PHYLOGENY, ADAPTIVE RADIATION, AND HISTORICAL BIOGEOGRAPHY IN Bromeliaceae: INSIGHTS FROM AN EIGHT-LOCUS PLASTID PHYLOGENY

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The family Bromeliaceae (58 genera, ca. 3140 species) constitute one of the most morphologically distinctive, ecologically diverse, and species-rich clades of flowering plants native to the tropics and subtropics of the New World (Fig. 1). Bromeliads range from mist-shrouded tepuis in Venezuela to sun-baked granitic outcrops of the Brazilian Shield, from cloud forests in Central and South America to the cypress swamps of the southern United States, and from the frigid Andean puna to the arid Atacama (Smith and Downs, 1974; Givnish et al., 1997; Benzing 2000). Their distinctive leaf rosettes often impound rainwater in central tanks, possess the CAM photosynthetic pathway, and bear absorptive trichomes, providing mechanisms to weather drought and obtain or conserve nutrients on rocks and exposed epiphytic perches (Pittendrigh, 1948; McWilliams, 1974; Crayn et al., 2004; Givnish et al., 2007; Schulte et al., 2009). Bromeliad tanks also house a great diversity of insects—including some with substantial impact on human health—and other arthropods, as well as crabs, frogs, salamanders, and snakes.
In a hectare of cloud forest, these tanks can sequester tens of thousands of liters of rainwater and trap hundreds of kilograms of humus high in the canopy and provide key food sources for many primates and birds (Paoletti et al., 1991; Leme, 1993; Sillett, 1994; Richardson, 1999; Benzing, 2000; Acevedo et al., 2008). Some tank bromeliads are directly carnivorous (Fish, 1976; Frank and O’Meara, 1984; Givnish et al., 1984, 1997), and at least one is known to benefit from the prey captured by inquiline spiders (Romero et al., 2006). Many tank bromeliads are protected and/or fed by ants (Benzing, 1970, 2000; McWilliams, 1974; Givnish et al., 1997). Pollinators include a wide variety of insects, as well as hummingbirds, bats, and a few perching birds (Benzing, 1980, 2000; Luther, 1993; Beamann and Judd, 1996; Smith and Till, 1998; Buzato et al., 2000; Krömer et al., 2006; Tschapka and von Helversen, 2007). The inflorescences of Puya raimondii are the most massive of any flowering plant, while those of some dwarf Brocchinia and Tillandsia are only a few centimeters in height (Fig. 1). Finally, bromeliads contribute a large share of the total species richness of vascular epiphytes in neotropical forests, are particularly diverse at mid-elevations, and exhibit increasingly narrow endemism at higher elevations (Kessler, 2001; Krömer et al., 2005; Linares-Palomino et al., 2009; Linares-Palomino and Kessler, 2009).

To understand the genesis of these patterns—and, more generally, the history of adaptive radiation and geographic diversification in bromeliads—we need a well-resolved, strongly supported phylogeny for this remarkable family. Progress toward this goal initially was slow, partly because bromeliads are taxonomically isolated, with no clear outgroup with which to polarize character-states (Gilmartin and Brown, 1987; Terry et al., 1997; Givnish et al., 2000; Pires and Sytsma, 2002); partly because bromeliad plastid DNA evolves at an unusually slow rate (Gaut et al., 1992, 1997; Givnish et al., 2004, 2005); and partly because previous studies had limited taxon sampling.

Over the last dozen years, however, these roadblocks have been mostly overcome, through a greater understanding of relationships among monocot families overall (Givnish et al., 2005; Chase et al., 2006; Graham et al., 2006) and, within Bromeliaceae, through the sequencing and analysis of one or a few rapidly evolving genes and gene spacers in the plastid genome by individual laboratories (e.g., Terry et al., 1997; Horres et al., 2000; Crayn et al., 2004; Givnish et al., 2004, 2007; Sass and Specht, 2010). Based on a thorough sampling of taxa in all three traditional subfamilies—especially the critical Pitcairnioideae (characterized by winged or unappendaged seeds) — Givnish et al. (2007) presented the most comprehensive view of bromeliad phylogeny and evolution to date, based on cladistic analyses of sequences of the plastid gene ndhF and calibration of the resulting molecular tree against the known ages of several monocot phylogeny and evolution to date, based on cladistic analyses of

**MATERIALS AND METHODS**

**DNA extraction, taxon sampling, and selection of molecular markers—**

Total genomic DNAs were extracted using the protocols of Crayn et al. (2004), Barfuss et al. (2005), Schulte et al. (2005), and Givnish et al. (2007). We sequenced eight rapidly evolving plastid regions (atpB-rbcL, matK, ndhF, psbA-trnH, rpl32-trnL, rps16, trnL intron, trnL-trnF) for 90 bromeliad species representing 46 genera, and three outgroups from Rapateaceae and Typhaceae (Appendix 1). An 81-gene analysis of relationships within Bromeliaceae (Schulte et al., 2005, 2009; Horres et al., 2007; Schulte and Zizka, 2008; Sass and Specht, 2010) and Tillandsioidae (Barfuss et al., 2005)—we formed an international consortium to produce a well-resolved, strongly supported phylogeny for Bromeliaceae based on multiple plastid loci and as comprehensive a sampling of bromeliad genera as could be managed.

Here we present the first results of that collaboration. To re-construct relationships across Bromeliaceae, we completed the sequencing of eight rapidly evolving plastid regions for representatives of 46 of 58 bromeliad genera. We then used the resulting phylogeny to (1) analyze relationships within the family and test the new eight-subfamily classification, (2) infer the timing of divergence of various clades and relate these dates to events in Earth history, and (3) determine the geographical origins of the family and patterns of subsequent spread outside this region by members of each subfamily. A companion paper will calculate the rate of net species diversification for each major bromeliad clade and relate the observed differences in diversification rate to differences among clades in morphology, ecology, geographic distribution, mode of seed dispersal, and time of adaptive radiation.
Fig. 1. Representative species of bromeliad subfamilies; images are at different scales. BROCCCHINOIDEAE: (A) Brocchinia prismatica, non-pounding species sister to all Brocchinia, found in wet, sandy savannas in SW Venezuela; (B) B. reducta, terrestrial carnivore of damp, sandy savannas in SE Venezuela and SW Guyana; (C) tree-like B. micrantha, SE Venezuela and SW Guyana. LINDMANIOIDEAE: (D) Lindmania guianensis, SE Venezuela and SW Guyana; (E) Connellia augustae, sandstone outcrops, Venezuela and Guyana. TILLANDSIOIDEAE: (F) Catopsis berteroniana, carnivorous epiphyte, Florida to Brazil; (G) Guzmania lingulata, epiphyte, Central and N South America; (H) Tillandsia dyeriana, epiphyte, Ecuador; (I) Tillandsia setacea (above branch) and T. usneoides (Spanish moss, below branch), widespread atmospheric epiphytes; (J) Vriesea heliconioides, epiphyte, Mexico to
We believe that our approach to higher-level bromeliad phylogenetics, based solely on sequences from the plastid genome, is justified because very few natural cases of hybridization among bromeliads are known, based on morphology or on more decisive comparisons of organelar vs. nuclear DNA markers (Wendt et al., 2008; Gonçalves and de Azevedo-Gonçalves, 2009). Partly this may be because nuclear ribosomal ITS—the nuclear locus used to screen for hybridization and/or introgression in many angiosperm lineages—has only rarely been amplified and sequenced in bromeliads, given its strong hairpin geometry in this group (T. M. Evans, personal communication). However, Schulte et al. (2009), Gonsiska (2010), Jabaily and Sytsma (2010), and Sass and Specht (2010), employing other nuclear markers (PhyC, PRK, and nDNA ETS) with plastid sequences to evaluate relationships among hundreds of species, have identified only a very small number of putative hybrids, most notably the ancestor of the Chilean clade of Puya and one species of Catopsis. Thus, here we rely on multiple loci from the plastome genome to reconstruct evolutionary relationships, recognizing that the validity of our plastid phylogeny should be tested when it becomes possible to sequence and align low-copy nuclear genes across all subfamilies.

**DNA amplification, sequencing, and alignment**—Methods for amplifying and cycle-sequencing different plastid regions from total DNA extracts followed Barfuss et al. (2005) for atpB-rbcL and rpl16; Crayn et al. (2004) for matK; Givnish et al. (2007) for ndhF; Horres et al. (2000, 2007) for the trnL intron and trnL-trnF; and Shaw et al. (2007) for psbA-trnH and rpl32-trnL. Sequences were visually aligned following Baum et al. (1994). Structures of DNA that were difficult to align (i.e., there were multiple conflicting alignments possible under the assumptions of Baum et al.) or had missing data for a substantial number of taxa were excluded from analysis. We were unable to complete 60 (9.2%) of 651 sequences. GenBank accession numbers were acquired for all new sequences; previously obtained sequences were downloaded from GenBank (Appendix 1). An aligned data set has been deposited in TreeBase (http://www.treebase.org/treebase-web/home.html; accessed 04-07-11), together with the maximum likelihood and Bayesian trees as case S11152.

**Phylogenetic analyses**—We inferred relationships from the nucleotide data using maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI). MP analyses were conducted using the program PAUP* (Sikes and Lewis, 2001), based on Parsimony Ratchet (Nixon, 1999) and implemented in the Cyberinfrastructure for Phylogenetic Research (CIPRES) portal 2 teragrid (http://www.phylo.org) (Miller et al., 2010). Individual bases were considered multistate, unordered characters of equal weight; unknown nucleotides were treated as uncertainties. Following Nixon (1999) and Goloboff (1999), we performed multiple (50) independent searches in PAUP* to cover tree space adequately. Each search involved 500 iterations, with the shortest trees from each search used to form a strict consensus tree and a majority-rule tree. Shortest trees from each successive search were combined with previous search trees to evaluate whether the combined search consensus tree had stabilized. Stabilization of a consensus tree based on multiple, independent searches in PAUP* supports the accuracy of the topology obtained (Goloboff, 1999). We used bootstrap analysis (Felsenstein, 1985) in the program PAUP* 4.0b10 (Swofford, 2002) to assess the relative support for each node in the strict consensus, using 1000 random resamplings of the data and retaining 200 trees per iteration. To determine the extent to which the lower support for the monophyly of Puyioideae and Bromelioidae in this study vs. Givnish et al. (2007) was due to our inclusion here of a number of Chilean Puya and Chilean bromelioids and Deinacanthion of the nearby Gran Chaco, respectively, we removed the latter from the analysis and recalculated support values for Puyioideae and Bromelioidae. Consistency indices, including autapomorphies (CI) and excluding them (CT), were calculated to evaluate the extent of homoplasy in the data (Givnish and Sytsma, 1997). Maximum-parsimony phylogenies were also formed for each plastid region, and incongruence length difference (ILD) tests (Farris et al., 1994) were conducted for each pair of regions (ndhF, matK, trnL-trnF, atpB-rbcL, psbA-trnH, rpl16, rpl32-trnL) in PAUP* after removing taxa not sequenced for either region, to assess potential conflicts between regions in phylogenetic structure.

Maximum-likelihood analyses used the program RAxML—(Genetic Algorithm for Rapid Likelihood Inference; Zwickl, 2006) in CIPRES. Multiple models for each gene partition are not allowed in GARLI, so the more complex model for a given set of genes was chosen. Maximum-likelihood bootstrapping (MLB) was completed using the program RAxML 7.0.4 (Stamatakis et al., 2005, 2008).

Bayesian inference was performed in the program MrBayes 3.1 (Ronquist and Huelsenbeck, 2003) allowing different models for each region. Four independent runs of 500 000 generations each were completed with a chain temp of 0.2. Trees were sampled every 1000 generations. The first 25% of runs were discarded as burn-in. A majority rule consensus of the remaining trees from the four runs was produced in PAUP* 4.0 and used as the Bayesian inference tree with posterior probabilities (PP). We also explored the mixture model of Pagel and Meade (2008) as implemented in the program BayesPhylogenies (Pagel and Meade, 2004). This model allows the fit of more than one model of evolution to each site in the alignment. We used the recommended GTR + I model with "patterns=2, pi=2true", allowing two rate matrices to be formed and allowing both rate parameters and base frequencies to vary.

**Dating radiations**—An indirect approach to calibrating the bromeliad phylogeny is required because almost all bromeliads occur in habitats that are poor in age constraints. We inferred the age of the crown group of the Bromeliaceae using the program BEAST 1.5 (Drummond and Rambaut, 2007) together with the maximum likelihood and Bayesian trees as case S11152.
for fossil preservation. There is only one macrofossil clearly assignable to Bromeliaceae, from Costa Rica 36 million years ago (Ma) (Smith and Till, 1998), long after both existing estimates of the origin of the family based on molecular data (Givnish et al., 2004, 2007). Lemé et al. (2005) recently erected a new family for a bromeliad-like fossil (Protananas lucenae) from northeastern Brazil in limestone 100–110 Ma old. The authors report, however, that this taxon appears to be a nonbromeliad close to the base of order Poales.

We conducted two analyses to assess the timing of the rise of the bromeliad stem lineage within Poales and of the crown radiation of the family. First, building on previous analyses of relationships and fossil dating (Bremer, 2000; Givnish et al., 2000, 2005; Janssen and Bremer, 2004), we used ndhF sequences of 333 taxa of monocots (including 71 from Bromeliaceae) and the outgroup Ceratophyllum to build a molecular phylogeny. The ML tree derived in GARLI using a model from jModelTest was used for subsequent fossil calibration. As ndhF alone does not have the power to resolve several key nodes, we constrained five areas of the monocot backbone based largely on the results of a recent monocot-wide study employing 81 plastid genes (Givnish et al., 2010). These constraints included (1) (Araceae, Tofieldiaceae, all other Alismatales); (2) (Lilaceae, Asparagales + commelinids); (3) (Dasygynogono- naceae, Arecaceae); (4) (Poales, Commelininales, Zingiberales)); and (5) (Bromeliaceae, Typhaceae, (Rapateae, all other Poales))). We used the Langley and Fitch (1974) method, as implemented in the program r8s (Sanderson 2004), to reconstruct divergence times on the ML tree (Bremer 2004) to find the optimal value of the smoothing parameter, based initially on minimizing the sum of the squared deviations between the observed and expected branch lengths derived by jackknifing each branch (Sanderson, 2002). We varied the smoothing parameter from 10 to 100 in steps of 0.25 of the exponent. The optimal value of the smoothing parameter was validated using the check-gradient algorithm in r8s. We can separate r8s analyses using a range of smoothing values near the optimum to examine the impact of different values on variation in the stem and crown age of Bromeliaceae and chose the final value of the smoothing parameter based on minimization of that variation within the window of values that yield similar, near-minimal sums of the squared deviations between observed and expected branch lengths (see above). To estimate uncertainties in node age due to uncertainties in the monocot-wide ndhF branching topology, we calculated the cross-validation algorithm in r8s (Sanderson 2004) to find the optimal value of the smoothness parameter, based initially on minimizing the sum of the squared deviations between the observed and expected branch lengths derived by jackknifing each branch (Sanderson, 2002). We varied the smoothing parameter from 10 to 100 in steps of 0.25 of the exponent. The optimal value of the smoothness parameter was validated using the check-gradient algorithm in r8s.

Six Cretaceous fossils were used to constrain the corresponding nodes as minimum ages (Janssen and Bremer, 2004; Givnish et al., 2005; Hesse and Zetter, 2007). The monocot root was fixed at 134 Ma (Bremer, 2000; Janssen and Bremer, 2004). Penalized likelihood smooths local rates in the difference of DNA evolution on different branches, taking into account branch lengths and branching topology and assigning a penalty for rate changes among branches that are too rapid or frequent, based on a smoothness parameter. We used the cross-validation algorithm in r8s (Sanderson 2004) to find the optimal value of the smoothness parameter, based initially on minimizing the sum of the squared deviations between the observed and expected branch lengths derived by jackknifing each branch (Sanderson, 2002). We varied the smoothing parameter from 10 to 100 in steps of 0.25 of the exponent. The optimal value of the smoothness parameter was validated using the check-gradient algorithm in r8s. We can separate r8s analyses using a range of smoothing values near the optimum to examine the impact of different values on variation in the stem and crown age of Bromeliaceae and chose the final value of the smoothing parameter based on minimization of that variation within the window of values that yield similar, near-minimal sums of the squared deviations between observed and expected branch lengths (see above). To estimate uncertainties in node age due to uncertainties in the monocot-wide ndhF branching topology, we calculated the cross-validation algorithm in r8s (Sanderson 2004) to find the optimal value of the smoothness parameter, based initially on minimizing the sum of the squared deviations between the observed and expected branch lengths derived by jackknifing each branch (Sanderson, 2002). We varied the smoothing parameter from 10 to 100 in steps of 0.25 of the exponent. The optimal value of the smoothness parameter was validated using the check-gradient algorithm in r8s.

To estimate variation in node age due to uncertainties in the derived node dates of the eight-locus tree and the ndhF crown nodes, we performed three further analyses. First, we calculated the standard deviation of inferred age at each node via 100 bootstrap resamplings of the eight-locus data set. Second, we calculated the standard deviation of both the stem and crown nodal dates for Bromeliaceae based on 100 bootstrap resamplings of the monocot-wide ndhF data; this allowed us to generate of the mean ± SD of the inferred ages for both the stem and crown nodes based directly on fossil calibration. Given that variation in inferred node ages is a function of random variation in the ages of the set-dates independent of random variation in node ages due to uncertainties in the eight-locus phylogeny, we employed a penalization for rate changes among branches of DNA evolution on different branches, assuming a molecular clock and conduct a χ² test of rate constancy to test for significant deviation from clocklike evolution. Given the nonclocklike pattern of evolution observed, we converted the ML tree into ultrametric form using penalized likelihood (PL) in r8s (Sanderson, 2002, 2004), calibrated against monocot-wide fossils.

Historical biogeography—To reconstruct spatial patterns of geographic diversification within Bromeliaceae, we employed three contrasting methods and accommodating assumptions implemented in the programs Statistical Dispersal-Vicariance Analysis (S-DIVA; Yu et al., 2010), BayesTraits (Pagel and Meade, 2007), and MacClade 4.08 (Maddison and Maddison, 2005). Given that the stem lineage of the family is already known to extend back to the Cretaceous but with a far more recent crown radiation (Givnish et al., 2004, 2007), and that bromeliads are clearly capable of long-distance dispersal—for example, from South America to the Galápagos (Racinaea insularis, Tillandsionidae), the Juan Fernandez Islands (Grellica biarteria and Ochagavia elegans, Bromeliaceae), and tropical West Africa (Pitcairnia felicina, Pitcairniaceae); see Smith and Downs 1974, 1977, 1979) and Givnish et al. (2007)—any assumption about the relative importance of vicariance vs. dispersal in Bromeliaceae would be difficult to justify. Programs to evaluate geographic diversification either favor vicariance (e.g., dispersal–vicariance analysis [DIVA, Ronquist, 1996, 1997; and S-DIVA] or allow any amount of dispersal between areas (e.g., BayesTraits or MacClade using BI and MP criteria, respectively). Explicit, model-driven analyses of geographic diversification are possible (Rée et al., 2005; Rée and Smith, 2008), especially in the context of well-known geological events (e.g., continental vicariance as in Clayton et al., 2009), but remain premature for examining diversification within and among areas of geologically complex South America.

To minimize some of the shortcomings inherent in DIVA (Nylander et al., 2008; Harris and Xiang, 2009; Kodandaramaiah, 2010), we instead used S-DIVA (Yu et al., 2010). DIVA optimizes distributions for each node by allowing vicariance but minimizing assumptions of dispersal and extinction. S-DIVA extends DIVA by permitting assessment of phylogenetic uncertainty by examining multiple trees (in our case, a random subset of post burn-in Bayesian trees), each of which may contain polytomies. Ranges of terminal taxa were atomized into recognized areas of endemism largely following Givnish et al. (2007) and (except for fusion of all Andean regions) Antonelli et al. (2009), including (1) Guayana Shield; (2) Brazilian Shield (including the Serra do Mar and Serra da Mantiqueira, as well as the adjacent Panchozeroc post-horn of the Horn of Brazil and the Rio de la Plata basin); (3) Amazonia; (4) Caribbean (including the coast of northern South America and the southeastern United States); (5) Central America (including shallow western Texas and eastern Mexico; and) (6) tropical West Africa. Distributional data were drawn from Smith and Downs (1974, 1977, 1979). Following the recommendation of Ronquist (1996), terminal species representing higher taxa (i.e., genera) were scored for ancestral area where possible (specifically, for Catopsis in Central America [Brown, 1993a, 1993b]; for Pitcairnia and Bromelia, where not justifiable, we scored single placeholders for all portions of the generic range (e.g., Bromelia) despite the known sacrifice in geographical resolution at deeper nodes in S-DIVA reconstructions (Ronquist, 1996). Multiple species per genus were each scored based on their own distribution. Vicariance between the Guayana Shield and the Andes, Caribbean, and Central America were excluded, as was
victa between tropical West Africa and any other region, due to the lack of any geographic contact between these regions over the inferred age of the bromeliad stem group. Due to the ancient split of Bromeliaceae from all other Poales, we performed several iterations of S-DIVA with respect to different outgroups (i.e., Rapateaceae and Typhaceae). Rapateaceae (and other lineages among the early splits in Poales) are Guayanans, whereas Typhaceae are cosmopolitan. We thus ran S-DIVA with the two outgroup families scored as Guayana Shield and polymorphic, respectively. We also ran analyses after scored both outgroups as Guayana Shield, due to the strong signal of Guayana Shield as basal in more Poales-wide biogeographic analyses (Givnish et al., 2000, 2004, 2007). Last, we removed Typhaceae entirely as an outgroup, as advocated by Bremer (2002), who removed this aquatic, easily dispersed group in DIVA analysis because it would be dangerous to base any conclusions regarding ancestral distributions on their present distributions. A random subset of 1000 Bayesian posterior probability trees from the phylogenetic analysis of the eight-locus data set was input into S-DIVA to estimate probabilities of ancestral areas at each node. We explored the impact of restricting the number of unit areas allowed in ancestral distributions by using the maxareas option (all possible areas, 4, and 2). The ancestral areas for all nodes were visualized on the ML tree with Puya constrained to be monophyletic.

We also analyzed the biogeographical data using ML and MP reconstructions that relax emphasis on vicariance by permitting dispersal between any pair of biogeographic areas. We implemented BI optimization of ancestral areas (Pagel, 1999) with the Markov chain Monte Carlo (MCMC)-based BayesMultiState option in the program BayesTraits v.1.0 (Pagel and Meade, 2007) using the ML tree with Puya constrained to be monophyletic to portray ancestral area reconstructions. To reduce some of the uncertainty and arbitrariness of choosing priors under MCMC, we used the hyperprior approach (the rjhp command) as recommended (Pagel et al., 2004; Pagel and Meade 2007). Combina- tion of hyperprior values (exponential or gamma, mean and variance) and rate parameter values were explored to find acceptance rates when running the Markov chains of between 20 and 40% (as recommended by Pagel and Meade, 2007). All subsequent analyses used the reversible-jump hyperprior command (rjhp gamma 0 30 0 10) that seeded the mean and variance of the gamma prior from uniform hyperpriors on the interval 0 to 30 and 0 to 10, respectively, and a rate parameter of 150 (ratedev 150). We reconstructed ancestral areas using MP by overlaying the ranges of individual species (or inferred ancestral area for Catopsis) using MacClade 4.08 (Maddison and Maddison, 2005), resolving all of the most parsimonious states at each node of the ML tree.

RESULTS

Phylogeny—We obtained an aligned data matrix of 94 taxa × 9341 characters; of the latter, 1210 were parsimony-informative and 1429 were variable but parsimony-uninformative (Table 1). The number of informative characters varied nearly 6-fold among loci, from 61 for psbA-trnH to 357 for ndhF. The fraction of informative sites varied from 8.8% (psbA-trnH) to 16.2% (rpl32-trnL). The numbers of informative vs. variable but uninformative characters were strongly correlated with each other across loci (r = 0.97, P < 0.0001 for two-tailed t test with 6 df), and the ratio of informative to variable but uninformative characters averaged 0.85 ± 0.074 (mean ± SD). Within Bromeliaceae, 1663 characters were variable, of which 766 were informative.

Maximum parsimony resulted in a single island of 1317600 trees of length 4546 steps, and a strict consensus tree that was well resolved outside subfamily Bromelioidae (Fig. 3). The consistency index CI for these trees was 0.70; CI′ (excluding autapomorphies) was 0.54. Branches that were unusually short (see below) were usually lost in the strict consensus tree relative to the majority-rule tree (Fig. 3).

The MP strict consensus tree supported the monophyly of all eight proposed subfamilies; each had 99–100% bootstrap support except Puyoideae and Bromelioidae (Fig. 3). Chilean Puya formed a clade with 100% bootstrap support; non-Chilean Puya had 99% support. Puya as whole—while resolved as monophyletic—had less than 50% support (Fig. 3). Bromelioidae had 59% bootstrap support. Bromelia, Fascicularia-Ochagavia, Deinacanthon, and Greigia formed a weakly supported clade sister to all other bromelioids in the MP majority-rule tree and a basal polytomy in the strict consensus tree. Pseudananas is sister to the remaining bromelioids (61% bootstrap), then Ananas. A core group of bromelioids, sister to and including Ananas, had 88% bootstrap support, but seven of 24 relationships within this core group were unresolved in the strict consensus (Fig. 3). The clade consisting of Bromelioidae and Puyoideae had 100% bootstrap support.

Support levels for the monophyly of each of the eight subfamilies in the strict consensus tree were generally much higher than those in the original ndhF phylogeny (Figs. 2, 3), except for Puyoideae and Bromelioidae. Experimental removal of taxa show that these two subfamilies had lower support in the current analysis due to our inclusion of Chilean Puya, Chilean bromelioids, and Deinacanthon from the nearby Gran Chaco. Relationships among the eight subfamilies agreed with those in the original ndhF phylogeny (Fig. 2) but were better supported. In addition, the eight-locus data set resolved the subfamilial trichotomy present in the ndhF phylogeny, placing Hechtioideae sister to (Navioideae, (Pitcairnioideae, (Bromelioideae, Puyoideae))), and Tillandsioideae sister to all five subfamilies (Fig. 3).

In both the strict consensus and majority-rule trees, Brocchinia, Guzmania, Hechitia, Deuterocohnia, Dyckia, Encholirium, Fosterella, Pitcairnia, Puya, Ananas, and Arecococcus emerged as monophyletic. In contrast, Lindmania, Tillandsia, Navia, and Ochogavia were paraphyletic; Mezobromelia, Vriesea, and especially Aechmea (with at least six apparent “origins”) were polyphyletic (Fig. 3). In the MP majority-rule tree, Acanthostachys was sister to taxa corresponding to the tank-bromelioid clade (“core bromelioids”) of Schulte et al. (2009) and its sister Cryptanthus; Acanthostachys, Cryptanthus, and the tank bromelioids formed an unresolved trichotomy in the strict consensus (Fig. 3).

MP trees based on individual plastid regions were less resolved and less well supported than the strict consensus phylogeny.

Table 1. Numbers of parsimony-informative, variable but parsimony-uninformative, and invariant sites for each of the plastid regions sequenced, as well as the consistency indices (with and without autapomorphies) and proportion of informative sites for those regions.

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<th>Region:</th>
<th>matK</th>
<th>ndhF</th>
<th>rps16</th>
<th>atpB-rbcL</th>
<th>psbA-trnH</th>
<th>rpl32-trnL</th>
<th>trnL-trnF, trnL intron</th>
<th>Total</th>
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<td>No. informative sites</td>
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<td>251</td>
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<tr>
<td>No. invariant sites</td>
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<td>1109</td>
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<td>937</td>
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<tr>
<td>Total aligned bp</td>
<td>1631</td>
<td>2098</td>
<td>1145</td>
<td>1377</td>
<td>900</td>
<td>1383</td>
<td>1147</td>
<td>9681</td>
</tr>
<tr>
<td>Consistency index (CI)</td>
<td>0.70</td>
<td>0.71</td>
<td>0.72</td>
<td>0.66</td>
<td>0.69</td>
<td>0.71</td>
<td>0.73</td>
<td>0.71</td>
</tr>
<tr>
<td>C'</td>
<td>0.56</td>
<td>0.54</td>
<td>0.57</td>
<td>0.49</td>
<td>0.55</td>
<td>0.56</td>
<td>0.59</td>
<td>0.55</td>
</tr>
<tr>
<td>Informative sites/base</td>
<td>0.131</td>
<td>0.118</td>
<td>0.115</td>
<td>0.089</td>
<td>0.078</td>
<td>0.140</td>
<td>0.141</td>
<td>0.119</td>
</tr>
</tbody>
</table>
based on the combined data set. Although ILD tests showed apparently significant differences in phylogenetic structure between some pairs of regions, such differences only occurred in comparisons when one or both regions with relatively small numbers of phylogenetically informative sites (Table 1). Furthermore, for each region, the MP strict-consensus tree did not
diverge from the combined-data phylogeny at nodes well supported (≥90% bootstrap support) in the former.

For maximum-likelihood analysis, the AIC identified the optimal models as TVM + Γ for ndhF; TVM + I + Γ for matK, trnL (plus intron), atpB, and rps16; and GTR + I + Γ for psbA-trnL and rpl32. The maximum-likelihood and Bayesian trees were nearly identical to each other in topology and mostly congruent with the MP majority-rule tree, but placed Bromelioidae in a paraphyletic Puya, sister to the non-Chilean taxa (Figs. 3–5). Both ML and BI placed Hechtia sister to Navioideae-Pitcairnioideae-Puyioideae-Bromeliodeae, congruent with the MP tree. Both placed Catopsis sister to Glomeropitcairnia at the base of the tillandsioids (Figs. 4, 5). The four areas of greatest phylogenetic uncertainty within bromeliads—judged by differences in topology among trees or the degree of resolution within each tree—correspond to the portions of those trees with exceedingly short branch lengths, including (1) early-divergent bromelioids, (2) late-divergent bromelioids, (3) relationships among Chilean and non-Chilean taxa (Figs. 3–5), and (4) relationships among Catopsis, Glomeropitcairnia, and all other tillandsioids (Figs. 3, 5). Conflicts among the three phylogenies generally did not occur at nodes that are well supported by each individually.

Molecular clocks and dating—Cross-verification of a penalized-likelihood calibration of the ndhF ML tree across monocots showed that smoothing parameters between 50 and 100 yielded very similar, nearly minimal sums of the squared deviations between the observed and expected branch lengths derived by jackknifing each branch. Within that range, a smoothing parameter of 75 minimized the variance in the apparent ages of the crown and stem node of Bromeliaceae. We used this value to calibrate the across-monomocot tree, producing estimates of the bromeliad stem age as 100.0 ± 5.2 million years ago (Ma) (and the corresponding crown age as 19.1 ± 3.4 Ma (Fig. 6). These dates were then employed to calibrate the eight-locus bromeliad tree; cross verification produced a smoothness parameter of 100. The resulting chronogram (Fig. 7) resolved clade-genetic events within Bromeliaceae from 19.1 to 0.64 Ma. The standard deviation of estimated ages for individual nodes generally varied from 0.5 to 2 Myr, with smaller estimated amounts of variation due to phylogenetic uncertainty in nodes closer to the present (Fig. 7). Regression of estimated ages for several representative nodes in Bromeliaceae from the eight-locus tree on those from the across-monomocots phylogeny (Table 2) yielded excellent agreement between the two sets of estimates (y = 1.060x – 0.032, r² = 0.80, P < 0.0001 for 25 df).

Historical biogeography—Reconstruction of ancestral areas using MP, BI, and S-DIVA generally agreed with each other, with the exception of a few nodes detailed below (Fig. 8). Based on our eight-locus chronogram and biogeographic reconstruction using MP, we infer that bromeliads arose in the Guayana Shield ca. 100 Ma, based on the restriction to this ancient craton—and in most cases, to highly leached marine sandstones of the overlying Precambrian Roraima Formation—of Brocchinoideae and Lindmaniaeae, nested sequentially at the base of the family. Brocchinoideae diverged from the ancestor of all other bromeliads ca. 19.1 Ma, and extant species of Brocchafia began to diverge from each other ca. 13.1 Ma (Fig. 8). All other extant bromeliad subfamilies began diverging from each other slightly before that, with the stem lindmaniaeae diverging from the ancestor of other bromeliads ca. 16.3 Ma. The stem tillandsioids arose shortly after that, ca. 15.4 Ma (Fig. 8). Based on MP, it is unclear whether tillandsioids arose on the northern littoral of South America, in the Andes, or in Central America (Fig. 8). Catopsis, sister to Glomeropitcairnia with it sister to the remaining tillandsioids, today grows in the Guayana Shield as well as the north coast of South America, the Caribbean, Central America, and southern Florida, but appears to have arisen in Central America (Fig. 8). Glomeropitcairnia is endemic to the Lesser Antilles, Trinidad, and Tobago, and the north coast of Venezuela, and appears to have diverged from Catopsis about 14.0 Ma. The ancestor of the remaining members of the subfamily—which we term the core tillandsioids—appears to have arisen in the Andes about 14.2 Ma, with the modern genera beginning to diverge from each other ca. 8.7 Ma, with evolution mainly in the Andes but with several subsequent invasions of Central America, the northern littoral of South America, and the Caribbean (Fig. 8).

Hechtia arose ca. 16.6 Ma and invaded Central America independently (Fig. 8). Extant species of Hechtia began differentiating from each other ca. 10.3 Ma. About 15.0 Ma, Navioidae arose in the Guayana and/or Brazilian Shields, with restriction to the Guayana Shield after 10.4 Ma, corresponding to the endemism there of Brewearia, Navia, and Sequencia and of Cotendorphia to the Brazilian Shield.

The common ancestor of the three remaining subfamilies evolved about 15.0 Ma in the Andes (Fig. 8), where Pitcairnia grows from near sea level to above treeline (with scattered occurrences elsewhere in the Guayana Shield and southeastern Brazil), Fosterella grows mostly at midelevations in mesic sites (with disjunct occurrences in Central America), Dyckia grows in drier sites from mid to high elevations and extends into the Brazilian Shield and the Río de la Plata basin (including the Gran Chaco within the latter), and Deuterocohnia occurs as cushion plants in arid, high-elevation sites just south of the “knee” of the Andes, in southern Bolivia and northern Argentina (Fig. 9). Pitcairnioideae arose ca. 13.4 Ma; Pitcairnia, ca. 12.0 Ma; Fosterella, ca. 11.3 Ma; and Deuterocohnia, ca. 8.5 Ma. Based on the taxa included in this study, the lineage leading to Pitcairnia feliciana dispersed to Guinea in west Africa from the Andes sometime in the last 9.3 Myr. Dyckia and Enchlorium (the latter restricted to southeastern Brazil) form a clade sister to Deuterocohnia and apparently invaded the Brazilian Shield from the Andes, beginning 8.5 Ma (Figs. 8, 9). Given the geographic overlap of Deuterocohnia, Dyckia, and Fosterella in south-central Bolivia (Fig. 9), it is likely that key cladogenetic events in Pitcairnioideae occurred there.

The common ancestor of Puya and the bromelioids arose about 13.4 Ma in the Andes (Fig. 8). Ancestral Puya diverged from the ancestral bromelioids ca. 10.1 Ma, with Puya splitting almost immediately (10.0 Ma) into two clades distributed in the Andes in low-elevation Chile vs. the rest of the cordillera at mid to high elevations. Present-day species of Puya began to diverge from each other during the last 3.5 Myr in the Andes, and during the last 2.5 Myr in Chile (Fig. 8). In the ML, BI, and MP majority-rule trees, a clade of five small bromelioid genera—mostly from Chile and the southern Andes—are sister to the remaining members of Bromelioidae (Fig. 8). Three of these genera (Fascicularia-Ochagavia and Greigia) are partly or wholly restricted to temperate regions at low elevations in the southern Andes, including low-elevation habitats just above high tide in Fascicularia bicolor and Ochagavia litoralis in continental Chile, and O. elegans in the Juan Fernandez Islands. Greigia grows in montane habitats from Central America to the Andes, and in the
understory of humid deciduous and evergreen forests in southern Chile and the offshore Juan Fernandez Islands. Two other genera—monotypic Deinocanthon and species-rich Bromelia—grow in the Gran Chaco (the southwestern portion of the Rio de la Plata basin, adjacent to the Andes) and throughout the Neotropics at low elevations, respectively (Fig. 8).

The remaining bromelioids form the "Brazilian Shield clade", which arose in the Brazilian Shield ca. 10.1 Ma via dispersal from the Andes (Fig. 8). Members of this clade subsequently dispersed repeatedly outside this region, notably in Ananas, Aechmea, Araeococcus, Billbergia, Neoregelia, and Ronnbergia, but most taxa are restricted to a narrow portion of the Brazilian Shield near the southeastern coast of Brazil, running ca. 1500 km from Minas Gerais to Rio Grande do Sol. This area includes the Brazilian Highlands (Serra do Mar and the more inland Serra da Mantiqueira) and adjacent coastal plain, with their extremely humid, highly diverse Atlantic rain forests and cloud forests, restingas on sandy soils, mangroves, campos de altitude, and drier vegetation inland (e.g., campos rupestres on rocky outcrops). The bromelioid tank-epiphyte clade—sister to

Fig. 4. Maximum-likelihood (ML) phylogram for Bromeliaceae based on concatenated sequenced data. Branch lengths are proportional to the inferred number of nucleotide changes down each branch. Puya (red branches) in paraphyletic in the ML tree, but monophyletic in the MP tree.
Fig. 5. Bootstrap support values (above each branch) and posterior probabilities (below each branch) for the maximum-likelihood/Bayesian inference tree.
Fig. 6. Cross-verified penalized-likelihood chronogram across monocots based on the maximum-likelihood analysis of *ndhF* sequence variation. A = age of monocot root = 134 Ma (Janssen and Bremer, 2004); B–G = ages of the six Cretaceous fossils (Givnish et al., 2004; Janssen and Bremer, 2004) used to calibrate the monocot phylogeny against time. Bromeliaceae are highlighted in green. Tan boxes indicate ±1 SD, based on bootstrap resamplings, around the estimated ages of several key nodes (red dots), including the core monocots (excluding Acorales and Alismatales), commelinid monocots, order Poales, families Bromeliaceae and Rapateaceae, and remaining Poales sister to Rapateaceae. Red branches indicate those whose topology was constrained based on the plastome tree of Givnish et al. (2010).
Cryptanthus-Acanthostachys—is nearly restricted to this region and arose 9.1 Ma, with present-day taxa diverging from each other ca. 5.5 Ma (Fig. 8).

Reconstruction of the geographic spread of bromeliads under Bayesian inference tells largely the same story. Bayesian inference is, however, somewhat more specific than maximum parsimony about the likely origins of the tillandsioids and navioids. This portion of the tree is the largest that is not fully resolved biogeographically under MP, involving the rapid-fire divergence of four major lineages between 15.4 and 15.0 Ma, and accounting today for all but 2% of all bromeliad species. Bayesian inference reconstructed this portion of the bromeliad spine as being most probably Andean in origin (Fig. 8). Together with the BI reconstruction of the distribution of the stem tillandsioids and navioids, this suggests that tillandsioids arose in the Andes with many subsequent dispersals to other regions, especially Central America, the northern littoral of South America, and the Caribbean. It also suggests that ancestral navioids were, at some point, restricted to the Guayana Shield, with later dispersal or vicariance leading to occupancy of the Brazilian Shield by *Cottendorphia* (Fig. 8). BI suggests that the Guayana Shield or the Andes characterized the stem group for all bromeliads except Brocchinioideae and Lindmanioideae. Maximum parsimony instead points to this group’s origin—as well as that of the common ancestor of Hechtioideae and its sister group—being in the Guayana Shield, Andes, or Central America. Maximum parsimony identifies these three areas, as well as the northern littoral of South America and the Caribbean, as possible ancestral areas for Tillandsioidae and *Catopsis-GLomeropitcairnia* (Fig. 8). Maximum parsimony identifies the Guayana Shield, Brazilian Shield, Andes, and Central America as possible ancestral areas for Hechtioideae and the common ancestor of Hechtioideae and the subfamilies to which it is sister. Bayesian inference is less certain than MP in reconstructing the biogeographic origins of *Pitcairnia*, assigning it to one of five areas while MP assigns it to the Andes. Bayesian inference is also less certain than MP in reconstructing the ancestral area of Bromelia and Greigia, making it equally likely that their common ancestor arose in Central America, the northern littoral of South America and the Caribbean, or the Andes. Bayesian inference reconstructs the stem region of Bromelioidae as being nearly equally likely to be the Andes or Brazilian Shield, with the taxa in the clade sister to the Brazilian Shield clade all being native to the southern Andes/Chile and the Gran Chaco, in the extreme southwest of the Rio de la Plata basin.

Finally, when outgroups are excluded, S-DIVA implies that the Guayana Shield is the ancestral area for Bromeliaceae, Brocchinioideae, and Lindmanioideae (Fig. 8). S-DIVA estimates the chance that the ancestral area for Tillandsioidae is the northern littoral of South America or Caribbean as 29%; that area fused to the Andes, 31%; and that same area fused to Central America, 40%. The chance that the ancestor of Tillandsioidae and its sister groups arose in the Guayana Shield fused to the northern American littoral and Caribbean is 31%; in the Andes alone, 33%; and in Central America alone, 36%. *Catopsis-GLomeropitcairnia* originated in Central America fused to the northern littoral of South America and Caribbean (Fig. 8). S-DIVA identifies the Andes fused to Central America as the ancestral area for Hechtioideae and its sister clade and the ancestral area of Navioidae and its sister clade as the Andes fused to the Brazilian Shield. Under this approach, Navioidae arose in the Guayana Shield fused to the Brazilian Shield, while the extant bromelioids arose in the Andes fused to the Brazilian Shield (Fig. 8). At other nodes, S-DIVA without outgroups usually reconstructs the same ancestral areas as MP and BI, except for *Pitcairnia*, which it implies arose in the Andes. Including outgroups changed the S-DIVA reconstruction little except at the base of Bromeliaceae, where a greater range of possible source regions were identified.

**DISCUSSION**

**Phylogenetic relationships**—Our analysis—based on more sequence data per taxon and wider sampling of genera than any previous study—supports the eight-subfamily classification advanced by Givnish et al. (2007) based on ndhF sequences (Fig. 2), and further clarifies the relationships among those subfamilies (Figs. 3–5). In the MP strict consensus, six subfamilies received bootstrap support ≥90%. Bromelioidae had 55% bootstrap support; Puyoideae, <50%. Support for five subfamilies increased relative to the ndhF study, but that for Lindmanioideae, Puyoideae, and Bromelioidae decreased as a result of the greater breadth of taxonomic sampling, including *Conellia*, the three Chilean *Puya* species, and several Chilean bromelioids. When we excluded the latter from our analysis, bootstrap support for both Puyoideae and Bromelioidae jumped to 100%; when we excluded *Conellia*, support for Lindmanioideae also reached 100%.

The MP, ML, and BI trees all support a stepped phylogeny for the bromeliad subfamilies: (Brocchinioideae, (Lindmanioideae, (Tillandsioidae, (Hechtioideae, (Navioidae, (Pitcairnioideae, (Puyoideae, Bromelioidae))))))). In Givnish et al. (2007), *Hechta* instead formed a hard trichotomy with Tillandsioidae and all subfamilies sister to and including Navioidae. Our results clarify the position of Hechtioideae and, thus, the relationships of all bromeliad subfamilies. Support for the position of Navioidae is less than 50% under maximum parsimony, compared with 69% under maximum likelihood and 93% under Bayesian inference (Fig. 5).

Our results concur with the general finding that tree resolution and support for most angiosperm clades increase in combined vs. separate plastid gene analyses (e.g., Solis et al., 1998, 2000; Savolainen et al., 2000; Olmstead et al., 2000, 2001; Bremer et al., 2002; Chase et al., 2006; Graham et al., 2006). Furthermore, simulations show that phylogenetic resolution and support can also improve with more taxa sampled within a given clade (Hillis, 1996; Graybeal, 1998), particularly when taxa are added strategically to break up long branches (Hendy and Penny, 1989; Leebens-Mack et al., 2005). While a number of ILS tests suggest that some plastid regions sequenced in this study show conflict in phylogenetic structures, we believe that this conflict is illusory. First, the plastid genome is inherited as a unit, so individual plastid regions should not conflict in the phylogenetic history their sequences reflect (Doyle, 1992). Second, trees based on each individual region generally do not differ from the combined-data phylogenies at nodes resolved and well supported in the individual-region trees. However, it must be realized that the limited number of informative sites in several data partitions (Table 1) result in few resolved and well-supported nodes in many individual-region trees. For example, we found that sequences for *atpB-rbcL* resolve only 40% of the nodes within Bromeliaceae; of those, 63% have bootstrap support from 50 to 90%, and only 21% (8 nodes) have bootstrap values greater than 90%. The whole point of concatenating plastid data is that individual genes and spacers each contain
Table 2. Stem and crown ages of bromeliad subfamilies and subsets thereof, based on penalized-likelihood analyses of the across-monocots ndhF tree and the eight-locus plastid phylogeny.

<table>
<thead>
<tr>
<th>Taxon</th>
<th>Stem age (Myr)</th>
<th>Crown age (Myr)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ndhF 8-locus</td>
<td>ndhF 8-locus</td>
</tr>
<tr>
<td>Brocchinioideae</td>
<td>19.1 19.1</td>
<td>14.2 13.1</td>
</tr>
<tr>
<td>Lindmanioideae</td>
<td>15.6 16.3</td>
<td>8.9</td>
</tr>
<tr>
<td>Tillandsioideae</td>
<td>14.0 15.4</td>
<td>11.8 14.2</td>
</tr>
<tr>
<td>Core tillandsioids</td>
<td>11.8 14.2</td>
<td>6.8 8.7</td>
</tr>
<tr>
<td>Hechtioideae</td>
<td>14.0 15.2</td>
<td>12.1 10.3</td>
</tr>
<tr>
<td>Navioideae</td>
<td>14.0 15.0</td>
<td>9.4 10.4</td>
</tr>
<tr>
<td><em>Navia-Brewcaria</em></td>
<td>9.3 8.3</td>
<td>8.6 7.0</td>
</tr>
<tr>
<td>Pitcairniodae</td>
<td>13.3 13.4</td>
<td>9.4 11.8</td>
</tr>
<tr>
<td>Pitcairnia</td>
<td>13.2 12.0</td>
<td>9.4 11.8</td>
</tr>
<tr>
<td>Puyoideae</td>
<td>9.8 10.1</td>
<td>8.7 10.0</td>
</tr>
<tr>
<td>Bromelioideae</td>
<td>9.8 10.1</td>
<td>9.5 8.9</td>
</tr>
<tr>
<td>Brazilian Shield clade</td>
<td>9.5 9.1</td>
<td>9.3 7.4</td>
</tr>
<tr>
<td>Tank epiphyte clade</td>
<td>7.1 5.7</td>
<td>5.7 5.5</td>
</tr>
<tr>
<td>Puyoideae + Bromelioideae</td>
<td>13.2 13.4</td>
<td>10.1 10.0</td>
</tr>
<tr>
<td>Puy + Brom + Ptc</td>
<td>13.4 15.0</td>
<td>13.2 13.4</td>
</tr>
</tbody>
</table>

We find relatively little phylogenetic signal in slowly evolving bromeliads, so several regions must be sampled to obtain a reliable phylogenetic estimate. Finally, the pairs of plastid regions showing “significant” conflict in the ILD tests in this study are those in which one or both regions have few informative sites (Table 1). Incongruence length difference tests involving such regions are inherently unstable due to sampling error in determining the universe of characters sampled; branches supported by limited data can easily be reversed in larger data sets as the signal in individual bases is overruled by that in additional bases sampled (e.g., see Darlu and Lecointre, 2002). The fact that the apparent conflict between regions occurred only among those involving one or two regions with limited numbers of informative characters in the combined analysis, combined with the fact that such conflict should be most likely when limited numbers of characters are sampled in a phylogeny with short branches argues that the “conflict” detected by ILD tests for some pairs of regions is simply a sampling artifact and should thus be ignored.

Implications for classification—Our results confirm that the traditional division of Bromeliaceae into three subfamilies—Pitcairnioideae s.l., Tillandsioideae, and Bromelioidae (Harms, 1930), defined by possession of winged seeds, plumose seeds, and fleshy fruits, respectively—must be abandoned. Pitcairnioideae sensu Harms (1930) is paraphyletic and must be split into Brocchinioideae, Lindmanioideae, Hechtioideae, Navioideae, Pitcairnioideae s.s., and Puyoideae to produce monophyletic subfamilies. Each of the new subfamilies is easily diagnosed based on morphology (Givnish et al., 2007), and the relationships among subfamilies found here are consistent with those demonstrated in other recent analyses (Terry et al., 1997; Crayn et al., 2000, 2004; Horres et al., 2000, 2007; Givnish et al., 2004, 2007; Barfuss et al., 2005; Schulte et al., 2005; Schulte and Zizka, 2008), but better resolved and more taxonomically inclusive.

Our results raise the question of *Puya’s* monophyly. *Puya* is monophyletic but weakly supported under MP, and paraphyletic under ML and BI (Figs. 3–5). Jabaily and Sytsma (2010) found support for the monophyly of *Puya* in a combined analysis of sequences for three plastid regions (*matK, rps16, trnS-trnG*) and one single-copy nuclear gene (*PhyC*) with a far more extensive sampling of the genus. *PhyC* alone supports the monophyly of *Puya*, while the plastid data do not contradict monophyly. Given these results, *Puya’s* monophyly in our MP trees, and *Puya’s* possession of a striking morphological synapomorphy—e.g., petals that spiral tightly after anthesis (Smith and Downs 1974)—we consider *Puya* and Puyoideae to be monophyletic, but recognize that further tests of relationships among Chilean *Puya*, other *Puya*, and Bromelioidae would be useful. The possibility of sinking *Puya* into Bromelioidae, as suggested by Terry et al. (1997), is not appealing, given that both Bromelioidae and Puyoideae as currently defined are characterized by obvious morphological synapomorphies, while the clade consisting of both subfamilies appears to lack such defining traits.

Our findings add to a growing case, developed by Schulte et al. (2005, 2009), Schulte and Zizka (2008), Zizka et al. (2009), and Jabaily and Sytsma (2010) that three small terrestrial genera from temperate Chile and the southern Andes (*Fascicularia, Ochagavia, Greigia*) are among the earliest-divergent members of subfamily Bromelioidae, together with two small terrestrial genera, wide-ranging *Bromelia* and monotopic *Deinacanthus* endemic to the semiarid Gran Chaco of southern Bolivia, Paraguay, and northern Argentina. These genera form a weakly supported clade in our ML, BI, and MP majority-rule trees, and a largely unresolved grade in our MP strict consensus tree (Figs. 3–5). All three analyses identify a further grade of small terrestrial genera sister to the remaining bromelioids, including *Pseudananas, Ananas*, and *Cryptanthus*; the single species of *Pseudananas* is epiphytic (but nontank forming) *Acanthostachys* is closely related to *Cryptanthus*. Taxa sister to and including *Pseudananas* form the Brazilian Shield clade (61% MP bootstrap support, 81% ML bootstrap support, 100% BI bootstrap support), which arose 9.1 Ma (see Results). In contrast to our results, Sass and Specht (2010) recovered *Ananas* and *Araeococcus* as not being monophyletic. However, this is a result solely of those authors sampling a far greater number of species in the known “trash-can” genus *Aechmea*; almost surely, their findings will result in the errant *Aechmea* species being reclassified as members of *Ananas* or *Araeococcus*.

Almost all species in the Brazilian Shield clade—represented by the 21 species in our study, sister to and including *Aechmea drakeana-A. lingulata-Ronnbergia petersii*—form a clade of tank epiphytes endemic to the Brazilian Shield, based on the possession of tanks and the epiphytic habit by almost all these species (see Smith and Downs, 1974, 1977, 1979; Schulte et al., 2009). All three analyses support this clade, with <50% support under MP, 73% under ML, and 99% under BI (Figs. 3–5). Among these taxa, only *Araeococcus pectinatus* lacks a tank; only *Aechmea bromeliifolia, A. spherocephala*, and *Billbergia...
Fig. 8. Geographic evolution of Bromeliaceae calibrated against time. Present-day distribution of individual species (or of genera, in cases where wide-ranging groups are represented by one or two placeholder taxa) indicated by colored boxes. Branch colors indicate the inferred distributions of ancestral taxa under maximum parsimony (MP); gray indicates ambiguity. Pie diagrams at nodes indicate the inferred ancestral distributions under Bayesian inference (BI), with width of wedges delimited by black lines showing likelihood of alternative inferences. Larger pie diagrams displaced northwest of nodes indicate the inferred ancestral distributions under S-DIVA, with wedges delimited by black lines showing likelihood of alternative inferences, and a blend of colors within wedges signifying vicariance involving a fusion of two regions represented by those colors. Analyses involving the possible fusion of more than two areas yield similar results except for a few backbone nodes.
decora are almost never epiphytic; and only Aechmea drakeana, A. haltoni, and Ronbergia petersonii are not native, at least in part, to the Brazilian Shield (Smith and Downs, 1974, 1977, 1979). Schulte et al. (2009) similarly found tanks ubiquitous (except in Araeococcus flagelliferolius) in a clade of 28 core bromelioids sister to Aechmea drakeana-Hohenbergia eriostachya based on sequence data from one nuclear gene (PRK) and five plastid loci. That clade has a membership consistent with our bromelioid tank-epiphyte clade, but also included species of Androlepis, Neoglaziovia, Portea, and Ursulaea—four of the 12 genera not included here. Schulte et al. (2009) found that two other genera—Orthophyllum and Fernseea, both species-poor terrestrial groups from the Brazilian Shield—are part of our Brazilian Shield clade. Fernseea is sister to all remaining elements of the Brazilian Shield clade, and Orthophyllum is sister to Cryptanthus; only one species of Fernseea from these three genera are epiphytes or tank-formers (Schulte et al., 2009).

Our study generally agrees with Barfuss et al. (2005) on relationships within Tillandsioideae. Consistent with our ML tree, Barfuss et al. (2005) found that Catopsis and Glomeropitcairnia were sister to each other and together sister to all other tillandsioids. Also largely consistent between the two studies is the split of the remaining taxa into the tribes Vrieseae (Alcantarea, Vriesea, Werauhia) and Tillandsieae (Guzmania, Racinaea, Tillandsia, Viridantha). However, in our study one species of Vriesea fell into Tillandsieae with 100% bootstrap support, and Mezobromelia pleiosticha—replacing a misidentified Guzmania variegata sequenced by Barfuss et al. (2005)—fell into Vrieseae with 95% bootstrap support (Fig. 3).

Brewcaria reflexa appears to be embedded in Navia (Figs. 3, 4). Holst (1997) moved several species from Navia into Brewcaria based on their possessing a spicate or paniculate inflorescence, rather than the capitulate inflorescences seen in other Navia. This decision is not supported in the case of Brewcaria reflexa, the only species of that genus included in this study. Our study confirms the highly polyphyletic nature of Aechmea, with six independent origins indicated by our study. Sass and Specht (2010) found an even greater degree of polyphyly and paraphyly in Aechmea based on a much more extensive sampling of species (150) within Bromelioidae.

In a way, our findings confirm the traditional view that bromelioids and tillandsioids arose from within Pitcairnioideae s.l. (Schimper, 1888; Mez, 1904; Pittendrigh, 1948; Tomlinson, 1969; Smith and Downs, 1974; Benzing et al., 1985; Smith, 1989; Benzing, 1990). Terry et al. (1997) reached a similar conclusion, but had a different view of relationships of bromelioids to tillandsioids and the seeming isolation of Brocchinia because they did not sample two of our subfamilies and undersampled two others. Terry et al. (1997) also concluded that Hechtia was closely allied to Dyckia, Encholirium, Abromeitiella, and Deuterocohnia, rather than being a convergent lineage. Horres et al. (2000) did not exclude a close tie of Hechtia to xeromorphic pitcairnioids and Puya, but their data placed Hechtia in a position consistent with that found here. Givnish et al. (2007) noted that the shared possession of four to six leaf anatomical traits by Hechtia with Puya and the xeromorphic pitcairnioids as a striking instance of concerted convergence.

The classical view that bromelioids and tillandsioids emerged from within Pitcairnioideae s.l. was based not on phylogenetic analysis, but on observing that epiphytism—a highly specialized habit, with several adaptations for life on twigs and branches—is almost absent among pitcairnioids as previously circumscribed. No early writer proposed that Brocchinia or Lindmania were sister to the rest of the family, or that Pitcairnioideae s.l. were not monophyletic. Terry et al. (1997) were the first to conclude that Brocchinia was sister to all other bromeliads and that the traditional Pitcairnioideae were paraphyletic. That view, based on an analysis including exemplars of only 28 of 58 bromeliad genera, is confirmed and greatly amplified by the present analysis.

The remarkably long period of ca. 81 My between the rise of the bromeliads and the divergence of modern lineages from each other suggests that much extinction occurred during the intervening period, and explains the morphologically isolated position of the family and the difficulty, even with extensive molecular data sets, of identifying its sister group (see Givnish et al., 2005, 2007; Chase et al., 2006; Graham et al., 2006). Restriction of Brocchinioideae and Lindmanioideae to the Guayana Shield, the occurrence of some Navioideae, the divergence of most bromelioid genera in just the last 5.5 Myr, coupled with very low rates of molecular evolution in bromeliads, explains the great difficulty investigators have had in ob-

Fig. 9. Geographic distribution of genera of Pitcairnioideae minus Pitcairnia; the latter is broadly distributed throughout the Andes and nearby regions. Note the regional overlap of three of the four genera in the "knee" of the Andes.
taining a well-resolved phylogeny for bromelioids (Terry et al., 1997; Horres et al., 2000, 2007; Crayn et al., 2004; Givnish et al., 2004, 2007; Schulte et al., 2005) and the relatively limited and homoplasic morphological variation in this group (Smith and Downs, 1979; Smith and Kress, 1989, 1990; de Faria et al., 2004; Schulte and Zizka, 2008; Sass and Specht, 2010).

**Historical biogeography**—Our analyses show that bromeliads arose in the Guayana Shield roughly 100 Ma, spread from that hyperhumid, extremely infertile center to other parts of tropical and subtropical America starting ca. 15.4 Ma, and arrived in tropical Africa ca. 9.3 Ma. Our PL chronology implies that the extant subfamilies began to diverge from each other beginning only about 19 Ma and that invasion of drier peripheral areas in Central America (*Hechtia*) and northern South America (*Tillandsioideae*) began roughly 15.2 to 15.4 Ma. Brocchinioideae, Lindmanioidae, and Navioidae except *Cottendorfia* remained entirely within the Guayana Shield. The northern Andes and Central America were independently colonized by two major lineages: the core tillandsioids (*Alcantarea, Tillandsia, Vriesea, Werauhia*) beginning about 14.2 Ma; and *Fosterella*, beginning about 11.3 Ma. In addition, *Puya* and the early-divergent bromelioids colonized throughout the Andes, extending into temperate coastal Chile, beginning ca. 10.1 Ma (Fig. 5; all calculated ages based on stem groups). Other groups—including some *Pitcairnia* and species in several bromelioid genera (e.g., *Aechmea, Aroacocceae, Neoregelia, Ronnbergia*)—also invaded the Andes independently, but we have not sampled enough taxa to estimate the timing and/or numbers of such events reliably. At least five additional colonizations, however, appear to be involved.

Uplift of the northern Andes beginning in the mid-Miocene, causing a shift in the course of the Amazon from a northerly route via the paleo-Orinoco toward Lake Maracaibo to an easterly course toward its present mouth (Hoorn, 1994; Hoorn et al., 1995, 2010; Potter, 1997), appears to correspond roughly to the uplift of the northern Andes and filling of the vast Pebas wetlands of western Amazonia, as well as erosion finally cutting through the Purus Arch in central Amazonia (Figueredo et al., 2009). Divergence of monotypic *Cottendorfia* from remaining Navioidae of the Guayana Shield about 10.4 Ma suggests that *Cottendorfia* may have arrived in the Brazilian Shield via long-distance dispersal. However, the timing of the deposition of Amazonian sediments separating the Guayana and Brazilian Shields on the Amazonian Platform is close enough in time, and the proximity of both shields close enough in space then that we should not exclude vicariance–short-distance dispersal as an alternative explanation. Three other groups also appear to have colonized the Brazilian Shield: *Dyckia-Encholirium* from the central Andes 8.5 Ma (Fig. 7); the Brazilian Shield bromelioids, most likely from the southern Andes ca. 9.1 Ma (see below); and certain species of *Bromelia*, probably from the Amazon basin, also ca. 9.1 Ma (Fig. 8). Individual species of several wide-ranging genera (e.g., *Guzmania, Tillandsia, Vriesea*) almost surely colonized the Brazilian Shield from other areas as well.

Our reconstruction suggests that Pitcairnioideae dispersed counterclockwise through time, first from the Guayana Shield to the (northern) Andes and its lowland slopes for *Pitcairnia*, then to the central Andes for the split between lineages giving rise to *Fosterella* and to the remaining genera, with a split between the puna cushion-plants of *Deuterocohnia* and arid-zone *Dyckia* in south-central Bolivia roughly 9.1 Ma, and subsequent dispersal of *Dyckia* to the Brazilian Shield and its divergence from *Encholirium* in the Horn of Brazil about 2.4 Ma (Figs. 7 and 8; see also Givnish et al., 2004, 2007).

The cradle of *Puya* appears to be Andean, but our analysis samples too few species within the genus to locate its geographic origin (see Jabaily and Sytsma, 2010). Jabaily (2009) used AFLP data to argue that *Puya* spread northward from the southern and central Andes soon after the split from the Chillean taxa. Based on our calculations, that split occurred around 10 Ma, soon after the uplift of the northern Andes began to accelerate. Divergence between Puyoideae and Bromelioideae seems likely to have occurred in and around the southern Andes, given the basal split in *Puya* between Chillean and Andean taxa, the apparent origin of *Puya* generally from the southern Andes, and the presence in the southern Andes and nearby Pacific lowlands of several members of basal grade or clade of bromelioids, including *Fascicularia, Greigia*, and *Ochagavia* (see Results and Schulte et al., 2005). Subsequent diversification of Bromelioideae entailed dispersal of *Bromelia* and *Ananas* throughout much of lowland South and Central America, with colonization of the Brazilian Shield independently by *Bromelia* and by the
ancestor(s) of *Fernseea* (see Schulte et al., 2005) and the large number of genera sister to it (Fig. 8). This last lineage—the Brazilian Shield clade—apparently arose 9.1 Ma (Fig. 8).

We propose that the origin of the bromelioid epiphytic clade in and around the Serra do Mar roughly 5.5 Ma corresponds to three key events, involving (1) uplift of the Serra do Mar mainly during Pliocene-Pleistocene times (Almeida, 1976; Amorim and Pires, 1996), (2) uplift of the central Andean Altiplano toward the end of the Miocene (Garzione et al., 2008), and (3) origin of a cooler, rainier climate in the Serra do Mar/Atlantic rain-forest region predicted to result from the impact of central Andean uplift on wind circulation, with increased advection of moisture from the Atlantic as winds from the Pacific were blocked (Ehlers and Poulsen, 2009). The climate models of Ehlers and Poulsen (2009) assume all other factors remained constant as the height of the Andes varied, so the actual uplift of the Serra do Mar mainly from the Pliocene to the present most likely would have caused the observed onset there of cooler, rainier, more humid conditions congenial to epiphytes starting around 5.6 Ma (Vasconcelos et al., 1992; Grazziotin et al., 2006), corresponding nearly exactly with the calculated time of origin of the bromelioid epiphytic clade. Today the Atlantic forest region, including highly diverse but largely destroyed Atlantic rain forests and cloud forests, sandy coastal restingsas, mangroves, campos de altitude, and granitic outcrops of the Serra do Mar and Serra da Mantiqueira and adjacent coastal plains, are the wettest part of eastern South America, and the montane habitats are the coolest (Safford, 1999). The Serra do Mar and Serra da Mantiqueira represent the elevated southeastern rim of the tilted Brazilian Shield, and these “seas of hills” (“mares do morros”) between roughly 22° and 29°S intercept heavy rainfall and fog from moisture carried by winds off the tropical south Atlantic, as well as occasional cold fronts spawned in Antarctica. Strong climatic fluctuations occurred in this montane region during the Pleistocene (e.g., Behling and Negrelli, 2001), much as they did in the northern Andes (van der Hammen, 1995).

Most bromelioids that arrived in the Brazilian Shield earlier than the origin of the epiphytic clade, during a drier phase and presumably by gradual, short-distance dispersal from the southern Andean region via a corridor of semiarid habitats, are highly xeromorphic terrestrial taxa (*Bromelia, Pseudananas, Ananas, Cryptanthus, Orthophytum*). *Fernseea*, sister to all other members of the Brazilian Shield clade (Schulte et al., 2009), is restricted to cool, moist, rocky microsites on the lofty Itataia Massif (2800 m a.s.l.) in the Serra da Mantiqueira (Medina et al., 2006), a mountain chain inland of the Serra do Mar in the Atlantic forest region and uplifted somewhat earlier (Amorim and Pires, 1996; Modenesi-Gauttieri and Motta de Toledo, 1996). *Fernseea* may thus have arrived directly from cool, moist habitats in the southern Andes via long-distance seed dispersal. Climatic oscillations throughout the Pleistocene included rainier phases during which the isolation of Amazonian and Atlantic rain forests from each other by semiarid vegetation may have been greatly reduced (Auler and Smart, 2001; Wang et al., 2004), which would have promoted the later dispersal of bromelioids from the Serra do Mar to other areas, and dispersal of other bromeliads (e.g., *Guzmania, Tillandsia, Vriesea*) into the Serra do Mar.

Dispersal of ancestral bromelioids from the southern Andes to the mountains of southeastern Brazil is consistent with the proposal of Schulte et al. (2005), although we envision at least two colonizations, involving a long-distance, mesic “high road” for *Fernseea* (as argued by Schulte et al., 2005) and a gradual, semiarid “low road” for the remaining taxa, with subsequent evolution of mesomorphic epiphytic taxa in the Atlantic forest region. The defining disjunction of Bromelioidae between the southern Andes and the Atlantic forest region is similar to that seen in several other plant groups, including *Araucaria, Cordyline, Drimys, Fuchsia* sect. *Quelusia*, and *Griselinia* (Zimmer, 1987; Berry, 1989; Katina et al., 1999; Berry et al., 2004). Most of these cases, however, probably involved a mesic “high road” to the Brazilian Shield, either via long-distance dispersal or (more likely in these ancient groups) as relics of more widespread mesic temperate forests in the southern hemisphere during the Tertiary. In more recently dispersed groups, gradual spread of mesic-adapted taxa from the Andes to the Brazilian Highlands during glacial cycles of the last few million years is another possibility (Safford, 1999). Although glacial/interglacial cycles had much less amplitude prior to ca. 2.8 Ma (Lisiecki and Raymo, 2005), Antarctic ice sheets are known to have advanced and retreated until at least ca. 4.9 Ma (Naish et al., 2009), so dispersal of bromelioids from the southern Andes to southeastern Brazil during a glacial period cannot be excluded.

The initial diversifications of the tillandsioid and epiphytic tank bromelioid radiations roughly 14.0–8.7 Ma and 5.5 Ma, respectively, associated with independent origins of the tank habit (Givnish et al., 2007), corresponds well with the independently derived dates of origin of diving-beetle lineages endemic to bromeliad tanks ca. 12 Ma in northern South America and ca. 4 Ma in the Serra do Mar region (Balke et al., 2008 and inferences regarding ancestral distributions). In addition, the estimated origin of *Bothrops* (fer-de-lance) species endemic to Atlantic rain forests ca. 3.8 Ma (Grazziotin et al., 2006) agrees fairly well with our estimate of the origin there of the epiphytic tank bromelioids in wet forests ca. 5.5 Ma.

*Pitcairnia feliciana* apparently arrived in tropical West Africa via recent long-distance dispersal from South America no earlier than about 9.3 Ma. This accords with *Maschalocephalus dinklagei* of Rapateaceae also being a product of recent long-distance dispersal, not ancient vicariance via continental drift (Givnish et al., 2000, 2004). Recent colonization might partly explain the lack of African speciation in both groups, but that seems quite unlikely; the bromelioid epiphytic clade spawned nearly 600 species in less than half the time that we estimate *Pitcairnia* and *Maschaloccephalus* have been in Africa. Historical cycles of aridity (Goldblatt, 1993; Querouil et al., 2003) probably played a more important role, given that neither Rapateaceae nor *Pitcairnia* are especially drought-tolerant (Givnish et al., 2004, 2007) and that neither clade contains species with fully developed CAM photosynthesis (Crayn et al., 2001, 2004).

The African endemics of these families occupy nearly adjacent ranges: *Maschaloccephalus* in savannas and forests on wet sand from Sierra Leone to Côte d’Ivoire; *Pitcairnia feliciana* on sandstone outcrops of the Fouta Djalon massif in Guinea a few hundred kilometers to the northwest (Porembski and Barthlott, 1999; Givnish et al., 2000, 2004). The Guinean Mountains maintained a wet climate during the Pleistocene, serving as a refuge for wet-climate taxa (Jahn et al., 1998; Dupont et al., 2000). Both Rapateaceae and Bromeliaceae are also likely to have been favored by infertile soils, given their origin and continued abundance in the Guayana Shield. Therefore, early vicariance of habitat—through rafting of sandstone deposits to either side of the Atlantic—followed, much later, by long-
distance dispersal appears to have caused the disjunct distributions of rapateads and bromeliads (Givnish et al., 2004). There are roughly 10 other angiosperm families with pantropical distributions (Thorner, 1972, 1973); the use of fossil-calibrated molecular clocks shows that recent, long-distance dispersal probably accounts for this pattern in Melaustomaceae (Renner and Meyer, 2001) and Vochysiaceae (Sytsma et al., 2004) as well, with trans-Atlantic dispersal having occurred in these families well before it did in bromeliads or rapateads.

It might be argued that, even with a sample of 90 bromeliad stratified across all subfamilies and most genera, that it would be premature to reconstruct biogeographic (or, in other contexts, morphological or ecological) ancestral character states, given that less than 3% of all extant bromeliad species are included in our analysis. We disagree. First, the full range of geographic distributions have been considered for all genera included, and less than 3% of bromeliad species have been excluded in that process. More importantly, a detailed study of biogeographic and morphological variation with Bromelioidae, based on a substantially denser sampling of taxa (150 species, ca. 17.5% of all bromelioids), showed that both groups of characters were phylogenetically highly conserved (Sass and Specht, 2010). Such conservatism supports the placeholder approach used here.

What morphological and physiological traits adapted bromeliads for life outside the Guayana Shield? How frequently did they arise? Were they acquired sequentially or nearly simultaneously? To what extent is variation among the eight bromeliad subfamilies in species number and diversification rate correlated with these traits and the environments invaded by those subfamilies? What factors make the Tillandsioideae and Bromelioidae, with 40 and 27% of all bromeliad species, respectively, especially diverse? Each of these questions will be addressed in a companion paper, building on the phylogenetic, chronological, and biogeographic reconstructions presented here and new reconstructions of the ancestral states of various morphological, physiological, and ecological characters.

LITERATURE CITED


Felsenstein, J. 1993. PHYLIP (Phylogeny Inference Package) version 3.5c [computer program]. Distributed by the author, Department of Genetics, University of Washington, Seattle, Washington, USA.


QUEROUIL, S., E. VERHEY, M. DILLON, AND M. COLYN. 2003. Patterns of diversification in two African forest shrews: Sylvisorex johnstoni and...


Wendt, T., T. S. Coser, G. Mattalana, and F. A. G. Guilherme. 2008. An apparent lack of prezygotic reproductive isolation among...
APPENDIX I. Species, vouchers, and GenBank accessions for taxa included in this study. Taxa are grouped by subfamily within Bromeliaceae and by family outside Bromeliaceae. Sequences newly generated for this study begin with HQ or JF. Taxa for which sequences were concatenated in the combined analyses are listed sequentially with an asterisk (*). Sequences for different loci obtained from different accessions of the same species are listed after the corresponding vouchers.

Missing sequences are indicated by ∼.

**Taxon**: Voucher specimen, Herbarium; GenBank accessions: matK; ndhF; rps16; atpB-rbcL; psbA-trnH; rpl32-trnL; trnL intron/trnl-trnf intergenic spacer