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Evolution of pollination syndromes and corolla symmetry in Balsaminaceae reconstructed using phylogenetic comparative analyses

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• **Background and Aims** Floral diversity as a result of plant–pollinator interactions can evolve by two distinct processes: shifts between pollination systems or divergent use of the same pollinator. Although both are pollinator driven, the mode, relative importance and interdependence of these different processes are rarely studied simultaneously. Here we apply a phylogenetic approach using the Balsaminaceae (including the species-rich genus *Impatiens*) to simultaneously quantify shifts in pollination syndromes (as inferred from the shape and colour of the perianth), as well as divergent use of the same pollinator (inferred from corolla symmetry).
• **Methods** For 282 species we coded pollination syndromes based on associations between floral traits and known pollination systems, and assessed corolla symmetry. The evolution of these traits was reconstructed using parsimony- and model-based approaches, using phylogenetic trees derived from phylogenetic analyses of nuclear ribosomal and plastid DNA sequence data.
• **Key Results** A total of 71 % of studied species have a bee pollination syndrome, 22 % a bimodal syndrome (Lepidoptera and bees), 3 % a bird pollination syndrome and 5 % a syndrome of autogamy, while 19 % of species have an asymmetrical corolla. Although floral symmetry and pollination syndromes are both evolutionarily labile, the latter shifts more frequently. Shifts in floral symmetry occurred mainly in the direction towards asymmetry, but there was considerable uncertainty in the pattern of shift direction for pollination syndrome. Shifts towards asymmetrical flowers were associated with a bee pollination syndrome.
• **Conclusion** Floral evolution in *Impatiens* has occurred through both pollination syndrome shifts and divergent use of the same pollinator. Although the former appears more frequent, the latter is likely to be underestimated. Shifts in floral symmetry and pollination syndromes depend on each other but also partly on the region in which these shifts take place, suggesting that the occurrence of pollinator-driven evolution may be determined by the availability of pollinator species at large geographical scales.

Key words: Asymmetry, floral morphology, floral symmetry, *Impatiens*, *Hydrocera*, molecular phylogenetics, pollinator.

INTRODUCTION

The evolution of floral diversity is traditionally thought to be driven by pollinators (Darwin, 1862; Grant, 1949, 1994; Grant and Grant, 1965; Stebbins, 1970). Two distinct processes of pollinator-driven evolution have been identified. First, populations may adapt to different pollination systems, resulting in the formation of pollination ecotypes (Armbruster, 1985; Johnson, 2006; Whitall and Hodges, 2007; Valente *et al.*, 2012; Van der Niet *et al.*, 2014a). Secondly, populations may diverge in the way in which a particular pollinator is utilized (divergent use of the same pollinators) (Armbruster *et al.*, 1994; Waterman *et al.*, 2011; Eaton *et al.*, 2012). These processes may eventually result in pollinator-driven speciation either through ethological isolation via pollination system shifts, or mechanical isolation

through divergent use of the same pollinator (Grant, 1994; Van der Niet *et al.*, 2014a). Although the two processes are both driven by pollinators, they are fundamentally different in their underlying drivers and their effect on floral evolution (Grant, 1994). During pollination system shifts, populations diverge in floral traits which reflect the sensory bias and morphological differences between different most effective functional pollinator groups, or lack of pollinators in the case of a shift to autonomous self-pollination (Robertson and Wyatt, 1990; Johnson, 1997; Johnson *et al.*, 1998; Moeller, 2006). This process is generally driven by geographical turnover in pollinator species (Johnson, 1997; Johnson and Steiner, 1997; Moeller, 2006; Van der Niet *et al.*, 2014b; Duffy and Johnson, 2017). In contrast, divergent use of the same pollinator is mainly associated with

divergence in floral traits which mediate the position on the pollinator where the pollen is deposited (character displacement), and is thought to be generally driven by local competition for pollinator services (Armbruster, 1985; Armbruster *et al.*, 1994).

Pollinator-driven evolutionary processes are best studied at the population level (Kay *et al.*, 2005; Boberg *et al.*, 2014; Cosacov *et al.*, 2014; Forest *et al.*, 2014; Gómez *et al.*, 2014; Peter and Johnson, 2014; Van der Niet *et al.*, 2014*b*), but this is not the most suitable way to quantify their importance in macroevolution. This requires a comparative perspective in a phylogenetic context (e.g. Smith and Kriebel, 2018; Dellinger *et al.*, 2019; Kriebel *et al.*, 2019, 2020; Xiang *et al.*, 2020). Inferences from such comparative studies have revealed that shifts in pollination systems are relatively frequent (reviewed in Van der Niet and Johnson, 2012). Fewer studies have considered the frequency of shifts in use of the same pollinator (e.g. Eaton *et al.*, 2012), and no macroevolutionary analysis has been carried out so far that quantified the overall frequency of pollinator-driven evolution, and the mode of evolution and relative importance of both pollination system shifts and divergent use of the same pollinator.

Perhaps one of the greatest challenges associated with comparitive phylogenetic studies of pollinator-driven evolution is the need for information on pollination systems (Van der Niet, 2020), and an understanding of which floral traits may be involved in divergent use of the same pollinator, for a relatively large number of species. One approach that has been used in this context is to infer pollination systems based on species' pollination syndromes. Although the use of pollination syndromes has been criticized (Ollerton, 1996; Waser *et al.*, 1996; Ollerton *et al.*, 2009; Van der Niet, 2020), there is evidence that in groups of species that are characterized by relatively high levels of specialization in pollination systems, floral syndrome traits may be indicative of pollination systems, at least at the level of functional pollinator groups (Johnson and Steiner, 2000; Fenster, 2004; Rosas-Guerrero *et al.*, 2014; Johnson and Wester, 2017). Similarly, divergent use of the same pollinator may be inferred from distinct differences in floral morphology which are known to be associated with different pollen placement sites on pollinators (Armbruster, 1985; Armbruster *et al.*, 1994; Waterman *et al.*, 2011; Eaton *et al.*, 2012).

Balsaminaceae consists of the monotypic *Hydrocera*, and its large sister genus *Impatiens* (Yuan *et al.*, 2004). The >1000 *Impatiens* species are characterized by a tremendous floral diversity (Grey-Wilson, 1980). The general architecture of Balsaminaceae flowers comprises various zygomorphic perianth parts, which are partially fused in *Impatiens* and unfused in *Hydrocera*, including a nectar-producing spur that is part of the lower sepal (Grey-Wilson, 1980). Grey-Wilson (1980) classified *Impatiens* species into several pollination syndromes. He suggested that flat-type flowers with a narrow entrance, shallow lower sepals, long spur and pale to deep pink colour are pollinated by butterflies; funnel-type flowers with a large entrance, deep lower sepals, hood-like dorsal petals, short spurs and yellow, white or pale pink colour are pollinated by bees; red or orange flowers with a large entrance are pollinated by birds; and white funnel-type flowers with a very long spur are pollinated by moths. Comparative studies have confirmed that variation in size and shape of the perianth parts is associated with predictable differences in pollination systems (Grey-Wilson, 1980; Kato *et al.*, 1991; Ruchisansakun *et al.*, 2016; Abrahamczyk *et al.*, 2017). Besides the presence of distinct pollination syndromes, species which share the same pollinator also vary in floral architecture. In particular, floral variation among these species is associated with precise placement of pollen on the pollinator bodies, as was confirmed independently among co-flowering bee-pollinated species in Asia and bird-pollinated species in Africa (Janeček *et al.*, 2015; Ruchisansakun *et al.*, 2016). In several cases, differential pollen placement on bees is achieved by a highly unusual mechanism of floral asymmetry in which the lower lateral petals are asymmetrical (Kato *et al.*, 1991; Ruchisansakun *et al.*, 2016). Floral asymmetry therefore mediates divergent use of the same pollinator. Based on the two distinct types of floral variation in association with different pollination systems and divergent use of the same pollinator, Balsaminaceae are an ideal family to evaluate the overall frequency and relative importance of two distinct processes of pollinator-driven evolution.

The aim of the current study is therefore to reconstruct the evolution of pollination syndromes and divergent use of the same pollinator in Balsaminaceae. For this study, we compiled all pollination studies of Balsaminaceae species to set up a predictive framework for assigning species sampled in the largest phylogeny of the genus to date to pollination syndromes. Together with data on floral symmetry, we used the phylogeny for evolutionary analyses of pollination syndromes and floral symmetry to assess their mode of evolution, the overall frequency and relative importance of shifts in these two features, and whether or not they evolved independently.

MATERIALS AND METHODS

Phylogenetic analyses

Taxon sampling. To reconstruct the evolution of pollination systems and corolla symmetry in Balsaminaceae, we included 282 accessions of Balsaminaceae species. Accessions comprised 281 *Impatiens* (approx. 25 % of all species in the genus) and *Hydrocera triflora*. Among the *Impatiens* specimens included in this study, 251 are from Asia (representing approx. 29 % of all Asian species), while 30 species are from Africa, Europe, Madagascar and North America (representing approx. 8 % of all species from these regions). The analysis is therefore biased towards species from Asia, which comprises three out of the five informal hotspots of *Impatiens* diversity. Furthermore, the pollination ecology of these species is arguably the most well understood. *Marcgravia umbellata* is used as outgroup (see Supplementary data Table S1).

DNA sequencing and phylogeny reconstruction. To reconstruct the phylogenetic tree of Balsaminaceae, DNA sequences from plastid (*atpB–rbcL* intergenic spacer, '*atpB–rbcL*' hereafter) and nuclear (ribosomal internal transcribed spacer, 'ITS' hereafter) genomes were used as characters. Most DNA sequences used for phylogeny reconstruction were obtained from GenBank (Yuan *et al.*, 2004; Ruchisansakun *et al.*, 2015; Utami and Ardiyani, 2015; Yu *et al.*, 2015; Shajitha, 2016*a*, *b*), but for 27 species DNA sequences were newly generated.

For these species, genomic DNA was extracted from fresh or silica-dried leaf material and herbarium specimens using the cetyltrimethylammonium bromide (CTAB) protocol (Doyle and Doyle, 1987). The ITS and *atpB–rbcL* regions were amplified following the protocols of Yuan *et al.* (2004) and Janssens *et al.* (2006), respectively. Standard DNA sequencing using the original amplification primers was done by Macrogen (Amsterdam, the Netherlands). The chromatograms of forward and reverse sequences were combined using the De Novo Assembly tool to create contigs in Geneious 10.2.2 (Biomatters Ltd, New Zealand) with default settings. Sequences were aligned using default settings in MUSCLE 3.8 (Edgar, 2004) and manually edited in Geneious 10.2.2 (Biomatters Ltd, New Zealand).

To obtain a set of ultrametric trees for analyses of character evolution, two sets of Bayesian phylogenetic analyses were implemented. The methods for analyses of separate datasets comprising nuclear and plastid DNA sequences are provided in Supplementary data Methods S1. A total evidence dataset combining plastid and nuclear DNA sequences was analysed using BEAST v.1.8.4 (Drummond and Rambaut, 2007), which was run on the CIPRES Science Gateway v. 3.3 (www.phylo.org). All parameters for the BEAST analysis were set in BEAUTI v.1.8.0 (Drummond and Rambaut, 2007) as described below. Based on the Akaike information criterion (AIC) as implemented in jModelTest2 v0.1.1 (Darriba *et al.*, 2012), the GTR+I+G model of sequence evolution was selected for ITS whereas the GTR+G model was specified for *atpB–rbcL*. We chose to analyse the combined dataset with a nuclear and plastid DNA sequence partition under the most complex model GTR+I+G with estimated base frequencies as suggested by Abadi *et al.* (2019). As input parameter, a log-normal relaxed clock model was implemented using the 'estimate' option in the clock model. In addition, a Yule speciation tree prior (Gernhard, 2008) was applied with a random starting tree. The length of the Markov chain Monte Carlo (MCMC) was set to 30 million generations. Parameters were sampled each 3000th generation, whereas trees were sampled each 30 000th generation with a 10 % burn-in, resulting in a set of 900 trees. The tree prior was set uniformly at 100 in order to create ultrametric trees with a similar root basis. A maximum clade credibility (MCC) tree was constructed in TreeAnnotator v1.8.0. Examination of chain convergence was carried out with Tracer v1.71 (Rambaut *et al.*, 2018). This resulted in effective sampling size (ESS) parameters exceeding 100 for all parameters, and 200 for most parameters apart from parameters related to the Yule process and substitution rates, indicating an adequate sampling and subsequent mixing for the topology estimation.

Character coding

Pollination syndromes. For 40 (14.2 %) of the Balsaminaceae species included in our analysis, the pollination systems are known, while all the other species included in the phylogenetic analysis had unknown pollination systems. We assigned species to pollination syndromes [suites of floral traits associated with attraction of, and pollination by, particular functional pollinator groups (Fenster *et al.*, 2004)]. To assign the species that were not studied in the field to pollination syndromes, we reviewed

all literature related to Balsaminaceae pollination to assess which floral characters were associated with particular pollination systems. We specifically focused on the following floral characters that were identified in previous comparative studies (Grey-Wilson, 1980; Ruchisansakun *et al.*, 2016; Abrahamczyk *et al.*, 2017): floral entrance width (<2 mm or >6 mm), spur length (shorter or longer than 10 mm, or spur absent) and petal colour. Pollination syndromes were assigned at the level of functional pollinator groups using a framework that integrates information from several comparative studies by Grey-Wilson (1980), Ruchisansakun *et al.*, (2016) and Abrahamczyk *et al.* (2017), and our own pollinator observations. As functional groups, we used bee pollination, bimodal pollination by bees and Lepidoptera, bird pollination and autonomous self-pollination, as these groups are represented by more than one empirical study. Although Abrahamczyk *et al.* (2017) assigned species with small flowers to a fly pollination syndrome, we do not recognize this syndrome for the following reason. In a study by Lozada-Gobilard *et al.* (2019), several species that conformed to the fly pollination syndrome were autogamous and sometimes cleistogamous. Furthermore, Abrahamczyk *et al.* (2017) showed that species with the fly pollination syndrome produce hardly any nectar. These traits are similar to those of the autogamous species studied by Ruchisansakun *et al.* (2016). Given that there are no studies available in the public domain which provide empirical evidence for the existence of specialized fly pollination in small-flowered *Impatiens* species, these are rather inferred to be autonomously selfing. Based on characters that were associated with particular pollination systems for species for which pollinator data were available, we assigned species to the bee pollination syndrome if they had a large floral entrance and short spur; to a bimodal pollination syndrome if species had a small floral entrance and long spur; to the bird pollination syndrome if species had a large floral entrance, short spur, red flowers and were native to Africa; and to the autogamy syndrome if they were spurless (Table 1). We then scored each of these floral characters for species in our analysis without pollinator data, and used these characters to characterize their pollination syndromes.

Corolla symmetry. To assess corolla symmetry (i.e. zygomorphic vs. asymmetrical flowers according to a different size or shape of lateral petals on either side of a vertical symmetry axis), we analysed fresh material, investigated photographs taken by the authors, or photographs of Balsaminaceae in books or on websites which were identified to species level by Balsaminaceae specialists, studied illustrations and descriptions in the literature and examined dried specimens or illustrations of herbarium specimens. Each species was classified as either 'zygomorphic' or 'asymmetrical'. Based on our personal observations, *Hydrocera* is polymorphic for corolla symmetry in which the zygomorphic form is much more common than the asymmetrical form. We therefore scored *Hydrocera* as 'zygomorphic'.

Character evolution analyses

Our character evolution analyses aimed at reconstructing ancestral character states, assessing patterns of transitions among both pollination syndromes and corolla symmetry,

TABLE I. *Summary of associations between floral traits and pollination systems based on empirical studies of* Impatiens

Entrance	Spur	Colour	Bee	Bird	Lepidoptera	Fly	Bee and Lepidoptera	Bee and hoverfly	Lepidoptera and long proboscid fly	Autogamy	Total
Large	Short	Yellow to orange	7	0	0	0	0	0	0	0	7
Large	Short	Pink	10	0	0	0	0	1	0	0	11
Large	Short	Red	0	7	0	0	2	0	0	0	9
Large	Short	White	2	0	0	0	0	0	0	0	2
Large	Long	Yellow to orange	1	0	0	0	1	0	0	0	2
Large	Long	Pink	2	0	0	0	0	0	0	0	1
Large	Long	Red	0	0	0	0	1	0	0	0	1
Large	Spurless	Yellow to orange	0	0	0	1	0	0	0	0	1
Large	Spurless	White	0	0	0	0	0	0	0	1	1
Small	Short	Yellow to orange	1	0	0	0	0	0	0	0	1
Small	Short	White	1	0	0	0	0	0	0	0	1
Small	Long	Pink	0	0	1	0	11	0	1	0	13
Small	Long	Red	0	0	0	0	1	0	0	0	1
Small	Long	White	0	0	0	1	2	0	0	0	3
Total			24	7	1	2	18	1	1	1	55

and testing for correlated evolution between these two characters.

A diverse array of methods exists for analysing character evolution, each with their own strengths and weaknesses. It is beyond the scope of this study to review these in detail, but we provide a brief justification for the choice of methods used here. Parsimony-based methods are known to perform well in datasets where character change is rare (e.g. Pirie *et al.*, 2012), but have been criticized due to implicit assumptions of character evolution such as that only one shift per branch is permitted (e.g. Schluter *et al.*, 1997). Approaches which explicitly implement models of character transitions are not constrained by the assumption of a single shift per branch, but have been shown to return model parameter values which are counter-intuitive, especially in cases where certain character states are rare (Pagel, 1999). Given the fact that two of the four pollination syndromes in our dataset are rare, we implemented both parsimony- and model-based methods. Although some authors have argued that accurate reconstruction of character evolution requires explicit modelling of whether and how character states affect diversification (through a family of methods referred to as SSE) (e.g. Maddison *et al.*, 2007), these methods have also been criticized for their performance (Raboski and Goldberg, 2015). Our own preliminary analyses suggested little impact of character states on speciation and extinction rates in our dataset (results not shown). Given the problems associated with SSE models, we therefore decided to implement Fitch parsimony (Fitch, 1971) and SIMMAP (Bollback, 2006) for ancestral character state reconstruction, and BayesTraits (Pagel *et al.*, 2004) for model selection and analyses of correlated evolution. These analyses were performed on the set of 900 BEAST trees from the analysis of combined nuclear and plastid DNA sequence data, as well as on similar sets of trees resulting from separate analyses of each genomic data partition (see Supplementary data Methods S1 for a description of the methods for the separate analyses and results).

To assess the optimal model of character evolution in terms of transition rates among character states, we implemented Bayesian analyses using the BayesTraits V3.0 software (Pagel *et al.*, 2004; Pagel and Meade, 2006) on the set of 900 BEAST trees. For all analyses in BayesTraits, we used the 'ScaleTrees' command (Pagel and Meade, 2006). For the binary character

'floral symmetry', we ran a test to assess the fit of two discrete models. The first included a discrete, unconstrained model, in which transition rates between the two states were allowed to vary independently. The second included a model in which only a single transition rate (equal forward and reverse rates) was modelled. Each model was run for 2 000 000 generations with a burn-in of 20 000 (ESSs of estimated parameters >200). For this analysis, we used an exponential hyperprior with a mean seeded from a uniform distribution on an interval ranging from 0 to 10. Marginal likelihoods were estimated by heating 100 stones for 10 000 iterations each. The Bayes factor (BF) between the independent and restricted model was subsequently calculated according to the formula: log BF = 2(log marginal likelihood complex model – log marginal likelihood restricted model). Log BF values of <2 indicate that the restricted (less complex) model should be preferred (and hence that transition rates between symmetrical and asymmetrical flowers are not significantly different).

Pollination syndrome is a multistate character with four states. Consequently, 12 transition rates and many model restrictions are possible, resulting in high model complexity. To accommodate this complexity, we used reverse jump (RJ) MCMC to select optimal models and parameters (Pagel and Meade, 2006). We ran 100 000 000 iterations (resulting in an ESS >200) with a burn-in of 10 000 000. The ten models that were most frequently sampled were considered for further interpretation. Both analyses also calculate the posterior probability of each state at the root node of Balsaminaceae, which is also reported.

The number and position of shifts under the parsimony criterion was reconstructed based on the set of 900 sampled BEAST trees. To summarize the frequency and direction of evolution, we used the function 'summarize state changes over trees' in Mesquite Version 3.6 (Maddison and Maddison, 2018) with 50 mappings sampled per tree.

To implement a model-based approach to reconstructing the frequency and position of shifts, we used the make.simmap function in the 'phytools' R package (Revell, 2012). Shifts were reconstructed onto a set of 100 randomly sampled post-burn-in BEAST trees using stochastic mapping. Prior to reconstruction, three different models were compared: an all rates different

(ARD) model, an equal rates (ER) model and a symmetrical rate (SR) model. Model comparison was based on the AIC, and the most fitting model (ARD) was used in subsequent analyses. Transition rates were estimated with the ARD model. For all analyses, we estimated the prior distribution of state probabilities at the root node. The transition rate matrix and mean and median total number of estimated shifts between states were calculated. Based on ten simulations, average probabilities of each state at each node were estimated and plotted on the MCC tree using 'ggtree' in R (Yu *et al.*, 2017).

To evaluate whether floral symmetry and pollination syndromes evolve in a correlated fashion or independently, we used Bayesian character evolution analyses implemented in BayesTraits V3.0 (Pagel and Meade, 2006). Analyses of correlated evolution for discrete traits can only be performed between two binary characters. We therefore first reduced the multistate character 'pollination syndrome' to multiple binary characters (e.g. bee pollination syndrome present/absent). Each of the four resulting binary character datasets (representing the four pollination syndromes present in our dataset) was then analysed separately for correlated evolution with the binary character 'floral symmetry'. We used the discrete independent and dependent option in the software and ran 10 000 000 iterations with a burn-in length of 1 000 000. Due to low ESS for the dependent model of the Autogamy data set, we ran this for 50 000 000 iterations with a burn-in of 5 000 000 (ESS all >100). We used an RJ MCMC with an exponential hyperprior

with a mean seeded from a uniform distribution on an interval ranging from 0 to 10. A stepping-stone sampling approach was used to calculate the marginal log-likelihood of both dependent and independent analyses. For this, a set of 100 stones were run for 10 000 iterations each. Two replicate runs were performed for each individual analysis to confirm consistency (only results from one run shown). The BF between the dependent and the independent model was then calculated. Log BFs <2 indicate that there is no evidence for correlated evolution between pollination syndrome and floral symmetry. The average and 95 % highest posterior density (HPD) transition rates among character states were subsequently calculated from the combined runs in the RJ MCMC analysis using Tracer v 1.71 and graphed.

RESULTS

Assignment of pollination syndromes and corolla symmetry

Data on pollination systems were available for 58 *Impatiens* species, 40 species of which were included in the phylogenetic analysis (Supplementary data Table S2). The majority of pollination studies were done on Asian species (*n* = 31), followed by African species (*n* = 10), species occurring in Europe (*n* = 8) and American species (*n* = 3). Most *Impatiens* species are pollinated by more than one pollinator species. Apart from African *Impatiens* species, the majority of species are
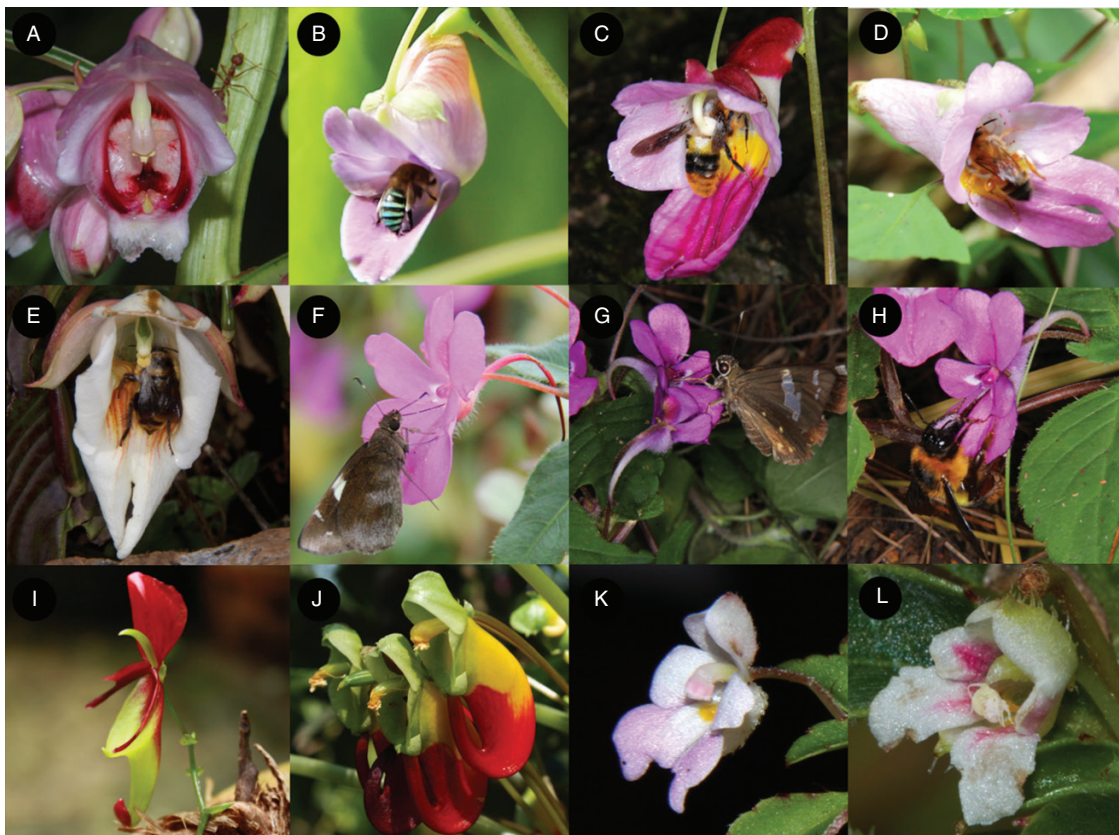

Fig. 1. Balsaminaceae flower diversity and pollination syndromes. (A) *Hydrocera triflora* flower. (B–E) Bee-pollinated species: (B). *I. jiewhoei*, (C) *I. psittacina*, (D) *I. daraneenae*, (E) *I. kerriae*. (F–H) Species pollinated by Lepidoptera and bees (bimodal): (F) *I. chiangdaoensis*, (G and H) *I. santisukii*. (I and J) Bird-pollinated species: (I) *I. hians*, (J) *I. niamniamensis*. (K and L) Autogamous species: (K) *I. decurva*, (L) *I. muscicola*.
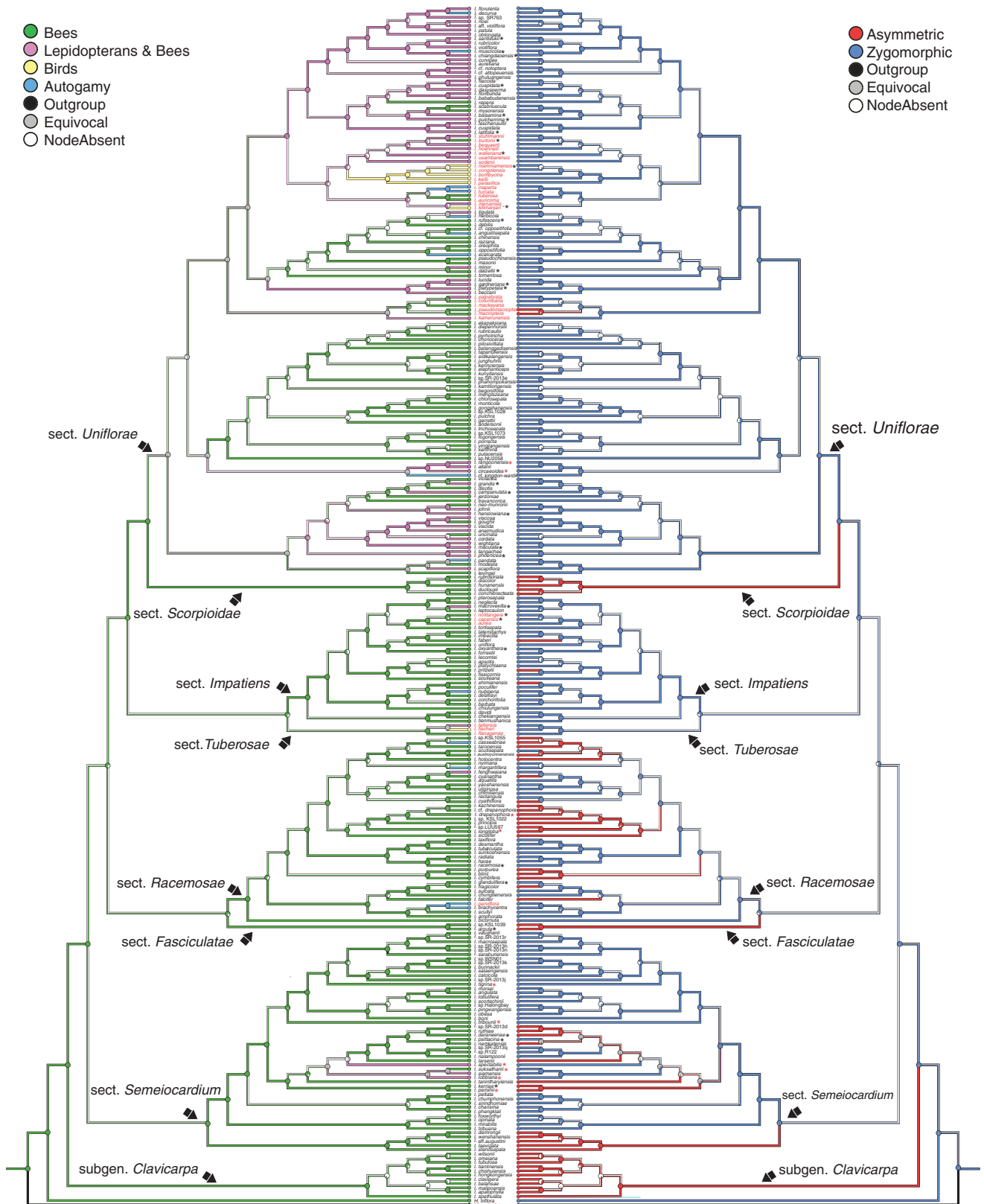
FIG. 2. Parsimony ancestral character state reconstruction of pollination syndromes (left) and corolla symmetry (right). Branch colours represent the most parsimonious ancestral character states reconstructed using the MCC tree of the combined analysis. Pie charts at nodes represent the proportion of BEAST trees for which a particular character state at each node was reconstructed. The names of species outside Asia are marked in red. Black asterisks (*) show species for which pollination systems are known (see Supplementary data Table S2). Red asterisks (*) show species for which pollinators were observed by Saroj Ruchisansakun.

predominantly bee pollinated. Furthermore, most species pollinated by Lepidoptera are also pollinated by bees (Fig. 1; Table 1; Supplementary data Table S2).

Variation in floral traits is associated with different pollination systems (Table 1). Asian, European and North American species with a short spur and large floral chamber are bee pollinated; species with a long spur and small floral chamber are mostly pollinated by both Lepidoptera and bees (bimodal pollination system) (Table 1); the species with small, spurless flowers are autogamous (Table 1). African species with a large floral entrance, short spur and red flowers are bird pollinated.

Based on these associations, among the *Impatiens* species sampled, 200 (70.9 %) are assigned to the bee pollination syndrome, 61 (21.6 %) species to the bimodal Lepidoptera and bee pollination syndrome, 14 (5.0 %) species to the autogamy syndrome and 7 (2.5 %) species to the bird pollination syndrome. Furthermore, 56 out of 282 (19.9 %) species have an asymmetrical corolla.

Phylogenetic analysis

The combined dataset consisted of 2703 bp: 1269 bp for the ITS region and 1434 bp for the *atpB–rbcL* region. Separate and combined BEAST MCC trees revealed some cases of topological incongruence (Supplementary data Figs S1 and S2), but the topologies are similar in terms of the placement of the main clades, and the MCC tree from the combined analysis is well resolved (Supplementary data Fig. S3). *Impatiens* can be divided into eight clades (Fig. 2). Species from outside Asia were distributed across several sections of *Impatiens*. In particular, African species were distributed among three clades: two of these are part of a big clade which comprises *I.* sect. *Uniflorae*, whereas some African species are members of the smaller clade which comprises *I.* sect. *Tuberosae*. Madagascan species form a monophyletic clade and are nested inside the largest African clade. North American species form a monophyletic clade within the clade of *I.* sect. *Impatiens*, whereas the European *I. parviflora* is part of *I.* sect. *Racemosae*. The remaining Asian species are scattered across all eight clades.

Character evolution

Models of character evolution. The analyses of floral symmetry evolution indicated that the simpler model with a single transition rate between zygomorphic and asymmetrical corollas was preferred over the model in which these rates vary independently for the combined (BF 0.43) and nuclear analyses (BF –0.51), but for the plastid analysis the unrestricted model was preferred (BF 8.99) with a mean rate bias in favour of transitions from asymmetrical to zygomorphic flowers of 6.3. The average probability of a zygomorphic ancestor in Balsaminaceae was 0.88 based on the combined dataset (nuclear, 0.95; plastid, 0.19). The RJ MCMC analysis of the combined dataset indicated that several transition rates among pollination syndromes were indistinguishable from 0 (Table 2), in particular rates involving shifts away from the bee pollination syndrome and shifts away from the Lepidoptera + bee pollination syndrome. Shifts towards the autogamy syndrome and from the autogamy syndrome to the bee and Lepidoptera + bee pollination syndromes were generally high and almost never 0. Results were similar for the separate analyses, although there were fewer cases where rates were 0 (Supplementary data Table S3). There was much uncertainty regarding the ancestral pollination syndrome in all three analyses, although for all of them the bee pollination syndrome had the highest probability (combined, 0.32; nuclear, 0.38; plastid, 0.29).

Shifts in floral symmetry and pollination syndromes. Based on the parsimony analysis of the combined dataset, the ancestral state of corolla symmetry in Balsaminaceae was zygomorphic in 91 % of all trees and the remaining reconstructions were equivocal (nuclear, 92 % zygomorphic, remainder equivocal; plastid, 29 % zygomorphic, remainder equivocal). There was a higher average number of shifts from a zygomorphic to an asymmetrical corolla for the combined analysis (Fig. 2; Table 3) and both separate datasets (Supplementary data Table S4). The positions of corolla symmetry shifts are scattered across several clades (i.e. *I.* subgen. *Clavicarpa*, *I.* sect. *Scorpioidae*, *I.* sect. *Impatiens*, *I.* sect. *Racemosae*, *I.* sect. *Fasciculatae* and *I.* sect. *Semeiocardium*), comprising only bee-pollinated species (Fig. 2), and almost never occurred in *I.* sect. *Uniflorae*.

TABLE 2. *Top ten models of transition rates (*q*) among pollination syndromes, ranked according to their sampling frequency in the RJ MCMC analysis of the combined dataset*

Model	q_{01}	q_{02}	q_{03}	q_{10}	q_{12}	q_{13}	q_{20}	q_{21}	q_{23}	q_{30}	q_{31}	q_{32}	Proportion	Cumulative proportion
1	Z	Z	0	Z	Z	0	Z	0	Z	1	0	0	0.07	0.07
2	Z	Z	0	Z	Z	0	Z	0	0	1	0	0	0.06	0.12
3	Z	Z	0	Z	Z	0	0	0	Z	1	0	0	0.05	0.18
4	Z	Z	0	Z	Z	0	0	0	0	1	0	0	0.04	0.21
5	Z	Z	0	0	0	0	Z	Z	1	1	1	Z	0.02	0.24
6	Z	Z	0	0	0	0	0	0	1	1	1	Z	0.02	0.26
7	Z	Z	0	0	0	0	Z	0	1	1	1	Z	0.02	0.28
8	Z	Z	0	0	0	0	0	Z	1	1	1	Z	0.02	0.30
9	Z	Z	0	0	0	0	0	1	0	1	1	Z	0.02	0.32
10	Z	Z	0	0	0	0	0	0	1	1	1	0	0.02	0.33

Subscript numbers indicate pollination syndromes (0 = bee, 1 = Lepidoptera + bee, 2 = bird, 3 = autogamy); numbers in sequence indicate shifts from one pollination syndrome to another. Symbols (Z, 0 or 1) in the table represent transition rates. A value of Z indicates a transition rate of 0, whereas values of 0 and 1 represent different positive transition rates. Within models, transitions sharing a symbol occur at the same rate, whereas transitions with different symbols occur at different rates

TABLE 3. *Summary of changes in corolla symmetry of Balsaminaceae*

	Zygomorphic to asymmetrical	Asymmetrical to zygomorphic	Total number of shifts
Parsimony	17.93 (7–23)	2.97 (0–15)	20.90
SIMMAP	18.42 (20) ± 4.41	9.45 (5) ± 8.96	27.88 (26) ± 5.74

For parsimony, the numbers represent the average number of shifts (min–max) of each kind across 50 mappings on a set of 900 BEAST trees. For SIMMAP, the numbers represent the average number of shifts (median) ± s.d. resulting from ten stochastic mappings on a random sample of 100 post-burn-in BEAST trees.

The results from the SIMMAP analysis of the combined dataset showed a much higher number of transitions from zygomorphic to asymmetrical flowers (Fig. 3; Table 3). The results from the nuclear dataset were consistent, but the number of shifts for the plastid dataset was higher in the opposite direction (Supplementary data Table S4).

Based on the parsimony analysis, the bee pollination syndrome is ancestral in *Impatiens*. Shifts in pollination syndrome appear phylogenetically concentrated in the clade that comprises sect. *Uniflorae* (Fig. 2). There were several shifts from a bee pollination syndrome to bimodal pollination syndrome, and towards the autogamy syndrome (Fig. 2; Table 4). Shifts from a bee to a bird pollination syndrome never occurred, but the shift from a bimodal to a bee pollination syndrome occurred relatively frequently. The bimodal pollination syndrome also shifted to the autogamy and bird pollination syndrome multiple times (Fig. 2; Table 4). Shifts between other pollination syndromes were almost absent (Fig. 2; Table 4). The average total number of shifts in pollination syndromes is 40.

The results from the SIMMAP analysis of the combined dataset differ in many ways. The most frequent shifts involve the autogamy syndrome, in particular shifts from a bee pollination syndrome towards an autogamy syndrome were common, as were shifts from a bimodal pollination syndrome to the autogamy syndrome, whereas shifts from the autogamy syndrome towards these two pollination syndromes were also frequent (Fig. 3; Table 4). All other types of shifts were rare or absent. The average total number of shifts was 140 (median 135) and thus much higher than those from the parsimony analysis. Results from the separate analyses are largely congruent with those of the combined analysis (Supplementary data Table S5).

Correlated evolution. Results from analyses of correlated evolution between floral symmetry and pollination syndromes showed that when pollination syndrome was coded as bee vs. other and Lepidoptera + bee vs. other, BFs indicated that a model of dependent evolution was preferred over a model in which all shifts occur independently of background character states (Table 5; Supplementary data Table S6). This was not the case when pollination syndromes were coded as bird vs. other or autogamy vs. other (Table 5; Supplementary data Table S6).

If pollination syndrome is coded as 'bee vs other', shifts towards asymmetrical flowers only happen against a background of a bee pollination syndrome (Fig. 4). This result was consistent across all three datasets. If pollination syndrome is coded 'bimodal vs. other', shifts towards asymmetrical flowers do not happen against a background of the bimodal syndrome, and neither do shifts towards this syndrome happen against a background of asymmetrical flowers (Fig. 4). This result was consistent across all three datasets.

DISCUSSION

Floral evolution in *Impatiens* is characterized by shifts in both pollination syndromes and floral symmetry (Figs 2 and 3). There are several uncertainties in terms of the frequency and direction of shifts, but some patterns were supported by almost all analyses. These included a predominance of shifts towards asymmetrical flowers with few reversals (Figs 2 and 3; Table 3; Supplementary data Table S4), as well as their occurrence in association with a bee pollination syndrome (Fig. 4).

The accuracy of our analyses of pollinator-driven evolution depends on the correct characterization of pollination syndromes, as the majority of sampled taxa have not been studied in the field. Although our inferences were based on pollination studies for >52 species (Table 1; Supplementary data Table S2), we acknowledge that our coding may still include some inaccuracies. In particular, pollination systems which are not represented among the studied species remain unknown and hence are likely to lead to underestimation of diversity in pollination systems and number of shifts in pollination syndromes (cf. Van der Niet, 2020). Given that most species in our analyses are from Asia (Figs 2 and 3), where most pollination studies were done (Supplementary data Table S2), we expect relatively few incorrect inferences. We also included pollination studies that were performed on non-native species (e.g. *I. glandulifera*, which is native in the Hymalayan mountains and invasive in many European countries, has been extensively studied in Europe) (Knuth, 1898; Erpenbach, 2006; Nienhuis *et al.*, 2009; Ugoletti *et al.*, 2013; Abrahamczyk *et al.*, 2017). Given that pollinators of invasive species are unlikely to have selected for large changes in floral syndrome traits over the relatively short time since the invasion, we think that studies done on invasive species can reveal useful information on morphological fit and pollinator types (cf. Abrahamczyk *et al.*, 2017). This is particularly the case if pollinators in the native and invaded range of an *Impatiens* species represent similar functional pollinator groups, as is the case, for instance, with bumble-bee species in Asia and Europe, which are both representatives of the genus *Bombus* [in fact, it is unlikely that a species with a relatively specialized floral morphology can invade a region without the presence of its functional pollinator niche, unless it is capable of autonomous self-pollination (see Duffy and Johnson, 2017)].

Impatiens is characterized by pollination by bees, Lepidoptera + bees, birds and autogamy (Grey-Wilson, 1980; Ruchisansakun *et al.*, 2016). In our analysis with a focus on Asian species, bee pollination is the most common pollination system, followed by bimodal pollination by Lepidoptera + bees, and autogamy. Bird pollination is the least common and only found in Africa. The distribution of pollination systems among Asian species appears to be different from that in African species, in which pollination by Lepidoptera + bees and pollination by birds is more common (Grey-Wilson, 1980; Janssens, 2008). This difference may to some extent reflect
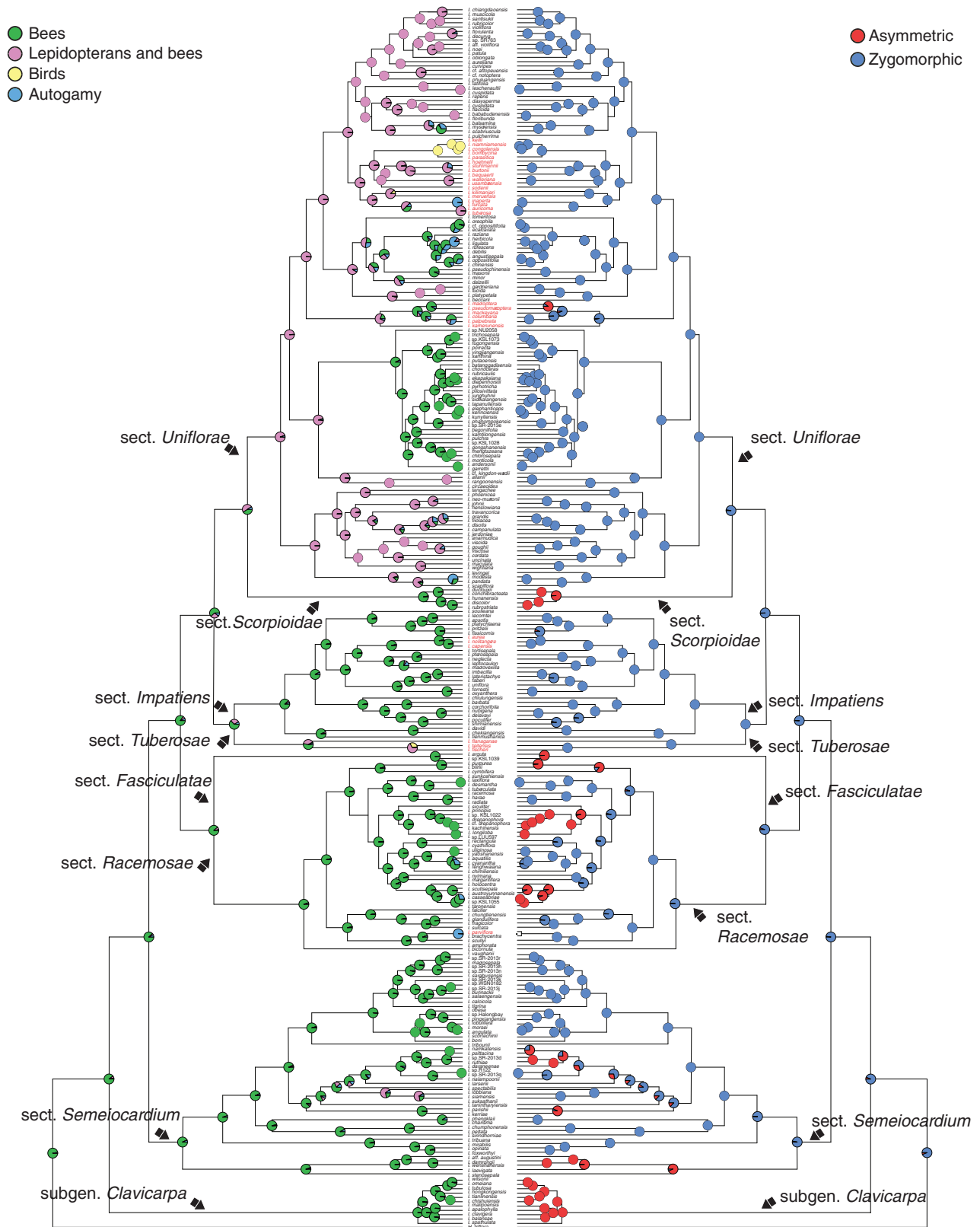
FIG. 3. SIMMAP ancestral character state reconstruction of pollination syndromes (left) and corolla symmetry (right) on the maximum clade credibility tree from the combined BEAST analysis. Pie charts at nodes represent the posterior probability of states based on ten stochastic mappings. The names of species outside Asia are marked in red.

TABLE 4. *Summary of changes in pollination syndromes of Balsaminaceae*

From:	To:	Parsimony	SIMMAP
Bees	Bimodal	12.73 (5–20)	3.51 (3) ± 2.91
Bees	Birds	0.69 (0–3)	0
Bees	Autogamy	8.33 (5–10)	36.87 (35) ± 14.57
Bimodal	Bees	11.03 (4–20)	6.22 (6) ± 4.56
Bimodal	Birds	2.28 (0–3)	3.71 (3) ± 1.09
Bimodal	Autogamy	3.65 (2–6)	24.21 (24) ± 6.26
Birds	Bees	0.02 (0–1)	0.14 (0) ± 0.82
Birds	Bimodal	0.37 (0–3)	1.49 (1) ± 2.56
Birds	Autogamy	0.02 (0–1)	0.46 (0) ± 1.64
Autogamy	Bees	0.43 (0–3)	49.24 (46) ± 15.90
Autogamy	Bimodal	0.56 (0–3)	13.86 (13) ± 5.23
Autogamy	Birds	0.00 (0–1)	0
Total shifts		40.11	139.71 (135) ± 31.83

For parsimony, the numbers represent the average number of shifts (min–max) of each kind across all mappings on a set of 900 BEAST trees. For SIMMAP, the numbers represent the average number of shifts (median) ± s.d. resulting from ten stochastic mappings on 100 randomly selected post-burn-in trees from the BEAST analysis

TABLE 5. *RJ MCMC model scores for the combined dataset when pollination syndromes are scored as binary traits (present/absent)*

Pollinator type	Model	Log marginal likelihood	BF
Bee	Dependent	–192.153686	12.01
	Independent	–198.156587	
Butterfly	Dependent	–184.335912	27.64
	Independent	–198.156587	
Bird	Dependent	–106.385056	–2.14
	Independent	–105.311592	
Autogamy	Dependent	–148.681805	–6.53
	Independent	–145.415361	

The dependent model indicates evolution of one trait dependent on the state in the other trait, whereas traits evolve independently in the independent model.

different animal distributions between the areas. For example, bee genera such as *Bombus* and *Apis*, which are important pollinators of Asian *Impatiens* species, are uncommon in tropical Africa (Williams, 1998; Gupta, 2014). Sunbirds, on the other hand, are an important pollination niche for tropical African plants, including many African *Impatiens* species (Bartoš and Janeček, 2014; Janecek *et al.*, 2015). However, pollinator distributions cannot be the only explanation for the differences in pollination systems as, despite the presence of sunbirds in Asia (Del Hoyo *et al.*, 2018), these do not pollinate *Impatiens* (Ruchisansakun *et al.*, 2016). For instance, based on floral traits, *I. phoenicea*, *I. coelotropis* and *I. platyadena* appear attractive to birds, but these species are pollinated by bees (Ramasubbu *et al.*, 2009, 2011) or by bees and Lepidoptera (bimodal) (Sreekala *et al.*, 2008*a, b*). We propose that the different frequencies of pollination systems can be understood in a context of historical biogeography. Phylogenetic evidence suggests that Balsaminaceae originated in Asia and dispersed from there to other regions (Janssens *et al.*, 2009). This, combined with the distribution of bees, may explain why bee pollination is so common in Asia. Colonization of tropical Africa,

where a limited number of large (forest) bee species currently occur, would then have to be associated with shifts to a new, locally available pollination niche (cf. Johnson, 1997; Van der Niet *et al.*, 2014*a*). Indeed, pollination syndrome shifts occur mostly in the clade of *I.* sect. *Uniflorae* which comprises most of the African and Malagasy *Impatiens* species in our analysis (Yuan *et al.*, 2004; Yu *et al.*, 2015). However, since some African species have a bee pollination syndrome, and many Asian species have a bimodal syndrome, this scenario does not provide a full explanation for the pattern of shifts in pollination syndrome.

The relatively smaller number of pollination syndrome shifts among Asian *Impatiens* species does not necessarily signal a low frequency of pollinator-driven evolution. Indeed, shifts in floral symmetry between zygomorphic and asymmetrical corollas occurred several times in Asian *Impatiens*. These shifts appear more rarely in African *Impatiens* as only a few asymmetric-flowered *Impatiens* species are described from there (but see Janssens *et al.*, 2015). Shifts in floral symmetry have occurred at least 20 times and appear to be reversible, although the number of shifts toward asymmetrical corollas is much higher than shifts toward zygomorphic corollas (Table 3) (apart from the model-based analysis of the plastid dataset). Furthermore, shifts in floral symmetry are biased to species with a bee pollination syndrome, and are almost entirely confined to Asian species (Figs 2–4) [interestingly, a mechanism of divergent use of the same pollinator appears to have evolved in African bird-pollinated *Impatiens* species, although the floral mechanism is not associated with asymmetrical corollas (Bartoš and Janeček, 2014)]. The specific evolutionary association between bee pollination and corolla asymmetry may be explained by the suitability of pollinator bodies for differential pollen placement. The relatively hairy bee bodies have many potential pollen placement sites (Armbruster *et al.*, 2014), whereas pollen placement sites on butterflies are more limited to the central region and proboscis (but see Butler and Johnson, 2020). Based on the presumed function of asymmetrical corollas in terms of mediating precise and different pollen placement, our result suggests several independent shifts in the use of the same pollinator (cf. Stebbins, 1970; Johnson, 2010; Eaton *et al.*, 2012; Armbruster, 2014). We probably underestimated the evolution of the divergent use of the same pollinator for two reasons. Firstly, divergent use of the same pollinator is not limited to asymmetrical flowers, as symmetrical bee-pollinated flowers also deposit pollen on different parts of the bee body (Ruchisansakun *et al.*, 2016). Secondly, the binary coding of floral symmetry probably does not do justice to cases where divergent use of the same pollinator may be mediated by the degree of corolla asymmetry. More field-based studies are required to fully understand the mechanism of corolla asymmetry in mediating divergent use of the same pollinator.

The presence of species with asymmetrical corollas in Balsaminaceae is relatively uncommon in angiosperms (Etcheverry *et al.*, 2008; Endress, 2012), and therefore provides a unique opportunity to investigate what drives its evolution. Ruchisansakun *et al.* (2016) showed that floral asymmetry results in different pollen placement sites on shared
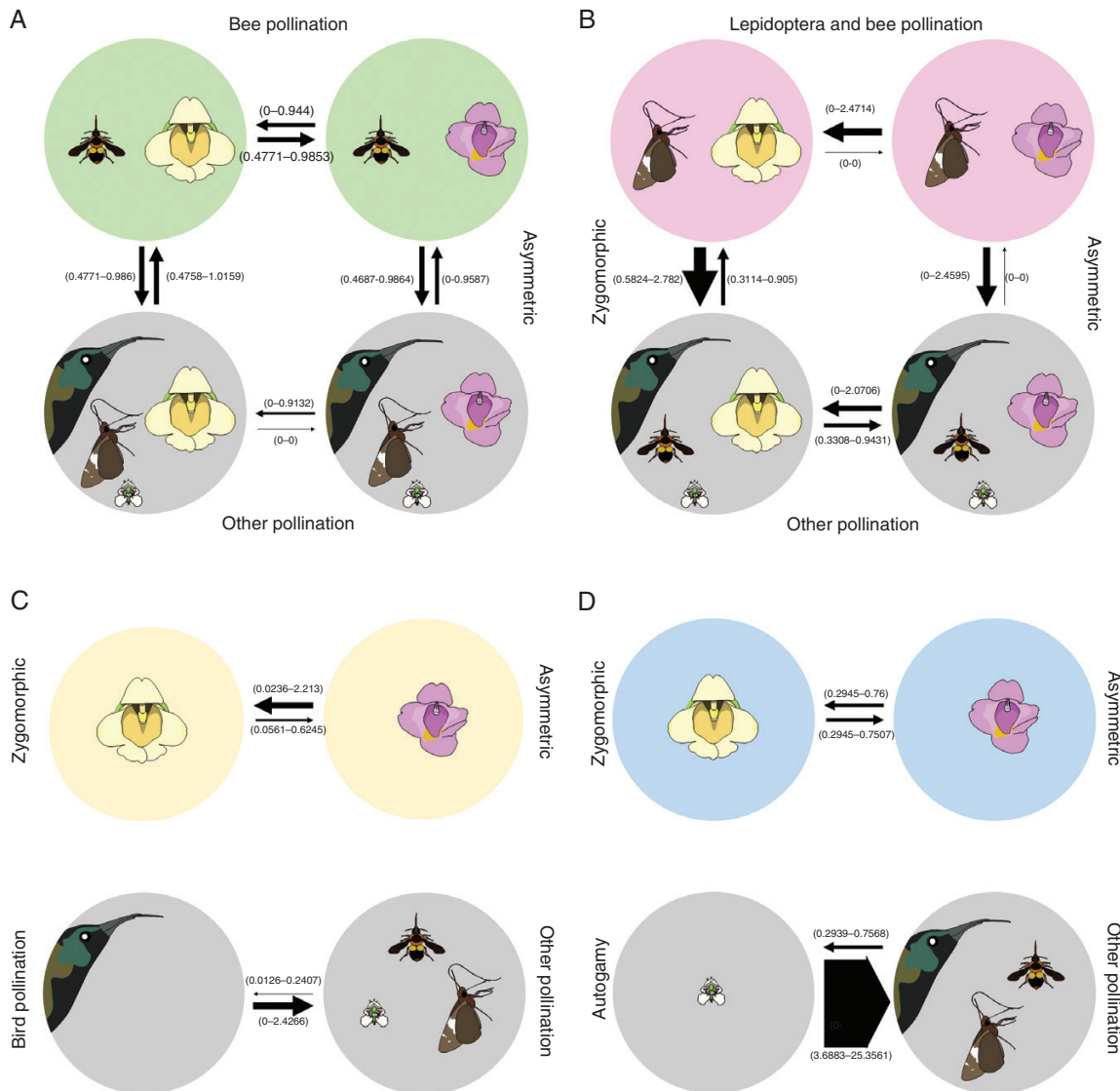
FIG. 4. Analyses of correlated evolution between pollination syndromes and floral symmetry. Pollination syndromes were coded as binary characters (present vs. other). (A and B) Cases where the evolution of pollination syndrome and floral symmetry are dependent on each other, whereas in (C) and (D) they evolve independently. Arrow thickness represents the magnitude of the average transition rates across the RJ MCMC analysis based on the set of 900 trees resulting from the combined BEAST analysis. Values in parentheses represent the 95 % HPD of transition rates. (A) Bee pollination syndrome vs. other pollination syndromes. (B) Bimodal (Lepidoptera + bee) pollination syndrome vs. other pollination syndromes. (C) Bird pollination syndrome vs. other pollination syndromes. (D) Autogamy syndrome vs. other pollination syndromes.

bee pollinators in species-rich *Impatiens* communities. It was hypothesized that asymmetrical flowers evolve in response to selection to avoid heterospecific pollen transfer. Three further hypotheses were proposed to explain the observation of multiple species with asymmetrical flowers. The phylogenetic analysis presented here can be used to distinguish among these hypotheses. The 'community invasion' hypothesis (cf. Sargent and Ackerly, 2008) postulates that asymmetrical flowers provide a key innovation which may facilitate successful invasion into Balsaminaceae communities, and hence allow clades with this trait to proliferate. Indeed, several relatively species-rich clades, such as sect. *Clavicarpa*, sect. *Scorpioidae* and several subclades of Sect. *Racemosae*, are characterized by the

evolution of asymmetrical flowers in their respective common ancestors. However, it remains to be tested whether this trait promotes diversification compared with lineages with zygomorphic flowers by performing formal analyses of state-dependent diversification. Frequent, repeated evolution of asymmetrical flowers may also be a signature of reproductive character displacement, either among closely related species (reinforcement) or not. Our phylogenetic analysis provides unambiguous support for repeated evolution of asymmetrical flowers, confirming ideas proposed in Ruchisansakun *et al.* (2016) based on the non-homologous nature of corolla asymmetry. To distinguish reinforcement from general character displacement requires an analysis of whether species with

asymmetrical flowers occur sympatrically with species with zygomorphic flowers, and whether they are cross-compatible. This is analysis was beyond the scope of this study, as it requires complete species-level sampling and data on the distribution of species and information on interspecific fertility. However, an informal analysis including five independently evolved asymmetrical species that are each sister to a (pair of) zygomorphic species suggests that only in one case (*I. faberi* vs. *I. imbecilla*/*I. lateristachys*) do the ranges of sister taxa overlap. On the other hand, in the remaining comparisons, the distribution of the asymmetrical species never overlaps with the (pair) of zygomorphic sister species. Our preliminary conclusion is therefore that the character displacement hypothesis (cf. Armbruster and Muchhala, 2009) would apply more frequently than the 'reinforcement' hypothesis (cf. Grant, 1994).

Shifts between pollination systems and floral symmetry can only partially explain the high diversity of *Impatiens*. In a meta-analysis of shifts in pollination systems, on average 25 % of cladogenic events were associated with pollination system shifts (Van der Niet and Johnson, 2012). In our study, we found that many branches in the phylogenetic tree are characterized by an absence of shifts. Although we argue that we may have underestimated the extent of pollinator-driven evolution, it seems likely that other drivers of speciation may be at play in *Impatiens*. Many *Impatiens* species are habitat specialists and consequently have a narrow and fragmented distribution. Such isolation may drive allopatric speciation (Janssens, 2008). Moreover, Yuan *et al.* (2004) showed that *Impatiens* species vary widely in their chromosome number, and that this trait is evolutionarily labile. This may be indicative of fast chromosomal evolution, leading to reproductive isolation and the evolution of species diversity without appreciable divergence in floral traits (White, 1968). More research into the relative importance of these different types of speciation is required to reconstruct and understand the evolution of species diversity in Balsaminaceae.

SUPPLEMENTARY DATA

Supplementary data are available online at https://academic.oup.com/aob and consist of the following. Table S1: species, localities, vouchers and GenBank accession numbers for the sequences used in this study. Table S2: list of studied Balsaminaceae species by country, floral traits and pollinators. Methods S1: methods and results associated with character evolution analyses based on separate nuclear and plastid datasets. Table S3: top five models ranked according to their sampling frequency. Table S4: summary of changes over trees in corolla symmetry of Balsaminaceae. Table S5: summary of changes over trees in pollination syndromes of Balsaminaceae. Table S6: RJ MCMC model scores for separate datasets when pollination syndromes are scored as binary traits. Figure S1: MCC nuclear dataset. Figure S2: MCC plastid dataset. Figure S3: MCC combined dataset.

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