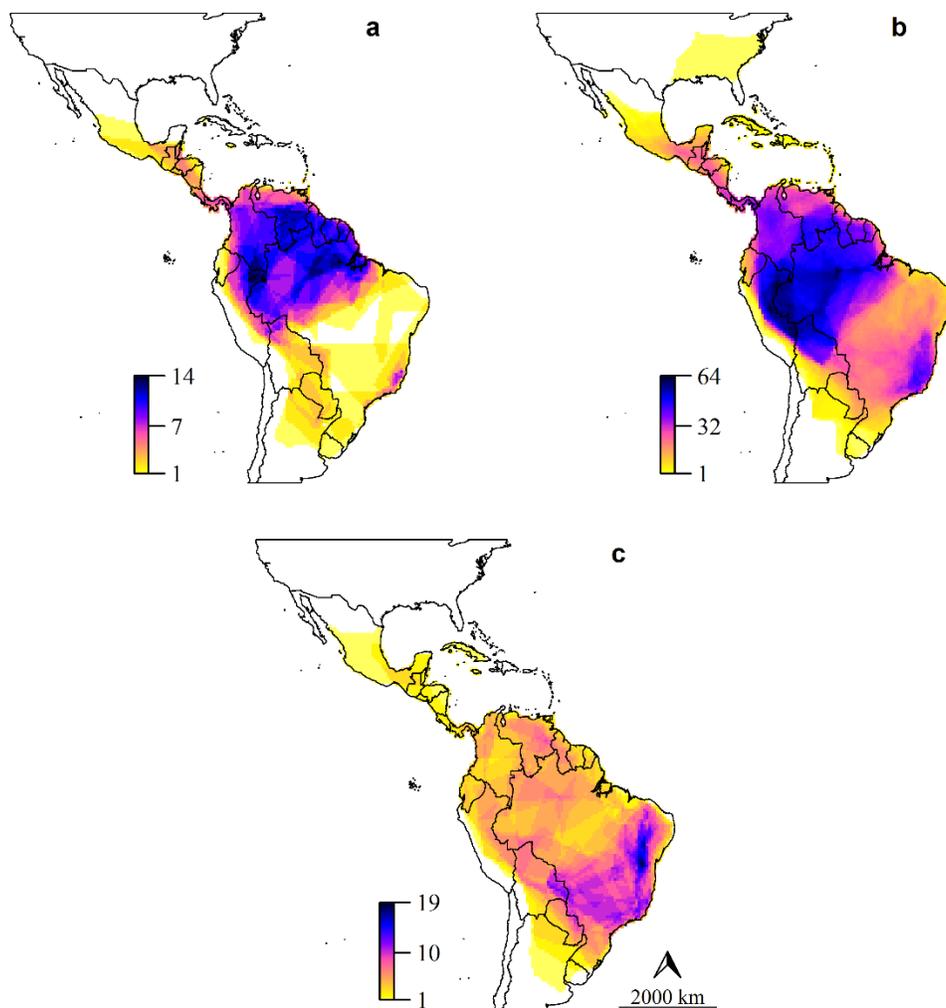
Figure S2.5. Richness deconstruction of the tribe Bignonieae according to the type of seed dispersion. (a) Richness pattern of species with water-dispersed seeds; (b) wind-dispersed seeds with linear wings; and (c) wind-dispersed seeds with ellipsoid wings.
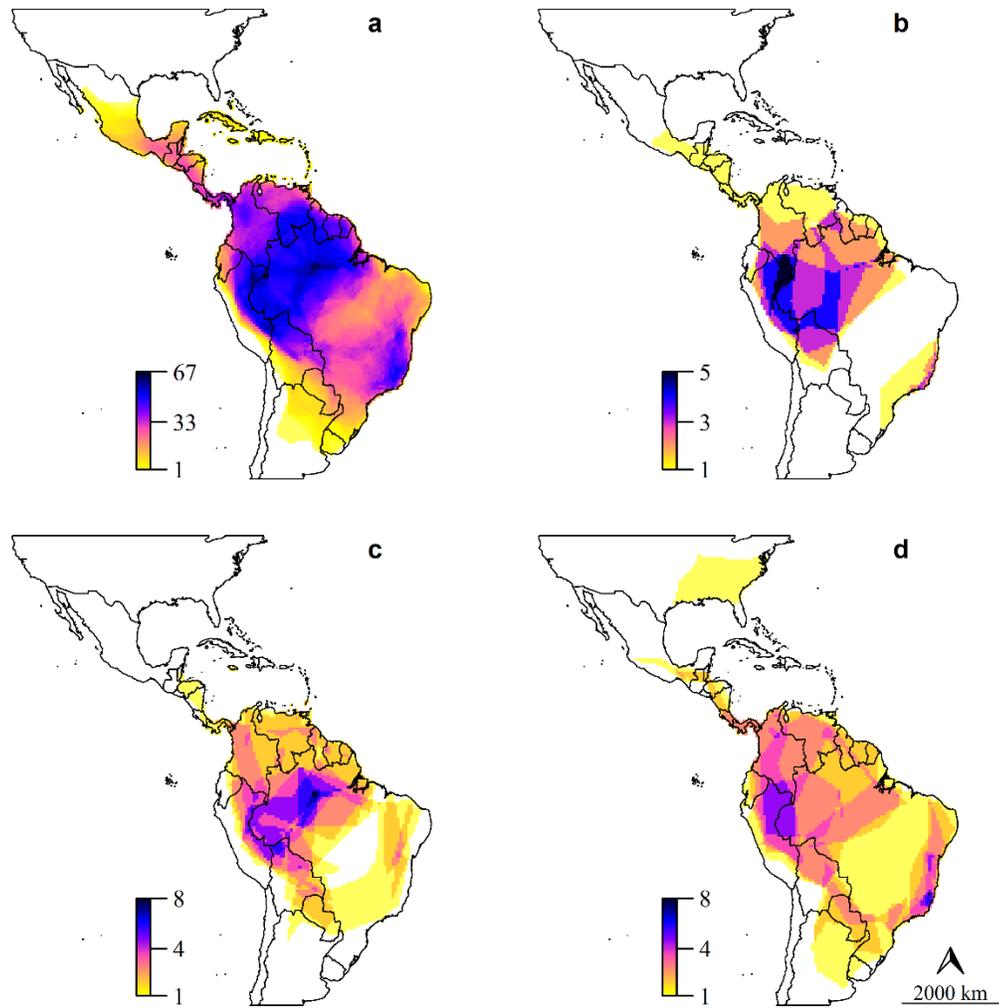
Figure S2.6. Richness deconstruction of the tribe Bignonieae according to the pollination syndrome. (a) Richness pattern of species pollinated by bees; (b) butterflies; (c) hawk moths; and (d) hummingbirds.
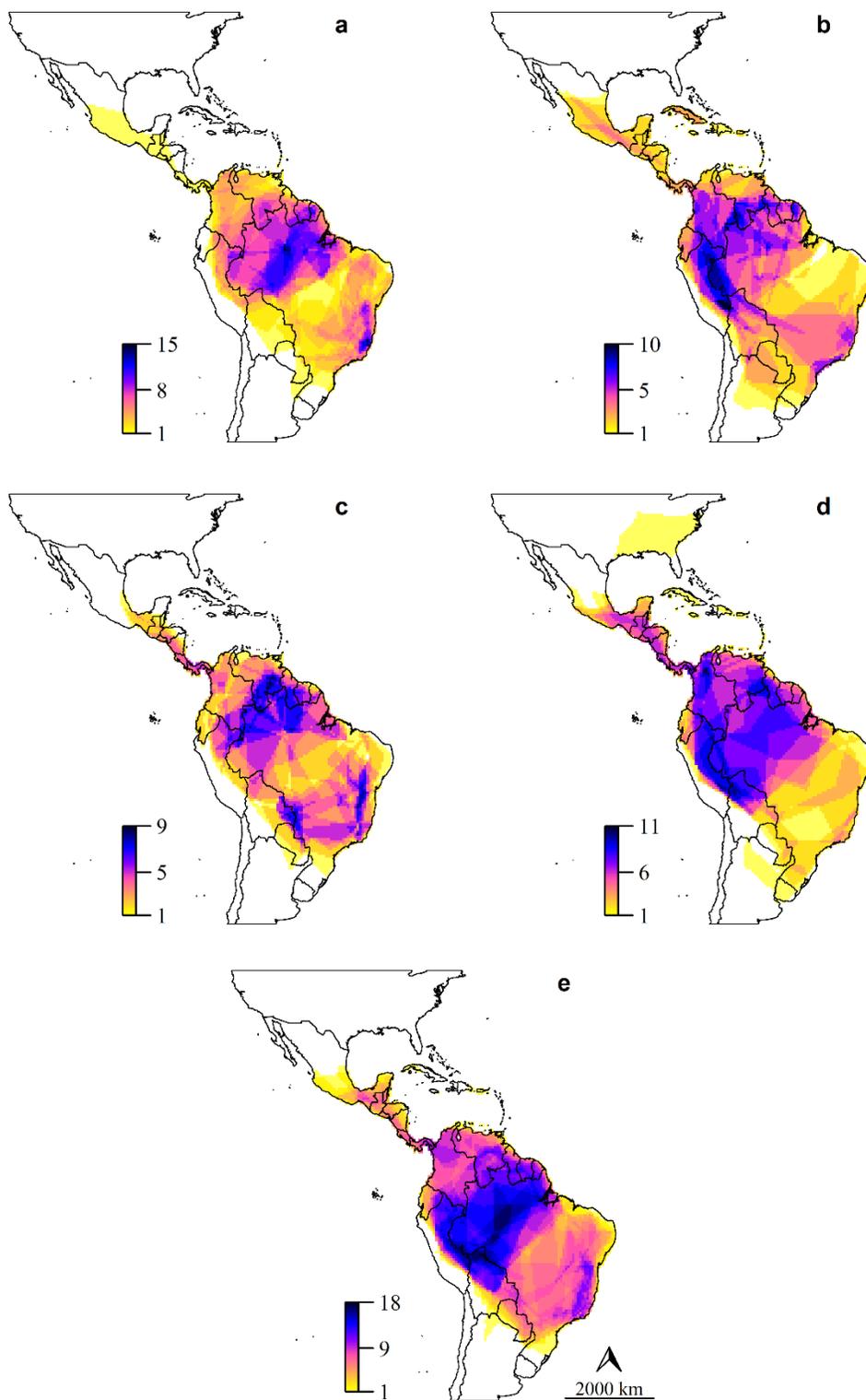
Figure S2.7. Richness deconstruction according to genus of the tribe that have more than 30 species. (a) Richness pattern of species belonging to *Adenocalymma*; (b) *Amphilophium*; (c) *Anemopaegma*; (d) *Bignonia*; and (e) *Fridericia*.

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Material suplementar – Capítulo 3

Table S3.1. Habitat classification of the liana species of the tribe Bignonieae (Bignoniaceae). F: species from forest habitats; R: riparian habitats; and S: savanna habitats.

Species name	F	R	S	Species name	F	R	S
Adenocalymma ackermannii			x	*Adenocalymma flaviflorum*	x		
Adenocalymma adenophorum	x			*Adenocalymma gibbosum*	x		
Adenocalymma albiflorum	x			*Adenocalymma gracielzae*	x		
Adenocalymma album		x		*Adenocalymma hatschbachii*	x		
Adenocalymma allamandiflorum	x			*Adenocalymma hirtum*	x		
Adenocalymma apparicianum			x	*Adenocalymma hypostictum*			x
Adenocalymma apurense	x			*Adenocalymma impressum*	x		
Adenocalymma arthropetiolatum	x			*Adenocalymma juliae*	x		
Adenocalymma aurantiacum	x			*Adenocalymma longilineum*	x		
Adenocalymma biternatum	x			*Adenocalymma magdalenense*	x		
Adenocalymma bracteatum	x	x	x	*Adenocalymma magnificum*	x		
Adenocalymma bracteolatum	x			*Adenocalymma marginatum*	x		
Adenocalymma bracteosum	x			*Adenocalymma mirabile*			x
Adenocalymma bullatum	x			*Adenocalymma molle*	x		
Adenocalymma calcareum	x			*Adenocalymma moringifolium*	x		
Adenocalymma chocoense	x			*Adenocalymma nodosum*			x
Adenocalymma cidii	x			*Adenocalymma patulum*	x		
Adenocalymma contractum	x			*Adenocalymma paulistarum*	x		
Adenocalymma coriaceum	x			*Adenocalymma peregrinum*			x
Adenocalymma cristicalyx		x		*Adenocalymma pubescens*			x
Adenocalymma cymbalum	x			*Adenocalymma salmoneum*	x		
Adenocalymma dichilum		x		*Adenocalymma saulense*	x		
Adenocalymma divaricatum		x		*Adenocalymma scabriusculum*			x
Adenocalymma dugandii	x			*Adenocalymma schomburgkii*	x		
Adenocalymma dusenii	x			*Adenocalymma subincanum*	x		

Species name	F	R	S
Adenocalymma subspicatum			x
Adenocalymma tanaeciicarpum	x		
Adenocalymma trifoliatum		x	
Adenocalymma ubatubense		x	
Adenocalymma uleanum	x		
Adenocalymma velutinum	x		
Amphilophium arenarium		x	
Amphilophium aschersonii	x		
Amphilophium bauhinioides	x		
Amphilophium blanchetii			x
Amphilophium bracteatum	x		
Amphilophium buccinatorium			x
Amphilophium carolinae			x
Amphilophium chocoense	x		
Amphilophium cremersii		x	
Amphilophium crucigerum	x		x
Amphilophium dasytrichum	x		
Amphilophium dolichoides	x		
Amphilophium dusenianum	x		
Amphilophium ecuadorense	x		
Amphilophium elongatum	x		
Amphilophium falcatum	x		
Amphilophium frutescens	x		
Amphilophium gnaphalanthum	x		
Amphilophium granulosum	x		
Amphilophium lactiflorum			x
Amphilophium laxiflorum	x		
Amphilophium lohmanniae	x		
Amphilophium magnoliifolium			x
Amphilophium nunezii	x		

Species name	F	R	S
Amphilophium obovatum	x		x
Amphilophium occidentale	x	x	
Amphilophium paniculatum	x	x	x
Amphilophium pannosum	x		
Amphilophium parkeri	x		
Amphilophium pauciflorum	x		
Amphilophium perbracteatum	x		
Amphilophium pilosum	x		
Amphilophium porphyrotrichum	x		
Amphilophium pulverulentum	x		
Amphilophium racemosum	x		
Amphilophium reticulatum		x	
Amphilophium rodriguesii	x		
Amphilophium sandwithii	x		
Amphilophium scabriusculum	x		
Amphilophium stamineum	x		
Amphilophium steyermarkii	x		
Anemopaegma alatum			x
Anemopaegma brevipes	x		
Anemopaegma chamberlaynii	x		x
Anemopaegma chrysanthum	x		
Anemopaegma chrysoleucum		x	
Anemopaegma citrinum	x		
Anemopaegma colombianum	x		
Anemopaegma flavum		x	
Anemopaegma floridum	x		
Anemopaegma foetidum			x
Anemopaegma gracile			x
Anemopaegma grandifolium	x		
Anemopaegma granvillei	x		

Species name	F	R	S	Species name	F	R	S
Anemopaegma heringeri	x			*Bignonia campanulata*	x		
Anemopaegma hilarianum	x			*Bignonia capreolata*	x		
Anemopaegma insculptum	x			*Bignonia cararensis*	x		
Anemopaegma ionanthum	x			*Bignonia corymbosa*	x		
Anemopaegma jucundum	x			*Bignonia costata*	x		
Anemopaegma karstenii		x		*Bignonia cuneata*	x		
Anemopaegma laeve			x	*Bignonia decora*	x		
Anemopaegma longidens	x			*Bignonia diversifolia*	x		
Anemopaegma longipetiolatum	x			*Bignonia hyacinthina*	x		
Anemopaegma mirabile			x	*Bignonia lilacina*	x		
Anemopaegma nebulosum			x	*Bignonia microcalyx*	x		
Anemopaegma oligoneuron	x			*Bignonia neoheterophylla*		x	x
Anemopaegma orbiculatum	x			*Bignonia neouliginosa*		x	
Anemopaegma pabstii			x	*Bignonia nocturna*	x		
Anemopaegma pachyphyllum	x			*Bignonia noterophila*		x	
Anemopaegma paraense		x		*Bignonia phellosperma*		x	
Anemopaegma parkeri	x			*Bignonia potosina*	x		
Anemopaegma patelliforme		x		*Bignonia prieurii*	x		
Anemopaegma prostratum	x			*Bignonia pterocalyx*	x		
Anemopaegma puberulum	x			*Bignonia ramentacea*			x
Anemopaegma robustum	x			*Bignonia sanctae-crucis*	x		
Anemopaegma rugosum	x			*Bignonia sciuripabulum*	x		
Anemopaegma santaritense	x			*Bignonia sordida*	x		
Anemopaegma setilobum	x			*Bignonia uleana*	x		
Anemopaegma velutinum			x	*Callichlamys latifolia*	x		
Anemopaegma villosum	x			*Cuspidaria argentea*			x
Bignonia aequinoctialis	x			*Cuspidaria bracteata*			x
Bignonia binata	x			*Cuspidaria bracteolata*	x		
Bignonia bracteomana	x			*Cuspidaria cinerea*			x
Bignonia callistegioides	x			*Cuspidaria convoluta*	x		

Species name	F	R	S
Cuspidaria emmonsii	x		
Cuspidaria floribunda	x		
Cuspidaria inaequalis	x		
Cuspidaria lasiantha	x		
Cuspidaria lateriflora	x		
Cuspidaria multiflora			x
Cuspidaria octoptera	x		
Cuspidaria pulchella			x
Cuspidaria pulchra			x
Cuspidaria sceptrum			x
Cuspidaria simplicifolia			x
Cuspidaria subincana	x		
Cuspidaria weberbaueri	x		
Dolichandra chodatii	x		
Dolichandra cynanchoides			x
Dolichandra dentata		x	
Dolichandra hispida	x		
Dolichandra quadrivalvis	x	x	x
Dolichandra steyermarkii	x		
Dolichandra uncata		x	
Dolichandra unguiculata		x	
Dolichandra unguis-cati	x		
Fridericia arthrerion	x		
Fridericia candicans	x		
Fridericia caudigera	x		
Fridericia chica	x		
Fridericia cinerea	x		
Fridericia cinnamomea	x		
Fridericia conjugata	x		
Fridericia crassa	x		

Species name	F	R	S
Fridericia craterophora			x
Fridericia cuneifolia			x
Fridericia egensis	x		
Fridericia elegans	x		
Fridericia fagoides	x		
Fridericia fanshawei	x		
Fridericia floribunda	x		
Fridericia florida	x		
Fridericia formosa	x		
Fridericia grosourdyana	x		
Fridericia japurensis	x		
Fridericia lauta	x		
Fridericia leucopogon	x		
Fridericia limae			x
Fridericia mollis	x		
Fridericia mollissima	x		
Fridericia mutabilis	x		
Fridericia nicotianiflora	x		
Fridericia nigrescens	x		
Fridericia oligantha	x		
Fridericia oxycarpa	x		
Fridericia patellifera	x		
Fridericia pearcei	x		
Fridericia podopogon	x		
Fridericia poeppigii			x
Fridericia prancei	x		
Fridericia pubescens	x	x	
Fridericia rego	x		
Fridericia samydoides	x		
Fridericia schumanniana	x		

Species name	F	R	S	Species name	F	R	S
Fridericia speciosa	x			*Mansoa glaziovii*	x		
Fridericia spicata	x			*Mansoa hirsuta*			x
Fridericia subexserta	x			*Mansoa hymenaea*	x		
Fridericia subincana	x			*Mansoa ivanii*			x
Fridericia subverticillata	x			*Mansoa lanceolata*	x		
Fridericia trachyphylla	x			*Mansoa longicalyx*			x
Fridericia trailii	x			*Mansoa minensis*	x		
Fridericia triplinervia	x		x	*Mansoa onohualcoides*	x		
Fridericia truncata			x	*Mansoa paganuccii*			x
Fridericia tuberculata	x			*Mansoa parvifolia*	x		
Fridericia viscida	x			*Mansoa sagotii*	x		
Fridericia whitei	x			*Mansoa standleyi*	x		
Lundia corymbifera	x			*Mansoa verrucifera*	x		
Lundia damazioi	x			*Martinella insignis*	x		
Lundia densiflora	x	x	x	*Martinella iquitoensis*	x		
Lundia erionema		x		*Martinella obovata*	x		
Lundia gardneri			x	*Pachyptera aromatica*	x		
Lundia helicocalyx			x	*Pachyptera erythraea*	x		
Lundia laevis	x			*Pachyptera kerere*	x	x	
Lundia longa			x	*Pachyptera ventricosa*	x		
Lundia nitidula	x			*Perianthomega vellozoi*	x		
Lundia obliqua	x			*Pleonotoma bracteata*		x	
Lundia puberula	x			*Pleonotoma castelnaei*			x
Lundia spruceana	x	x		*Pleonotoma clematis*		x	
Lundia virginalis	x		x	*Pleonotoma dendrotricha*	x		
Manaosella cordifolia	x			*Pleonotoma echitidea*	x		
Mansoa alliacea	x			*Pleonotoma exserta*			x
Mansoa angustidens	x			*Pleonotoma fissicalyx*	x		
Mansoa difficilis	x			*Pleonotoma fluminensis*	x		
Mansoa gentryi		x		*Pleonotoma jasminifolia*		x	

Species name	F	R	S
Pleonotoma longiflora	x		
Pleonotoma melioides	x		
Pleonotoma orientalis			x
Pleonotoma pavettiflora	x		
Pleonotoma stichadenia	x		
Pleonotoma tetraquetra	x		
Pleonotoma variabilis	x		
Pyrostegia millingtonioides	x		
Pyrostegia venusta	x		
Stizophyllum inaequilaterum	x		
Stizophyllum perforatum	x		
Stizophyllum riparium	x		
Tanaecium affine	x		
Tanaecium apiculatum	x		
Tanaecium bilabiatum		x	
Tanaecium caudiculatum	x		
Tanaecium crucigerum	x		
Tanaecium cyrtanthum			x
Tanaecium dichotomum	x		x
Tanaecium duckei	x		
Tanaecium exitiosum	x		
Tanaecium jaroba		x	
Tanaecium neobrasiliense			x
Tanaecium ornithophilum	x		
Tanaecium paradoxum			x
Tanaecium parviflorum			x
Tanaecium pyramidatum	x		x
Tanaecium revillae		x	
Tanaecium selloi	x		
Tanaecium tetragonolobum	x		

Species name	F	R	S
Tanaecium truncatum	x		
Tanaecium xanthophyllum	x		
Tynanthus cognatus	x		
Tynanthus croatianus	x		
Tynanthus densiflorus	x		
Tynanthus espiritosantensis	x		
Tynanthus fasciculatus	x		
Tynanthus guatemalensis	x		
Tynanthus labiatus	x		
Tynanthus macranthus	x		
Tynanthus micranthus	x		
Tynanthus panurensis	x		
Tynanthus polyanthus	x		
Tynanthus pubescens	x		
Tynanthus sastrei	x		
Tynanthus schumannianus	x		
Xylophragma corchoroides	x		
Xylophragma heterocalyx			x
Xylophragma seemannianum	x		

Table S3.2. Pearson's r correlation between climatic variables and the first three axes of a principal component analysis with all 19 bioclimatic variables.

Variable	Code	PCA 1	PCA 2	PCA 3
Annual mean temperature	Bio1	**0.96**	-0.18	-0.13
Mean diurnal range	Bio2	-0.47	-0.18	0.39
Isothermality	Bio3	0.39	0.56	0.08
Temperature seasonality	Bio4	**-0.74**	-0.51	-0.06
Max temperature of warmest month	Bio5	0.61	-0.47	-0.05
Min temperature of coldest month	Bio6	**0.96**	0.11	-0.18
Temperature annual range	Bio7	-0.65	-0.43	0.16
Mean temperature of wettest quarter	Bio8	0.67	-0.52	-0.22
Mean temperature of driest quarter	Bio9	**0.92**	-0.06	-0.20
Mean temperature of warmest quarter	Bio10	0.69	-0.55	-0.22
Mean temperature of coldest quarter	Bio11	**0.98**	0.09	-0.06
Annual precipitation	Bio12	0.08	**0.89**	-0.06
Precipitation of wettest month	Bio13	0.27	**0.81**	0.22
Precipitation of driest month	Bio14	-0.49	0.24	**-0.80**
Precipitation seasonality	Bio15	0.54	0.07	**0.76**
Precipitation of wettest quarter	Bio16	0.19	**0.83**	0.25
Precipitation of driest quarter	Bio17	-0.32	0.40	**-0.80**
Precipitation of warmest quarter	Bio18	-0.39	0.65	0.06
Precipitation of coldest quarter	Bio19	0.23	0.47	-0.23

Table S3.3. Direct effect (Dir.), indirect effect via canopy height (Ind.), and total effect (Tot.) of environmental variables on species richness of total lianas of the tribe Bignonieae (Bignoniaceae) and richness of subsets of lianas from different habitats. Values were extracted from structural equation.

	Total lianas			Forest species			Riparian species			Savanna species		
	Dir.	**Ind.**	**Tot.**	**Dir.**	**Ind.**	**Tot.**	**Dir.**	**Ind.**	**Tot.**	**Dir.**	**Ind.**	**Tot.**
Canopy height	0.57	-	0.57	0.65	-	0.65	0.33	-	0.33	-0.43	-	-0.43
Temperature	0.39	0.09	0.49	0.33	0.08	0.43	0.20	-0.01	0.23	0.17	-0.05	0.17
Precipitation	0.17	0.15	0.33	0.17	0.17	0.34	0.11	0.06	0.18	-0.04	-0.17	-0.17
Precipitation seasonality	0.04	-0.18	-0.10	0.01	-0.20	-0.15	-0.33	-0.07	-0.39	0.08	0.14	0.27
Cation exchange capacity	-0.09	-0.09	-0.18	-0.06	-0.10	-0.16	-0.07	-0.07	-0.13	-0.23	0.07	-0.15
Number of soil types	0.04	-	0.04	0.03	-	0.03	0.08	-	0.08	0.04	-	0.04
R^2		0.65			0.68			0.36			0.29	

Table S3.4. Direct effect of environmental variables on canopy height. Values were extracted from structural equation models.

Variables	Total lianas	Forest species	Riparian species	Savanna species
Temperature	0.15	0.13	-0.02	0.11
Precipitation	0.27	0.26	0.19	0.39
Precipitation Seasonality	-0.32	-0.32	-0.22	-0.32
Cation exchange capacity	-0.16	-0.16	-0.21	-0.17
Number of soil types	-	-	-	-
R^2	0.21	0.19	0.15	0.34

Table S3.5. Results of structural equation models (SEM) and ordinary least squares models with inclusion of Moran's eigenvector maps (OLS+MEMs) for the total liana species richness of the tribe Bignonieae (Bignoniaceae) and richness of subsets of lianas from different habitats. ENV: pure environmental component; ENV & SPA: spatially structured environmental component; SPA: spa pure spatial component; and type of spatial weighting matrix represents the spatial structure used to account for the spatial autocorrelation, which was generated combining a connectivity matrix (DNEAR: distance-based matrix connecting all site at a distance equals to once and a half the largest edge of the minimum spanning tree), a weight matrix (Binary: without weight between connections; Fdow: concave-down function; or Fup: concave-up function) and a connective style ("W" or "B").

|	Total lianas		Forest species		Riparian species		Savanna species	
	SEM	OLS+MEMs	SEM	OLS+MEMs	SEM	OLS+MEMs	SEM	OLS+MEMs
Standardized partial regression coefficients								
Canopy height	0.57	0.42	0.65	0.48	0.33	0.20	-0.43	-0.40
Temperature	0.39	0.56	0.33	0.52	0.20	0.37	0.17	-0.16
Precipitation	0.17	0.23	0.17	0.21	0.11	0.61	-0.04	-0.23
Precipitation seasonality	0.04	0.05	0.01	-0.04	-0.33	-0.05	0.08	0.15
Cation exchange capacity	-0.09	< 0.01	-0.06	0.01	-0.07	-0.03	-0.23	-0.16
Soil types	0.04	0.04	0.03	0.04	0.08	0.04	0.04	0.06
Variation partitioning components								
Only ENV	-	0.54	-	0.57	-	0.45	-	0.34
Shared ENV & SPA	-	0.11	-	0.11	-	-0.09	-	-0.05
Only SPA	-	0.22	-	0.18	-	0.45	-	0.13
Residuals	-	0.13	-	0.14	-	0.18	-	0.58
Type of spatial weighting matrix	DNEAR – Binary – W		DNEAR – Fdown – W		DNEAR – Fup – W		DNEAR – Binary – B	
Number of selected MEMs	-	22	-	22	-	33	-	1
Global Moran's I of residuals	0.43	< 0.05	0.33	< 0.05	0.46	< 0.05	0.09	< 0.05
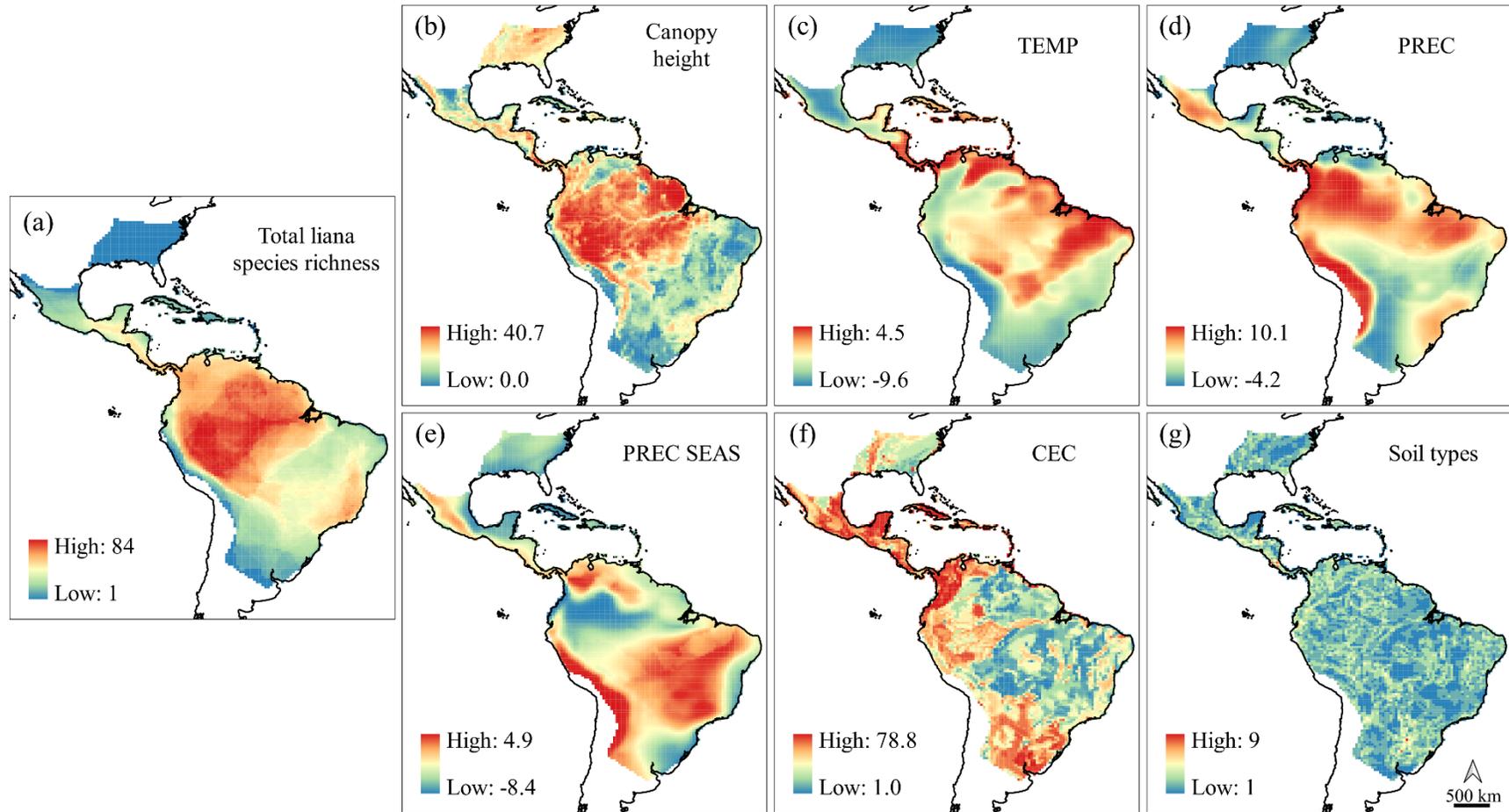
Figure S3.1. Total liana species richness of the tribe Bignonieae (Bignoniaceae). Spatial distribution of: (a) species richness in N°. of species; (b) canopy height in meters; (c) climate PCA 1 representing mean annual temperature; (d) climate PCA 2 representing annual precipitation; (e) climate PCA 3 representing precipitation seasonality; (f) cation exchange capacity in cmol/kg; and (g) N°. of soil types.
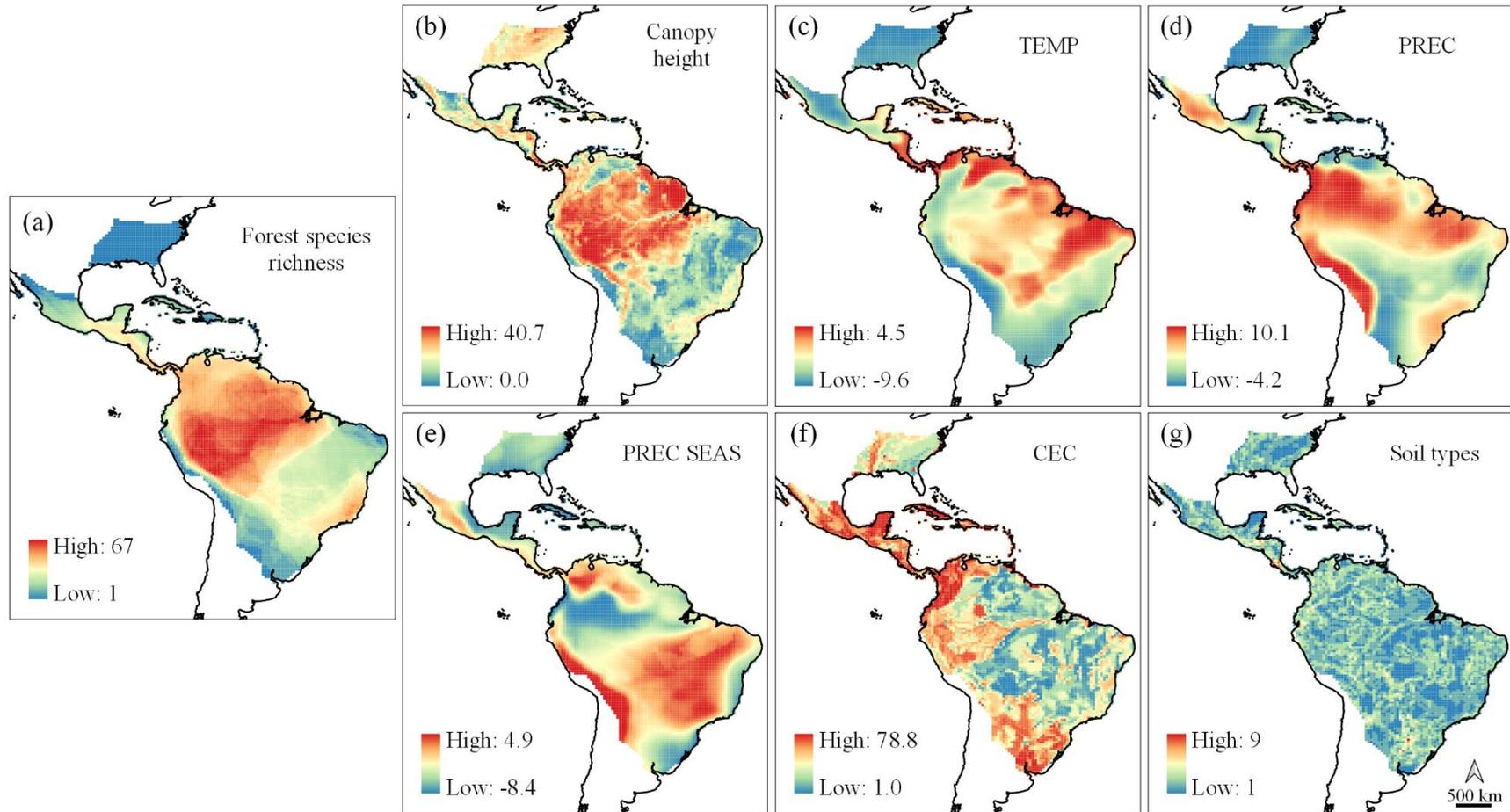
Figure S3.2. Species richness of forest lianas of the tribe Bignonieae (Bignoniaceae). Spatial distribution of: (a) species richness in N°. of species; (b) canopy height in meters; (c) climate PCA 1 representing mean annual temperature; (d) climate PCA 2 representing annual precipitation; (e) climate PCA 3 representing precipitation seasonality; (f) cation exchange capacity in cmol/kg; and (g) N°. of soil types.
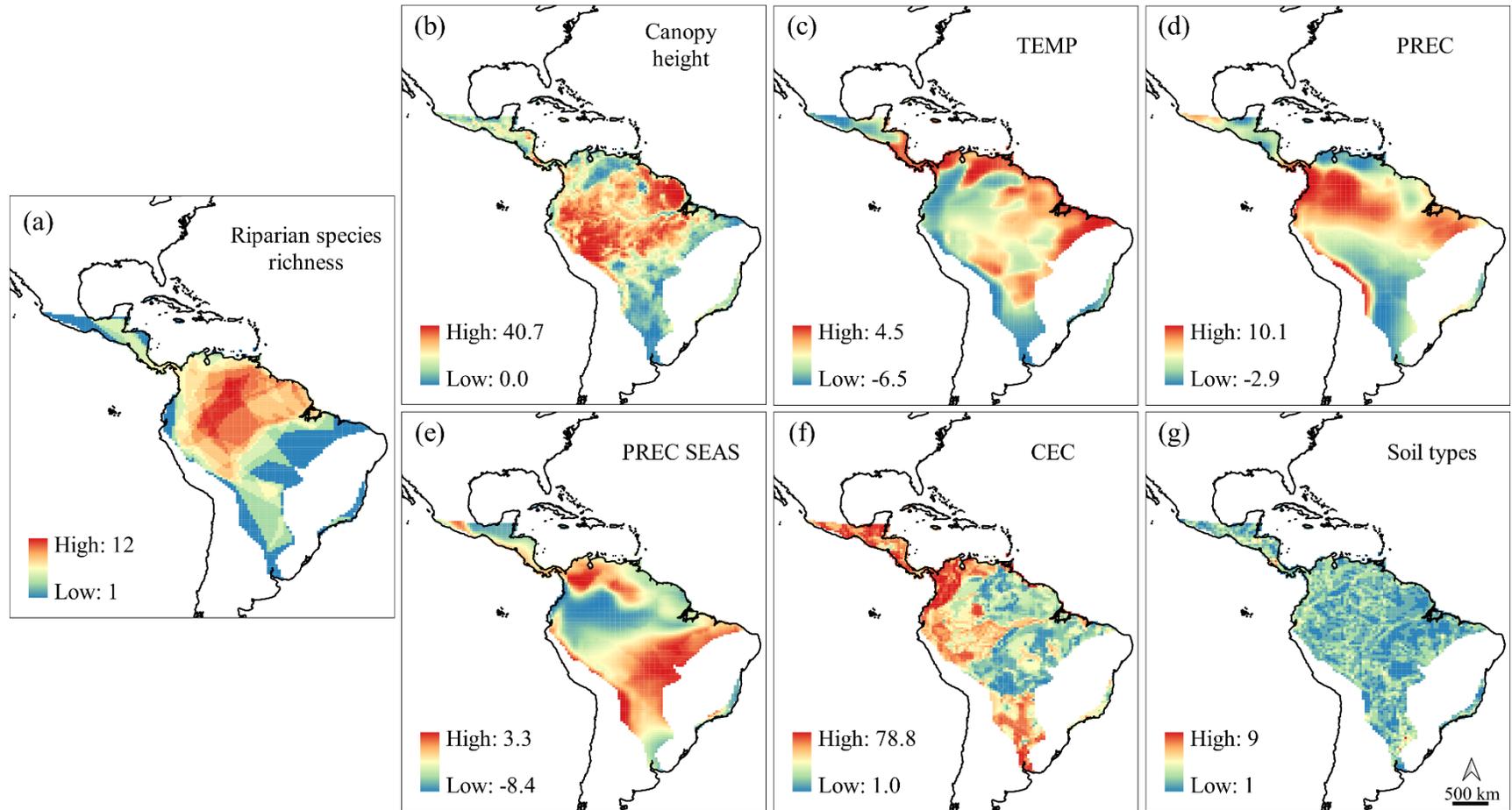
Figure S3.3. Species richness of riparian lianas of the tribe Bignonieae (Bignoniaceae). Spatial distribution of: (a) species richness in N°. of species; (b) canopy height in meters; (c) climate PCA 1 representing mean annual temperature; (d) climate PCA 2 representing annual precipitation; (e) climate PCA 3 representing precipitation seasonality; (f) cation exchange capacity in cmol/kg; and (g) N°. of soil types.
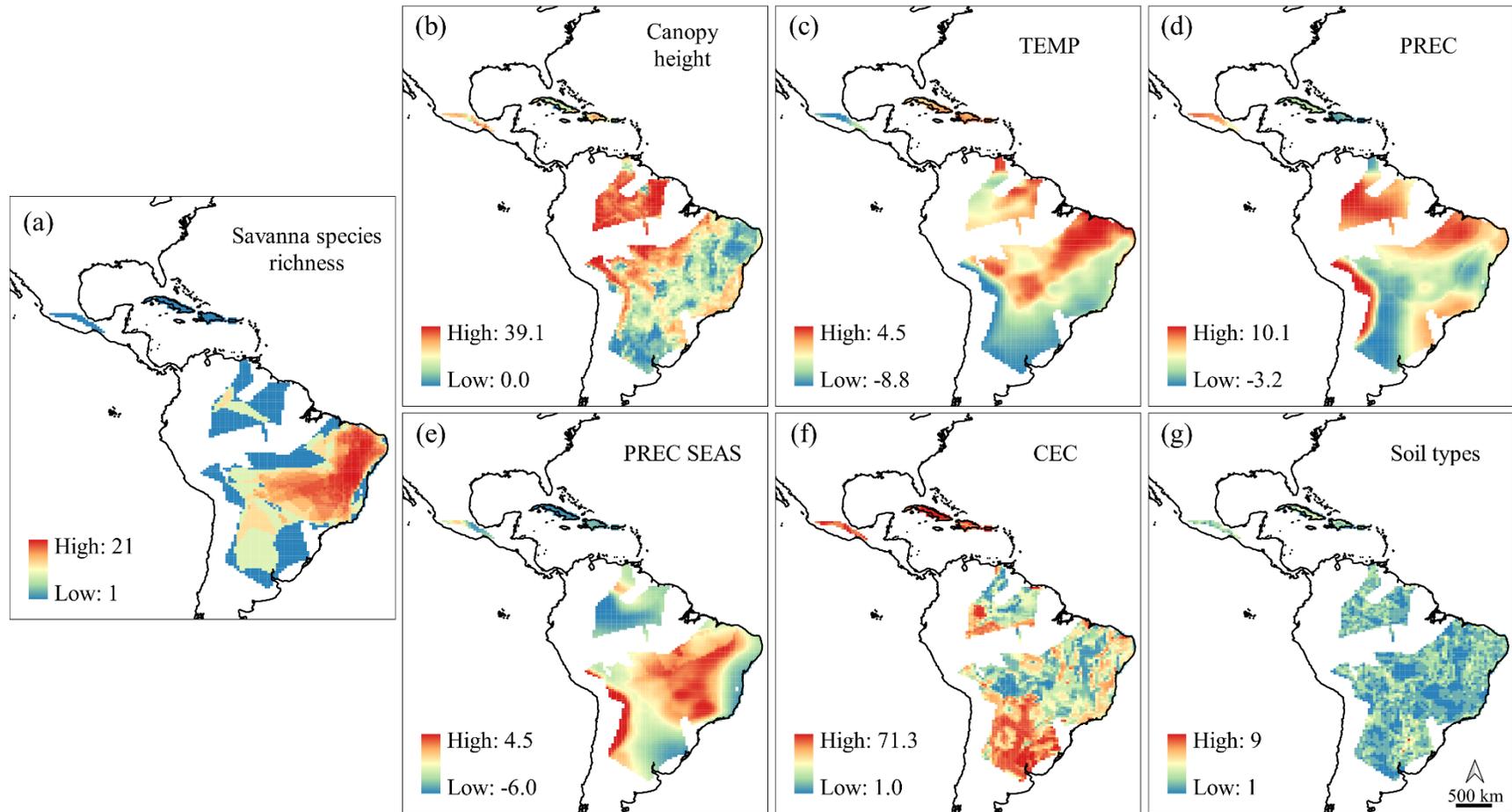
Figure S3.4. Species richness of savanna lianas of the tribe Bignonieae (Bignoniaceae). Spatial distribution of: (a) species richness in N°. of species; (b) canopy height in meters; (c) climate PCA 1 representing mean annual temperature; (d) climate PCA 2 representing annual precipitation; (e) climate PCA 3 representing precipitation seasonality; (f) cation exchange capacity in cmol/kg; and (g) N°. of soil types.
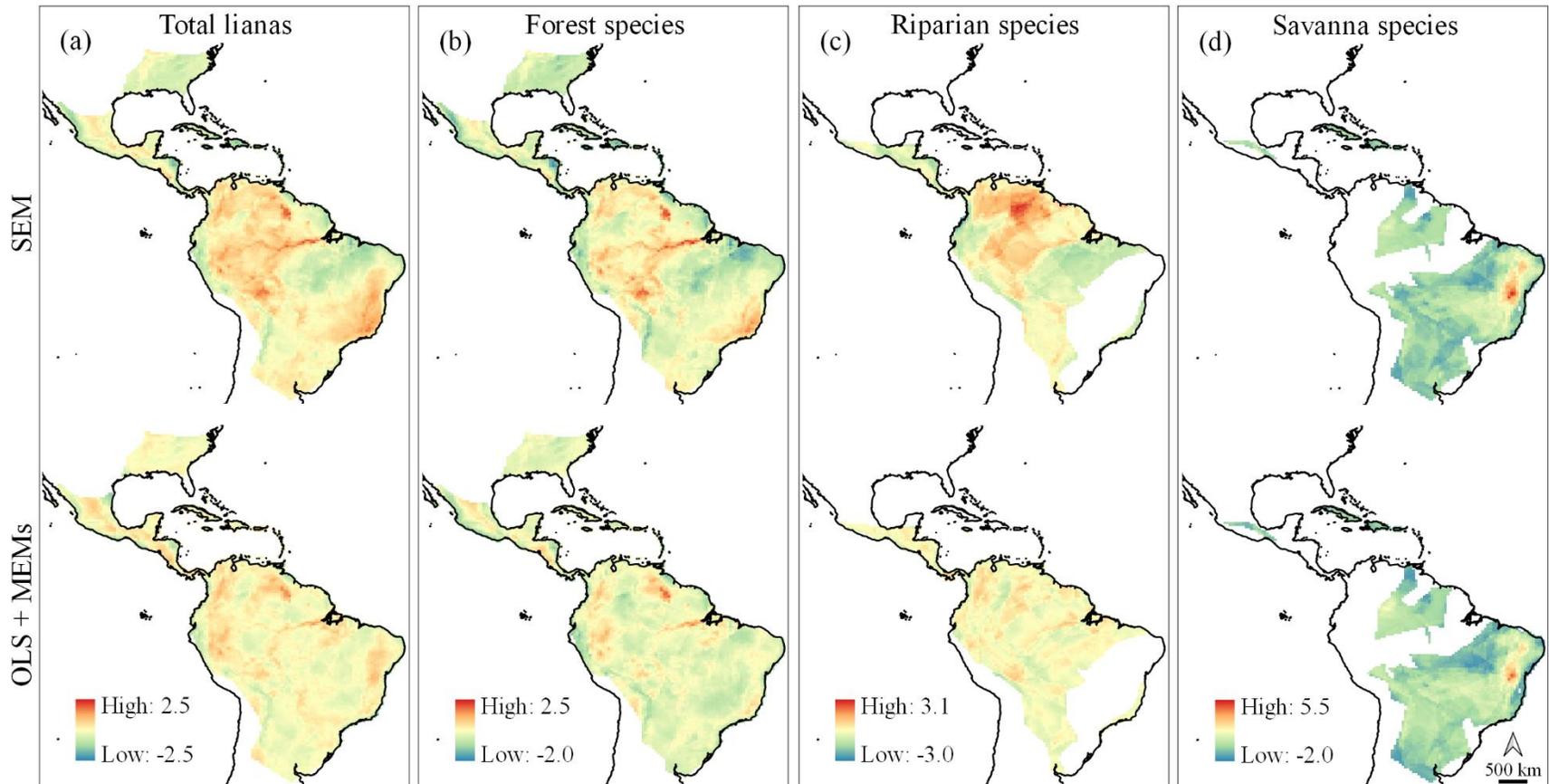
Figure S3.5. Residuals of structural equation model (SEM – not accounting for the spatial structure) and ordinary least squares model with inclusion of Moran's eigenvector maps (OLS+MEMs – accounting for the spatial structure) for the total liana species richness of the tribe Bignonieae (Bignoniaceae) and richness of subsets of lianas from different habitats. The predictor variables of each richness model were canopy height, temperature, precipitation, precipitation seasonality, cation exchange capacity and soil type.