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Radiation following long-distance dispersal: the contributions of time, opportunity and diaspore morphology in *Sicyos* (Cucurbitaceae)

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ABSTRACT

Aim To infer the most plausible explanations for the presence of 14 species of the Neotropical cucurbit genus *Sicyos* on the Hawaiian Islands, two on the Galápagos Islands, two in Australia, and one in New Zealand.

Location Neotropics, the Hawaiian and Galápagos archipelagos, Australia and New Zealand.

Methods We tested long-problematic generic boundaries in the tribe Sicyoeae and reconstructed the history of *Sicyos* using plastid and nuclear DNA sequences from 87 species (many with multiple accessions) representing the group's generic and geographic diversity. Maximum likelihood and Bayesian approaches were used to infer relationships, divergence times, biogeographic history and ancestral traits.

Results Thirteen smaller genera, including *Sechium*, are embedded in *Sicyos*, which when re-circumscribed as a monophyletic group comprises 75 species. The 14 Hawaiian species of *Sicyos* descended from a single ancestor that arrived *c*. 3 million years ago (Ma), Galápagos was reached twice at *c*. 4.5 and 1 Ma, the species in Australia descended from a Neotropical ancestor (*c*. 2 Ma), and New Zealand was reached from Australia. Time since arrival thus does not correlate with *Sicyos* species numbers on the two archipelagos.

Main conclusions A plausible mechanism for the four trans-Pacific dispersal events is adherence to birds of the tiny hard fruit with retrorsely barbed spines found in those lineages that underwent long-distance migrations. The Hawaiian clade has lost these spines, resulting in a lower dispersal ability compared with the Galápagos and Australian lineages, and perhaps favouring allopatric speciation.

Keywords

Australia, bird dispersal, diversification, Galápagos, Hawaiian radiation, Miocene, New Zealand, trans-Pacific dispersal.

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The geographic origin and speed of diversification of flowering plant clades occurring on the archipelagos of the Pacific Ocean have attracted much recent attention (e.g. Wright *et al.*, 2000; Cronk *et al.*, 2005; Harbaugh & Baldwin, 2007; Clark *et al.*, 2008; Harbaugh *et al.*, 2009; Keppel *et al.*, 2009). Especially striking are radiations on the Hawaiian Islands, including the

Lobelioideae with 126 species, *Cyrtandra* (Gesneriaceae) with 59, *Melicope/Platydesma* (Rutaceae) with 52, and eight more genus-level clades each with \geq 19 species (Baldwin & Wagner, 2010). Most Hawaiian lineages are younger than five million years (Myr) old (Lindqvist & Albert, 2002; Price & Clague, 2002; Clark *et al.*, 2009; Havran *et al.*, 2009; Willyard *et al.*, 2011), and, compared with other angiosperm rates so far reported, some of them have diversified at a higher rate

http://wileyonlinelibrary.com/journal/jbi doi:10.1111/j.1365-2699.2012.02695.x (Baldwin & Sanderson, 1998). The Galápagos Islands by contrast have produced few plant radiations, the largest among them the daisy genus *Scalesia* with 15 species going back to a common ancestor living 1.9–6.2 million years ago (Ma) (Schilling *et al.*, 1994) and *Varronia* with four species going back 1.12–4.5 Myr (Weeks *et al.*, 2010). The difference in the number and size of plant radiations on the two archipelagos could reflect the time available for diversification, ecological opportunity, and the propensity of particular clades to form isolated populations prone to interruption of gene flow. Other possible explanations include different extinction effects (e.g. resulting from different palaeoclimatic histories) or taxonomic bias (different species concepts applied on different archipelagos; Carine & Schaefer, 2010; Schaefer *et al.*, 2011).

Clades occurring on both the Hawaiian and Galápagos archipelagos should in principle allow the contribution of time and ecological opportunity to be disentangled from cladespecific propensities to form new species. The latter may correlate with dispersal ability, mating system, ease of hybridization, and speed of karyotype rearrangements (see also Price & Wagner, 2004). The indigenous floras of the Hawaiian and Galápagos archipelagos share only 24 genera, with 13 having endemic species on both archipelagos (Table 1). Among them

Table 1 Shared native angiosperm genera of the Hawaiian and Galápagos Islands. Genera in bold have endemic species on both archipelagos (data from Wiggins & Porter, 1971; Wagner *et al.*, 1990; Carr, 2006; Bungartz *et al.*, 2009).

	Family	Hawaii		Galápagos	
Genus		Endemic	Native	Endemic	Native
Abutilon	Malvaceae	3	1	1	0
Acacia	Mimosaceae	2	0	0	3
Amaranthus	Amaranthaceae	1	0	4	1
Cordia/Varronia	Boraginaceae	0	1	4	2
Cuscuta	Cuscutaceae	1	0	2	0
Dodonaea	Sapindaceae	0	1	1	0
Chamaesyce	Euphorbiaceae	15	0	8	0
Gossypium	Malvaceae	1	0	2	0
Heliotropium	Boraginaceae	0	2	1	3
Іротаеа	Convolvulaceae	1	4	2–3	3
Lobelia	Campanulaceae	13	0	0	1
Lycium	Solanaceae	0	1	1	0
Peperomia	Piperaceae	23	2	4	2
Phyllanthus	Euphorbiaceae	1	0	0	1
Phytolacca	Phytolaccaceae	1	0	0	1
Pilea	Urticaceae	0	1	1	1
Pisonia	Nyctaginaceae	2	3	1	0
Plantago	Plantaginaceae	3	0	1	0
Plumbago	Plumbaginaceae	0	1	0	2
Portulaca	Portulacaceae	3	1	1	0
Psychotria	Rubiaceae	11	0	2	0
Sesuvium	Aizoaceae	0	1	1	1
Sicyos	Cucurbitaceae	14	0	2	0
Solanum	Solanaceae	3	1	1	1
Waltheria	Sterculiaceae	0	1	0	1

is Sicvos, the focal clade of this study. Sicvos is a genus in the Cucurbitaceae that has 14 endemic species on the Hawaiian Islands (Wagner & Shannon, 1999), two species on the Galápagos Islands (Sebastian et al., 2010a), two in Australia, one in New Zealand, and between 41 and 56 species in the Americas, depending on the taxonomic concept applied: several small genera have been included in Sicvos or segregated from it based mostly on fruit characters. Species of Sicyos are climbing or trailing annual or perennial vines that often occur in disturbed habitats. All Sicyos species are monoecious, with male and female flowers on each individual; the flowers are diurnal and depend on wasps and short-tongued bees for pollination (LaBerge & Hurd, 1965; Fig. 1a) because automatic selfing is precluded by their unisexuality. Fruit and seed morphology in the Sicvos alliance is exceptionally variable, and traits such as fleshy or hard fruits, with smooth surfaces or surfaces bearing barbed or hooked spines (Fig. 1e-i), are likely to influence dispersal.

The *Sicyos* clade, including the segregate genera, is especially diverse in Mexico, where several new species have been discovered in the recent past (Lira, 1994; Lira & Rodríguez-Arévalo, 1999; Rodríguez-Arévalo & Lira, 2001; Rodríguez-Arévalo, 2003; Rodríguez-Arévalo *et al.*, 2004, 2005). *Sicyos* is the name-giving taxon of the Sicyoeae, a tribe with 265 species in perhaps a dozen genera (Schaefer & Renner, 2011a,b). Family-wide molecular phylogenies relying on plastid and recently also nuclear data suggest that Sicyoeae are monophyletic (Kocyan *et al.*, 2007; Schaefer *et al.*, 2009; Schaefer & Renner, 2011b). However, none sampled more than a few species of *Sicyos*.

Here we use *Sicyos* to study whether time since arrival, ecological opportunity, or different fruit morphologies more plausibly explain the different species numbers produced in regions reached by long-distance dispersal, namely Hawaii (14 species), Galápagos (2), Australia (2) and New Zealand (1). A single medium-sized clade having produced species in all these areas provides a rare opportunity to disentangle the relative effects of age, traits and ecological opportunity on diversification.

MATERIALS AND METHODS

Taxon sampling, DNA sequencing, alignment and phylogenetic analysis

We used 112 accessions representing 87 species of Sicyoeae, including the type species of all relevant generic names so as to be able to decide the taxonomic fate of the previously segregated genera *Anomalosicyos* Gentry (7 species, Central to South America), *Cladocarpa* (H. St John) H. St John (20 species, Hawaii), *Costarica* L.D. Gómez (1 species, Costa Rica), *Microsechium* Naudin (2–4 species, Mexico and Guatemala), *Parasicyos* Dieterle (2 species, Guatemala), *Pterosicyos* Brandegee (1 species, Mexico and Guatemala), *Sarx* H. St John (2 species, Hawaii), *Sechiopsis* Naudin (5 species, Mexico and Guatemala), *Sechium* P. Browne (5 species, Mexico),



Figure 1 Habitats, flowers, and armed or unarmed fruits of *Sicyos* species from Hawaii, Australia and the continental mainland: (a) *S. angulatus* visited by *Vespula germanica* (USA), (b) *S. pachycarpus* (Hawaii), (c) *S. maximowiczii* growing in a colony of great frigatebird (*Fregata minor*), (d) *S. undara* (Australia), (e) *S. pachycarpus* (Hawaii), (f) *S. weberbaueri* (Peru), (g) *S. australis* (Australia), (h) *S. acarieanthus* (Peru), (i) *Microsechium ruderale* (Guatemala). Scale bar = 1 cm. Photographs by: Forest & Kim Starr (a, e), T. Rau (b; Carr, 2006), H. Schaefer (b), P. Sebastian (d), M. Weigend (f, h), A. Lyne (g; APII) and M. Nee (i).

Sicvocarva (A. Grav) H. St John (25 species, Hawaii), Sicyocaulis Wiggins (1 species, Galápagos Islands), Sicyosperma A. Gray (1 species, Mexico and Arizona) and Skottsbergiliana H. St John (2 species, Hawaii). No previous taxonomic fusions or segregations were based on molecular data. We were able to sample all species known from the Galápagos Islands, Australia and New Zealand, and 13 of the 14 known from the Hawaiian Islands. The missing Hawaiian species, Sicyos semitonsus, is close to S. herbstii, S. hispidus and S. maximowiczii, judging from the shared hairy fruit protuberances, but may actually be a hybrid (Telford, 1990; Starr & Martz, 1999). The type specimen of Costarica hamata was unavailable for sequencing, and instead we used material collected at the type locality on the slopes of the Irazú Volcano in Costa Rica. Appendix S1 in the Supporting Information lists all included species with their authors, geographic origin of the sequenced sample, voucher deposition and GenBank accession numbers. A total of 420 chloroplast and 98 nuclear sequences were newly generated for this study and have been submitted to GenBank (accession numbers JN560179-JN560696).

Genomic DNA was isolated from herbarium specimens or from silica-dried leaves, using the NucleoSpin plant kit (Machery-Nagel, Düren, Germany). Polymerase chain reaction (PCR) protocols and primers were the same as in Sebastian *et al.* (2010b). The plastid DNA regions sequenced were the

Journal of Biogeography **39**, 1427–1438 © 2012 Blackwell Publishing Ltd trnL intron, the adjacent trnL-trnF intergenic spacer, the rpl20-rps12 intergenic spacer, the trnS-trnG intergenic spacer, the psbA-trnH intergenic spacer and the rbcL gene; the nuclear region sequenced was the complete internal transcribed spacer (ITS) region of the ribosomal DNA. For amplification of the psbA-trnH intergenic spacer, we used the primers listed in Volz & Renner (2009). The PCR products were purified with the PCR Wizard clean-up kit (Promega GmbH, Mannheim, Germany) or ExoSap (Fermentas, St Leon-Rot, Germany). Cycle sequencing was performed with the BigDye Terminator cycle sequencing kit on an ABI Prism 3100 Avant automated sequencer (Applied Biosystems, Foster City, CA). Sequencing primers were the same as those used for DNA amplification. The ITS region yielded single bands and unambiguous base calls, and we therefore refrained from cloning. Sequence assembly of forward and reverse strands was carried out with SEQUENCHER 4.7 (Gene Codes, Ann Arbor, MI), and sequences were aligned by eye using MACCLADE 4.08 (Maddison & Maddison, 2003).

The aligned plastid DNA matrix comprised 4527 nucleotides, and the aligned ITS matrix 872 nucleotides. In eight cases, we combined plastid and nuclear sequences from different samples (Appendix S1). Maximum likelihood (ML) analyses and ML bootstrap searches (using 500 replicates) were carried out using RAxML 7.2.8 (Stamatakis, 2006). RAxML searches relied on the GTR + Γ model, with model parameters estimated over the duration of specified runs. Analyses of the separate plastid and nuclear datasets (gene trees not shown) with one exception yielded congruent tree topologies, with differences restricted to tip nodes with low statistical support (bootstrap < 75%); the sole difference concerned *Microsechium gonzalo-palomae* (see Results).

Molecular clock analyses and diversification rates

To obtain age ranges for the nodes of biogeographic interest we used Bayesian time estimation and a relaxed clock uncorrelated-rates model as implemented in BEAST 1.6.1 (Drummond & Rambaut, 2007). Species with nearly identical sequences were excluded from the dating analysis to reduce stochastic error and rate heterogeneity, yielding an alignment of 81 species, including the early-diverging Sicyoeae Luffa aegyptiaca, Nothoalsomitra suberosa and Trichosanthes ovigera for rooting purposes (Schaefer & Renner, 2011b). The pollen Hexacolpites echinatus from the Oligocene (33.9 to 23 Ma) of Cameroon (Salard-Cheboldaeff, 1978) is the oldest known hexacolpate echinate Sicyoeae-type pollen and was used as a calibration point. The most conservative assignment of this pollen is to the split between Linnaeosicyos with 4-colporate reticulate pollen (Schaefer et al., 2008a) and the remaining New World Sicyoeae with 4-16 colpate/colporate and mostly echinate pollen. To cover the uncertainty in the pollen age, we applied a normally distributed prior probability distribution of 28.5 Ma \pm 6 Myr to this node, as there is little justification for weighting the probability towards the minimum bound of the stratum in which the pollen was found (Ho & Phillips, 2009). The root of the Sicyoeae was constrained to 37 Ma \pm 3 Myr (again with a normal prior distribution) based on the age found for this node in the family-wide analysis by Schaefer et al. (2009). All BEAST runs used a Yule tree prior and the GTR + Γ model with six rate categories; Monte Carlo Markov chains (MCMC) were run for 20 million generations, sampling every 1000th generation. Mixing of the chains and convergence were checked using TRACER 1.5 (Rambaut & Drummond, 2007); of the 20,001 posterior trees, the first 5000 were discarded as burn-in based on inspection of the TRACER files. Final trees were edited in FIGTREE 1.3.1 (Rambaut, 2006).

We modelled diversification as a time-homogeneous birth/ death process, with a net diversification rate λ and a relative extinction rate $\kappa = 0$ or $\kappa = 0.9$ (Magallón & Sanderson, 2001). Rates were calculated using the rate.estimate algorithm implemented in the R package GEIGER 1.3.1 (Harmon *et al.*, 2008).

Ancestral area reconstruction

To infer the biogeographic history of Sicyoeae we used Bayesian MCMC searches in BEAST and the continuous-time Markov chain (CTMC) biogeographic reconstruction approach proposed by Lemey *et al.* (2009). The advantage of this approach is that it incorporates branch length information as well as uncertainty in the tree topology. Priors for migration rates used a Γ distribution for the relative rate parameter (shape parameter = 1.0) and an exponential distribution (mean = 1.0) for the geosite model parameter as recommended by Lemey *et al.* (2009). The CTMC phylogeographic model assumes that ancestral ranges are limited to single regions, making it particularly relevant for clades in which dispersal plays a larger role than vicariance, as is the case for oceanic island archipelagos. The geographic regions coded were: (1) North American plate, (2) Caribbean plate, (3) South American plate, (4) Hawaii, (5) Galápagos, and (6) Australia/ New Zealand.

Evolution of habitat occupation and fruit armature

To assess whether habitat diversity in a region is correlated with diversification we categorized habitats into (1) shrublands and coastal vegetation, (2) tropical deciduous forest, (3) tropical evergreen forest, (4) tropical wet montane or cloud forest, (5) *Pinus–Quercus* forest, and (6) dry montane forest, and then coded each species for its preferred habitat(s). Data on habitat preferences came from specimen labels and taxonomic and floristic treatments (Macbride, 1960; Wiggins & Porter, 1971; Wagner *et al.*, 1990; Jeffrey & Trujillo, 1992). Preferences were plotted on a ML phylogeny for the same 81 taxa as used for the molecular clock dating.

To infer ancestral states of fruit armature in *Sicyos*, we used ML as implemented in MESQUITE 2.74 (Maddison & Maddison, 2009), employing the Markov k-state one-parameter model (Lewis, 2001). The coded character states were: (1) armed, (2) unarmed, (3) winged, and (4) variable withinspecies (this was relevant for *Sicyos edulis*; Lira *et al.*, 1999). Transition parameters were estimated on the 81-taxon ML phylogeny.

RESULTS

Phylogenetic relationships of the Sicyoeae

The ML phylogeny for the Sicyoeae (Fig. 2) shows that almost all species of Anomalosicyos, Cladocarpa, Costarica, Microsechium (only the type species, M. ruderale), Parasicyos, Pterosicyos, Sarx, Sechiopsis, Sechium, Sicyocarya, Sicyocaulis, Skottsbergiliana and Sicyosperma are embedded among species of Sicyos, a clade that itself has 100% bootstrap support. In addition, all the segregate genera that had more than one species (Anomalosicyos, Microsechium, Parasicyos, Sechiopsis, Sechium) turn out to be polyphyletic, and Frantzia, which traditionally was seen as close to Sechium, instead constitutes a genetically distant lineage (Fig. 2). From now on, we focus on the monophyletic genus Sicyos as circumscribed in Fig. 2, that is, including all the former segregates. The Hawaiian species of Sicyos form a robustly supported monophyletic group, and this is also supported by a 6-bp deletion in their trnL intron. The single New Zealand species groups with the two Australian species. By contrast, the two species on the Galápagos



Figure 2 Maximum likelihood phylogram for 86 species of Sicyoeae (excluding *Microsechium gonzalo-palomae*; see Results) based on 5399 aligned nucleotides of plastid and nuclear sequences analysed under a GTR + Γ model. The tree is rooted on *Nothoalsomitra*. Values at nodes give likelihood bootstrap support \geq 75% based on 500 replicates. Boxes around clades and arrows in the inset mark the four long-distance dispersals to: Hawaii (blue), Galápagos (yellow) and Australia/New Zealand (pink). Stars indicate type species of currently or formerly accepted genera. Inset: Geographic origins of the sequenced plant material. Circles, *Sicyos*; stars, other Sicyoeae.

archipelago result from independent dispersals to the islands (Fig. 2).

The Mexican species *Microsechium gonzalo-palomae* is the only species placed differently in the plastid and nuclear (ITS) gene trees: based on its plastid sequences it clusters with the *Frantzia* clade, but based on its nuclear sequences it belongs in *Sicyos*. Two ITS sequences from duplicates of one of the two

existing herbarium collections of this species showed 10 nucleotide differences but nevertheless clustered together, suggesting multiple coexisting ITS copies, such as would be expected following hybridization. We excluded this species from our further combined analyses, as investigating the nature of this species or hybrid population will require fieldwork to collect more material.

Divergence times, direction of dispersal and diversification rates

Sicyos originated in North America (probably Mexico, see inset in Fig. 2) during the early Miocene, 23.6–15.1 Ma (Fig. 3). The common ancestor of the Hawaiian radiation is inferred to have diverged from a North American (Mexican) lineage 5.5-1.9 Ma and to have given rise to the extant Hawaiian species around 3 (4.1-1.3) Ma (Fig. 3). The Galápagos species Sicvos villosus is part of a clade occurring in Ecuador, Peru, Chile, Bolivia, Argentina and southern Brazil from which it diverged about 4.5 (6.4-2.8) Ma. The other Galápagos species, Sicvocaulis pentagonus, is nested in a separate clade among species from Ecuador, Peru and Brazil from which it diverged 1 (1.5-0.08) Ma, so the ancestral areas of both Galápagos species were probably in South America, possibly in adjacent mainland Ecuador (Fig. 3). The Australia/New Zealand clade is sister to species from the south-western United States, Mexico and Bolivia, and diverged from a North American ancestor 5.6-1.7 Ma. The Australian Sicyos undara is about 1 (3.6-0.5) Myr old, and its close relatives, S. australis and S. mawhai, the latter endemic to New Zealand, are about 0.7 (1.6-0.1) Myr old. The two new species, S. mawhai and S. undara, differ from S. australis in fruit morphology, number of flowers per inflorescence, and flower size and peduncle length (Telford et al., 2012).

The net diversification rate (λ) of the *Sicyos* crown group in the Hawaiian Islands is $\lambda = 0.47-1.45$ species Myr⁻¹, assuming no extinction ($\kappa = 0$), or $\lambda = 0.18-0.58$ species Myr⁻¹ if extinction rates are high ($\kappa = 0.9$; Table 2, which also summarizes the characteristics of the four trans-Pacific disjunctions). In the Australian/New Zealand clade, the diversification rate is $\lambda = 0.11-0.81$ species Myr⁻¹ ($\kappa = 0$) or $\lambda = 0.03-0.24$ species Myr⁻¹ ($\kappa = 0.9$). Of course, it is zero for the two singlespecies Galápagos lineages.

Habitat diversity and fruit morphology

Habitat preferences in Sicyos are variable even within very young clades and notably so in the Hawaiian clade (Fig. 1 and Appendix S2). We did not code disturbed versus undisturbed habitats; however, Sicyos species often grow in disturbed sites. Some of the widespread species, such as Sicyos angulatus and S. polyacanthus, occur in a wide range of habitats in their native ranges and are locally invasive in the Old World. The Hawaiian species are found in coastal areas, in arid or moist shrublands, or in openings in rain forest up to 2000 m elevation. Sicyocaulis pentagonus on the Galápagos is known only from a few collections in moist forests of the Scalesia zone between 130-200 and 400-550 m. The other Galápagos endemic, Sicvos villosus, is known from a single collection made by Charles Darwin on Floreana, which lacks habitat details. Habitats on Floreana, which has a maximum elevation of 640 m a.s.l., could have been coastal vegetation, arid shrublands, and/or moist Scalesia forest.

Of the two Australian species, *Sicyos australis* is widespread from northern Queensland to Tasmania, where it occurs in deciduous vine thickets, eucalypt forest, and in montane and near-coastal habitats; it has also been collected on New Zealand's North Island, Lord Howe (now extinct) and Norfolk Islands. The second Australian species, *S. undara*, is known only from the Undara Volcanic National Park in Queensland, where it grows in clay loam in boulder gullies of collapsed lava tubes in tropical deciduous forest. The New Zealand endemic, *S. mawhai*, is restricted to islands adjacent to the North Island and the Kermadec Islands, where it occurs in scrubs or forest margins of near-coastal sites.

Ancestral state reconstruction suggests that fruits armed with spines or hooks and winged fruits evolved several times (Appendix S3). Both Galápagos species as well as the Australian and New Zealand species have spiny fruits and are derived from relatives with such fruits (Fig. 1g and Appendix S3). By contrast, the Hawaiian clade lost the spines and instead has smooth fruits (Fig. 1e) or fruits with stubby, hairy protuberances (*Sicyos maximowiczii, S. hispidus, S. herbstii* and *S. semitonsus*).

DISCUSSION

Here we use a medium-sized clade (the genus Sicyos, which comprises 75 species in its new monophyletic circumscription) in order to study whether ecological opportunity or time available for diversification more plausibly explain the strikingly different species numbers in four regions reached by long-distance dispersal. Our dense species sampling allowed identification of the geographic origins of the disjunct species on Hawaii, the Galápagos, Australia and New Zealand. The distances from North America to Hawaii (3800 km) and from the South American mainland (Ecuador) to Galápagos (930 km) should favour plant arrival on the Galápagos, but hardly make it so frequent as to retard speciation. Indeed, based on our biogeographic reconstruction, Hawaii and Australia/New Zealand were reached a single time, while Galápagos was reached twice. The finding that more distant archipelagos have fewer arrivals and larger radiations fits with findings from archipelagic birds (Ricklefs & Bermingham, 2007).

We estimate that the genus *Sicyos* is about 19 Myr old, the Hawaiian radiation occurred 3 Ma, the Australian species are 2 Myr old, the New Zealand species 0.7 Myr old, and the two Galápagos species *Sicyos villosus* and *Sicyocaulis pentagonus* are 4.5 and 1 Myr old, respectively (for error margins see Table 2 and Fig. 3). Time *per se* therefore cannot explain the different species numbers in the four areas reached by long-distance dispersal. Instead, the species build-up on the Hawaiian Islands clearly exceeded that in the other regions, although the Hawaiian diversification rate of *Sicyos* is not exceptional compared with other plant radiations (Valente *et al.*, 2010). Morphologically, the Hawaiian *Sicyos* species are distinct from each other (Wagner & Shannon, 1999), although their genetic divergence is low (Fig. 2), a combination also found in other



Figure 3 Chronogram and ancestral area reconstruction for *Sicyos* and related Sicyoeae obtained under a Bayesian relaxed clock and a continuous-time Markov chain biogeographic reconstruction applied to the data set used for Fig. 2 but excluding five Hawaiian species with almost identical sequences. Bars at nodes indicate the 95% confidence intervals around the estimated times. Numbers above branches give the node age, stars mark the calibration nodes, and arrows the four long-distance dispersals discussed in the text. Branch colour indicates character states for ancestral areas with the highest posterior probability (all \geq 0.92, except for a few outgroups), with the coding explained in the inset.

Table 2 Characteristics of the four Sicyos disjunctions compared here.

Characteristic	Hawaii	Australia/New Zealand	Galápagos 1 (<i>Sicyos villosus</i>)	Galápagos 2 (Sicyocaulis pentagonus)
Number of extant species	14	3	1	1
Distance from likely region of origin [km]	3800	6000	930	930
Relative habitat diversity	High	High	Low	Low
Dispersal ability (diaspore morphology)	Low	High	High	High
Stem age [Ma]	5.5-1.9	5.6-1.7	6.4–2.8	1.5-0.08
Crown age [Ma]	4.1-1.3	3.6-0.5	NA	NA
Diversification rate ($k = 0$) [species Myr ⁻¹]	0.47-1.45	0.11-0.81	0	0
Diversification rate ($k = 0.9$) [species Myr ⁻¹]	0.18-0.58	0.03–0.24	0	0

NA, not applicable.

Hawaiian radiations (Baldwin & Robichaux, 1995; Lindqvist et al., 2003).

As time for speciation can be discounted as a strong explanation for the numbers of species in the four areas reached following long-distance dispersal, it might be extrinsic factors that make the Hawaiian Islands especially conducive to Sicyos speciation. Available area per se may influence diversification in island archipelagos (Ricklefs & Bermingham, 2007; Price & Wagner, 2011). The land area of the Hawaiian archipelago (16,300 km²) is more than twice that of the Galápagos (8000 km²). This could explain the larger species number on Hawaii compared with the Galápagos but certainly not that only three species evolved in Australia and New Zealand. However, extrapolation from land surface to number of suitable habitats is difficult (see also Price & Wagner, 2011). The Hawaiian archipelago harbours many types of plant formations (Mueller-Dombois & Fosberg, 1998), and species of Sicyos occupy most of them (Appendix S2). Especially relevant may be the extreme breadth of rainfall regimes on Hawaii. High islands, such as Kaua'i and Hawai'i, receive on their windward slopes as much as 12 m annual precipitation, whereas their leeward slopes experience warm-season droughts and as little as 250 mm annual precipitation, in common with some of the low islands. The Hawaiian soils derived from volcanism have accordingly experienced very different weathering (Cuddihy, 1989).

The Galápagos archipelago by comparison has fewer climate and vegetation types. Aridification there set in *c*. 3 Ma, while before that conditions were warmer and moister (Wara *et al.*, 2005; Federov *et al.*, 2006), potentially supporting rain forest vegetation. Today, the climate of the Galápagos Islands is characterized by highly variable convective rainfall during the hot season and by a prolonged cool season (June to December), with only little orographic rainfall on the higher windward sides of the islands and frequent droughts at lower elevations with arid-adapted vegetation types (Mueller-Dombois & Fosberg, 1998). The overall more arid climate on Galápagos compared with Hawaii, combined with fewer habitat types on smaller islands, may explain the absence of any large plant radiations on Galápagos. Among the 13 angiosperm genera with endemic species in both archipelagos (Table 1) the Hawaiian genera usually have more species, and radiations of more than four species are almost entirely restricted to Hawaii.

An even broader range of climatic and edaphic conditions in the Australian region than in the Hawaiian Islands, however, did not result in a radiation of Sicyos, although further collecting and sequencing efforts may well reveal additional Australian species. The limited diversification of Australian Sicyos resembles the situation in the remaining Cucurbitaceae on that continent. These go back to some 20 independent arrivals from the Malesian region that occurred at different times over the past 35 Myr, with none currently having more than four living descendant species (Schaefer et al., 2008b, 2009). The largest cucurbit radiations in Australia are Austrobryonia, with four species in the arid and semi-arid regions of the continent (Schaefer et al., 2008b), and Cucumis, with two radiations of two/three species in tropical savanna habitats (Sebastian et al., 2010b; Telford et al., 2011). The reasons for the limited cucurbit diversification in Australia remain unclear.

In New Zealand, Cucurbitaceae had no endemic species before the discovery of *Sicyos mawhai*. This is surprising because Cucurbitaceae are successful transoceanic dispersers (Schaefer *et al.*, 2009; Duchen & Renner, 2010; Schaefer & Renner, 2010), and the distance of 2100 km between Australia and New Zealand has been overcome by many other disjunctly distributed Australia/New Zealand clades (Pole, 1994). Nor is *Sicyos* the only angiosperm genus disjunctly distributed between the Americas and the Australian/New Zealand region: Californian species of *Lepidium* (Brassicaceae) are phylogenetically closest to Australian/New Zealand species, which has been explained by transoceanic dispersals (Mummenhoff *et al.*, 2004).

Seabirds can act as dispersal agents across the Pacific Ocean (Falla, 1960; Carlquist, 1967) because at least some of them, such as storm petrels, shearwaters and frigate birds, nest on the ground or in burrows in coastal vegetation where they may contact fruiting plants [Marks & Leasure, 1992; Starr & Martz, 1999; our Fig. 1c shows a great frigatebird (*Fregata minor*) nesting among *Sicyos maximowiczii* on Laysan Island, Hawaii]. Some petrel populations migrate between Mexico, Central and

South America, the Galápagos and Hawaii, and one race of the white-faced storm-petrel (Pelagodroma marina) migrates across the Pacific between New Zealand and the Humboldt Current (off the coast of Peru), then west past the Galápagos Islands (Tomkins, 1982). Species of Siycos have fleshy fruits (fresh up to c. 10 cm long) or hard fruits (5-10 mm long) that are smooth or barbed with hooked spines (Fig. 1 and Appendix S3). As the spiny Sicyos fruits are presented in multi-seeded infructescences, one contact with a bird can lead to several seeds being transported. Fruit morphology has been evolutionarily labile, and even fairly large wings have arisen several times (Appendix S3), the latter surprisingly not linked to any long-distance dispersal events. All lineages or species involved in long-distance dispersal to Hawaii, the Galápagos, Australia or New Zealand have spiny fruits. The spines, however, are readily lost; in Sicyos edulis, natural populations can contain individuals with spiny or smooth fruits (Lira et al., 1999). Spines were also lost in the Hawaiian clade, where fruits are unarmed or in four species retain stubby outgrowths (Telford, 1990). Loss or reduction of dispersal ability is well documented in other insular plant and animal species (Carlquist, 1965, 1966a,b, 1974), the prime example being Bidens, which on the Hawaiian Islands lost the barbed awns responsible for long-distance dispersal in the mainland species (Carlquist, 1966a, 1967). Selection for loss of dispersibility should be strong because the majority of propagules that are dispersed away from islands will be lost at sea. In Hawaiian Sicyos, such limited dispersal ability could have promoted the isolation of populations and thus allopatric speciation in the diverse habitats and species build-up.

CONCLUSIONS

Sicyos, a clade of 75 species once the names in the segregate genera are transferred to the genus *Sicyos*, includes four trans-Pacific disjunctions. Small-scale habitat diversity and morphological adaptations (loss of spines leading to reduced dispersal ability) are the most plausible factors that could account for the significantly higher and more rapid accumulation of species on the Hawaiian Islands compared with the Galápagos, Australia or New Zealand.

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SUPPORTING INFORMATION

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

Appendix S1 List of Sicyoeae species with their authors, geographic origin of the sequenced sample, voucher deposition, and GenBank accession numbers for all sequences included in this study.

Appendix S2 Habitat types of Sicyoeae species plotted on an 86-species maximum likelihood phylogeny.

Appendix S3 Evolution of armed fruits and unarmed fruits in the Sicyoeae inferred on an 86-species maximum likelihood phylogeny under maximum likelihood optimization.

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BIOSKETCH

Patrizia Sebastian is a PhD student in the laboratory of Susanne Renner at the University of Munich (LMU), where she is working on the evolution of *Cucumis*, *Sicyos* and other Cucurbitaceae.

The main research interests of the authors are the evolution, biogeography and systematics of plants.

Author contributions: P.S. and S.R. designed the research; P.S. collected and analysed the data; H.S., I.T. and R.L. selected and supplied plant materials; P.S., H.S. and S.R. wrote the paper.

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