

Appendix 1. Greater landmass at extreme latitudes is not driving the difference in range size for selfing and outcrossing sister species

We find that selfers have larger geographic ranges and occupy higher maximum latitudes than their outcrossing sister species (Fig S2, left panels). Together, we interpret this to mean that selfing allows migration to higher latitudes, and these range expansions partially explain the larger range sizes of selfers. That is, larger range size is a direct effect of selfing, mediated by presence at higher latitude without a corresponding absence at lower latitude.

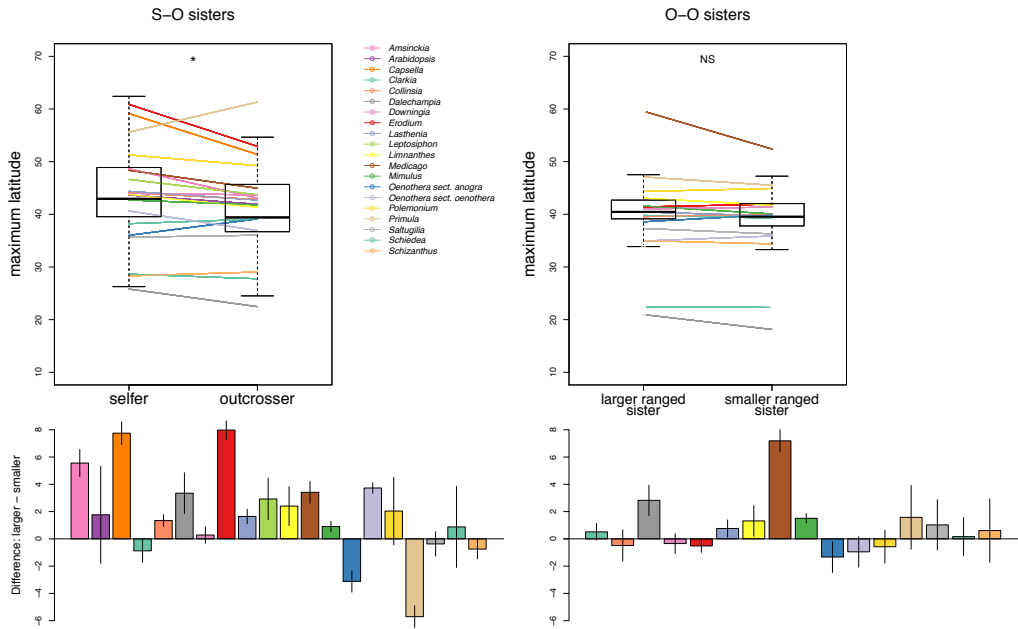
An alternative explanation may be that there is simply more landmass at higher latitudes (particularly in the northern hemisphere) and therefore, any species that have shifted their ranges into high latitudes have greater opportunity to achieve larger ranges. In this view, the direct cause of larger range is occupation of higher latitudes, and mating system is only an indirect cause. This landmass bias is unlikely to be driving our results for two reasons.

First, if selfing merely causes ranges to shift to higher latitudes and it is then the landmass bias that is responsible for the larger range size of selfers, we would expect to see the entire latitudinal distribution of selfers (minimum, midpoint, and maximum latitudes) shifted towards higher latitudes. This was not the case, as selfing and outcrossing sister species occupied similar minimum and midpoint latitudes (see main text Fig 2). It thus appears that selfing facilitates occupation of higher latitudes without reduced presence at lower latitudes, and thus that the larger range of selfers is directly connected to mating system, rather than driven by landmass bias.

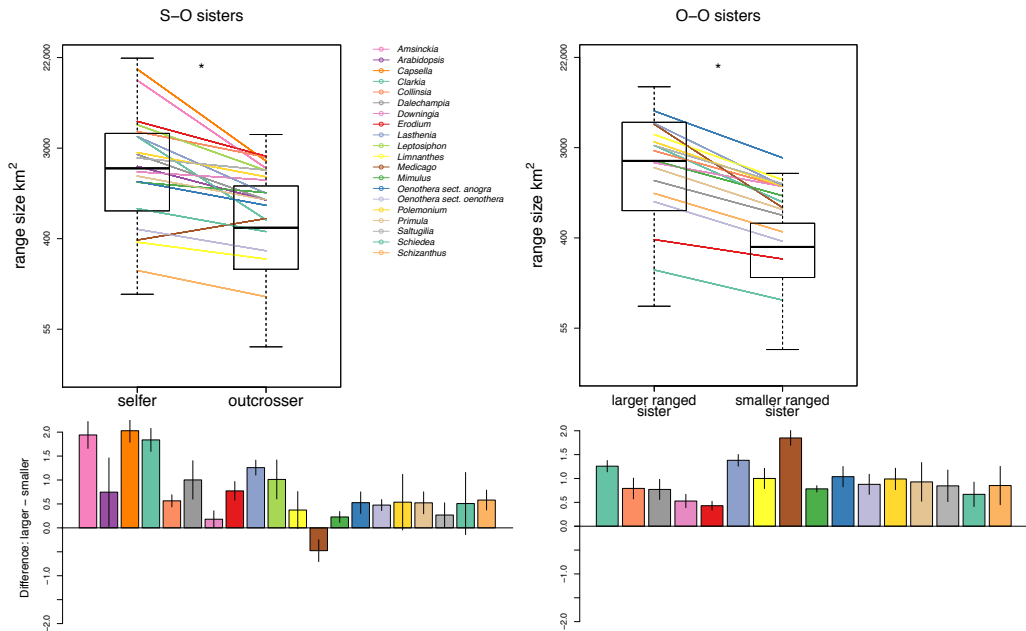
Second, the land mass bias should apply equally to outcrossing-outcrossing (O-O) and selfing-outcrossing (S-O) sister pairs. In particular, the land area effect predicts that the larger-ranged member of O-O sister pairs should also occur at higher maximum latitudes. This is not the case, however (Fig S2 right panels). Using the same basic model as described in the main text, we identified 193 O-O sister pairs and compared the maximum latitudes of the larger and smaller ranged sister. We found that there was no significant difference in maximum latitude for O-O sisters ($P=0.24$; Fig S2A right panel), despite the range size difference of larger and smaller members of O-O pairs being comparable to that of S-O pairs (Fig S2B).

Figure S2. Box plots of **(A)** maximum latitudinal distributions and **(B)** range sizes of S-O (left panels) and O-O (right panels) sister species. * $P < 0.05$

(A) Maximum Latitude



(B) Range Size



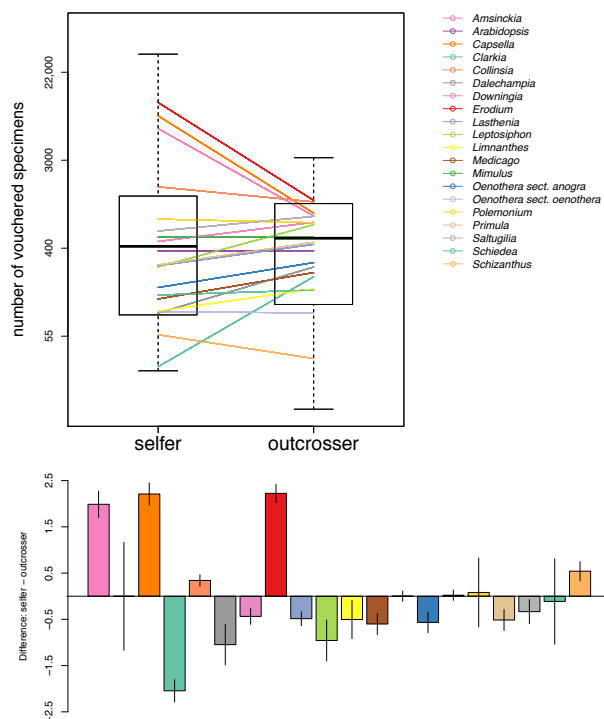
Note: Colored line segments indicate predicted slopes for 20 clades. Bottom bar charts represent the predicted average sister species difference in latitude (selfer – outcrosser, or larger-smaller range size) for each of 20 clades, with vertical lines representing standard errors.

Appendix 2. No differences in sampling effort for selfing and outcrossing sister species

Sampling bias with regards to voucher specimens is an important consideration that could influence range size estimation. There are two opposing sampling biases that could impact our study. On the one hand, selfers may occur more often in human-disturbed habitats, and thus may be oversampled relative to outcrossers. Alternatively, given their diminutive flowers and total size, selfers may be more likely to be overlooked and thus under-sampled relative to outcrossers.

To explore whether there is sampling bias, we examine the total number of voucher specimens for selfing and outcrossing sister species (using the same model as described in the main text for assessing range size differences, but with the response variable “Log number of voucher specimens”). We find that the number of voucher specimens was not significantly different for selfers than outcrossers ($P=0.97$; Fig S3). Thus, it is unlikely that sampling bias is influencing our primary result of selfers having larger ranges than their outcrossing sister species.

Figure S3. Box plot of predicted number of voucher specimens for selfing and outcrossing members of S-O sister pairs.



Note: Colored line segments indicate predicted slopes for 20 clades. Vertical axis is natural logarithmic scale (back-transformed number of vouchered specimens). Bottom bar charts represent the predicted average difference in sampling effort ($\ln(\text{selfer}) - \ln(\text{outcrosser})$) for each of 20 clades, with vertical lines representing standard errors.

Figure S1. Evolutionary relationships and native distributions of 20 clades. Trees represent bayesian consensus phylogenies with tips colored by mating system (red selfers, black outcrossers, green mixed). Geographic distributions represent species' occurrences, obtained from the global biodiversity information facility (www.gbif.org).

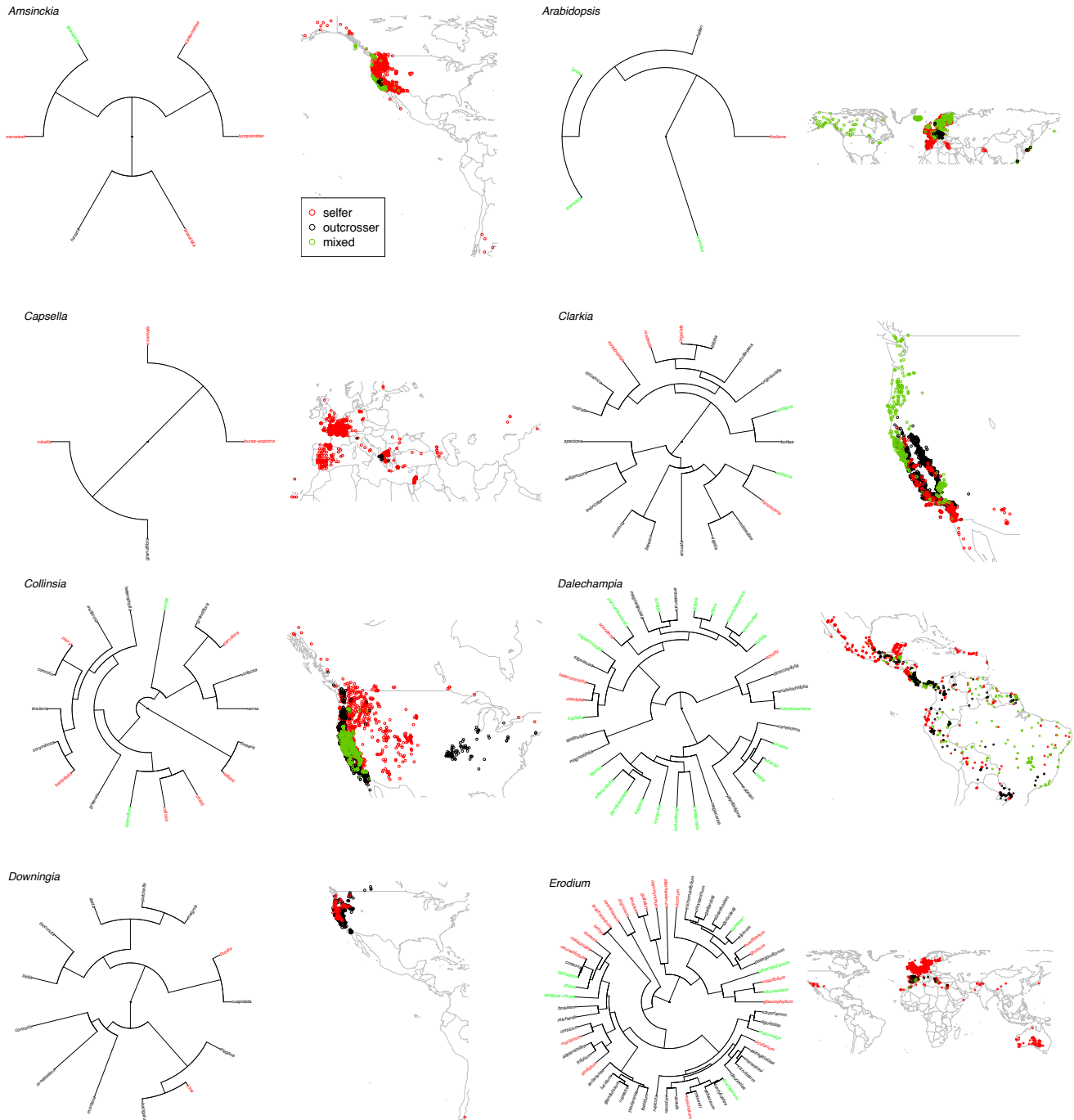


Figure S1 continued

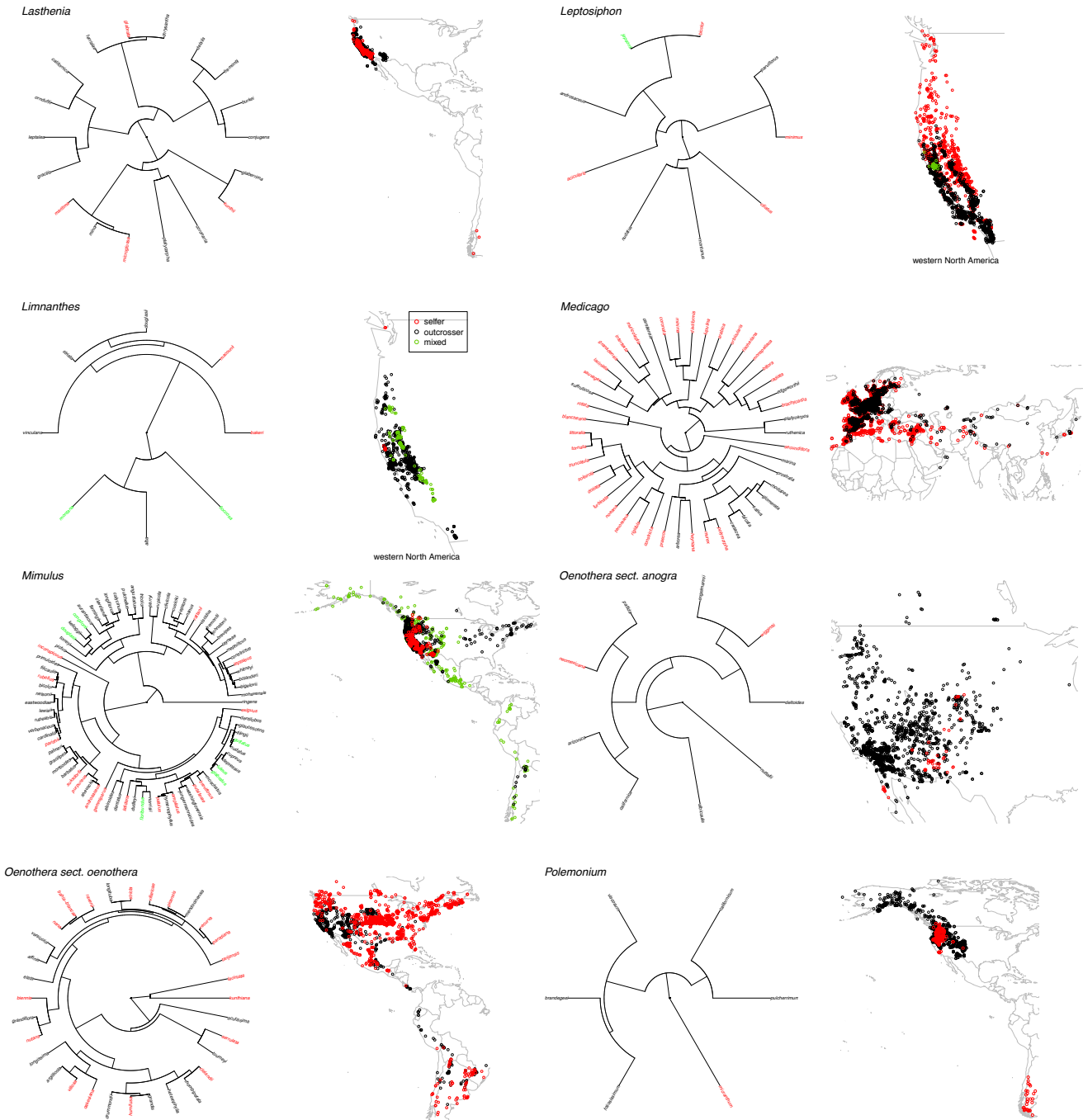
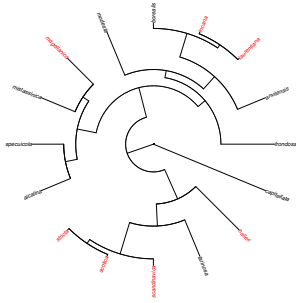
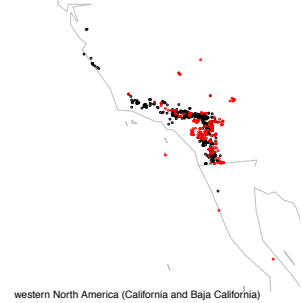
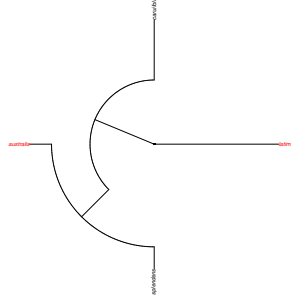


Figure S1 continued.

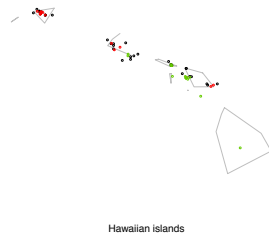
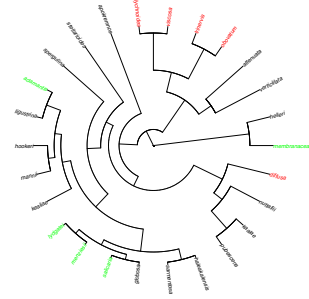
Primula



Saltugilia



Schiedea



Schizanthus

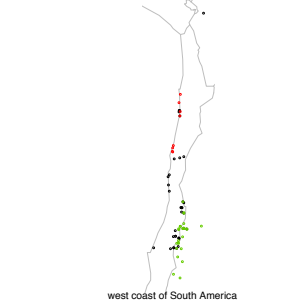
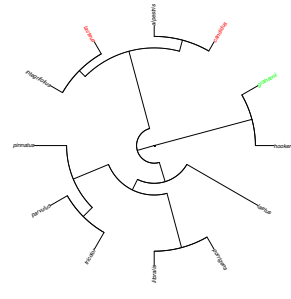


Table S1. The specific methods, software and packages used for each analysis.

Analysis aim	Method (Citation)
Align multiple sequences	The MUSCLE package in R, version 3.8.31-4 (Edgar 2004)
Conduct Bayesian estimation of phylogenetic relationships and the absolute divergence times among species	BEAST v1.6.2 (Drummond et al. 2012)
Assess convergence and mixing of the MCMC	Tracer v. 1.5 (Rambaut et al. 2014)
Run linear mixed effects models	The lmer function in the lme4 R package (Bates et al. 2012)
Calculate marginal and conditional R^2 values	Following Johnson (2014)
Determine significance using likelihood ratio tests with single term deletions	Implementation in the R package <i>afex</i> (Singmann 2014).
Divide the world into a series of rectangular cells by grid lines that follow longitude and latitude	The “raster” R package version 2.3-0 (Hijmans et al. 2011)
Perform a sign-test	The binom.test function in core stats package in R

Bates, Douglas; Maechler, Martin; Bolker, B. & Walker, S. (2014). {lme4}: Linear mixed-effects models using Eigen and S4. *R Packag. version 1.1-7*.

Drummond, A.J., Suchard, M. a, Xie, D. & Rambaut, A. (2012). Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Mol. Biol. Evol.*, 29, 1969–73.

Edgar, R.C. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.*, 32, 1792–1797.

Hijmans, R.J., Phillips, S., Leathwick, J. & Elith, J. (2011). dismo: Species distribution modeling. R package version 0.7–23.

Johnson, P.C.D. (2014). Extension of Nakagawa & Schielzeth’s R2GLMM to random slopes models. *Methods Ecol. Evol.*, 5, 944–946.

R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org/>.

Rambaut, A., Suchard, M., Xie, D. & Drummond, A. (2014). Tracer v1.6. *Available from <http://beast.bio.ed.ac.uk/Tracer>*.

Singmann, H. (2014). afex: Analysis of factorial experiments. R package version 0.9-109.

Table S2. Phylogenetic information for 20 clades included in our study.

Clade total species (proportion in our phylogeny)	Previously published phylogeny [number of loci]	Predominant life history strategy: herbaceous(H) woody(W)	Subst. model	Chain length X 10 ⁶	min. ESS	posterior ESS
<i>Amsinckia</i> 14(0.57)	Schoen et al. 1997 [0nuc,1cp]	H	GTR +gamma	200	3207	6259
<i>Arabidopsis</i> 10(0.6)	Beck et al. 2007 [1nuc,0cp]	H	GTR + gamma	20	790	1367
<i>Capsella</i> 5 (1.0)	Hurka et al. 2012 [1nuc,4cp]	H	GTR + gamma	100	1066	1128
<i>Clarkia</i> ±41(0.51)	Kay et al. in prep [2nuc,0cp]	H	GTR + gamma	20	856	3257
<i>Collinsia</i> ±20(0.95)	Baldwin et al. 2011 [2nuc,1cp]	H	GTR + gamma	20	766	3929
<i>Dalechampia</i> 120 (0.5)	Armbruster et al 2009 [2nuc,2cp]	W	GTR + gamma	200	4179	7435
<i>Downingia</i> 15 (0.87)	Schultheis 2001 [1nuc,1cp]	H	GTR + gamma	20	884	2709
<i>Erodium</i> ±74(0.80)	Fiz-Palacios et al. 2010 [1nuc,1cp]	H	GTR + gamma	20	734	1713
<i>Lasthenia</i> 18 (1.0)	Chan et al. 2001 [2nuc,1cp]	H	GTR + gamma	20	697	2680
<i>Limnanthes</i> 8 (1.0)	Meyers et al. 2010 [1nuc,2cp]	H	HKY + gamma	100	2588	6690
<i>Leptosiphon</i> 30 (0.83)	Goodwillie 1999 [1nuc,0cp]	H	GTR + gamma	20	602	3610
<i>Medicago</i> 83 (0.70)	Maureira-Butler et al. 2008 [2nuc, 1mito]	H	GTR + gamma	20	880	3148
<i>Mimulus</i> ±120(0.94)	Beardsley et al. 2004 [2nuc,1cp]	H	GTR + gamma	152	1974	4892
<i>Oenothera sect.</i> <i>Anogra</i> 10 (0.9)	Theiss et al. 2010 [1nuc,5cp]	H	GTR + gamma	200	602	2243
<i>Oenothera sect.</i> <i>Oenothera and</i> <i>Calylophus*</i> 65 (0.51)	Johnson et al. 2009 [2nuc,3cp]	H	GTR + gamma	200	602	2243
<i>Polemonium</i> 30 (0.63)	Worley et al. 2009 [afip]	H	GTR + gamma	20	834	3343
<i>Primula sect.</i> <i>Aleuritia</i> 21 (0.81)	Guggisberg et al. 2006 [0,4]	H	GTR + gamma	20	882	2949
<i>Saltugilia</i> 4 (1.0)	Johnson et al. 2007 [1nuc,2cp]	H	HKY + gamma	200	4264	6655

<i>Schiedea</i> 34 (0.76)	Soltis et al. 1996 [1nuc,1cp]	W	HKY + gamma	20	740	5438
<i>Schizanthus</i> 12 (1.0)	Perez and Arroyo 2006 [2nuc,1cp]	H	GTR + gamma	20	674	2223

1.

Armbruster, W.S., Lee, J. & Baldwin, B.G. (2009). Macroevolutionary patterns of defense and pollination in Dalechampia vines: adaptation, exaptation, and evolutionary novelty. *Proc. Natl. Acad. Sci.*, 106, 18085–90.

2.

Baldwin, B.G., Kalisz, S. & Armbruster, W.S. (2011). Phylogenetic perspectives on diversification, biogeography, and floral evolution of *Collinsia* and *Tonella* (Plantaginaceae). *Am. J. Bot.*, 98, 731–53.

3.

Beardsley, P. (2004). Patterns of evolution in western North American *Mimulus* (Phrymaceae). *Am. J. Bot.*, 91, 474–489.

4.

Beck, J.B., Al-Shehbaz, I. a, O’Kane, S.L. & Schaal, B. a. (2007). Further insights into the phylogeny of *Arabidopsis* (Brassicaceae) from nuclear *Atmyb2* flanking sequence. *Mol. Phylogenet. Evol.*, 42, 122–30.

5.

Chan, R., Baldwin, B. & Ornduff, R. (2001). Goldfields revisited : A molecular phylogenetic perspective on the evolution of *Lasthenia* (Compositae : Heliantheae sensu lato). *Int. J. Plant Sci.*, 162, 1347–1360.

6.

Fiz-Palacios, O., Vargas, P., Vila, R., Papadopoulos, A.S.T. & Aldasoro, J.J. (2010). The uneven phylogeny and biogeography of *Erodium* (Geraniaceae): radiations in the Mediterranean and recent recurrent intercontinental colonization. *Ann. Bot.*, 106, 871–84.

7.

Goodwillie, C. (1999). Multiple origins of self-compatibility in *Linanthus* section *leptosiphon* (Polemoniaceae): Phylogenetic evidence from Internal-Transcribed-Spacer sequence data. *Evolution*, 53, 1387–1395.

8.

Guggisberg, A., Mansion, G., Kelso, S. & Conti, E. (2006). Evolution of biogeographic patterns, ploidy levels, and breeding systems in a diploid-polyploid species complex of *Primula*. *New Phytol.*, 171, 617–32.

9.

Hurka, H., Friesen, N., German, D. a, Franzke, A. & Neuffer, B. (2012). “Missing link” species *Capsella orientalis* and *Capsella thracica* elucidate evolution of model plant genus *Capsella* (Brassicaceae). *Mol. Ecol.*, 21, 1223–38.

10.

Johnson, L. (2007). Transfer of the western north American species *Gilia splendens* to *Saltugilia* (Polemoniaceae), and the taxonomic affinities of *Gilia scopulorum*, *Gilia stellata*, and *Gilia*. *Novon A J. Bot. Nomencl.*, 17, 193–197.

11.

Johnson, M.T.J., Smith, S.D. & Rausher, M.D. (2009). Plant sex and the evolution of plant defenses against herbivores. *Proc. Natl. Acad. Sci.*, 106, 18079–84.

12.

Maureira-Butler, I.J., Pfeil, B.E., Muangprom, A., Osborn, T.C. & Doyle, J.J. (2008). The reticulate history of *Medicago* (Fabaceae). *Syst. Biol.*, 57, 466–82.

13.

Meyers, S., Liston, A. & Meinke, R. (2010). A molecular phylogeny of *Limnanthes* (Limnanthaceae) and investigation of an anomalous *Limnanthes* population from California , U . S . A . *Syst. Bot.*, 35, 552–558.

14.

Pérez, F. & Arroyo, M. (2006). Ancestral reconstruction of flower morphology and pollination systems in *Schizanthus* (Solanaceae). *Am. J. Bot.*, 93, 1029–1038.

15.

Schoen, D., Johnston, M., L’Heureux, A. & Marsolais, J. (1997). Evolutionary history of the mating system in *Amsinckia* (Boraginaceae). *Evolution*, 51, 1090–1099.

16.

Schultheis, L. (2001). Systematics of *Downingia* (Campanulaceae) based on molecular sequence data: implications for floral and chromosome evolution. *Syst. Bot.*, 26, 603–621.

17.

Soltis, P., Soltis, D., Weller, S., Sakai, A. & Wagner, W. (1996). Molecular phylogenetic analysis of the Hawaiian endemics *Schiedea* and *Alsinidendron* (Caryophyllaceae). *Syst. Bot.*, 21, 365–379.

18.

Theiss, K.E., Holsinger, K.E. & Evans, M.E.K. (2010). Breeding system variation in 10 evening primroses (Oenothera sections Anogra and Kleinia; Onagraceae). *Am. J. Bot.*, 97, 1031–9.

19.

Worley, A., Ghazvini, H. & Schemske, D. (2009). A phylogeny of the genus *Polemonium* based on amplified fragment length polymorphism (AFLP) markers. *Syst. Bot.*, 34, 149–161.

Table S3. Description of how mating system was determined for each clade. The proportion of species assigned as outcrossers, mixed maters, and selfers are included in brackets, [outcrosser/mixed/selfer].

<i>Amsinckia</i>	Outcrossing rates were estimated with molecular markers and shown to be correlated with style type for a subset of species (e.g. Schoen et al. 1997). Distylous species are predominantly outcrossing or mixed mating; homostylous species are predominantly selfing. Style type was thus used to estimate mating system for additional species in this clade. [0.64/0.00/0.36]
<i>Arabidopsis</i>	Outcrossing and self-incompatibility rates were estimated using molecular data and experimental hand-pollinations (e.g., Claus and Koch 2006). [0.20/0.40/0.40]
<i>Capsella</i>	Outcrossing and self-incompatibility rates were estimated using molecular data and experimental hand pollinations (e.g., Brandvain et al. 2013, Hurka et al. 2012). [0.33/0.00/0.66]
<i>Clarkia</i>	Automatic selfing rates and outcrossing rates (estimated with molecular data for a few species) were correlated with herkogamy (e.g., Lewis and Lewis 1955). Herkogamy was used to estimate mating system for the remainder of species. [0.48/0.08/0.45]
<i>Collinsia</i>	Outcrossing rates were estimated with molecular markers for all species and shown to be correlated with timing of stigma receptivity and flower size (e.g., Kalisz et al 2012). [0.58/0.05/0.37]
<i>Dalechampia</i>	Automatic seed set for bagged flowers was shown to correlate with herkogamy for a subset of species (e.g., Armbruster 1988 and 1993). Herkogamy was used to estimate mating system for the remainder (Armbruster 1993). [0.33/0.51/0.16]
<i>Downingia</i>	Automatic seed set in the greenhouse was correlated with stigma exertion and flower size in a subset of species (Schultheis 2001). Stigma exertion was used to estimate mating system for the remainder. [0.85/0.00/0.15]
<i>Erodium</i>	Automatic fruit set (% fruit production on bagged plants; unbagged plants were used as a control) was highly correlated with pollen ovule ratios for a subset of species (Alarcon et al 2011). Pollen ovule ratios were used to estimate mating system for the remaining species. [0.53/0.12/0.35]
<i>Lasthenia</i>	Self-incompatibility rates were determined for all species presumably using experimental hand pollinations (e.g., Orundorf 1966). For those species that were self compatible, rates of automatic selfing were high (presumably when flowers were bagged) on a subset of species (Orundorf 1966; Chan et al. 2001). [0.79/0.00/0.21]
<i>Limnanthes</i>	Protandry and gynodioecy was correlated with high outcrossing rates, while cleistogamy was correlated with high selfing rates in a subset of species (e.g., McNeil and Jain 1983). A range of field pollination studies and molecular studies have been used to confirm this across the majority of taxa. [0.44/0.33/0.22]
<i>Leptosiphon</i>	Self-incompatibility was determined using experimental hand pollinations for all

	species (e.g., Goodwillie 1999). For a subset of the self-compatible species, outcrossing rates were estimated with molecular markers and were either low (consistent with predominant selfing) or intermediate (consistent with mixed mating) (e.g., Goodwillie 2001). [0.50/0.00/0.50]
<i>Medicago</i>	Degree of automatic fruit set in the greenhouse was used to categorize species as "selfers" or "outcrossers" (Maureira-Butler et al. 2008) and was found to be consistent with previously published reports for a subset of the species. [0.72/0.00/0.28]
<i>Mimulus</i>	Outcrossing rates were estimated with molecular markers and were correlated with the degree of herkogamy for a subset of species (e.g. Ritland and Ritland 1989). The degree of herkogamy was then used to estimate mating system across other species (e.g. Grossenbacher and Whittall 2011). [0.71/0.07/0.23]
<i>Oenothera sect. Anogra</i>	Self-incompatibility rates were estimated using experimental hand pollinations for all species (e.g. Theiss et al. 2010). For self-compatible species, herkogamy was used to estimate whether species were predominantly selfing or outcrossing. [0.90/0.00/0.10]
<i>Oenothera sect. Oenothera and Calylophus*</i>	Species were classified as either sexual, or functionally asexual due to a permanent translocation whereby plants self-fertilize but do not undergo segregation and recombination (Johnson et al. 2009). For species defined as sexual, experimental crosses showed that about half were self-incompatible and thus outcrossing. The remaining half displayed partial self-incompatibility and may be mixed mating. For the purposes of the present study, sexual species are assumed to be outcrossing relative to asexual species. [0.42/0.00/0.58]
<i>Polemonium</i>	Self-incompatibility rates were determined using experimental hand pollinations on a subset of species (Worley pers. com.). Species were classified as outcrossing when the combined fruit x seed set of selfed flowers was <25% of that in outcrossed flowers. For species that were self-compatible, automatic selfing rates were assessed in the field or greenhouse (e.g., Worley pers. com., Hill et al. 2008). [0.85/0.00/0.15]
<i>Primula sect. Aleuritia</i>	Self-incompatibility was correlated with style type for a subset of species (discussed in Guggisberg et al. 2006). Distylous species were found to be self-incompatible, homostylous species self-compatible and autogamous (e.g., Tremayne and Richards 2000). [0.56/0.00/0.44]
<i>Saltugilia</i>	Self-incompatibility and autogamy rates were assessed for all 4 species (Grant and Grant 1965). [0.50/0.00/0.50]
<i>Schiedea</i>	Species were determined to be dioecious, subdioecious, gynodioecious, or hermaphroditic (Weller et al 1995). Dioecious and subdioecious species were reported as mostly outcrossing. For gynodioecious and hermaphroditic species, outcrossing and automatic selfing rates (measured using molecular data and presumably bagging experiments) ranged from mostly outcrossing to mostly selfing. [0.66/0.17/0.17]
<i>Schizanthus</i>	Automatic selfing rates in the field were correlated with pollen dehiscence and other reproductive characters for the majority of species (e.g., Perez et al. 2009). These

	correlated characters were used to estimate mating system in the remaining 3 species. [0.75/0.08/0.17]
--	--

1.

Alarcón, M.L., Roquet, C. & Aldasoro, J.J. (2011). Evolution of pollen/ovule ratios and breeding system in *Erodium* (Geraniaceae). *Syst. Bot.*, 36, 661–676.

2.

Armbruster, W. (1988). Multilevel comparative analysis of the morphology, function, and evolution of *Dalechampia* blossoms. *Ecology*, 69, 1746–1761.

3.

Armbruster, W. (1993). Evolution of plant pollination systems : Hypotheses and tests with the neotropical vine *Dalechampia*. *Evolution*, 47, 1480–1505.

4.

Brandvain, Y., Slotte, T., Hazzouri, K.M., Wright, S.I. & Coop, G. (2013). Genomic identification of founding haplotypes reveals the history of the selfing species *Capsella rubella*. *PLoS Genet.*, 9.

5.

Chan, R., Baldwin, B. & Ornduff, R. (2001). Goldfields revisited : A molecular phylogenetic perspective on the evolution of *Lasthenia* (Compositae : Heliantheae sensu lato). *Int. J. Plant Sci.*, 162, 1347–1360.

6.

Clauss, M.J. & Koch, M. a. (2006). Poorly known relatives of *Arabidopsis thaliana*. *Trends Plant Sci.*, 11, 449–59.

7.

Goodwillie, C. (1999). Multiple origins of self-compatibility in *Linanthus* section *leptosiphon* (Polemoniaceae): Phylogenetic evidence from Internal-Transcribed-Spacer sequence data. *Evolution*, 53, 1387–1395.

8.

Goodwillie, C. (2001). Pollen limitation and the evolution of self-compatibility in *Linanthus* (Polemoniaceae). *Int. J. Plant Sci.*, 162, 1283–1292.

9.

Grant, V. & Grant, K.A. (1965). *Flower pollination in the phlox family*. Columbia University Press, New York.

10.

Grossenbacher, D.L. & Whittall, J.B. (2011). Increased floral divergence in sympatric monkeyflowers. *Evolution*, 65, 2712–2718.

11.

Guggisberg, A., Mansion, G., Kelso, S. & Conti, E. (2006). Evolution of biogeographic patterns, ploidy levels, and breeding systems in a diploid-polyploid species complex of *Primula*. *New Phytol.*, 171, 617–32.

12.

Hill, L.M., Brody, A.K. & Tedesco, C.L. (2008). Mating strategies and pollen limitation in a globally threatened perennial *Polemonium vanbruntiae*. *Acta Oecologica*, 33, 314–323.

13.

Hurka, H., Friesen, N., German, D. a, Franzke, A. & Neuffer, B. (2012). “Missing link” species *Capsella orientalis* and *Capsella thracica* elucidate evolution of model plant genus *Capsella* (Brassicaceae). *Mol. Ecol.*, 21, 1223–38.

14.

Johnson, M.T.J., Smith, S.D. & Rausher, M.D. (2009). Plant sex and the evolution of plant defenses against herbivores. *Proc. Natl. Acad. Sci.*, 106, 18079–84.

15.

Kalisz, S., Randle, A., Chaiffetz, D., Faigeles, M., Butera, A. & Beight, C. (2012). Dichogamy correlates with outcrossing rate and defines the selfing syndrome in the mixed-mating genus *Collinsia*. *Ann. Bot.*, 109, 571–82.

16.

Lewis, H. & Lewis, M.E. (1955). *The genus Clarkia*. University of California Press Berkeley, California, USA.

17.

Maureira-Butler, I.J., Pfeil, B.E., Muangprom, A., Osborn, T.C. & Doyle, J.J. (2008). The reticulate history of *Medicago* (Fabaceae). *Syst. Biol.*, 57, 466–82.

18.

McNeill, C. & Jain, S. (1983). Genetic differentiation studies and phylogenetic inference in the plant genus *Limnanthes* (section *Inflexae*). *Theor. Appl. Genet.*, 257–269.

19.

Ornduff, R. (1966). *A biosystematic survey of the goldfield genus Lasthenia (Compositae: Helenieae)*. University of California Press Berkeley, California, USA.

20.

Pérez, F., Arroyo, M.T.K. & Armesto, J.J. (2009). Evolution of autonomous selfing accompanies increased specialization in the pollination system of *Schizanthus* (Solanaceae). *Am. J. Bot.*, 96, 1168–76.

21.

Ritland, C. & Ritland, K. (1989). Variation of sex allocation among 8 taxa of the *Mimulus guttatus* species complex (Scrophulariaceae). *Am. J. Bot.*, 76, 1731–1739.

22.

Schoen, D., Johnston, M., L'Heureux, A. & Marsolais, J. (1997). Evolutionary history of the mating system in *Amsinckia* (Boraginaceae). *Evolution*, 51, 1090–1099.

23.

Schultheis, L. (2001). Systematics of *Downingia* (Campanulaceae) based on molecular sequence data: implications for floral and chromosome evolution. *Syst. Bot.*, 26, 603–621.

24.

Theiss, K.E., Holsinger, K.E. & Evans, M.E.K. (2010). Breeding system variation in 10 evening primroses (*Oenothera* sections *Anogra* and *Kleinia*; Onagraceae). *Am. J. Bot.*, 97, 1031–9.

25.

Tremayne, M. & Richards, A. (2000). Seed weight and seed number affect subsequent fitness in outcrossing and selfing *Primula* species. *New Phytol.*, 34, 149–161.

26.

Weller, S., Wagner, W. & Sakai, A. (1995). A phylogenetic analysis of *Schiedea* and *Alsinidendron* (Caryophyllaceae : Alsinoideae): Implications for the evolution of breeding systems. *Syst. Bot.*, 20, 315–337.

Table S5. Accounting for ploidy and life history effects. Results of 14 separate linear mixed models analyzing the effect of mating system on species' range size (estimated at 4 different spatial scales) and latitude. (A) Subsetted dataset of s-o sister pairs with the same ploidy, e.g., both are diploid or both are tetraploid (N=129). (B) Subsetted dataset of s-o sister pairs with the same life history, e.g., both are annuals or both are perennials (N=107).

Response	LR	<i>P</i>	Marginal R^2	Conditional R^2	Predicted value	
					Selfer	Outcrosser
(A) subsetted dataset by ploidy						
Natural log Range Size (km ²)						
~25 km ² grid cell	7.47	0.006	0.225	0.939	1890	930
~100 km ² grid cell	7.18	0.007	0.212	0.935	5988	3097
~2500 km ² grid cell	6.15	0.01	0.178	0.931	60,458	36,743
~10,000 km ² grid cell	6.09	0.01	0.133	0.934	141,917	94,306
Absolute Latitude (decimal degree)						
minimum	1.92	0.17	0.030	0.964	32.98	34.28
midpoint	0.05	0.83	<0.001	0.985	38.45	38.31
maximum	1.38	0.24	0.016	0.983	44.22	42.89
(B) subsetted dataset by life history						
Natural log Range Size (km ²)						
~25 km ² grid cell	10.42	0.001	0.198	0.953	1553	763
~100 km ² grid cell	10.42	0.001	0.192	0.946	5033	2575
~2500 km ² grid cell	10.49	0.001	0.187	0.925	55,955	32,523
~10,000 km ² grid cell	11.28	0.0008	0.172	0.910	136,968	85,289
Absolute Latitude (decimal degree)						
minimum	0.01	0.91	<0.001	0.979	32.04	32.10
midpoint	0.58	0.45	0.003	0.992	36.25	35.74
maximum	1.51	0.22	0.009	0.987	40.77	39.73

Significance of fixed effects was assessed by likelihood ratio tests (LR) using single term deletions. Marginal R^2 values are the proportion of variance explained by mating system (fixed effect). Conditional R^2 values are the variance explained by mating system and the random effects of clade and sister pair. Predicted values for range size are back-transformed.

Table S6. Sign tests of predicted clade-average difference in range size and latitude (selfing minus outcrossing member of sister pair). Positive values indicate that, within a clade, selfers have larger range sizes and occupy higher latitudes than their outcrossing sister species.

We report results **(A)** the full s-o sister pair data set, **(B)** subsetting dataset of s-o sister pairs with the same ploidy, e.g., both are diploid or both are polyploid, and **(C)** subsetting dataset of s-o sister pairs with the same life history, e.g., both are annuals or both are perennials.

	(A) full dataset			(B) subsetting dataset by ploidy			(C) subsetting dataset by life history		
	Number of clades		<i>P</i>	Number of clades		<i>P</i>	Number of clades		<i>P</i>
	-	+		-	+		-	+	
Natural log Range Size (km²)									
~25 km ² grid cell	1	19	<0.001	0	16	<0.001	1	15	<0.001
~100 km ² grid cell	1	19	<0.001	0	16	<0.001	1	15	<0.001
~2500 km ² grid cell	1	19	<0.001	1	15	<0.001	0	16	<0.001
~10,000 km ² grid cell	1	19	<0.001	0	16	<0.001	1	15	<0.001
Absolute Latitude (decimal degree)									
minimum	12	8	0.503	12	4	0.077	9	7	0.804
midpoint	5	15	0.042	5	11	0.210	6	10	0.455
maximum	5	15	0.042	4	12	0.077	5	11	0.210