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ARTICLE

Biogeographical diversification of mainland Asian *Dendrobium* (Orchidaceae) and its implications for the historical dynamics of evergreen broad-leaved forests

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ABSTRACT

Aim Evergreen broad-leaved forests (EBLFs) occupy most tropical and subtropical regions of mainland Asia and exhibit high species diversity, productivity and richness. Understanding the historical dynamics of EBLFs is important for biodiversity conservation and regional carbon storage and cycling under global climate change. However, little is known about the historical dynamics of EBLFs in mainland Asia. *Dendrobium*, an epiphytic orchid genus found in EBLFs, was used to gain new insights of the historical establishment and extension of EBLFs in mainland Asia.

Location Mainland Asia.

Methods We sampled c. 80% of the currently recognized species of *Dendrobium* found in mainland Asia. A phylogeny was generated using maximum parsimony, maximum likelihood and Bayesian inference methods. A calibrated chronogram was obtained using a Bayesian relaxed-clock model approach. Biogeographical scenarios were investigated using the statistical dispersal–vicariance analysis and dispersal–extinction–cladogenesis methods. Ancestral states were constructed by MESQUITE and BAYESTRAITS, and diversification of *Dendrobium* was investigated by APE and LASER packages.

Results Our results indicate that Asian *Dendrobium* was present on mainland Asia since the Oligocene, after which this genus diversified in this region and dispersed into higher elevations. The ancestral habit of *Dendrobium* was epiphytic and terrestrial and lithophytic habits each have multiple, recently independent origins.

Main conclusions Our results support the hypothesis that EBLFs have been established in mainland Asia at least since the Oligocene and further suggest that the EBLFs of mainland Asia expanded into higher elevations prior to the late Cenozoic. The diversification of Asian *Dendrobium* coincided with a warmer climate during the late Oligocene and middle Miocene and the expansion of key groups (including Fagaceae, Lauraceae, Magnoliaceae and Theaceae) of EBLFs during the early Cenozoic.

Keywords

Biogeography, *Dendrobium*, evergreen broad-leaved forests, mainland Asia, molecular dating, Orchidaceae

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INTRODUCTION

Evergreen broad-leaved forests (hereafter EBLFs), including tropical rain forest, tropical seasonal rain forest and subtropical EBLFs, occupy most regions of tropical and subtropical mainland Asia and are very important terrestrial ecosystems in terms of species diversity and ecosystem functioning (Fang & Yoda, 1991; Wu, 1995; He *et al.*, 1998; Ying, 2001; Zhu, 2013). Species of several woody families, such as Fagaceae, Lauraceae, Magnoliaceae and Theaceae, dominate EBLFs, which appear to be unique in terms of their climate characteristics, forest structure and species composition (Wu, 1995). In contrast to the EBLFs of Asia, most regions around the world at similar latitudes are occupied by savanna vegetation or even hot, dry deserts (Good, 1974). Evergreen broad-leaved forests provide considerable social and ecological benefits (Ying, 2001; Piao *et al.*, 2009). Recent results have demonstrated that they play critical roles in biological conservation and regional carbon storage and cycling, and a better understanding of the establishment and the historical dynamics of the EBLFs is important for biodiversity conservation and carbon sequestration, especially with respect to global climate change (Fang *et al.*, 1998, 2014; Myers *et al.*, 2000; Ying, 2001; Zhang *et al.*, 2007; Piao *et al.*, 2009; Pan *et al.*, 2011).

Currently, there is little knowledge regarding the historical dynamics of the development of Asian EBLFs. The frequent hybridization, complicated evolutionary histories (Samuel, 1999; Wu *et al.*, 2003; Zhang *et al.*, 2014), and taxonomic confusion in keystone forest tree families, notably Fagaceae (Samuel, 1999), Lauraceae (Rohwer, 2000; Chanderbali *et al.*, 2001), Magnoliaceae (Nie *et al.*, 2008) and Theaceae (Luna & Ochoterena, 2004; Zhang *et al.*, 2014), present major obstacles in tracing the historical dynamics of EBLFs. Understanding the historical dynamics of the development of Asian EBLFs is further complicated by complex geographical events, including the uplift of the Himalayas (An *et al.*, 2001), and by climatic changes, such as the establishment of the Asian monsoon (Sun & Wang, 2005) and climate changes during the Neogene (Zhou, 1999; Jacques *et al.*, 2011).

Recent results of fossil and molecular dating analyses have indicated that the woody families that dominate EBLFs diverged after the middle Cretaceous (Friis *et al.*, 1987; Magallón & Castillo, 2009; Smith *et al.*, 2011) and diversified during the early Cenozoic (Xiang *et al.*, 2014). The prevailing view is that EBLFs in tropical region began to appear after the K-Pg boundary (e.g. Upchurch & Wolfe, 1987; Morley, 2000; Johnson & Ellis, 2002; Schuettpelz & Pryer, 2009; Wang *et al.*, 2012). Therefore, it is logical to propose the hypothesis that the EBLFs have been established in mainland Asia since the early Cenozoic.

The orchid genus *Dendrobium* (Epidendroideae, Orchidaceae) is among the largest genera of flowering plants, with 1200–1500 species that are mainly distributed in Asia and Oceania (Cribb & Govaerts, 2005; Wood, 2006; Zhu *et al.*,

2009; Pridgeon *et al.*, 2014). Of the c. 200 species of *Dendrobium* in mainland Asia, most are typically epiphytic and grow on the trees of EBLF keystone groups, such as Fagaceae, Lauraceae, Magnoliaceae and Theaceae (Tsi, 1999; Wood, 2006; Zhu *et al.*, 2009). Like most epiphytic orchids, *Dendrobium* species have tiny wind-dispersal seeds with a high dispersal capacity (Hamrick & Godt, 1996; Alcantara *et al.*, 2006; Phillips *et al.*, 2012). Several species extend to the northern limits of EBLFs (Tsi, 1999; Wood, 2006; 2001–2013 our field observations). Therefore, *Dendrobium* species can be considered characteristic of these forests (Wood, 2006; Zhu *et al.*, 2009). The results of recent morphological and molecular analyses have indicated that *Dendrobium* s.l. is monophyletic and is divided into two clades: an Asian clade and an Australasian clade (Yukawa *et al.*, 1993, 2000; Clements, 2003, 2006; Burke *et al.*, 2008; Schuiteman, 2011; Xiang *et al.*, 2013). However, there is little knowledge about the historical biogeography and diversification of *Dendrobium*. The discovery of *Dendrobium* leaf fossils in New Zealand indicated the expansion of *Dendrobium* into Zealandia by the middle Cenozoic (Early Miocene, 23–20 Ma) (Conran *et al.*, 2009), which shed new insights on the spatial and temporal evolution of *Dendrobium*. Therefore, *Dendrobium* offers a remarkable and unique opportunity for studying the historical dynamics of the development of EBLFs in mainland Asia.

Our major aims are (1) to infer the historical biogeography and diversification of the epiphytic orchid *Dendrobium* and use this as a model to (2) infer the historical establishment and extension of EBLFs in mainland Asia and to (3) test the hypothesis that EBLFs have been established in mainland Asia since the early Cenozoic. To achieve these objectives, we first reconstructed a robust phylogenetic framework for *Dendrobium*, focusing on the mainland Asian groups and using more extensive sampling than that of any previous study. We then investigated the temporal and spatial diversification of mainland Asian *Dendrobium* by integrating phylogenetic, biogeographical and molecular dating methods.

MATERIALS AND METHODS

Sampling and molecular data

To fully understand the diversification of mainland Asian *Dendrobium*, we sampled all sections present in mainland Asia based on previous phylogenetic results, thus representing the geographical and taxonomic diversity of the genus (Clements, 2003, 2006; Wood, 2006; Burke *et al.*, 2008; Xiang *et al.*, 2013). Approximately 80% of the species from mainland Asia were sampled, and all relevant sequences were downloaded from GenBank (last download in 11 August 2015). The matrix contained 319 species (taxonomy of *Dendrobium* following Wood, 2006; Xiang *et al.*, 2013; Pridgeon *et al.*, 2014), of which 40 species were from the Australasian group and 10 species were outgroups. Four chloroplast DNA

sequences (*matK*, *rbcl*, *trnH-psbA* spacer and *trnL-F* region) and the nuclear internal transcribed spacer (ITS) region were used for analyses. Voucher information and GenBank accession numbers are listed (see Table S1 in Appendix S1 of Supporting Information).

Phylogenetic analyses

In order to assess the impact of missing data on phylogenetic reconstruction, five different matrixes of *Dendrobium* were generated and analysed using the same methods: matrix 1 with 80 taxa, each taxon with five loci (80 taxa, 5 loci), matrix 2 (91 taxa, 4–5 loci), matrix 3 (129 taxa, 3–5 loci), matrix 4 (281 taxa, 2–5 loci) and matrix 5 (319 taxa, 1–5 loci).

The alignment was performed in CLUSTALX 1.83 (Thompson *et al.*, 1997) and then adjusted manually in BIOEDIT (Hall, 1999). The data were partitioned as follows: ITS1, 5.8S rDNA, ITS2, *matK*, *rbcl*, *trnH-psbA* and *trnL-F*. Phylogenetic analyses were carried out using MRBAYES 3.2.1 (Ronquist & Huelsenbeck, 2003) for Bayesian inference (BI), PAUP v4.0b10 (Swofford, 2003) for maximum parsimony (MP) and RAXML 7.0.4 (Stamatakis, 2006) for maximum likelihood (ML).

MODELTEST 3.7 (Posada & Crandall, 1998) was used to determine the best-fit model under the Akaike information criterion (AIC). The GTR+I+ Γ model was selected for ITS, *rbcl* and the combined matrix while the TVM+I+G model was selected for all other loci. In the BI analysis, we used default priors and set the option *prset ratepr* as variable. The Markov chain Monte Carlo (MCMC) algorithm was run for 6,000,000 generations with one cold chain and three heated chains, starting from a random tree. The convergence was assessed using TRACER v1.5 (Rambaut & Drummond, 2007). With the first 25% trees discarded as burn-in, the 50% majority-rule consensus tree and posterior probabilities (PP) were calculated from the remaining trees.

For the MP analysis, heuristic searches were performed using 1000 random-addition-sequence replicates and tree-bisection-reconnection branch swapping with MulTrees in effect and steepest descent off. Bootstrap support values were calculated by conducting heuristic searches using 1000 replicates.

For the ML analysis, the GTR+GAMMA model was set for all partition, but all model parameters were estimated for each partition respectively. 1000 rapid bootstrap inferences were executed before a thorough ML search.

Molecular age estimation

Dendrobium divergence times were estimated in two steps. First, we used a phylogeny representing the major orchid lineages to estimate the crown group age of a monophyletic clade that included *Dendrobium*. We then used the estimated crown age to calibrate the rate corrected phylogeny of the *Dendrobium* species used in this study.

Divergence time estimation in Orchidaceae

We downloaded *matK* and *rbcl* sequences from GenBank to estimate the divergence times in Orchidaceae. Of 203 species included in the analysis, 195 represented 186 genera from five subfamilies in Orchidaceae and 8 taxa were outgroups selected from closely related families in Asparagales (see Table S2 in Appendix S1 in Supporting Information). Divergence times were estimated using a Bayesian uncorrelated relaxed-clock model implemented in BEAST 1.7.4 (Drummond & Rambaut, 2007). Four fossil calibration points were used: (1) the age of the oldest known monocot fossil (110–120 Ma) for the root, following Friis *et al.* (2004) and Ramírez *et al.* (2007) with a normal prior distribution (mean: 115 Ma, and a standard deviation of 3.05), for a normal distribution can be used to reflect the non-directional uncertainty on radiometric dating (Ho & Phillips, 2009); (2) 15 Ma as the minimum age for the monophyletic Goodyerinae Klotzsch (Orchidoideae, Orchidaceae) with exponential distribution (offset: 15, mean: 10) (Ramírez *et al.*, 2007); (3) 23.2 Ma as the minimum divergent age of the Asian and Australasian *Dendrobium* clades with exponential distribution (offset: 23.2, mean: 8) (Conran *et al.*, 2009; Pole, 2014); and (4) a leaf fossil of *Earina* (23.2 Ma) as the minimum stem age of *Earina* Lindl. (Epidendroideae, Orchidaceae) with exponential distribution (offset: 23.2, mean: 8) (Conran *et al.*, 2009; Pole, 2014). Except for the root age for which a normal distribution was used, an exponential distribution was used for the other three calibration points, which was decided by the characteristics of the exponential distribution and the greatest prior weight placed on node ages very close to the age of the fossil with diminishing probability to ∞ (Ho & Phillips, 2009). MCMC searches were run for 50,000,000 generations and sampled every 5000 generations. Convergence was monitored using TRACER 1.5 (Rambaut & Drummond, 2007). The effective sample sizes (ESSs) of all parameters were assessed. The maximum clade credibility tree was computed using TREEANNOTATOR 1.7.4 (Drummond *et al.*, 2012).

Divergence time estimation in *Dendrobium*

A likelihood ratio test was performed to estimate whether *Dendrobium* evolved at a homogeneous rate along all branches of the phylogeny. The result rejected a constant rate for *Dendrobium* ($\delta = 1683.39$, d.f. = 319, $P < 0.001$).

Previous results indicated that there are only 'soft' conflicts between the nuclear versus plastid trees in *Dendrobium* (Xiang *et al.*, 2013). Divergence times within *Dendrobium* were therefore estimated using the combined ITS, *matK*, *rbcl*, *trnH-psbA* and *trnL-F* matrix and the following tree priors: (1) based on the results of the chronogram of Orchidaceae (above), the root age was set to a normal prior distribution with a mean of 47.56 Ma and a standard deviation of 5.75 (resulting in a 95% CI ranging from c. 39–57 Ma); (2) a minimum age (23.2 Ma) was used for the stem age of the

Australasian clade of *Dendrobium* (Conran *et al.*, 2009; Pole, 2014) with an exponential prior distribution (mean = 3.0, SD = 0.5). The Yule process was chosen as the speciation process, and GTR+I+ Γ was used for the best-fitting evolutionary model (see MODELTEST). Markov chain Monte Carlo searches were run for 100,000,000 generations sampled every 5000 generations. Convergence, ESS of parameters and the calculation of the maximum clade credibility tree followed the methods outlined above.

Diversification analyses

Birth–death likelihood (BDL) models were used to test the significance of heterogeneity or the consistency of the temporal diversification rate (Rabosky, 2006a,b). The model selection was based on the difference in the AIC scores between the best-fitting rate-constant and rate-variable models ($\Delta\text{AIC}_{\text{RC}}$). The calculations were performed using LASER 2.3 (Rabosky, 2006a).

To visualize the temporal variation in the diversification rates, semi-logarithmic lineage-through-time (LTT) plots were constructed using the R package APE 2.5-1 (Paradis *et al.*, 2004). One thousand trees were sampled randomly from the converged BEAST trees and used to calculate a 95% credibility interval.

Ancestral area reconstructions

Based on the floristic regions delimited by Takhtajan (1986) and the extant distribution of *Dendrobium* and outgroups, four main regions were defined: A, mainland Asia (including Eastern Asia, India, Indo-China and Myanmar); B, Malesia (including Malaysia, Indonesia, Philippines, Singapore and New Guinea); C, Australasia (including Australia, New Zealand, New Caledonia and Tasmania); and D, circumpolar (for outgroups). The ancestral areas at internal nodes within the phylogenetic tree were inferred using two methods: (1) a statistical dispersal–vicariance analysis (S-DIVA) (Ronquist, 1997) implemented in RASP (Yu *et al.*, 2013) and (2) a likelihood approach using the dispersal–extinction–cladogenesis (DEC) model implemented in RASP with the source code of the C++ version of LAGRANGE (Ree & Smith, 2008). All analyses were based on the 1001 output trees and the maximum clade credibility tree from the BEAST analyses. The outgroups were included in the analyses. Neither analysis was performed with constraints on the maximum number of areas per node.

Ancestral states reconstruction

We inferred the elevation range of each species of *Dendrobium* according to Zhu *et al.* (2009), Wood (2006), the Orchids Species (<http://www.orchidspecies.com/>, last assessed in 11 August 2015) and our field observations (see Table S1 in Appendix S1 in Supporting Information). Shifts in *Dendrobium* elevation ranges was reconstructed using the squared-change parsimony option for continuous characters

using the continuous method with MESQUITE 2.74 (Maddison & Maddison, 2011). The maximum clade credibility tree obtained from BEAST was used in the analysis.

Species habit data were also obtained from the sources above (see Table S1 in Appendix S1). We defined three habit categories: epiphytic, lithophytic and terrestrial. The ancestral habit of *Dendrobium* and the direction of habit shifts were reconstructed using the MCMC approach in BAYESTRAITS (Pagel *et al.*, 2004) using a set of 1000 chronograms chosen randomly from the post-burn-in BEAST trees.

RESULTS

Phylogenetic analyses

Our results indicated that the backbones of the five phylogenetic topologies from analyses based on different taxon and character sampling strategies are similar, with differences only in clades that are weakly supported (Fig. 1; see Fig. S1 in Appendix S1). Matrix 5 with 319 *Dendrobium* taxa (each taxon with 1–5 loci) was therefore used in followed analyses and discussion. The aligned combined data set consisted of 7010 bp, 20% of which were parsimony-informative, and 56.1% of which contained missing data. The parsimony strict consensus tree of *Dendrobium* was largely consistent to the topologies of ML and BI analyses with differences only in weakly supported clades.

Dendrobium was divided into two main clades (MP-BS = 90, ML-BS = 100, PP = 1.00): an Asian clade and an Australasian clade (Fig. 1). The results were consistent with those of previous studies (Clements, 2003, 2006; Burke *et al.*, 2008; Xiang *et al.*, 2013). Twelve major clades were recognized within the Asian group, and all of these clades were recognized by Xiang *et al.* (2013) and Takamiya *et al.* (2014). However, the relationships among these clades are not well resolved and show a similar level of resolution to previous results (Clements, 2003, 2006; Burke *et al.*, 2008; Xiang *et al.*, 2013).

Age estimates

Family-level molecular dating indicated that Orchidaceae diverged at 93 Ma [95% highest posterior density (HPD): 83–102] and the four subfamilies (except subfamily Apostasioideae) diverged during the late Cretaceous (see Fig. S2 in Appendix S1). Divergence time analysis of *Dendrobium* using the combined data set (Fig. 2) showed that the stem age of *Dendrobium* was 30.34 Ma (95% HPD: 26.92–34.03), with the split between the Asian and Australasian clades occurring at 28.17 Ma (95% HPD: 25.1–31.63). The crown age of the Asian clade was 25.20 Ma (95% HPD: 20.96–29.31). Given the inferred credibility intervals of the divergence times, our estimates indicated that 10 clades/sections within the mainland Asian *Dendrobium* (i.e. all except clade VII and VIII) arose or diverged between the late Oligocene and the middle Miocene (Fig. 2; Table 1).



Figure 1 Strict consensus maximum parsimony tree of *Dendrobium* based on 319 species and five loci. Numbers on branches are maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI) support values respectively. Asterisk (*) indicates support value at a node is 100%, dash (–) indicates support value at a node < 50%, and blank indicates that a node does not appear in the ML or BI trees.

Diversification analyses

The BDL analysis rejected the null hypothesis of temporally homogeneous diversification rates within the Asian clade ($\Delta\text{AIC}_{\text{RC}} = 5.1$, $P < 0.001$). The yule3rate model, which included two diversification rate shifts and no extinction, was found to best fit the data and suggest that *Dendrobium* started to diversify with a rate $r_1 = 0.2177 \text{ sp Ma}^{-1}$. A decrease in the diversification rate to $r_2 = 0.1493 \text{ sp Ma}^{-1}$ occurred at $\text{ts}_1 = 5.21 \text{ Ma}$ (95% HPD: 2.70–7.21), followed by a further decrease at $\text{ts}_2 = 0.33 \text{ Ma}$ (95% HPD: 0.02–1.35) to $r_3 = 0.0225 \text{ sp Ma}^{-1}$ (Fig. 3). The LTT plots also indicated that *Dendrobium* did not exhibit a constant speciation rate: an acceleration in speciation of the Asian lineages occurred from the late Oligocene to the middle Miocene with a slight decrease after the late Miocene.

Ancestral area reconstruction

The reconstructions obtained for the major clades of interest using the DEC model and S-DIVA were highly congruent (Table 1). The optimal ancestral area reconstructions under S-DIVA are shown in Fig. 2. Our results suggest that *Dendrobium* most likely originated in mainland Asia and then diverged into Malesia and Australasia (Fig. 2). The most recent common ancestor (MRCA) of the Asian group was likely located in mainland Asia (Fig. 2, Table 1). The MRCAs of clades X, XI and XII originated in Malesia (Fig. 2), which have been connected to mainland Asia since the Eocene (Lomolino *et al.*, 2005).

The reconstruction of *Dendrobium* elevation ranges (Fig. 4) illustrated that the early lineages were distributed primarily in low-elevation regions (< 1000 m) and then spread to higher elevations ($\geq 1000 \text{ m}$) in both the Asian and Australasian clade. Of the 309 *Dendrobium* species sampled, 94.84% are typically epiphytic, 4.19% are lithophytic, and 0.97% are terrestrial. An epiphytic habit was the ancestral habit of *Dendrobium*, the lithophytic evolved independently 11 times in four clades and terrestrial habit evolved 3 times (see Fig. S3 in Appendix S1).

DISCUSSION

According to our results, the crown age of Orchidaceae diverged at 93 Ma (95% HPD: 83–102), and it is younger

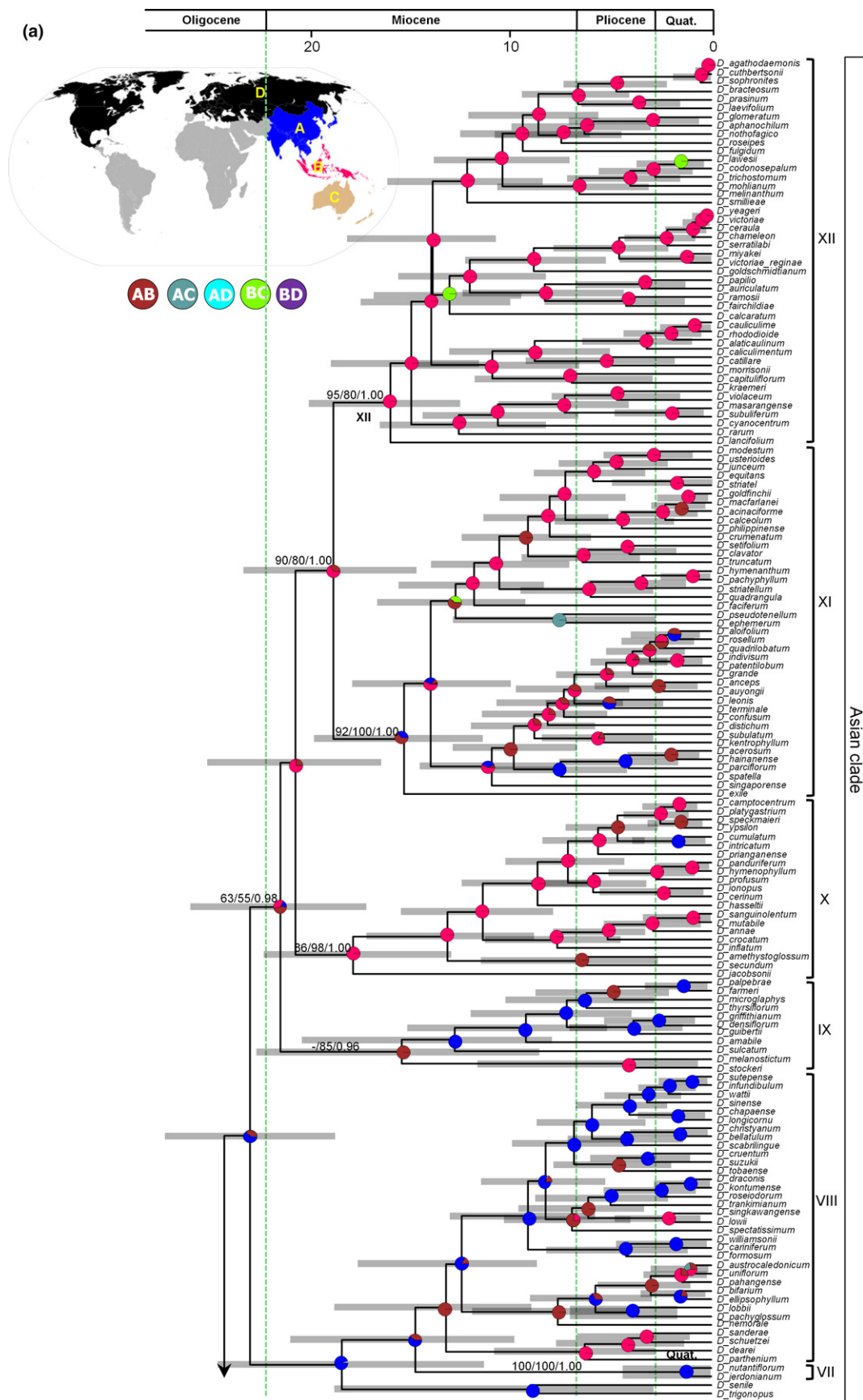
than the crown age estimated by Janssen & Bremer (2004) (111 Ma), but older than the estimates of Ramírez *et al.* (2007) and Bouetard *et al.* (2010) [76 ± 5 and 83 Ma (95% HPD: 68–104) respectively]. Four previous studies estimated the divergence times in Orchidaceae subfamilies (Ramírez *et al.*, 2007; Gustafsson *et al.*, 2010; Guo *et al.*, 2012; Givnish *et al.*, 2015). Our results for the divergence of the subfamilies are older than the results of Ramírez *et al.* (2007) and Gustafsson *et al.* (2010), but close to those of Guo *et al.* (2012) and Givnish *et al.* (2015) (see Table S3 in Appendix S1). The latter four studies of Orchidaceae subfamilies had different sampling strategies (60, 70, 200 and 201 taxa respectively), whereas we included 203 taxa. Our results indicated that similar sampling strategies have yielded similar molecular phylogenetic inferences and molecular dating.

The concatenated alignment (matrix 5, including 319 taxa and 1–5 loci for each taxon) contains 56.1% missing data, but it appears that this has limited impact on phylogenetic reconstruction as the backbone of the topology is consistent with that for other matrices with fewer taxa but less missing data (Fig. 1; Fig. S1 in Appendix S1) and also for other studies (Clements, 2003, 2006; Burke *et al.*, 2008; Xiang *et al.*, 2013; Takamiya *et al.*, 2014).

Dendrobium most likely originated in mainland Asia during the early Oligocene (30.34 Ma, 95% HPD: 26.92–34.03) (Fig. 2, Table 1). The results of the divergence time analysis indicated that the Asian clade started to diverge at 25.20 Ma (95% HPD: 20.96–29.31), soon after the initial origin of Asian *Dendrobium* in the middle Oligocene (28.17 Ma, 95% HPD: 25.10–31.63) (Fig. 2, Table 1). There were two important expansion events in the Asian group. First, in addition to the diversification of clades I–VII in Asian clade, the ancestor of clades X–XII dispersed from the mainland Asia into Malesia, and clades VIII and XI diversified in mainland Asia and the Malesia (Fig. 2). Second, Asian *Dendrobium* spread from low altitudes to higher altitudes from the beginning of the Miocene (Fig. 4).

The test for heterogeneity of the temporal diversification rate identified a model with no extinction and two rate shifts that fit the LTT plot (Fig. 3). The first rate change was at 5.21 Ma (95% HPD: 2.70–7.21), which was during the early Pliocene. The second rate change, a decrease at 0.33 Ma,

Figure 2 Timing of the diversification of *Dendrobium*. Chronogram derived from the maximum clade credibility tree estimated by using the uncorrelated exponential method in BEAST. Grey bars indicate 95% highest posterior density (HPD) intervals of the age estimates. The red star and orange star represent the root and fossil calibration node respectively (see Materials and methods). Clades I–XII represent the sections/clades recognized in Xiang *et al.* (2013) and Takamiya *et al.* (2014). Biogeographical region abbreviations: A, Mainland Asia; B, Malesia; C, Australasia; D, circumpolar.



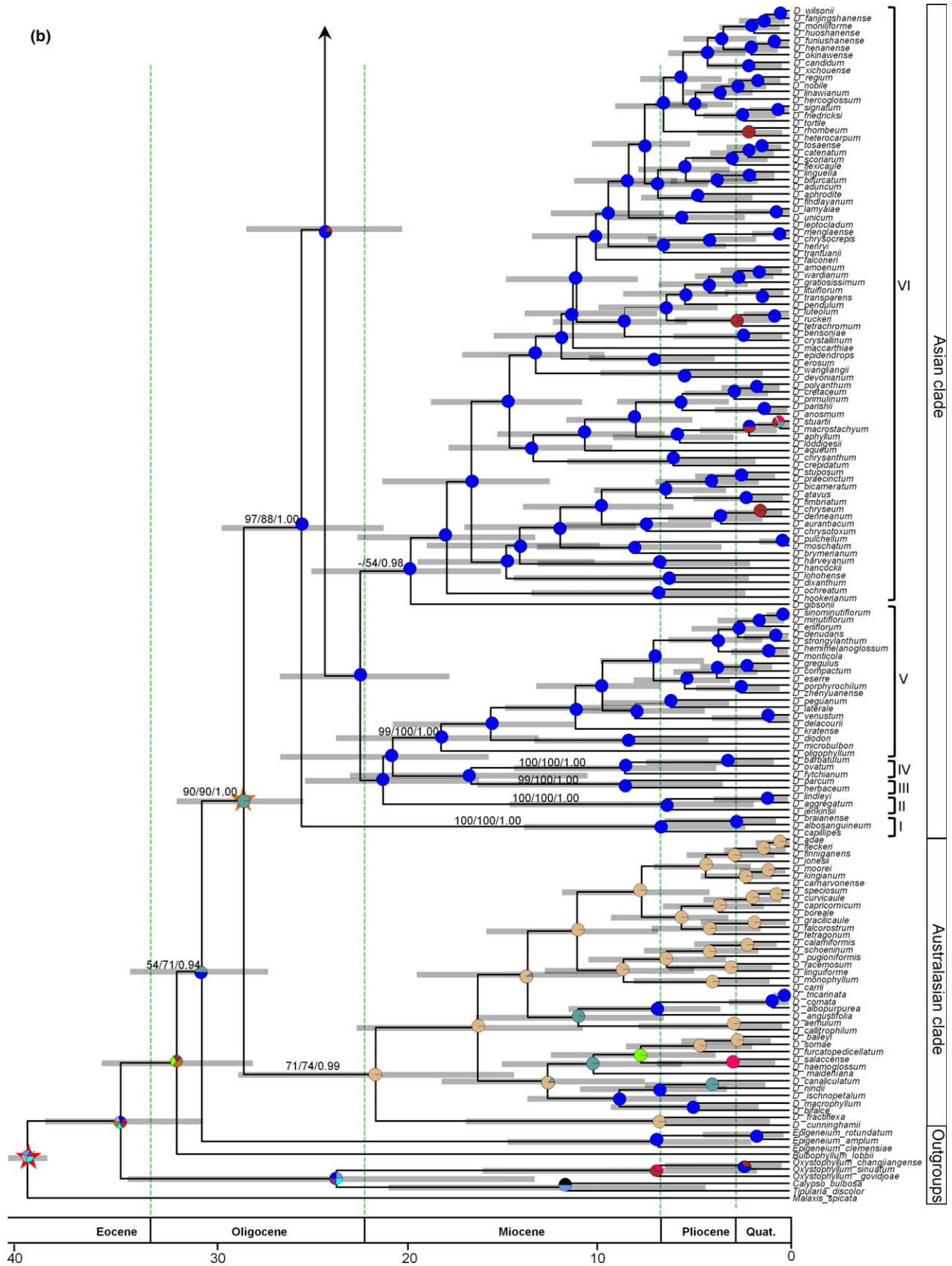


Figure 2 Continued.

Table 1 Clade support under maximum parsimony, maximum likelihood and Bayesian inference (MP, ML and PP respectively), divergence age estimates and ancestral area reconstructions for *Dendrobium*. RP, relative probability; MP, maximum probability. Clades names follow Figs 1 and 2; area codes follow Fig. 2 as follows: A, Mainland Asia; B, Malesia; C, Australasia; D, circumpolar.

Clade	Clade support (MP/ML/PP)	BEAST (95% HPD) (Ma)	Likelihood-DEC (RP)			S-DIVA (MP)		
			1	2	3	1	2	3
<i>Dendrobium</i> stem	54/71/0.94	30.34 (26.92–34.03)	A A: 0.70	AC A: 0.14		A: 0.51	AC: 0.49	
<i>Dendrobium</i> crown	90/100/1.00	28.17 (25.1–31.63)	A A: 0.49	C A: 0.31		AC		
I stem	NA	25.20 (20.96–29.31)	A A: 0.87			A		
I crown	100/100/1.00	6.63 (2.29–13.74)	A A: 0.85	A AB: 0.15		A		
II stem	NA	20.99 (16.05–25.01)	A A: 1			A		
II crown	100/100/1.00	6.39 (1.87–14.47)	A A: 0.84	A AB: 0.15		A		
III/IV stem	NA	16.45 (10.43–22.70)	A A: 0.99			A		
III crown	99/100/1.00	8.52 (3.81–14.24)	A A: 0.85	AB A: 0.13		A		
IV crown	100/100/1.00	8.48 (3.47–16.14)	A A: 1			A		
V stem	NA	20.49 (15.54–26.29)	A A: 1			A		
V crown	99/100/1.00	18.00 (12.96–23.43)	A A: 1			A		
VI stem	NA	22.17 (17.58–26.32)	A A: 1			A		
VI crown	–/54/0.98	19.57 (14.91–24.68)	A A: 1			A		
VII/VIII stem	NA	14.60 (9.74–20.74)	A A: 0.49	AB A: 0.34	B A: 0.17	A: 0.63	AB: 0.37	
VII crown	100/100/1.00	13.10 (8.89–18.58)	AB B: 0.72	B B: 0.17	A B: 0.10	B		
VIII crown	NA	1.56 (0.08–4.42)	A A: 1			AB		
IX stem	NA	21.22 (17.01–25.65)	B AB: 0.54	B B: 0.22		AB: 0.47	B: 0.33	A: 0.20
IX crown	–/85/0.96	15.26 (8.5–22.42)	A B: 0.66	AB B: 0.23	B B: 0.12	AB		
X stem	NA	20.49 (16.47–24.84)	B AB: 0.79	AB B: 0.20		B		
X crown	86/98/1.00	17.66 (12.84–22.06)	B B: 0.99			B		
XI/XII stem	90/80/1.00	18.63 (14.54–23.05)	B B: 0.688	AB B: 0.182	A B: 0.115	B: 0.57	AB: 0.43	
XI crown	92/100/1.00	15.16 (11.28–19.59)	A AB: 0.754	A A: 0.107		B: 0.57	AB: 0.43	
XII crown	95/80/1.00	15.82 (12.4–19.83)	B B: 0.999			B		

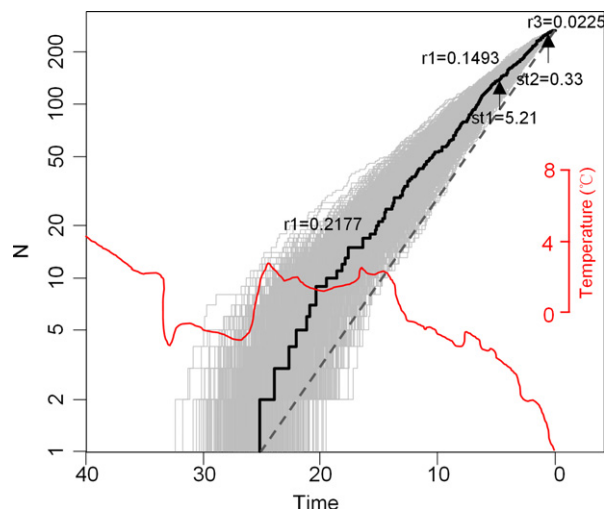


Figure 3 Semi-logarithmic lineage-through-time (LTT) plots and the rate shifts in Asian *Dendrobium* under the best rate-variable model. Grey lines represent the LTT plots for 1000 trees randomly selected from the BEAST analysis. The black line shows the maximum clade credibility tree. The red line represents the temperature curve since the Oligocene. The arrows highlight the two rate shifts identified, st_1 and st_2 are the time of the rate shift (in Ma) and r_1 , r_2 and r_3 the three speciation rates inferred (in $sp\ Ma^{-1}$).

appeared as a flattening of the LTT plot as the time approached the present (Fig. 3) but might reflect sampling gaps as many species are younger than 5 Ma. Clearly, a high

speciation rate has characterized the diversification of Asian *Dendrobium* through time.

Many factors, such as pollinators, mycorrhizal fungi and epiphytic habitats (e.g. EBLFs), may have affected the diversification of Orchidaceae (including *Dendrobium*) (Darwin, 1877; van der Cingel, 1995; Cozzolino & Widmer, 2005). Although few studies have focused on the roles of mycorrhizal fungi and the pollinators of this genus, recent results have indicated a low specificity of mycorrhizal fungi in some species of *Dendrobium* and in epiphytic orchids more generally (Xing *et al.*, 2013). Moreover, while several pollination mechanisms have been illustrated in *Dendrobium*, including autogamy, deceptive pollination and possible sleeping site rewards (Brodmann *et al.*, 2009; Kowalkowska & Margonska, 2012; Pang *et al.*, 2012), it seems that most *Dendrobium* species rely on deceptive pollination (van der Cingel, 2001; Jersáková *et al.*, 2006), which indicates that EBLFs provide rewards for deceived pollinators. The habitat of *Dendrobium*, is therefore likely crucial for supporting *Dendrobium* and their pollinators.

Furthermore, most species of *Dendrobium* in mainland Asia are strictly epiphytic plants in EBLFs and our reconstruction of habit indicates that the epiphytic state is ancestral in *Dendrobium*. The historical establishment and extension of EBLFs would have provided the necessary and potential habitats for the diversification of *Dendrobium* in mainland Asia and the diversification of *Dendrobium* is

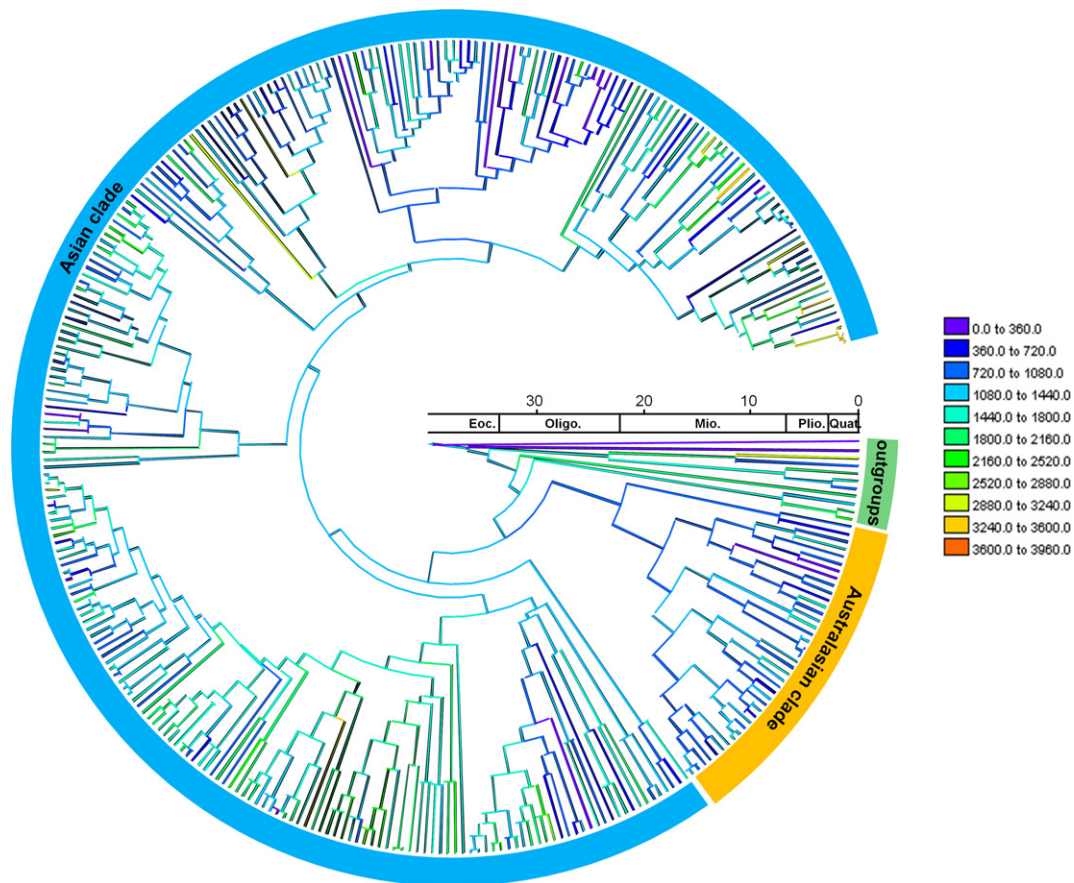


Figure 4 Ancestral reconstruction of *Dendrobium* elevation ranges. The order of the taxa is the same as in Fig. 2. Eoc., Eocene; Oligo., Oligocene; Mio., Miocene; Plio., Pliocene; Quat., Quaternary.

likely to reflect the minimum age of the establishment and extension of EBLFs. Our results indicated that Asian *Dendrobium* originated during the middle Oligocene, diversified mainly in mainland Asia and spread to Malesia by dispersal, followed by considerable expansion northwards and colonization of habitats up to at least 1400 m elevation during the late Oligocene (Fig. 4). This coincided with a warming climate during the late Oligocene to middle Miocene (see Zachos *et al.*, 2001). Fossil evidence has indicated that the EBLFs spread northwards to high latitudes and migrated to high altitudes during the warming climate of the Cenozoic (Zhou, 1999; Jacques *et al.*, 2011; Wang & Shu, 2013; Wen *et al.*, 2013). Furthermore, the distribution and diversity of several keystone families of EBLFs, such as Fagaceae, expanded widely during the early Cenozoic (Friis *et al.*, 1987, 2011; Zhou *et al.*, 2003). Molecular dating analyses indicated that Fagaceae evolved during the late Cretaceous and diversified during the early Cenozoic (Xiang *et al.*, 2014). Based on the findings of the present study, we suggest that the EBLF ecosystem in mainland Asia may have been present at higher altitudes and higher latitudes since the early Miocene.

CONCLUSION

Dendrobium, an epiphytic component of EBLFs, diverged at the beginning of the Oligocene and then radiated rapidly until the middle Miocene. The MRCA of Asian *Dendrobium* likely existed in mainland Asia, and then diversified *in situ* and spread northwards and into higher altitudes during the Miocene. A burst of diversification of the Asian *Dendrobium* group occurred during the late Oligocene to middle Miocene, which coincided with global warming. Moreover, the diversification of key groups of EBLFs (including Fagaceae, Lauraceae, Magnoliaceae and Theaceae) in the early Cenozoic provided new niches for *Dendrobium*. Based on these results, our multiple lines of evidence collectively support the hypothesis that EBLFs have been established in mainland Asia since the beginning of the Oligocene.

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SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

Appendix S1 Additional tables (Tables S1–S3) and figures (Figs S1–S3).

Appendix S2 Nexus file for Orchidaceae dating.

BIOSKETCH

Xiaoguo Xiang is an assistant professor at the State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany (CAS). Her research is focused on understanding the temporal and spatial evolution of orchids by integrating phylogenetic, biogeographical, dating estimation and diversification approaches.

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