

Retracing the contours of the early angiosperm environmental niche

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• **Background and Aims** Our aim was to understand the environmental conditions of the emergence and radiation of early angiosperms. Such a question has long remained controversial because various approaches applied in the past have drawn conflicting images of early angiosperm ecology.

• **Methods** We provided a new perspective on the question by using support vector machines to model the environmental niche of 51 species belonging to ten genera of extant lineages that diverged early during angiosperm evolution (basal angiosperms). Then, we analysed the resulting pattern of niche overlap and determined whether this pattern deviates from what would be expected on the basis of a null model or whether it might mirror a legacy of a common primitive niche based on a phylogenetic reconstruction.

• **Key Results** The niche of three-quarters of the species and all genera converged towards tropical montane cloud forests (TMCFs). The latitudinal pattern of basal angiosperm richness indeed culminated in the tropics, and the elevational pattern revealed a humpback curve peaking between 2000 m and 3500 m when accounting for the effect of area. At first glance, this diversity pattern does not significantly differ from null predictions. However, we revealed a tendency for the basal-most taxa to occur in TMCFs so that phylogenetic reconstructions indicated that the niche of the common ancestor of the sampled basal angiosperms had a probability of 0.85–0.93 to overlap with TMCFs.

• **Conclusions** Our new approach indicates that the environmental convergence of extant basal angiosperms towards TMCFs would reflect a legacy of an ancestral niche from which the least basal taxa would have diverged following a random pattern under geometric constraints.

Key words: Angiosperm evolution, biogeography, biome, life-history traits, maximum likelihood phylogenetic reconstruction, macro-ecology, mid-domain effect, niche modelling, relict angiosperms, species distribution models.

INTRODUCTION

Flowering plants (angiosperms) are undoubtedly the most species-rich and ecologically dominant clade of plants that has ever occurred. Their diversity and abundance in most ecosystems worldwide mirror their evolutionary success. The rapid diversification of angiosperms during the Cretaceous has fascinated generations of botanists since the time of Charles Darwin who referred to them as an 'abominable mystery' (Darwin and Seward, 1903; Friedman, 2009). Despite many attempts to depict the conditions in which angiosperms emerged within ecosystems formerly dominated by gymnosperms and ferns, the nature of the environment in which this radiation has begun remains enigmatic.

The long-held approaches based on fossil plant records have generated a variety of hypotheses about the habitat from which early angiosperms have radiated, sometimes thought to be semixerophytic shrublands (Stebbins, 1974), stream-channel margins at the early successional stage in arid regions (Doyle and Hickey, 1976; Hickey and Doyle, 1977), coastal deltas, lagoons and tidal flats (Retallack and Dilcher, 1986) or swampy woodlands (Coiffard *et al.*, 2007). It is perhaps not surprising that no emerging consensus has been delivered regarding the challenging task of reliably reconstituting paleoenvironments from fossils of extinct plants and their life-history traits.

Another historical image of the early angiosperm ecology has been inferred from current distributional patterns of modern representatives of angiosperm groups thought to be 'primitive' (Takhtajan, 1969; Thorne, 1976). This approach led to the view that the ancestral habitat of flowering plants would have borne a resemblance to extant tropical rain forests. However, biogeographical mechanisms such as extinctions subsequent to arid paleoclimatic events or dispersal barriers might skew such inference (Morley, 2000; Coiffard *et al.*, 2007).

Alternatively, the ecological distribution of flowering plants which diverged from the lineage leading to most flowering plants (basal angiosperms) has been viewed as reflecting many of the environmental attributes of early angiosperms (Feild *et al.*, 2000, 2004, 2009; Feild and Arens, 2005, 2007). Because the ecological diversification of angiosperms probably parallels the diversification of the main angiosperms clades, as highlighted by fossils (Doyle *et al.*, 2008), the extant members of the basal grade represented by terrestrial woody species might represent the best living models of the ecology of the earliest angiosperms (Feild *et al.*, 2011).

The current image of early angiosperm ecology drawn from extant basal angiosperms is primarily based on analyses of their eco-morphological traits (xylem structure, leaf mesophyll, growth habit and seed size) and eco-physiological performance (photosynthetic rate and stomatal conductance) as well as functional inferences from Early Cretaceous angiosperm fossil leaves. This suite of traits argues for an origin of angiosperms in habitats with conditions similar to what we know today as tropical rain forests (Feild *et al.*, 2000, 2004, 2009; Feild and Arens, 2005, 2007).

Traits were found to be useful to infer the biome distribution of early angiosperms, but the trait-based approach is of limited relevance for a quantitative assessment of the environment per se. As various classification schemes of tropical rain forests and other biomes have been proposed in the past on the basis of climatic variables (e.g. Whittaker and Robert, 1962; Bailey, 1983; Walter, 1984; Olson et al., 2001), it remains difficult to delimit the contours of the early angiosperm climatic envelope. The use of innovative and integrative approaches is essential to understand the first steps of angiosperm evolutionary history (Katz, 2017). Several lines of evidence suggest that niche conservatism in climatic tolerance can be observed over a long a evolutionary time scale and limit geographical range expansion of extant taxa (Ackerly, 2004, 2009; Crisp 2009; Buckley, 2010). Thus, an environment-focused approach searching for signatures that might remain in plant distributions and preferences that are vestiges of history is likely to complement the view of the ecology of early angiosperms drawn from plant-focused approaches.

Species distribution models (SDMs; niche models or habitat suitability models) have been designed to correlate geographic records of species occurrence with spatially explicit environmental variables (Elith and Leathwick, 2009). By delimiting a region of the environmental hyperspace (hypervolume) that encompasses observed species occurrences, these models have been interpreted to be in compliance with the Hutchinsonian concept of an environmental niche (Warren, 2012).

Basal angiosperms (*Amborella*, Austrobaileyales and Chloranthaceae) are most widespread and often restricted to the tropics (Morley, 2001; Feild *et al.*, 2009). At first sight, this pattern seems not to deviate from the global distribution of species richness where the richest areas are found in tropical regions. An influential idea to explain this pattern has been the tropical conservatism hypothesis. This hypothesis suggests that most extant clades originated in the tropics and, as such, are specialized to tropical climates (Wiens and Donoghue, 2004). As a result, most taxa might have difficulties dispersing out of the tropics because of niche conservatism, and most speciation events might have occurred in the tropics as a consequence of longer presence and greater available area (Kerkhoff *et al.*, 2014).

Another recurrent distributional feature of many extant basal angiosperms is their distribution above 1000 m elevation (e.g. Todzia, 1988; Feild *et al.*, 2009; Pouteau *et al.*, 2015), which tends to support another biogeographical model that could be behind the higher species richness in tropical regions: the mid-domain effect (MDE). According to the MDE hypothesis, random species placement over bounded gradients would predict an increasing niche overlap towards mid-domains (Colwell and Hurtt, 1994). Regarding latitudinal and elevational gradients, the theory predicts the tropics (mid-domain between the poles) and mid-elevations (mid-domain between sea level and the highest summits) to be the richest areas. Thus, one can argue that the ecological distribution of extant basal angiosperms might simply reflect geometric constraints that might be expected from a simple null model.

In this study, we address the question of whether SDMs applied to modern basal angiosperms can contribute to reconstruct the environmental distribution of early angiosperms. In this respect, we built an individual SDM for the most prevalent terrestrial extant basal angiosperm species on a global scale. We then searched for environmental convergence that might deviate from what would be expected on the basis of a null hypothesis and might mirror environmental requirements of basal angiosperms as a potential witness of early angiosperm ecology.

MATERIALS AND METHODS

Focal extant basal angiosperms

All terrestrial extant basal angiosperm species belonging to the ANA grade and the Chloranthales order were considered (Angiosperm Phylogeny Group IV, 2016; Moore *et al.*, 2010). The root of angiosperm phylogeny is composed of *Amborella*, Nymphaeales and Austrobaileyales. Nymphaeales were discarded because their aquatic habit is thought to be derived rather than ancestral in this clade (Endress *et al.*, 1994; Feild *et al.*, 2003). We included Chloranthales occupying an uncertain position at the base of the phylogeny, often branching immediately above the ANA grade. Congruent phylogenies place Chloranthales as sister to eumagnoliids (magnoliids + eudicots) (Qiu *et al.*, 2000; Soltis *et al.*, 2000; Zanis *et al.*, 2002).

Species occurrence records were extracted from the Global Biodiversity Information Facility (GBIF) database (http://www. gbif.org/). We removed invalid entries, occurrences out of the recognized natural range of the species (e.g. in botanical gardens) and occurrences duplicated on the same pixel to avoid spatial autocorrelation. Subspecies and varieties were merged at the species level because many specimens have not been identified at infraspecific ranks in the GBIF.

Within each genus, the third of all species with the highest number of occurrence records were used in the subsequent analyses and the remaining two-thirds of species were discarded. The most widespread extant basal angiosperm species were expected to reflect the ecological diversification of the group and to have a distribution shaped by ecological rather than geographical boundaries (e.g. small island endemics) while maximizing the accuracy of SDMs (Stockwell and Peterson, 2002). For monospecific genera (Amborella, Austrobaileya and Sarcandra), we used the only species available. This method led to the selection of 51 basal angiosperm species belonging to ten genera and five families (Supplementary data Appendix 1). The number of occurrences ranged from 256 for *Chloranthus* serratus (Chloranthaceae) to four for Illicium verum and Kadsura philippinensis (Schisandraceae) with a mean of 75 occurrences per species. To ensure that unbalanced numbers of species within genera did not bias the following analyses, they were computed at two taxonomic levels: the species level and the genus level.

Niche fitting

Species' niche was described in an environmental space with two dimensions: annual mean temperature (°C) and annual rainfall (mm) to enable correspondence with the well-known biome-type classification scheme of Whittaker (Whittaker and Robert, 1962). Using a higher number of environmental dimensions would also have decreased our chance of finding a common niche pattern with, ultimately, no niche intersection. Current climate variables (averaged for the period 1960–1990) were downloaded from the WorldClim website (Hijmans *et al.*, 2005; http://www.worldclim.org/) at 2.5 arcminute resolution, i.e. 4.75 km at the equator, 3.25 km at 45° (BIO1 and BIO12).

Species presences projected in the 2-D environmental space were fitted using support vector machines (SVMs), a nextgeneration machine learning algorithm presenting numerous computational advantages including non-linearity, no assumption on the statistical distribution of training data, ability to be trained on presence-only data (i.e. without absences or pseudoabsences) and good performance when trained on few occurrence records (Guo et al., 2005; Drake et al., 2006; Pouteau et al., 2012). SVMs model the support of the statistical distribution of environments from which the species presence observations are drawn, i.e. an environmental hyperspace, which is consistent with the classical definition of a niche as a multidimensional environmental space (Hutchinson 1965). In contrast, logistic regression (Keating and Cherry, 2004), MAXENT (Phillips et al., 2006), ecological niche factor analysis (ENFA; Hirzel et al., 2002) and other models based on probability densities represent the relative frequency of habitat use and are related rather to the idea of resource utilization or resource selection (Drake et al., 2006).

We used the one-class SVM implementation found in the package 'e1071' (Meyer *et al.*, 2019) of the R software (R Development Core Team, 2019). SVM fitting depends on a regularization parameter, *C*, which controls niche breadth and a kernel function that manages the shape of the niche. We chose the Gaussian radial basis function as kernel which relies on tuning only one kernel-specific hyperparameter, γ , while outputting accurate results (Hsu *et al.*, 2010). The 'tune.svm' function was used to search for the optimal couple of *C* and γ in the range [2⁻¹⁰, 2⁻⁹, ..., 2¹⁰] after 4-fold cross-validation in order to maximize model accuracy while preventing overfitting.

Niche overlap

Once fitted, individual species niches were stacked so that they expressed the local potential richness of basal angiosperms over each site of the combined map or each region of the environmental space (Guisan *et al.*, 1999). We then computed a niche overlap index (*NO*) as the proportion of co-occurring basal angiosperm species or genera. At the genus level, niches were defined by merging species-based models rather than by building new models from merged species occurrences because it was easier to manage species' unbalanced occurrences and this procedure was more consistent with the species-specific concept of environmental niche. Thereafter, we focused our attention on regions of maximum niche overlap at the species and genus ranks, denoted as 'species NO_{max} region' and 'genus NO_{max} region', respectively.

Phylogenetic reconstruction

The term 'basal', used to describe the phylogenetic position of early diverging lineages of angiosperms, is often incorrectly interpreted as a synonymous for 'primitive', yet one cannot assume that a basal group retains more ancestral features and most of basal taxa bear many derived features (Crisp and Cook, 2005). Ancestral character states might nevertheless be captured by being mapped on a phylogeny so that any character that is shared by successively branching lineages can reasonably be posited as putatively ancestral (Felsenstein, 1985). To distinguish whether occupation of a biome stemmed from a convergent evolution in angiosperms towards a derived environment (niche evolution) or from a legacy of a common primitive niche (niche conservatism), we assembled a composite phylogenetic tree of extant basal angiosperms using as a backbone the phylogenetic relationships available in Smith and Brown (2018), including the branch length calibration proposed in Magallón et al. (2015). These relationships coincide with the topology proposed by Doyle and Endress (2000), who presented complete and fully resolved relationships of the sampled genera. We mapped NO_{max} at the species and genus ranks. We used Brownian motion-based maximum likelihood estimations of ancestral states considering NO_{max} as a continuous variable. We used the packages 'ape' (Paradis and Schliep, 2018) and 'phytools' (Revell, 2012) for the production of phylogenetic trees, to perform ancestral state reconstructions and to visualize ancestral states on the phylogeny.

Testing for a mid-domain effect

We built a null model to test whether NO_{max} regions mirrored ecological preferences of basal angiosperms or a purely stochastic MDE according to which species ranges thrown randomly within a bounded range are expected to overlap more in the centre of the domain (mid-latitudes and elevations) than at the borders (low and high latitudes and elevations) (Colwell and Lees, 2000).

First, we corrected the area effect according to which differences in land area along the global latitudinal gradient can influence the pool of species found in each latitudinal band or according to which the schematically conical shape of mountains provides smaller habitats for species as elevation increases. This phenomenon is a direct consequence of the basic species richness–habitat size relationship equated by Arrhenius (1921):

$$S = cA^z \tag{1}$$

where S is the empirical species richness, c a constant that equals the number of species that the latitudinal or elevational band would support if it was confined to a one square unit, A is the regional area of the elevational zone and z is a constant describing the slope in a double-log species–area plot (McCain, 2007).

We used eqn (1) to account for the area effect on the global latitudinal and elevational patterns of basal angiosperm richness. S, the area-dependent basal angiosperm richness, was estimated using the range overlap of species within bands of 2° latitude and 100 m elevation. A was the planar area occupied by 2° latitudinal and 100 m elevational zones. Elevation was derived from a Shuttle Radar Topographic Mission digital elevation model (DEM) aggregated to 2.5 arcminutes resolution using the nearest-neighbour resampling method. We empirically determined z as the slope of the linear regression of the species richness (S)-area (A) plot on a log-log scale, and subsequently calculated c, the area-independent basal angiosperm richness, by solving the power model $c = SA^{z}$ (see McCain, 2007 for further details). For visual interpretation, c was multiplied by a constant so that the maximal empirical richness matched the maximal area-corrected richness.

In order to test whether the MDE explains the richness pattern of basal angiosperms within latitudinal and elevational boundaries of their distribution, area-corrected values of richness were compared with the average of 10 000 Monte Carlo simulations of a null model (McCain, 2007). Simulations of species richness were obtained using the software RangeModel 5.0 (Colwell, 2008) with empirical range size of species and random range mid-points. We assumed that basal angiosperm latitudinal and elevational distribution reflected an MDE if richness simulations were significantly correlated to area-corrected observations.

RESULTS

Widespread terrestrial basal angiosperms occurred in a large climatic envelope where annual mean temperature ranged from -3 °C to 30 °C and within a rainfall interval of 700 to 7500 mm (Fig. 1A). This climatic envelope covered all Whittaker's biomes with the only exception of sub-tropical desert and tundra (Fig. 1C). The niche of 39 species out of the 51 (77 %) overlapped in a most occupied region of the environmental hyperspace (species NO_{max} region) described by an annual mean

temperature of 17 °C and annual precipitation in the range 2300–2400 mm year⁻¹. The species NO_{max} region was located in the biome Whittaker referred to as 'temperate rain forest' (Fig. 1C). The ten basal angiosperm genera converged into a larger region (genus NO_{max} region) characterized by annual mean temperature in the range of 17–22 °C and annual rainfall in the range of 2000–2800 mm (Fig. 1B). The genus NO_{max} region intersected four biomes: 'tropical rain forest', 'temperate rain forest' (Fig. 1C).

This pattern in which more than three-quarters of the selected basal angiosperm species and all genera intersected in a similar environmental space was unexpected regarding the fact that all genera never co-occur (poor geographic overlap) and occupy altogether different biogeographical regions (Fig. 2). Two genera occur exclusively in the tropics (Amborella and Austrobaileya), five genera were represented by species occurring in both tropical and temperate regions (Ascarina, Chloranthus, Hedvosmum, Sarcandra and Trimenia) and the three genera belonging to the Schisandraceae were represented by species only occurring in temperate regions (Illicium, Kadsura and Schisandra). Illicium and Schisandra are distributed in the Northern hemisphere, Chloranthus, Kadsura and Sarcandra in Eastern Asia and in the Pacific, Hedyosmum in the Neotropics, Ascarina and Trimenia in the South Pacific, Amborella is endemic to New Caledonia and Austrobaileya is endemic to Queensland, Australia.

The number of species per genus explained little of the variation in the proportion of species within each genus whose niche intersected the species and genus NO_{max} regions ($r^2 = 0.02$ for the species NO_{max} region and $r^2 = 0.20$ for the genus NO_{max} region; *P*-value = 0.73 and 0.20, respectively). The niche of the monospecific genera *Amborella* and *Austrobaileya* as well as those of a high percentage of species in the Chloranthales (*Sarcandra, Chloranthus* and *Ascarina*) crossed both NO_{max} regions (5–100 %) (Fig. 3), the two exceptions being *Ascarina lucida*, endemic to New Zealand, and the Andean *Hedyosmum angustifolium*. In contrast, Austobaileyales (*Illicium, Kadsura*,

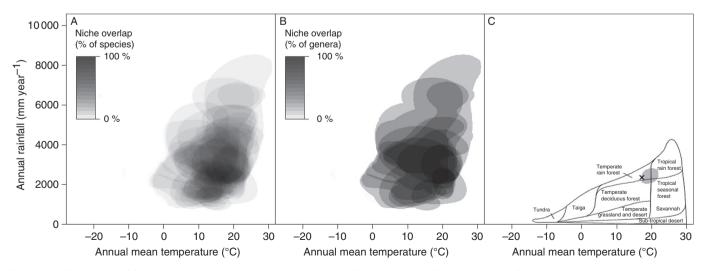


FIG. 1. (A) Niche overlap of 51 widespread terrestrial basal angiosperm species. (B) Niche overlap of the ten corresponding genera (see the Materials and methods for computational details). (C) Black lines represent contours of Whittaker's biome-type classification scheme. The centre of the black cross indicates the region of maximum species niche overlap (species NO_{max} region) occupied by 39 species (77 %). The grey-shaded area indicates the region of maximum genus niche overlap (genus NO_{max} region) where all genera (ten) co-occur.

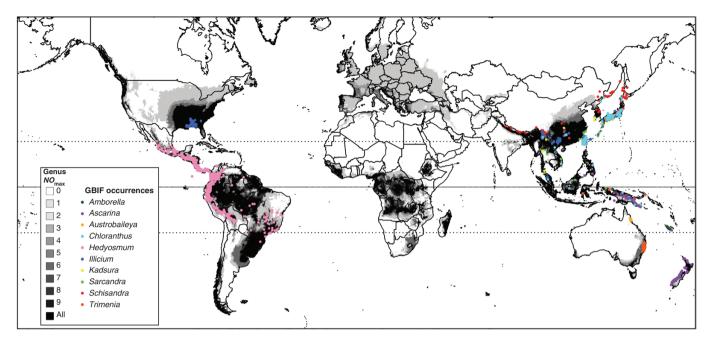


FIG. 2. Distribution of the ten terrestrial basal angiosperm genera according to herbarium records from the GBIF database. Genera are represented by the most prevalent third of all species found in each genus (or the only species available for monospecific genera). Grey levels denote the proportion of basal angiosperm genera whose climate envelopes overlap in a given region.

Schisandra and Trimenia) less frequently occupied the species NO_{max} region (40–80 %). Within this group, both Trimenia species T. moorei and T. papuana, however, intersected the genus NO_{max} region, while Schisandraceae (*Illicium, Kadsura* and Schisandra) were found to be less prevalent in that region (63–80 %) and to occur more frequently under cooler and drier temperate climates (Fig. 3). Coincidently, maximum likelihood phylogenetic reconstructions indicated that the putative common ancestor of the sampled basal angiosperms had a species NO_{max} value of 0.85, and a genus NO_{max} value of 0.93 (Fig. 3). Therefore, both reconstructions suggested high probability for a high niche overlap in the putative common ancestor of the sampled basal angiosperms.

At a global scale, the latitudinal pattern of basal angiosperm richness was poorly affected by the area effect as empirical and area-corrected patterns were highly correlated ($r^2 = 0.89$ at the species level and $r^2 = 0.90$ at the genus level; *P*-value <0.05 in both cases) and culminated in the tropics between 10° south and 30° north (Fig. 4A, C). However, correction of the area on the global elevational pattern of basal angiosperm richness revealed a humpback curve peaking between 2000 and 3500 m (Fig. 4B, D). At all taxonomic levels, area-corrected patterns along both latitudinal and elevational gradients fell within the prediction curve of the MDE model ($r^2 > 0.55$; *P*-value <0.05).

DISCUSSION

Most widespread extant basal angiosperms appeared limited in their latitudinal distribution by temperature and precipitation: areas with mean annual temperature below -3 °C and annual rainfall below 700 mm are never occupied. This limited distribution could be explained by their ecophysiological requirements. For instance, basal angiosperms might have a restricted

distribution due to their sensitivity to hydraulic failure derived from xylem embolisms (Trueba *et al.*, 2017), which result from the very high xylem tensions experienced under drought stress. Moreover, they also present low hydraulic competitiveness compared with vessel-bearing eudicot angiosperms with greater hydraulic efficiency (Sperry *et al.*, 2007), which might have restricted basal angiosperms to more hydraulically permissive environments.

Many basal angiosperms bear tracheids or vessels composed of vessel elements with long scalariform perforation plates and various degrees of pit membrane remnants (Carlquist and Schneider, 2002). Vessels with scalariform perforation plates exhibit hydraulic performances similar to those of tracheids, driving low hydraulic conductance and high vulnerability to drought-induced embolisms (Sperry et al., 2007; Trueba et al., 2019). Because of the physiological impact of anatomical traits such as a tracheid-based wood or vessels with long scalariform perforation plates, hydraulically permissive habitats with low evapotranspirative demands are expected to be particularly suitable for many basal angiosperm taxa (Feild and Wilson, 2012; Pouteau et al. 2015; Trueba et al., 2017). Given that these types of vascular conduits seem to be maintained in most basal angiosperms (ANA and Chloranthaceae), they are considered as a plesiomorphic state in angiosperms, and therefore basal taxa have been suggested to occupy mesic to wet environments since their origin (Carlquist, 2012).

We noticed a discernible preference of extant basal angiosperms for intermediate mesic to moist and cool environments located in the tropics at mid-elevation (2000–3500 m). This most occupied environment is typical of tropical montane cloud forests (TMCFs) that do not appear *per se* in the bidimensional biome classification of Whittaker (Whittaker and Robert, 1962), probably because they cover a marginal proportion of the Earth's terrestrial area (1.4 % of tropical forest area;

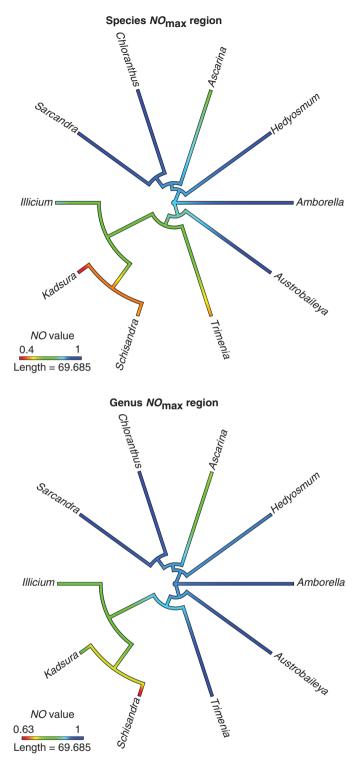


FIG. 3. Maximum likelihood estimation of ancestral states occupying NO_{max} regions at the species and genus levels. The continuous colour gradient shows the most probable NO_{max} values across the basal angiosperm phylogeny.

Bruijnzeel *et al.*, 2011). TMCFs are characterized by frequent cloud presence, low light transmittance, cool temperature, reduced vapour pressure deficit, and thus a low evaporative demand (Bruijnzeel *et al.*, 2011). The elevation of TMCFs shows considerable variation as it depends on many meteorological

(moisture content of the air, velocity and direction of the wind) and oro-topographical effects (mountain size, distance to the sea). However, a typical elevation for TMCFs on large, inland mountains is between 2000 and 3500 m while on coastal and isolated mountains, as on oceanic islands, the cloud forests is found at much lower elevations (e.g. 1000 m in Hawaii) (Hamilton *et al.*, 1995). The question then arises as to whether the occupancy of TMCFs reflects a random distribution or a legacy of a common ancestral niche.

The global latitudinal and elevational distribution of richness in extant basal angiosperms converging in TMCFs was statistically correlated with predictions of the MDE within the ecological limits of basal angiosperms imposed by their requirements for hydraulically permissive habitats. Thus, at first glance, the abundance of extant basal angiosperms in TMCFs appears not better explained by a deterministic niche perspective than by a purely null model within these boundaries. However, phylogenetic mapping of biome occupation revealed that the occupation of TMCFs is likely to have been shared with a common ancestor. This finding stems from the fact that the most basal taxa tend to occupy TMCFs more frequently than the least basal taxa, which is not predicted by the MDE. The convergence towards TMCFs of the environmental niche of the basal-most terrestrial woody angiosperms such as that of the monospecific genera Amborella and Austrobaileva indicates a legacy of an ancestral mesic to moist and cool ecological niche that might have been conserved over time. Nevertheless, less basal genera such as Kadsura, Schisandra and Illicium have both higher species and ecological diversification as they tend to comprise more species and to diverge from this ancestral niche following a random pattern under physiological and geometric constraints.

The Austobaileyales indeed decreased the probability that the common ancestor would have occupied the species NO_{max} region. However, this may arise from the poor sampling of certain genera such as Trimenia in which many less widespread species, not sampled in this study, are known to be restricted to TMCFs. This is the case of the two Trimenia endemic to the Marquesas archipelago, T. nukuhivensis found above 760 m on the islands of Nuku Hiva and Ua Pou, T. marquesensis found above 790 m on Hiva Oa and Tahuata (Wagner and Lorence, 2002), of T. weinmanniifolia found above 700 m in Fiji and Samoa, of T. bougainvilleensis found above 1500 m in the Solomon Islands (Rodenburg, 1971) and of T. neocaledonica occurring above 700 m in New Caledonia (Morat and MacKee, 1977). It is perhaps not surprising that many basal angiosperms have persisted on islands over time as island TMCFs have been shown to be much less sensitive to climate change than mainland TMCFs (Pouteau et al., 2018). These findings support the idea that TMCFs is the biome with the highest probability to have hosted early angiosperms.

Our niche reconstruction therefore challenges the assumption built from fossil records that early angiosperms emerged in arid to semi-arid biomes (Stebbins, 1974; Doyle and Hickey, 1976; Hickey and Doyle, 1977) and tends to support the idea developed from biogeographical patterns (Takhtajan, 1969; Thorne, 1976) and eco-morphological traits of extant basal angiosperms (Feild *et al.*, 2000, 2004, 2009; Feild and Arens, 2005, 2007) suggesting that the origin of angiosperms would be in tropical rain forests. However, our approach tells

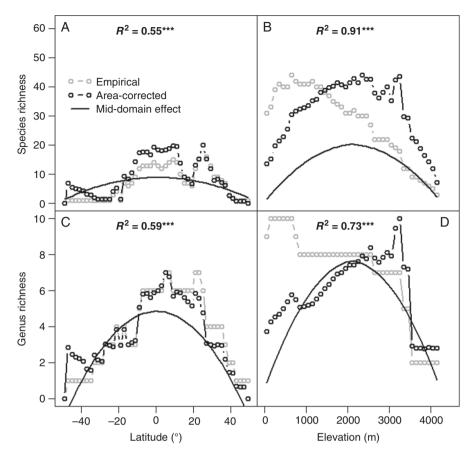


FIG. 4. Comparison of basal angiosperm richness patterns with a null mid-domain effect (MDE) model along latitudinal (A, C) and elevational gradients (B, D) at the species (A, B) and genus levels (C, D). R^2 are determination coefficients between area-corrected species richness (dashed black line) and MDE simulations (continuous black line).

a slightly different story as it identified tropical temperatelike rain forests (approx. 17 °C mean annual temperature and approx. 2300–2400 mm year⁻¹) as the most likely ancestral habitat, which is typically represented by TMCFs. If former approaches based on extant basal angiosperms were shown to be useful to draw an overall picture of the early angiosperm biome, our direct assessment of the environmental distribution of extant basal angiosperms enabled a more detailed delimitation of the contours of the early angiosperm environmental niche.

SUPPLEMENTARY DATA

Supplementary data are available online at https://academic. oup.com/aob and consist of Appendix 1: list of basal angiosperm species belonging to the ANA grade and the Chloranthales order used in this study.

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CORRIGENDUM

Retracing the contours of the early angiosperm environmental niche

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In the originally published version of this article a mistake was made in the first sentence of the discussion section on page 5. This sentence should read: 'Most widespread extant basal angiosperms appeared limited in their latitudinal distribution by temperature and precipitation: areas with mean annual temperature below -3 °C and annual rainfall below 700 mm are never occupied' and not '700 m are never occupied'. This has now been corrected.