

Supporting Information 1

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Article title: Extinction pulse at Eocene–Oligocene boundary drives diversification dynamics of the two Australian temperate floras

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Methods

Assembly of data and criteria for selection

Temperate IBRA regions with >300 mm average annual rainfall were included (Table S1). The IBRA defined region for SEA (1.34 million km²) is 4.5 times larger than SWA (0.30 million km²), and is substantially larger than that defined by Thiele and Prober (2014). Many temperate plant groups in SEA range widely from southeastern South Australia and Tasmania to northern New South Wales and southern Queensland. The broader definition of the area in this study allows for a broader assessment of dynamics between the two regions.

The twenty-one most species-rich flowering plant families with substantial endemic lineages in both regions were selected (Table 1). The compiled dataset includes 71% (5645/8000 spp.) and 75% (3607/4810 spp.) of the total extant plant species diversity for SWA and SEA respectively. Dilleniaceae was not included even though it is among the top 20 species-rich families in Australia (*Hibbertia* has c. 150 Australian species), as species concepts for SWA and SEA may be non-comparable, with two different taxonomists working on the genus in the two regions. Similarly, Thymelaeaceae was not included (*Pimelea* has c. 110 Australian species) as insufficient genetic data was available at the time of this study.

Entire families were selected when infra-familial Australian lineages are non-monophyletic and scattered across their respective family phylogenetic trees (e.g. Proteaceae) or have a majority of their lineages in Australia (e.g. Goodeniaceae, Proteaceae, Restionaceae). Sub-families of cosmopolitan families (e.g. Apiaceae: Mackinlayoideae, Asteraceae: Gnaphalieae) were used when

these are monophyletic and largely Australian. Families that have the highest disparity in richness between the two regions (i.e. having many more species in one region than the other) were selected for further analysis. For SWA these were Proteaceae, Myrtaceae, Fabaceae and Ericaceae (the four most species-rich families in SWA) and Restionaceae, while for SEA these were Asteraceae, Cyperaceae and Rutaceae.

We assembled checklists of species in each region (SEA, SWA) for each family (or infra-family) and each genus within the families, from the Australian Virtual Herbarium online database (AVH; <http://avh.chah.org.au>, accessed December 2017–January 2018), filtered by the respective IBRA regions. Introduced and cultivated taxa were pruned from the data set. For clades that also occur outside of Australia, numbers of species were obtained from the Angiosperm Phylogeny Website (<http://www.mobot.org/MOBOT/research/Apweb>, accessed January 2018) (Supplementary Material 2). Species numbers in groups undergoing substantial revision or with multiple conflicting estimates were cross-checked with relevant taxonomic experts and amended as required.

Genera with less than 75% of extant species diversity occurring within the region of interest (SWA or SEA) were discarded. This criterion is more conservative than the 50% cutoff adopted by Sauquet *et al.* (2009), but should increase the diversification signal specific to each region and reduces the likelihood that species disparity between the regions is the result of chance alone. The sensitivity of our analyses to different levels of cutoff was assessed by running similar analyses with the compiled dataset at four other minimum thresholds (50%, 65%, 90%, and 100%).

Dating and molecular analyses

For families or infra-families that lacked published dated phylogenies or were represented by multiple phylogenies, and that had sufficient available published sequences in GenBank, we constructed time-calibrated combined phylogenies using Bayesian approaches implemented in BEAST v2.4.7. (Bouckaert *et al.*, 2014). Phylogenies were calibrated with fossils sourced from the literature, following recommended best practice (Ho & Phillips, 2009; Parham *et al.*, 2011) (Table S3). BEAUTi v2.4.7 was used to create input files for BEAST. We used a GTR+I+G substitution model, Yule tree model, and a relaxed lognormal clock model. Calibration points were derived from the fossil data; flat priors were applied for the remaining parameters. For each tree, two BEAST runs were performed with 10 million Markov Chain Monte Carlo (MCMC) generations, sampling every 1000 generations. The first 20% of runs were discarded as burn-in. Tracer v1.6.0 (Rambaut *et al.*, 2015) was used to assess convergence using effective sample size values and a cutoff of 200.

Tree output files were combined using LogCombiner v2.4.7 and summarised in TreeAnnotator v2.4.7. Trees were visualised using FigTree v1.4.3 (Rambaut, 2012).

BAMM diversification analyses

For our BAMM analyses, BEAST v2.4.7 was used to reconstruct phylogenetic relationships and estimate divergence times across the phylogenies using the fossil calibrations and model settings as above (Table S3). For each tree, two BEAST runs were performed with the number of runs tailored to the size of the phylogeny (50, 10, and 20 million generations of MCMC for *Acacia*, *Eucalyptus*, and Epacridoideae respectively), sampling every 1000 generations. The first 20% of runs were discarded as burn-in. BEAST analyses were run on the CIPRES Science Gateway portal (Miller *et al.*, 2010). BAMM analyses were implemented as reversible jump Markov Chain Monte Carlo (rjMCMC) simulations and accounted for incomplete taxon sampling by specifying the sampling fraction according to current species estimates derived from the literature (0.5 for *Acacia* and Epacridoideae, 0.9 for *Eucalyptus*) (Mishler *et al.*, 2014; Puente-Lelièvre *et al.*, 2016; Thornhill *et al.*, 2019). We also accounted for this by running BAMM analyses of the three groups across a range of different global sampling fractions following the approach of Gubry-Rangin *et al.* (2015) (Figs. S10–12). While BAMM has been criticised as providing unreliable estimates of diversification rate shifts (Moore *et al.*, 2016; Meyer & Wiens, 2018), the problem applies to diversification models more broadly (Kodandaramaiah & Murali, 2017; Rabosky, 2017; Rabosky *et al.*, 2017) and can be addressed by identifying posterior estimates that are strongly supported independently from the prior (Rabosky *et al.*, 2017). We accounted for these limitations by running the analyses with different specified numbers of expected rate shifts (from 1–5). Two independent runs of 10 million rjMCMC generations using the fossil-calibrated BEAST trees were conducted for each group, sampling every 1000 generations. Post-run analyses and visualisations were conducted using the R package BAMMTools v2.5.0 (Rabosky *et al.*, 2014).

Diversification rate analyses

Diversification rates of stem groups were calculated using equation 6 from Magallón and Sanderson (2001) under both no extinction ($\kappa = \lambda/\mu = 0$) and high relative extinction ($\kappa = 0.9$) rates. The diversification rate of each genus was calculated using the stem age of the genus and number of extant species within the genus. The background diversification rate of each family or infra-family was calculated using the stem age of the oldest genus and total number of extant genera in the family. Similarly, region-specific diversification rates of each family or infra-family were calculated using the stem age of the oldest genus and total number of extant genera found in each of

the two respective regions. 95% confidence intervals on clade size based on stem age were calculated using equation 10 (Magallón & Sanderson, 2001) calculated using the “geiger” package (Harmon *et al.*, 2007; Pennell *et al.*, 2014) in R (R Core Team, 2016). This allowed identification of genera or clades that are unusually species-rich or species-poor relative to the background diversification rate of their respective families.

Statistical analyses

We conducted Shapiro-Wilks tests for normality for the compiled dataset, with variables log-transformed where necessary. Parametric tests (paired t-test, linear regression, and ANOVA) were conducted for datasets that were found to be normally distributed, while non-parametric tests (Wilcoxon signed rank and Kruskal-Wallis tests) were conducted for datasets that were skewed even after log transformation. Specifically, we tested for differences in average diversification rates across the two regions, and across different families. Tests were also carried out on the subset of the data comprising only large genera (> 30 species each) to reduce noise from species-poor lineages. Monotypic genera were excluded from the tests and analysed separately, as by definition they have a net diversification of zero. Chi-square tests for independence were conducted to assess differences in the distributions of diversification rates across the two regions. *Caladenia* (Orchidaceae) found to be an outlier, with a diversification rate an order of magnitude higher than any other genus, and was removed from further analyses.

Spearman rank correlation coefficients were calculated to test relationships between diversification rates of genera, divergence time, and the number and percentage of species found in each region. Relationships were visualised using bubble plots. All analyses were conducted in R (R Core Team, 2016), using the “nlme” (Pinheiro *et al.*, 2014) and “multcomp” (Hothorn *et al.*, 2008) packages.

Results

Diversification of genera

The SWA region has more genera ($n = 108$) than SEA ($n = 50$) in 18 out of the 20 families based on our applied $>75\%$ cutoff threshold. The region also has a greater number of large genera (> 40 spp., $n = 17$) compared to SEA ($n = 7$). The diversification of both total and endemic genera within families was significantly higher in SWA than SEA, under both pure birth ($\kappa = 0.0$) and high relative extinction models ($\kappa = 0.9$) ($p < 0.05$; Table S4). Of the 19 families, only four families showed lower rates of diversification for total and endemic genera in SWA under the pure birth

model (Table S5). Six and three families showed lower rates of diversification in SWA under the high relative extinction model for total and endemic genera respectively (Table S5).

More lineages (including monotypic genera) diversified in SWA than in SEA at any given time from 80 Ma to the present (Fig. 2). The diversification of genera was highest at *c.* 20 Ma and 5 Ma for SWA and SEA respectively (Fig. 2a). The ratio between diversification rates in the two regions peaked at 4.5 at *c.* 30 Ma, immediately after the Eocene–Oligocene (E–O) boundary, with the least number of genera in SEA diverging during that time period (35–30 Ma) (Fig. 2a). This decrease in diversification in SEA is apparent across all major plant groups (seven dominant families) and across different-sized genera (Fig. 2b–i), and was found whatever cutoff value was used (50% to 100% of extant species diversity occurring in each region) (Fig. S2). In contrast, these groups did not show a decrease in diversification in SWA during this time period with the exception of Proteaceae, Mirbelioids (Fabaceae), and Cyperaceae (Fig. 2c,d,h).

Major plant groups (Proteaceae, Fabaceae: Mirbeleae, Ericaceae, Asteraceae: Gnaphalieae, Myrtaceae: Chamelaucieae, Restionaceae, Hemerocallidaceae) showed an increase in diversification in SEA after *c.* 20 Ma, during the mid-Miocene Climatic Optimum period (MMCO, 18–16 Ma) except for Rutaceae (Figs 2). By contrast, four out of nine families (Ericaceae, Myrtaceae: Chamelaucieae, Cyperaceae: Schoenaeae, Hemerocallidaceae) showed a decrease in diversification in SWA during that period (Fig. 2). The ratio of divergences for monotypic genera in SWA and SEA peaked at the MMCO (*c.* 15 Ma), with the greatest number of monotypic divergences occurring during the Pliocene (5–0 Ma) for both regions (Fig. 2b).

Diversification rate distribution of SWA and SEA taxa

There are more genera in SWA at any given value of diversification rate than in SEA (from low, medium, to high rates) (Fig. 3). The diversification rate categories with the most genera were 0.03 and 0 net speciation events per Myr per lineage (i.e. monotypic genera) for SWA and SEA respectively, under the high relative extinction model. There was no significant difference ($p > 0.05$) in diversification rate distribution between the two regions across all genera (Table S7).

Diversification of species

Net species diversification rate averaged across all genera was significantly higher for SEA than SWA under the pure birth model ($p < 0.05$) (Table S6). However, *Caladenia* (Orchidaceae) was an outlier, with a diversification rate a magnitude higher than any other genus. With *Caladenia* removed, the regions were not significantly different ($p > 0.05$) under both pure birth and high

extinction scenarios. Differences in diversification rates were more pronounced between different plant families than between the two regions ($p < 0.05$) (Table S6).

The eight families with a high disparity in richness between the two regions had higher rates of diversification in the region in which they were richest, except for Asteraceae, which had a higher diversification rate under the pure birth model in SWA despite having a higher number of species in SEA. The five families that were disproportionately rich in SWA (Restionaceae, Proteaceae, Myrtaceae, Ericaceae, Fabaceae) had significantly higher combined rates of diversification than in SEA ($p < 0.05$) under both pure birth and high extinction models (Table S6). However, these differences were non-significant ($p > 0.05$) when each family was analysed separately. By comparison, the three families that were disproportionately rich in SEA (Cyperaceae, Asteraceae, Rutaceae) had higher rates of diversification compared to SWA, but the differences were non-significant ($p > 0.05$) in both combined and individual analyses across both pure birth and high extinction scenarios (Table S6).

Correlates of diversification

Diversification rates across genera were positively correlated with number of species and negatively correlated with divergence time ($p < 0.05$) across both regions under both pure birth and high extinction models (Table S8 & Fig. S3). For large genera (>40 species), there was a negative correlation ($p < 0.05$) between diversification rate and divergence time. Diversification rates were positively correlated ($p < 0.05$) with the percentage of species occurring in SEA; that is, genera with a greater fraction of their species found within SEA had higher diversification rates compared with genera that had a greater fraction of species found within SWA (Table S8 & Fig. S4). Similar trends were shown for genera with >30 species, but the differences were not significant ($p > 0.05$) (Table S8 & Fig. S4).

Expected clade-age diversity

Under the most conservative diversification model ($\kappa = 0.9$, i.e. high extinction), eight and five of the 21 families had genera that are unusually species-rich in SWA and SEA respectively, falling above the 95% confidence interval (Table S9, Fig. S5). Under the pure birth model ($\kappa = 0.0$), 12 and seven families had genera that are unusually species-rich in SWA and SEA respectively (Table S9, Fig. S5). Four and two of the five families that are disproportionately rich in SWA had genera that are unusually species-rich under the pure birth and high extinction models respectively. Three and one of the three families that are disproportionately rich in SEA had genera that are unusually species-rich under the pure birth and high extinction models respectively.

By comparison, under the most conservative model ($\kappa = 0.9$) 17 and 11 families had genera that are unusually species-poor in SWA and SEA respectively (Table S10, Fig. S5) while under the pure birth model ($\kappa = 0.0$) 16 and 11 families had genera that are unusually species-poor in SWA and SEA. Most of these species-poor genera are monotypic. When monotypic genera were excluded, only four and six families had genera that are unusually species-poor in SWA and SEA respectively under the high extinction model ($\kappa = 0.9$), and seven families are unusually species-poor in each region under the pure birth model ($\kappa = 0.0$) (Table S10, Fig. S5).

Lineages-through-time

Diversification decreased in both regions at the Paleocene–Eocene Thermal Maximum (PETM, *c.* 55 Ma) (Fig. S8). The lineage-through-time plots for each region have similar slopes except for the interval across the E-O boundary (40–30 Ma), when SEA plateaued then recovered after 30 Ma (Fig. 4). This pattern is the result of multiple groups (Proteaceae, Goodeniaceae, Myrtaceae, Mirbelieae; Fabaceae, Asparagaceae, Apiaceae, Rutaceae, Cyperaceae, and Orchidaceae) showing a similar response at the E-O boundary. (Fig. S9).

Similarly, the slopes for the diversification of both endemic and monotypic genera are parallel for each region until the E-O boundary, when diversification decreased in SEA but remained constant in SWA. Diversification decreased after *c.* 20 Ma for endemic genera, and increased markedly after 20 Ma for monotypic genera (Fig. S8b,c).

Fourteen of the 20 lineages (Droseraceae, Goodeniaceae, Asparagaceae, Fabaceae: Mirbelioideae, Hemerocallidaceae, Apiaceae, Rhamanaceae, Rutaceae, Cyperaceae, Orchidaceae, Loganiaceae, Haemodoraceae, and Elaeocarpaceae) showed a subsequent increase in diversification after *c.* 20 Ma across both regions (Fig. S9). Others (e.g. Asteraceae and Malvaceae) showed a more recent increase after the mid-Miocene to the Pliocene (10–1 Ma) (Fig. S9g,p).

BAMM diversification analyses

The time-dependent analysis in BAMM identified clades that underwent significant diversification rate shifts in all three major groups tested. Rate shifts identified across the three groups were consistent under different global sampling fraction regimes (Figs. S10–15).

Acacia

Significant accelerations in net species diversification were noted for two clades in *Acacia*, one of which includes entirely eastern Australian species (*Botrycephala* clade) showing a significant

increase in diversification rate during the Pliocene (*c.* 4 Ma) (Fig. 4a). The other clade contains largely arid zone *Acacia* species within subg. *Plurinerves* *p.p.* and *Juliflorae* *p.p.* showed a significant increase in diversification rate around the MMCO (*c.* 15 ± 5 Ma) (Fig. 4b).

Epacridoideae

Two clades were identified to have undergone significant accelerations in net speciation rate for the Epacrids. One of the clade is associated with species confined to SWA (*Leucopogon* species) that started diversifying significantly higher than the background rate in the early Miocene (*c.* 20 Ma ± 5 Ma) (Fig. 4b). The other clade with a recent diversification includes the *Dracophyllum* clade (mostly in New Zealand, and 13 % in SEA) that started diversifying in the late Miocene (*c.* 10 Ma) (Fig. 4b).

Eucalyptus

A clade that comprise taxa in subg. *Syphomyrtus* (Mallee species) underwent a significant positive shift in net diversification from the early Miocene (*c.* 20 Ma) (Fig. 4c). The significant increase in speciation rate within the genus immediately after 20 Ma was attributed to the radiation of this clade (Fig. S6a).

Table S1a IBRA regions included in each region and their area size.

Table S1b Twenty-one most species-rich plant families with major components across the temperate regions of Australia that were selected for this study. Number of genera and species in each subgroup of the respective families are listed. Species numbers were filtered through the defined IBRA regions of both regions and sourced from the Australasian Virtual Herbarium (AVH) (see text). *The subtribal classification within Chamaeleaceae is currently undergoing revision (B.Rye pers. comm. 2018), taxonomic estimates below were cross-checked with B.Rye and amended as necessary. **Species numbers for *Caldenia* were sourced from Phillips *et al.* (2009) and species no. for *Diuris* were omitted due to the taxonomic uncertainty within the genus.

Table S2 Sources of node ages for the respective plant groups, cross-checked with the database on TimeTree (Kumar *et al.*, 2017).

Table S3 Details of fossil and secondary calibrations used in the Bayesian divergence-dating analyses of the respective plant groups, compiled gene regions, and source of the datasets.

Table S4 Summary statistics of Wilcoxon signed rank tests of diversification rate at the family level across the two regions. Units are net speciation events per Myr per lineage ($\text{sp sp}^{-1} \text{My}^{-1}$). Values shown are p-values. **, and *** represent significance levels of $p < 0.001$ and < 0.0001 respectively.

Table S5 Differences in diversification rate for each family across the southwest and southeastern regions. * indicates families with a higher net diversification rate in the southeast region.

Table S6 Summary statistics of Kruskal Wallis tests for each of the eight families and all genera within the families across the two regions, and paired t-tests for the combined analyses. Values shown are degrees of freedom (DF), Chi-squared and p-values. ^a indicates the 5 dominant families in the southwest. ^b indicates the 3 dominant families in the southeast. * represents significance levels of $p < 0.01$. The eight dominant families were selected based on the criteria of having substantial endemic components (i.e. many endemic species) in the southwest and/or southeast, high species disparity between the two regions, and where sufficient data was available.

Table S7 Summary statistics of chi-squared tests for the diversification rates distributions of all and monotypic genera across the two regions. Values shown are degrees of freedom (DF), X-squared and p-values.

Table S8 Summary statistics of spearman rank correlation coefficient tests for number of species, divergence time and percentage of species (50–100%) in each region: **a)** all genera, **b)** genera with > 30 species each, **c)** genera with > 40 species each. Values shown are degree of correlation (ρ) and p-values. *, **, and *** represent significance levels of $p < 0.01$, 0.001 , and 0.0001 respectively.

Table S9 Genera that are unusually species-rich compared to the background diversification rate of their respective families in the southwest and southeast, under pure birth and high relative extinction models. κ = relative extinction rates.

Table S10 Genera that are unusually species-poor compared to the background diversification rate of their respective families in the southwest and southeast, under pure birth and high relative extinction models. κ = relative extinction rates. '*' marks non-monotypic genera.

Fig. S0 BAMM estimates of diversification rate for **a)** *Acacia* (Fabaceae); **b)** Epacrids (Ericaceae); **c)** *Eucalyptus* (Myrtaceae). Stars indicate significant accelerations of net diversification (i.e. speciation rate) over the background diversification rate – green star = southwestern clade, orange

star = southeastern clade, blue star = clade with both southwest and southeastern taxa, black star = non-temperate clade. Estimated rates of net species diversification ($\text{sp sp}^{-1} \text{My}^{-1}$) are colour-coded as indicated (red–blue; high–low rate). Illustrations were sourced from www.plantillustrations.org and modified under the Creative Commons Attribution 2.0 license: **a)** *Acacia buxifolia*; **b)** *Epacris*; **c)** *Eucalyptus obliqua*.

Fig. S1 Chronograms constructed through BEAST for the respective plant families, including error bars on node age estimates (95% CI): **a)** Apiaceae, **b)** Droseraceae, **c)** Fabaceae (Mirbelioids), **d)** Lamiaceae (Prostantherioideae), **e)** Orchidaceae (Diuridieae).

Fig. S2 Different cutoffs for genera diversification through time, with number of genera divergence across 10–5 Myr time-bins for the southwest and southeast Australian temperate regions: **a)** > 50% species diversity in each genera, **b)** > 65%, **c)** > 90%, **d)** > 100%. The trend lines show the moving average across each time-bin (green – southwest, orange – southeast). Grey horizontal trend line tracks the change in mean sea surface temperature, adapted from Zachos *et al.* (2001). Vertical grey line marks the Eocene–Oligocene boundary.

Fig. S3 Relationship between clade age and **a)** total species richness, **b)** diversification rate under the high relative extinction model ($\kappa = 0.9$), **c)** species richness of genera younger than 30 Myr, **d)** diversification rate under the high relative extinction model ($\kappa = 0.9$) of genera younger than 30 Myr, **e)** species richness of genera with > 40 species each, **f)** diversification rate under the high relative extinction model ($\kappa = 0.9$) of genera with > 40 species each.

Fig. S4 Relationship between the percentage of species (50–100%) in each region and diversification rate under the high relative extinction model ($\kappa = 0.9$) across: **a)** all genera, **b)** genera with > 30 species each. Circle size is proportional to species richness within each genus.

Fig. S5 Confidence intervals of expected clade species diversity according to the age of stem group, given a fixed background diversification rate (r) for each of the respective families or subfamilies/tribes. The black dashed lines are the 95% confidence intervals in the absence of extinction ($\kappa = 0$). The red lines are the 95% confidence intervals under the high relative extinction model ($\kappa = 0.9$). Green diamonds represent genera with > 75% of their species diversity in the southwest biodiversity hotspot. Orange squares represent genera with > 75 % of their species diversity in the southeast Australian temperate region. Blue diamonds represent genera with less than 75% diversity in each of the regions; **a)** *Drosera* sections (Droseraceae), **b)** Restionaceae, **c)** Proteaceae, **d)** Goodeniaceae, **e)** Epacrid tribes (Ericaceae), **f)** Epacrids (Ericaceae), **g)** Chamaeleacieae (Myrtaceae), **h)** Melaleuceae (Myrtaceae), **i)** Leptospermeae (Myrtaceae), **j)** Malvaceae, **k)** Asparagaceae, **l)** *Acacia* (Fabaceae), **m)** Mirbelioids (Fabaceae). **n)** Prostantherioideae (Lamiaceae), **o)** Elaeocarpaceae, **p)** Hemerocallidaceae, **q)** Mackinlayoideae (Apiaceae), **r)** Rhamnaceae, **s)** Boronieae (Rutaceae), **t)** Schoeneae (Cyperaceae); **u)** Gnaphalieae (Asteraceae); **v)** Diuridieae (Orchidaceae), **w)** Haemodoraceae, **x)** Loganiaceae, **y)** Stylidiaceae. See accompanying supplementary material 2 for specific details of all genera (species numbers, stem age, and proportion found in the southwest/southeast). Background illustrations were sourced from www.plantillustrations.org and modified under the Creative Commons Attribution 2.0 license: **a)** *Drosera*; **b)** Restionaceae; **c)** *Banksia coccinea*; **d)** *Lechenaultia biloba*; **e)** *Epacris*; **f)** *Styphelia triflora*; **g)** *Darwinia macrostegia*; **h)** *Beaufortia sparsa*; **i)** *Leptospermum scoparium*; **j)** *Lasiopetalum glutinosum*; **k)** *Thysanotus isantherus*; **l)** *Acacia*; **m)** *Gompholobium*; **n)** *Prostanthera phylicifolia*; **o)** *Tetratheca*; **p)** *Dianella ensifolia*; **q)** *Xanthosia rotundifolia*; **r)** *Cryptandra alpina*; **s)** *Diplolaena dampieri*; **t)** *Schoenus nigricans*; **u)** *Rhodanthe manglesii*; **v)** *Pterostylis*; **w)** *Anigozanthos manglesii*; **x)** *Logania albiflora*; **y)** *Stylium violaceum*.

Fig. S6 Speciation rate (lineages per Myr⁻¹) plotted through time for extant lineages through the BAMM analyses of **a,b)** *Eucalyptus* (Myrtaceae), **c,d)** *Acacia* (Fabaceae), **e,f)** Epacrids (Ericaceae). Red lines represent mean rate and blue envelop represents the 95% confidence interval from the Bayesian posterior. **a,c,e:** specified number of rate shifts = 1, **b,d,f:** specified number of rate shifts = 5.

Fig. S7 Lineage-through-time plots of eight dominant species-rich families and proportion of missing taxa (species) through time of **a)** Proteaceae, **b)** Mirbelioids (Fabaceae), **c)** Epacrids (Ericaceae), **d)** Chamelaucieae (Myrtaceae), **e)** Restionaceae, **f)** Schoeneae (Cyperaceae), **g)** Rutaceae, **h)** Asteraceae. The proportion of missing taxa was calculated by subtracting the number of genera sampled from the sum of their extant species diversity at each cumulative time interval. Illustrations were sourced from www.plantillustrations.org and modified under the Creative Commons Attribution 2.0 license: **a)** *Banksia coccinea*; **b)** *Gompholobium*; **c)** *Styphelia triflora*; **d)** *Darwinia macrostegia*; **e)** Restionaceae; **f)** *Schoenus nigricans*; **g)** *Boronia heterophylla*; **h)** *Rhodanthe manglesii*.

Fig. S8 Lineage-through-time plots of extant genera in the southwest (green) and southeast (orange) temperate region of Australia **a)** genera with > 75% species diversity in each of the respective regions; **b)** endemic genera and genera not found in the other region; **c)** monotypic genera. Illustration **b)** *Cephalotus follicularis* is sourced from www.plantillustrations.org and modified under the Creative Commons Attribution 2.0 license.

Fig. S9 Lineage-through-time plots (LTT) **a)** *Drosera*; **b)** Restionaceae; **c)** Proteaceae; **d)** Goodeniaceae; **e)** Ericaceae; **f)** Chamelaucieae; Myrtaceae; **g)** Malvaceae; **h)** Asparagaceae; **i)** Mirbelieae, Fabaceae; **j)** Lamiaceae; **k)** Hemerocallidaceae; **l)** Apiaceae; **m)** Rhamnaceae; **n)** Rutaceae; **o)** Cyperaceae; **p)** Asteraceae; **q)** Orchidaceae; **r)** Haemodoraceae; **s)** Loganiaceae; **t)** Elaeocarpaceae; **u)** species LTT for *Utricularia* (Lentibulariaceae). Illustrations were sourced from www.plantillustrations.org and modified under the Creative Commons Attribution 2.0 license: **a)** *Drosera*; **b)** Restionaceae; **c)** *Banksia coccinea*; **d)** *Lechenaultia biloba*; **e)** *Styphelia triflora*; **f)** *Darwinia macrostegia*; **g)** *Lasiopetalum glutinosum*; **h)** *Thysanotus isantherus*; **i)** *Gompholobium*; **j)** *Prostanthera phylicifolia*; **k)** *Dianella ensifolia*; **l)** *Xanthosia rotundifolia*; **m)** *Cryptandra alpina*; **n)** *Boronia heterophylla*; **o)** *Schoenus nigricans*; **p)** *Rhodanthe manglesii*; **q)** *Corybas pictus*; **r)** *Anigozanthos manglesii*; **s)** *Logania albiflora*; **t)** *Tetratheca*; **u)** *Utricularia longifolia*.

Fig. S10 BAMM estimates of diversification rate for *Acacia* (Fabaceae) under different global sampling fraction regimes: **a)** 20%; **b)** 40%; **c)** 60%; **d)** 80%; **e)** 100%. Estimated rates of net species diversification ($\text{sp sp}^{-1} \text{My}^{-1}$) are colour-coded as indicated (red–blue; high–low rate).

Fig. S11 BAMM estimates of diversification rate for Epacrids (Ericaceae) under different global sampling fraction regimes: **a)** 20%; **b)** 50%; **c)** 80%; **d)** 100%. Estimated rates of net species diversification ($\text{sp sp}^{-1} \text{My}^{-1}$) are colour-coded as indicated (red–blue; high–low rate).

Fig. S12 BAMM estimates of diversification rate for *Eucalyptus* (Myrtaceae) under different global sampling fraction regimes: **a)** 20%; **b)** 50%; **c)** 70%; **d)** 90%. Estimated rates of net species diversification ($\text{sp sp}^{-1} \text{My}^{-1}$) are colour-coded as indicated (red–blue; high–low rate).

Fig. S13 BAMM 95% credible rate shift configurations for *Acacia* (Fabaceae) under different global samplping fraction regimes: **a)** 20%; **b)** 40%; **c)** 60%; **d)** 80%; **e)** 100%. F = probability; percentage of samples in posterior assigned to shift configurations.

Fig. S14 BAMM 95% credible rate shift configurations for Epacrids (Ericaceae) under different global sampling fraction regimes: **a)** 20%; **b)** 50%; **c)** 80%; **d)** 100%. F = probability; percentage of samples in posterior assigned to shift configurations.

Fig. S15 BAMM 95% credible rate shift configurations for *Eucalyptus* (Myrtaceae) under different global sampling fraction regimes: **a)** 20%; **b)** 50%; **c)** 70%; **d)** 90%. F = probability; percentage of samples in posterior assigned to shift configurations.

Table S1a.

southwest		Area (ha)	southeast		Area (ha)
AW	Avon wheatbelt	9,517,104	AA	Australian Alps	1,232,981
ESP	Esperance Plains	2,921,327	BEL	Ben Lomond	657,500
GS	Geraldton sandplains	3,142,149	BBS	Brigalow Belt S	27,219,776
JF	Jarra Forest	4,509,074	CP	Cobar peneplain	7,385,346
MAL	Mallee	7,397,559	DRP	Darling Riverine Plains	10,699,769
SWA	Swan coastal plain	1,525,798	EYB	Eyre york block	6,120,409
WAR	Warren	844,771	FLI	Flinders	
			FLB	Flinders Lofty block	6,615,765
			KAN	Kanmantoo	812,415
			KIN	King	425,567
			MDD	Murray darling depression	19,958,349
			NAN	Nandewar	2,701,977
			NET	New England Tablelands	3,002,213
			NNC	NSW N Coast	3,996,591
			NSS	NSW South western slopes	8,681,126
			RIB	Riverina	
			SCP	SE Coastal Plain	1,749,237
			SEC	SE Corner	2,532,053
			SHE	SE Highlands	8,375,961
			SEQ	SE Qld	7,804,921
			SB	Sydney Basin	3,629,597
			TCH	Tas Central highlands	767,849
			TNS	Tas N Slopes	623,103
			TSR	Tas S ranges	757,228
			TSE	Tas SE	1,131,822
			TWE	Tas W	1,565,077
			VVP	Vic volcanic fields	2,440,340
			VM	Victorian Midlands	3,469,789
Total area (ha)		29,857,782			134,356,761

Table S1b

Family	southwest		southeast	
	no. of genera	no. of species	no. of genera	no. of species
1) Apiaceae (Mackinlayoideae subf.)	8	51	5	28
2) Asparagaceae (Lomandrioideae subf.)	7	100	5	52
3) Asteraceae (Gnaphalieae tribe)	55	201	52	277
4) Cyperaceae (Schoeneae tribe)	13	205	13	128
5) Droseraceae (<i>Drosera</i>)	1	84	1	13
6) Elaeocarpaceae (Tremandraceae)	3	37	1	23
7) Ericaceae (Epacrids)	23	398	31	303
8a) Fabaceae (<i>Acacia</i>)	1	472	1	352
8b) Fabaceae (Mirbelioids)	23	505	21	285
9) Goodeniaceae	11	215	8	97
10) Haemodoraceae	6	76	1	5
11) Hemerocallidaceae	12	40	9	34
12) Lamiaceae (Prostantherioideae subf.)	16	174	9	111
13) Loganiaceae	5	37	7	34
14) Malvaceae (Lasiopetaleae tribe)	7	114	6	33
15a) Myrtaceae (Chamelaucieae tribe*)	30	559	15	111
15b) Myrtaceae (<i>Eucalyptus</i>)	1	263	1	314
15c) Myrtaceae (Leptospermeae tribe)	6	69	2	86
15d) Myrtaceae (Melaleuceae tribe)	9	1481	2	428
16) Orchidaceae (Diurideae tribe)	21	366**	24	500**
17) Proteaceae	15	810	26	309
18) Restionaceae	28	146	17	51
19) Rhamnaceae (Pomaderreae tribe)	11	101	6	122
20) Rutaceae (Boronieae tribe)	14	130	12	216
21) Stylidiaceae	2	211	5	27

Note: Dilleniaceae was not included even though it is among the top 20 species-rich families in Australia (*Hibbertia* has c. 150 Australian species), as the taxonomic species concepts for SWA and SEA are non-comparable, with two different taxonomists working on the genus in the two regions. Similarly, Thymelaeaceae was not included (*Pimelea* has c. 110 Australian species) as not enough genetic data was available at the time of this study.

Table S2.

Family	References
Asparagaceae (Lomandrioideae subf.)	Chen <i>et al.</i> (2013)
Asteraceae (Gnaphalieae tribe)	Bergh and Linder (2009); Nie <i>et al.</i> (2016)
Cyperaceae (Schoeneae tribe)	Besnard <i>et al.</i> (2009); Escudero and Hipp (2013); Hoffmann <i>et al.</i> (2015)
Elaeocarpaceae (Tremandraceae*)	Crayn <i>et al.</i> (2006); Heibl and Renner (2012)
Ericaceae (Epacrids)	Wagstaff <i>et al.</i> (2010); Puente-Lelièvre <i>et al.</i> (2013); Liu <i>et al.</i> (2014)
Goodeniaceae	Beaulieu <i>et al.</i> (2013); Jabaily <i>et al.</i> (2014); Barreda <i>et al.</i> (2015)
Haemodoraceae	Janssen and Bremer (2004); Hopper <i>et al.</i> (2009)
Hemerocallidaceae	McLay and Bayly (2016)
Lentibulariaceae (<i>Utricularia</i>)	Jobson <i>et al.</i> (2017)
Loganiaceae	Foster <i>et al.</i> (2014)
Malvaceae (Lasiopetaleae tribe)	Richardson <i>et al.</i> (2015)
Myrtaceae	Thornhill <i>et al.</i> (2012); Thornhill <i>et al.</i> (2015)
Proteaceae	Sauquet <i>et al.</i> (2009)
Restionaceae	Litsios <i>et al.</i> (2014)
Rhamnaceae (Pomaderreae tribe)	Onstein <i>et al.</i> (2015)
Rutaceae (Boronieae tribe)	Salvo <i>et al.</i> (2010); Bayly <i>et al.</i> (2013)
Styliadiaceae	Wagstaff and Wege (2002); Beaulieu <i>et al.</i> (2013); Barreda <i>et al.</i> (2015)

Note: Dating estimates were derived from comparable studies that have similar calibration points only. Only one study was selected (included above) when different calibration points were used in different studies.

Table S3.

Group	Age (Ma)	Node constrained	Prior distribution of node	References	Gene regions and source
Apiaceae (Mackinlayoideae subf.)	87	Stem node of Mackinlayoideae	Log-normal Mean: 1.0 SD: 0.3 Offset: 84.5	Nicolas and Plunkett (2009)	<i>rpl16, trnD</i> ; GenBank
Orchidaceae (Diurideae tribe)	56.2	Stem node of Diurideae	Log-normal Mean: 0.01 SD: 1.0 Offset: 56.2	Chomicki <i>et al.</i> (2015)	ITS, <i>trnL-trnF, matK</i> ; GenBank
Droseraceae (<i>Drosera</i>)	70	Stem node of Droseraceae	Log-normal Mean: 0.01 SD: 2.0 Offset: 70	Fiz-Palacios <i>et al.</i> (2011)	ITS, <i>rbcL</i> ; Rivadavia <i>et al.</i> (2003)
Droseraceae (<i>Drosera</i>)	25	Stem node of <i>Drosera</i>	Log-normal Mean: 0.01 SD: 2.0 Offset: 25	*Biswal <i>et al.</i> (2017)	ITS, <i>rbcL</i> ; Rivadavia <i>et al.</i> (2003)
Fabaceae (Mirbelioids)	54.1	Stem node of Mirbelioids	Log-normal Mean: 54.1 SD: 0.5 Offset: 0.0	Lavin <i>et al.</i> (2005)	ITS, <i>trnL</i> ; GenBank
Fabaceae (Mirbelioids)	43.9	Stem node of <i>Daviesia</i>	Log-normal Mean: 43.9 SD: 0.4 Offset: 0.0	Cook <i>et al.</i> (2015)	ITS, <i>trnL</i> ; GenBank
Fabaceae (<i>Acacia</i>)	23	Stem node of <i>Acacia s.s.</i>	Log-normal Mean: 0.01 SD: 10 Offset: 23.0	Miller <i>et al.</i> (2013)	ITS, ETS, <i>rpl32-trnL, matK, psbA-trnH, trnL</i> and <i>trnL-F</i> ; Mishler <i>et al.</i> (2014)
Myrtaceae (<i>Eucalyptus</i>)	53.2	Crown of Eucalypts (<i>Eucalyptus, Angophora, Corymbia</i>)	Exponential Mean: 1.03 Offset: 53.2	Thornhill <i>et al.</i> (2012); Thornhill <i>et al.</i> (2015)	ITS, ETS, <i>matK npsbA</i> ; González-Orozco <i>et al.</i> (2016)
Myrtaceae (<i>Eucalyptus</i>)	53.2	Crown of Eucalypts (<i>Eucalyptus, Angophora, Corymbia</i>)	Exponential Mean: 1.03 Offset: 53.2	Thornhill <i>et al.</i> (2012); Thornhill <i>et al.</i> (2015)	ITS, ETS, <i>matK npsbA</i> ; González-Orozco <i>et al.</i> (2016)
Myrtaceae (<i>Eucalyptus</i>)	46.7	Crown of <i>Angophora</i> and <i>Corymbia</i>	Exponential Mean: 2.17 Offset: 45	Thornhill <i>et al.</i> (2012); Thornhill <i>et al.</i> (2015)	ITS, ETS, <i>matK npsbA</i> ; González-Orozco <i>et al.</i> (2016)
Myrtaceae (<i>Eucalyptus</i>)	33.9	Crown of <i>Eucalyptus</i>	Exponential Mean: 0.895 Offset: 33.9	Thornhill <i>et al.</i> (2012); Thornhill <i>et al.</i> (2015)	ITS, ETS, <i>matK npsbA</i> ; González-Orozco <i>et al.</i> (2016)

Table S3 continued.

Group	Age (Ma)	Node constrained	Prior distribution of node	References	Gene regions and source
Ericaceae	40.5	Minimum constraint on stem of <i>Rhododendron</i> separating <i>Cassiope</i>	Log-normal Mean: 60.0 Offset: 1.25	Wagstaff <i>et al.</i> (2010)	<i>atpB-rbcL</i> , <i>psbA</i> , <i>psbA-trnH</i> , <i>trnH</i> ; GenBank
Ericaceae (Epacrids)	21.5	Stem node of Stypheliaeae	Log-normal Mean: 21.5 SD: 0.1 Offset: 0.0	Puente-Lelièvre <i>et al.</i> (2013)	ITS, <i>rbcL</i> , <i>matK</i> , <i>trnH-psbA</i> , <i>atpB-rbcL</i> ; Puente-Lelièvre <i>et al.</i> (2016)
Ericaceae (Epacrids)	23.3	Stem node of Richeae	Log-normal Mean: 23.3 SD: 0.8 Offset: 7.0	Liu <i>et al.</i> (2014)	ITS, <i>rbcL</i> , <i>matK</i> , <i>trnH-psbA</i> , <i>atpB-rbcL</i> ; Puente-Lelièvre <i>et al.</i> (2016)
Lamiaceae (Prostantheroideae subf.)**	56	Stem node of Lamiaceae	Log-normal Mean: 14.0 SD: 1.25 Offset: 49.0	Roy and Lindqvist (2015); Kumar <i>et al.</i> (2017)	ETS, <i>trnT</i> , <i>ndnF</i> ; GenBank

*older fossils have been noted for *Drosera* however these are unpublished (J.Conran pers. comm.), nevertheless, the relative ages of selected *Drosera* clades can be estimated from these analyses and assess for different responses in diversification dynamics within the genus.

**Similarly, the paucity of Lamiaceae fossils limits accurate estimates of absolute node ages within the family (Roy & Lindqvist, 2015). More detailed studies are needed within the family to assess for the accuracy of the dated node ages.

Table S4.

	Pure birth model ($\kappa = 0$)	High extinction model ($\kappa = 0.9$)
	p-value	p-value
All genera	0.0002**	0.0002**
endemic genera	< 0.0001***	< 0.0001***

Table S5.

Family	Pure birth model ($\kappa = 0$)		high extinction model ($\kappa = 0.9$)	
	all genera	endemic genera	all genera	endemic genera
Apiaceae	0.0071	0.0355	0.0029	0.0067
Asparagaceae	0.0213	0.0630	0.0075	0.0086
Asteraceae	0.0043	0.0289	NA	0.0138
Cyperaceae	0.0115	0.0038	0.0031	0.0001
Droseraceae	0.0055	0.0732	0.0023	0.0129
Elaeocarpaceae	0.0289	NA	0.0047	NA
Ericaceae	0.0069	-0.0108*	-0.0016*	-0.0081*
Fabaceae	0.0008	-0.0156*	0.0005	-0.0011*
Goodeniaceae	0.0052	0.0355	0.0026	0.0067
Haemodoraceae	NA	NA	NA	NA
Lamiaceae	-0.0106*	0.0525	-0.0017*	0.0127
Loganiaceae	0.0090	NA	-0.0009*	NA
Malvaceae	0.0202	0.0630	0.0067	0.0086
Myrtaceae	0.0259	0.0334	0.0129	0.0147
Orchidaceae	-0.0034*	0.0260	-0.0024*	0.0043
Proteaceae	-0.0104*	-0.0163*	-0.0056*	-0.0073*
Restionaceae	0.0078	0.0192	0.0050	0.0084
Rhamnaceae	-0.0254*	0.0229	-0.0036*	0.0048
Rutaceae	0.0030	0.0130	0.0015	0.0036
Hemerocallidaceae	0.0067	-0.0693*	0.0034	-0.0095*
Styliadiaceae	NA	NA	NA	NA

Note: Diversification estimates for Haemodoraceae could not be completed as only one genus (*Haemodorum*) was present in the southeast (this analyse require at least one genus per region). Similarly, estimates for Styliadiaceae could not be obtained due to insufficient data.

Table S6.

Family	Pure birth model ($\kappa = 0$)			High extinction model ($\kappa = 0.9$)		
	DF	Chi-squared	p-value	DF	Chi-squared	p-value
Restionaceae ^a	1	0.8333	0.3613	1	0.5333	0.4652
Proteaceae ^a	1	2.8571	0.09097	1	3.4571	0.06298
Myrtaceae ^a	1	0.5302	0.4665	1	0.0589	0.8082
Ericaceae ^a	1	0.5952	0.4404	1	1.5238	0.217
Fabaceae ^a	1	0.1837	0.7347	1	0.7347	0.3914
Cyperaceae ^b	1	0.2143	0.6434	1	0.2143	0.6434
Asteraceae ^b	1	0.1865	0.6658	1	0.0342	0.8533
Rutaceae ^b	1	0.2143	0.6434	1	0.8571	0.3545
^aCombined analysis: southwest 5 dominant families	4	-	0.0213*	4	-	0.0226*
^bCombined analysis: southeast 3 dominant families	2	-	0.3628	2	-	0.4128
All genera	1	3.8538	0.0496*	1	1.7609	0.1845
All genera without <i>Caladenia</i>	1	3.1609	0.0754	1	1.2827	0.2574

Table S7.

	DF	X-squared	p-value
All genera	7	7.0103	0.4278
monotypic genera	11	6.0871	0.8675

Table S8a.

	Pure birth model ($\kappa = 0$)		High extinction model ($\kappa = 0.9$)	
	ρ	p-value	ρ	p-value
southwest				
number of species	0.4400	<0.0001***	0.6643	<0.0001***
divergence time (Myr)	-0.7333	<0.0001***	-0.5143	<0.0001***
% of species (50–100)	-0.3229	0.0002**	-0.4355	<0.0001***
southeast				
number of species	0.5903	<0.0001***	0.7392	<0.0001***
divergence time (Myr)	-0.8021	<0.0001***	-0.6503	<0.0001***
% of species (50–100)	0.2545	0.0265*	0.2439	0.0337

Table S8b.

	Pure birth model ($\kappa = 0$)		High extinction model ($\kappa = 0.9$)	
	ρ	p-value	ρ	p-value
southwest				
number of species	0.0497	0.7985	0.1845	0.3381
divergence time (Myr)	-0.9242	<0.0001***	-0.8843	<0.0001***
% of species (50–100)	0.0193	0.921	-0.0383	0.8437
southeast				
number of species	-0.2310	0.5208	-0.1945	0.5902
divergence time (Myr)	0.9394	<0.0001***	0.9394	<0.0001***
% of species (50–100)	0.5515	0.0984	0.5152	0.1276

Table S8c.

	Pure birth model ($\kappa = 0$)		High extinction model ($\kappa = 0.9$)	
	ρ	p-value	ρ	p-value
southwest				
divergence time (Myr)	-0.7881	0.0002**	-0.7605	0.0004**
divergence time < 30 (Myr)	-0.9862	<0.0001***	-0.9118	<0.0001***
southeast				
divergence time < 30 (Myr)	-0.9643	0.0004**	-0.8929	0.0068**

Table S9

southwest hotspot		southeast non-hotspot	
$\kappa = 0.0$	$\kappa = 0.9$	$\kappa = 0.0$	$\kappa = 0.9$
Droseraceae	Droseraceae	Ericaceae	Ericaceae
<i>Drosera</i> sect. <i>Lamprolepis</i>	<i>Drosera</i> sect. <i>Lamprolepis</i>	<i>Epacris</i>	<i>Epacris</i>
<i>Drosera</i> sect. <i>Erythrorhiza</i>		<i>Trochocarpa</i>	
<i>Drosera</i> sect. <i>Stolonifera</i>		<i>Melichrus</i>	
Proteaceae	Proteaceae	Fabaceae	Fabaceae
<i>Banksia</i> ser. <i>Dryandra</i>	<i>Banksia</i> ser. <i>Dryandra</i>	<i>Acacia</i> subg.	<i>Acacia</i> subg.
Ericaceae	Ericaceae	<i>Botrycephalae</i>	<i>Botrycephalae</i>
<i>Leucopogon</i> <i>sen. lat.</i>	<i>Leucopogon</i> <i>sens. lat.</i>	<i>Pultenaea</i>	
<i>Andersonia</i>		Rhamnaceae	Rhamnaceae
<i>Astroloma</i>		<i>Pomaderris</i>	<i>Pomaderris</i>
Myrtaceae		Rutaceae	
<i>Darwinia</i>		<i>Zieria</i>	
<i>Verticordia</i>		Cyperaceae	
Malvaceae	Malvaceae	<i>Baumea</i>	
<i>Lasiopetalum</i>	<i>Lasiopetalum</i>	Asteraceae	Asteraceae
<i>Thomasia</i>	<i>Thomasia</i>	<i>Leiocarpa</i>	<i>Leiocarpa</i>
<i>Guichenotia</i>		<i>Cassinia</i>	
Asparagaceae		Orchidaceae	Orchidaceae
<i>Thysanotus</i>		<i>Caladenia</i>	<i>Caladenia</i>
Fabaceae			
<i>Gastrolobium</i>			
Cyperaceae			
<i>Schoenus</i>			
Asteraceae	Asteraceae		
<i>Asteridea</i>	<i>Asteridea</i>		
<i>Actinobole</i>			
<i>Pithocarpa</i>			
Orchidaceae	Orchidaceae		
<i>Diuris</i>	<i>Diuris</i>		
Haemodoraceae	Haemodoraceae		
<i>Conostylis</i>	<i>Conostylis</i>		
<i>Anigozanthos</i>			
Styliadiaceae	Styliadiaceae		
<i>Styliodium</i>	<i>Styliodium</i>		

Table S10

southwest hotspot		southeast non-hotspot	
$\kappa = 0.0$	$\kappa = 0.9$	$\kappa = 0.0$	$\kappa = 0.9$
Rhamnaceae	Rhamnaceae	Fabaceae	Fabaceae
<i>Siegfriedia</i>	<i>Siegfriedia</i>	<i>Stonesiella</i>	<i>Stonesiella</i>
<i>Blackalnia</i>	<i>Blackalnia</i>	<i>Goodia*</i>	<i>Goodia*</i>
Fabaceae	Fabaceae	<i>Viminaria</i>	<i>Viminaria</i>
<i>Erichsema</i>	<i>Erichsema</i>	Malvaceae	Malvaceae
<i>Viminaria</i>	<i>Viminaria</i>	<i>Seringia</i>	<i>Seringia</i>
<i>Euchilopsis</i>	<i>Euchilopsis</i>	<i>Trochocarpa</i>	
<i>Callistachys</i>	<i>Callistachys</i>	<i>Melichrus</i>	
<i>Ptychosema</i>	<i>Ptychosema</i>	Ericaceae	Ericaceae
Ericaceae	Ericaceae	<i>Prionotes</i>	<i>Prionotes</i>
<i>Needhamiella</i>	<i>Needhamiella</i>	<i>Montitega</i>	<i>Montitega</i>
<i>Oligarrhena</i>	<i>Oligarrhena</i>	Myrtaceae	Myrtaceae
<i>Cosmelia</i>	<i>Cosmelia</i>	<i>Ochrosperma*</i>	<i>Ochrosperma*</i>
Lamiaceae	Lamiaceae	Asteraceae	Asteraceae
<i>Brachysola*</i>	<i>Brachysola*</i>	<i>Acanthocladium</i>	<i>Acanthocladium</i>
	<i>Physopsis*</i>	<i>Pterygopappus</i>	<i>Pterygopappus</i>
	<i>Cyanostegia*</i>	<i>Calomeria</i>	<i>Calomeria</i>
Myrtaceae	Myrtaceae	<i>Triptilodiscus</i>	<i>Triptilodiscus</i>
<i>Actinodium*</i>	<i>Actinodium*</i>	<i>Leucophyta</i>	<i>Leucophyta</i>
	Elaeocarpaceae	<i>Parantennaria</i>	<i>Parantennaria</i>
	<i>Tremandra*</i>	<i>Polycalymma</i>	<i>Polycalymma</i>
Goodeniaceae	Goodeniaceae	<i>Lemooria</i>	<i>Lemooria</i>
<i>Diaspasis</i>	<i>Diaspasis</i>	<i>Ewartia*</i>	<i>Ewartia*</i>
<i>Pentaptilon</i>	<i>Pentaptilon</i>	Cyperaceae	Cyperaceae
Asteraceae	Asteraceae	<i>Ptilothrix</i>	<i>Ptilothrix</i>
<i>Argyroglossis</i>	<i>Argyroglossis</i>	<i>Costularia*</i>	<i>Costularia*</i>
<i>Decazesia</i>	<i>Decazesia</i>	Restionaceae	Restionaceae
<i>Hyalochlamys</i>	<i>Hyalochlamys</i>	<i>Eurychorda</i>	<i>Eurychorda</i>
<i>Triptilodiscus</i>	<i>Triptilodiscus</i>	<i>Winifredia</i>	<i>Winifredia</i>
<i>Leucophyta</i>	<i>Leucophyta</i>	<i>Coleocarya</i>	<i>Coleocarya</i>
<i>Feldstonia</i>	<i>Feldstonia</i>	<i>Calorophus*</i>	<i>Calorophus*</i>
<i>Lemooria</i>	<i>Lemooria</i>	Hemerocallidaceae	Hemerocallidaceae
<i>Pterochaeta</i>	<i>Pterochaeta</i>	<i>Herpolirion</i>	<i>Herpolirion</i>
<i>Fitzwillia</i>	<i>Fitzwillia</i>	Orchidaceae	Orchidaceae
<i>Gilruthia</i>	<i>Gilruthia</i>	<i>Leporella</i>	<i>Leporella</i>
<i>Quinqueremulus</i>	<i>Quinqueremulus</i>	<i>Burnettia</i>	<i>Burnettia</i>
<i>Cephalosorus</i>	<i>Cephalosorus</i>	<i>Rimacola</i>	<i>Rimacola</i>
<i>Bellida</i>	<i>Bellida</i>	<i>Leptoceras</i>	<i>Leptoceras</i>
<i>Gilberta</i>	<i>Gilberta</i>	<i>Pheladenia</i>	<i>Pheladenia</i>
Rutaceae	Rutaceae	<i>Caleana</i>	<i>Caleana</i>
<i>Chorilaena</i>	<i>Chorilaena</i>	Droseraceae	Droseraceae
Cyperaceae	Cyperaceae	<i>Drosera sect. Bryastrum</i>	<i>Drosera sect. Bryastrum</i>
<i>Tetraria*</i>	<i>Tetraria*</i>		<i>Drosera sect. Arcturia*</i>
	<i>Evandra*</i>	Proteaceae	Proteaceae
	<i>Mesomelaena*</i>	<i>Bellendena</i>	<i>Bellendena</i>
Restionaceae	Restionaceae	<i>Cenarrhenes</i>	<i>Cenarrhenes</i>
<i>Catacolea</i>	<i>Catacolea</i>	<i>Agastachys</i>	<i>Agastachys</i>
<i>Taraxis</i>	<i>Taraxis</i>	<i>Floydia</i>	<i>Floydia</i>
<i>Cytogonidium</i>	<i>Cytogonidium</i>	<i>Sympilionema*</i>	<i>Sympilionema*</i>
<i>Tyrbastes</i>	<i>Tyrbastes</i>		
<i>Kulinia</i>	<i>Kulinia</i>		
	<i>Platychorda*</i>		

	<i>Tremulina</i> *
	<i>Alexgeorgea</i> *
Hemerocallidaceae	Hemerocallidaceae
<i>Hodgsoniola</i>	<i>Hodgsoniola</i>
	<i>Stypandra</i> *
	<i>Chamaescilla</i> *
Apiaceae	Apiaceae
<i>Chlaenosciadium</i>	<i>Chlaenosciadium</i>
<i>Homalosciadium</i>	<i>Homalosciadium</i>
<i>Schoenolaena</i>	<i>Schoenolaena</i>
Orchidaceae	Orchidaceae
<i>Leporella</i>	<i>Leporella</i>
<i>Spiculaea</i>	<i>Spiculaea</i>
<i>Leptoceras</i>	<i>Leptoceras</i>
<i>Epiblema</i>	<i>Epiblema</i>
<i>Praecoxanthus</i>	<i>Praecoxanthus</i>
Droseraceae	Droseraceae
<i>Drosera</i> sect. <i>Stelogyne</i>	<i>Drosera</i> sect. <i>Stelogyne</i>
Haemodoraceae	Haemodoraceae
<i>Blancoa</i>	<i>Blancoa</i>
<i>Macropidia</i>	<i>Macropidia</i>
Proteaceae	Proteaceae
<i>Acidonia</i>	<i>Acidonia</i>
<i>Franklandia</i> *	<i>Franklandia</i> *

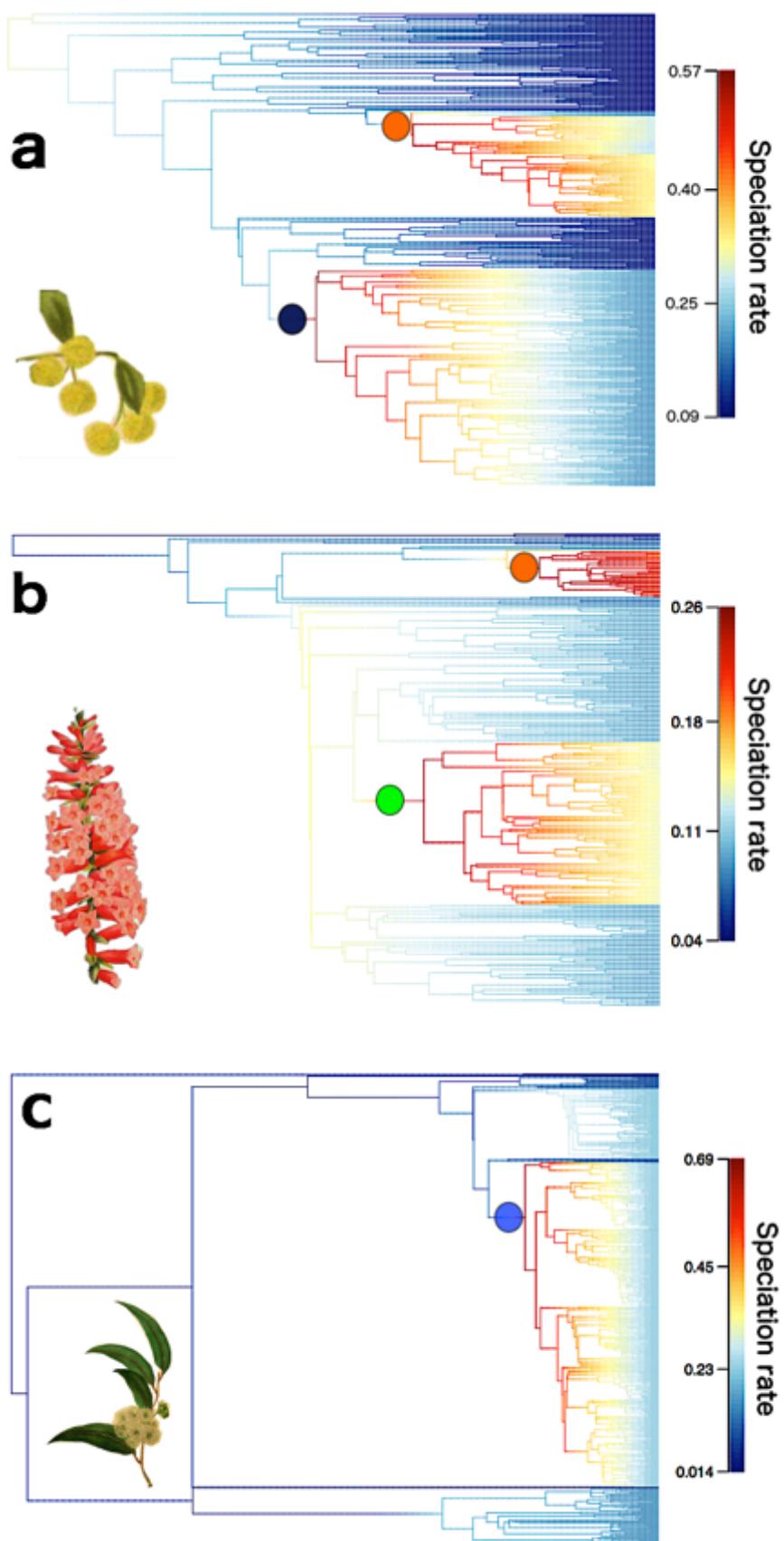


Fig. S0

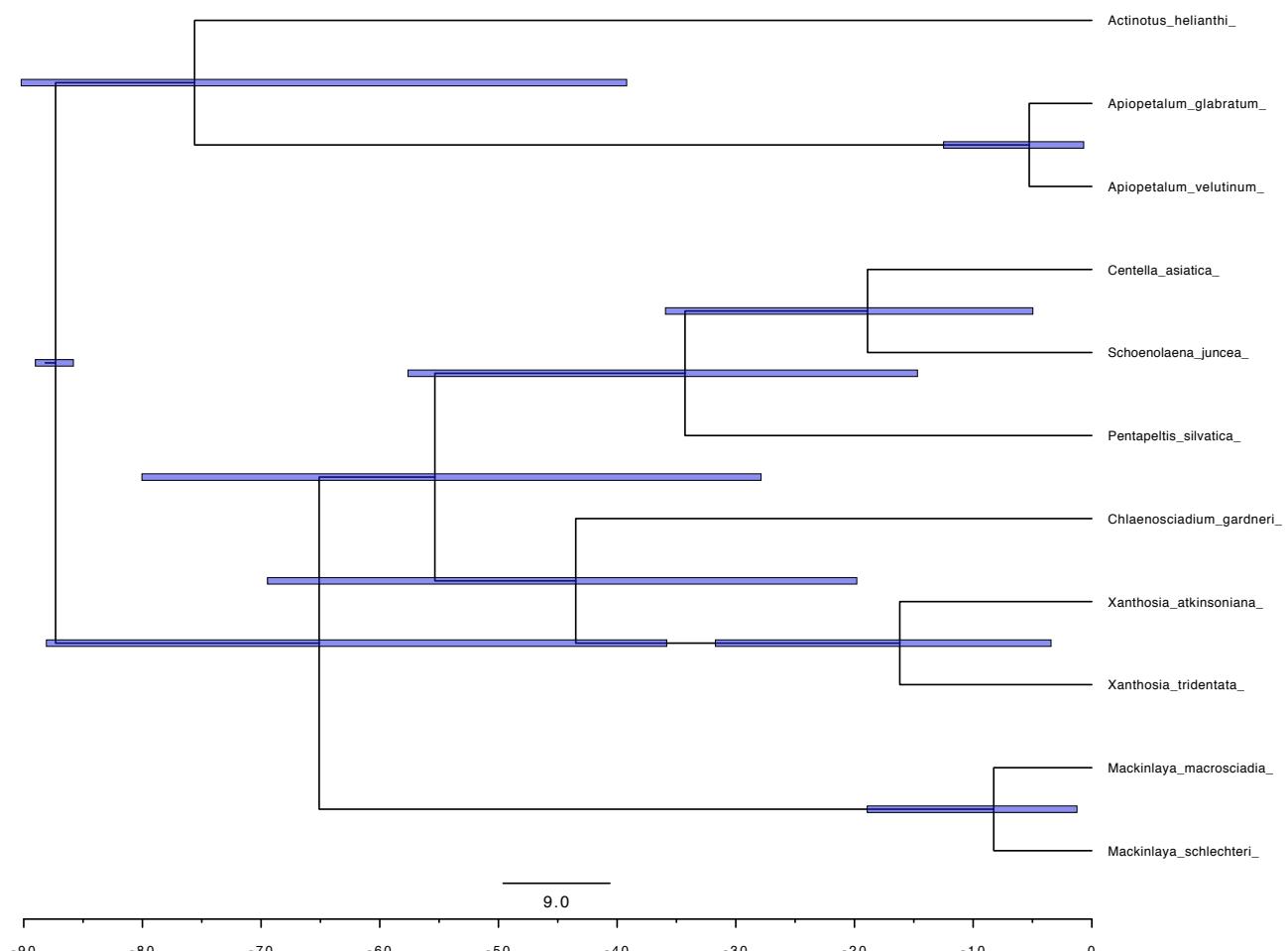


Fig. S1a Mackinlayoideae (Apiaceae) chronogram.

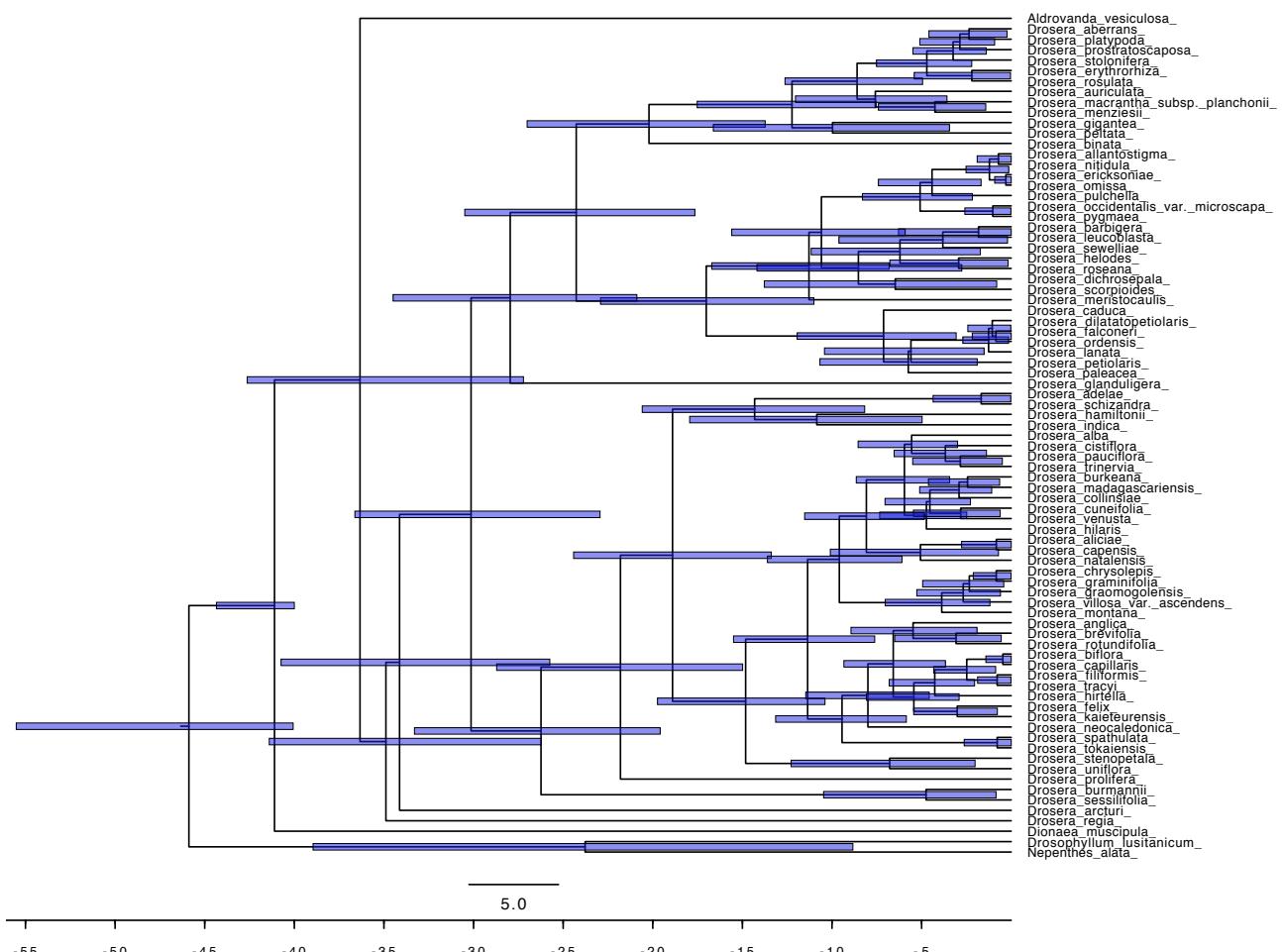


Fig. S1b *Drosera* (Droseraceae) chronogram.

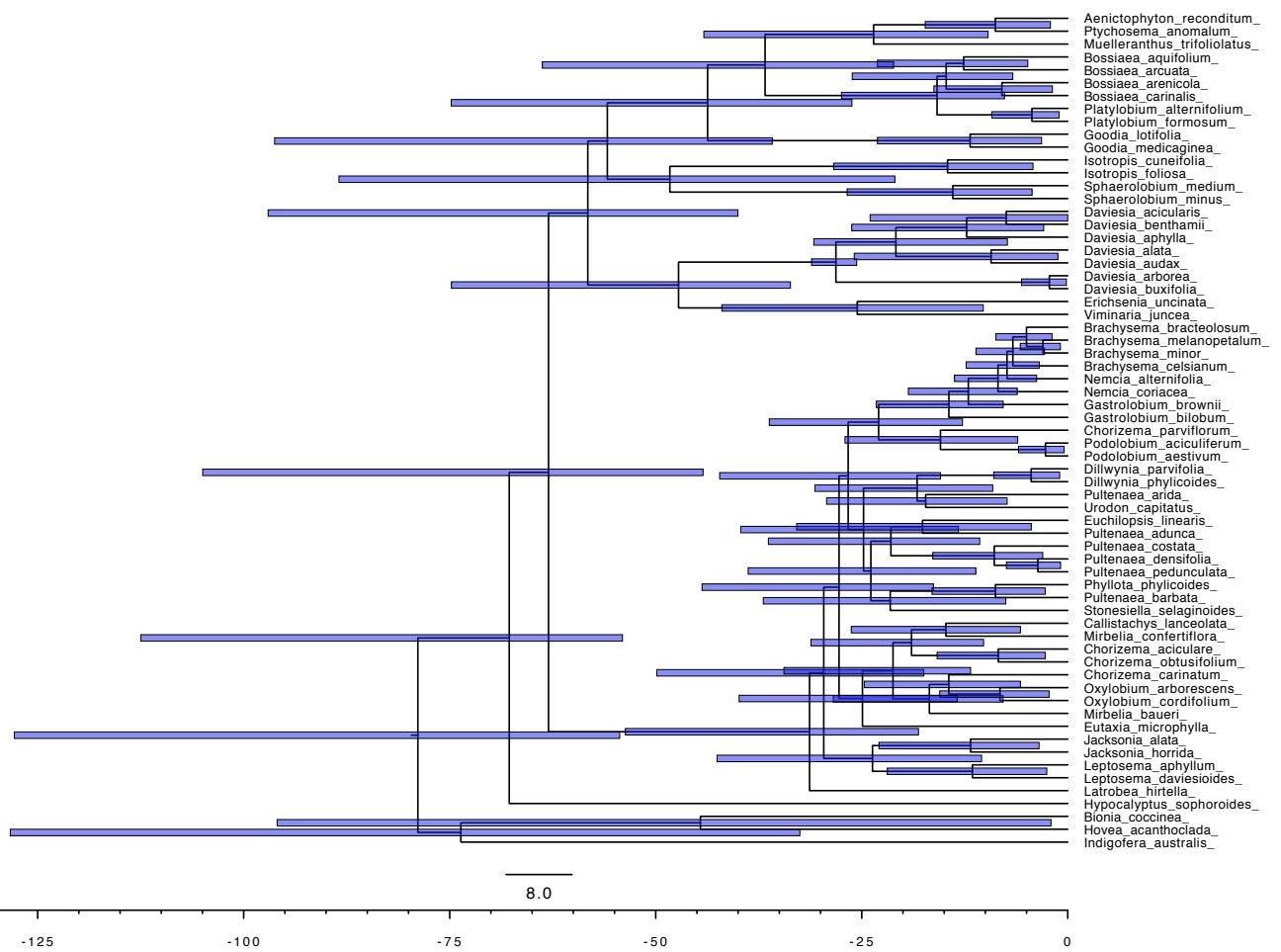


Fig. S1c Mirbelioids (Fabaceae) chronogram.

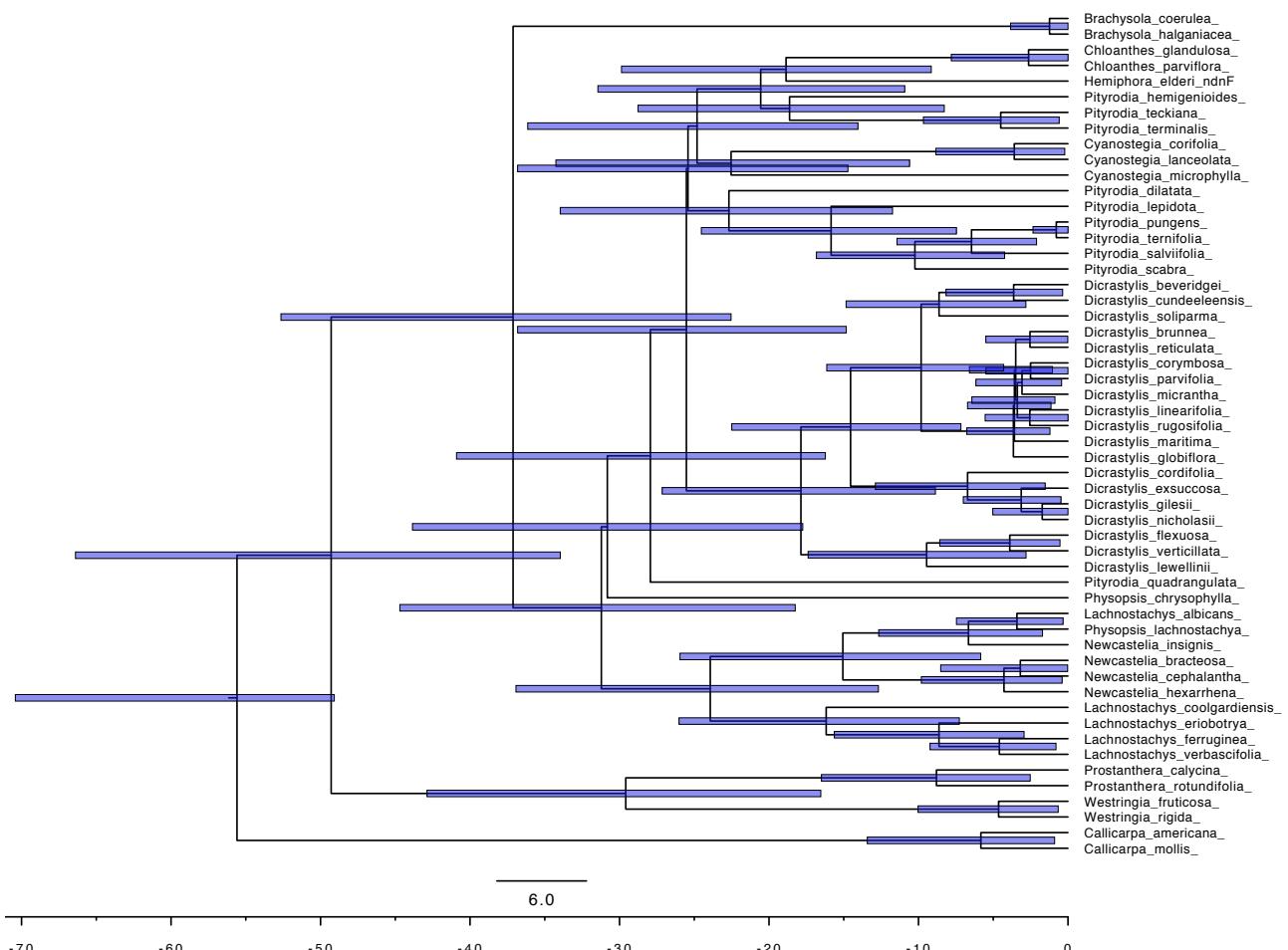


Fig. S1d Prostantherioideae (Lamiaceae) chronogram.

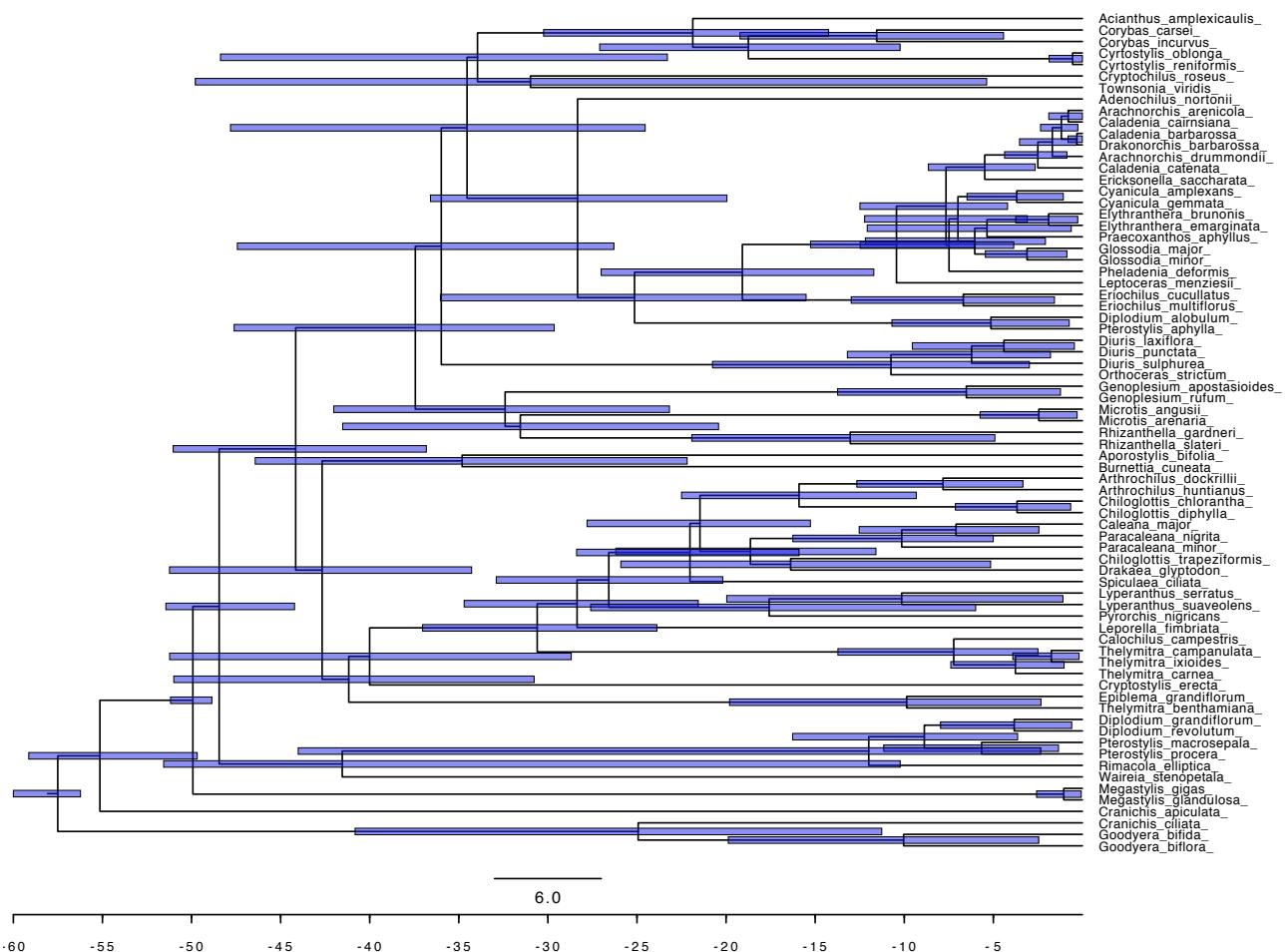


Fig. S1e Diuridieae (Orchidaceae) chronogram.

Fig. S2

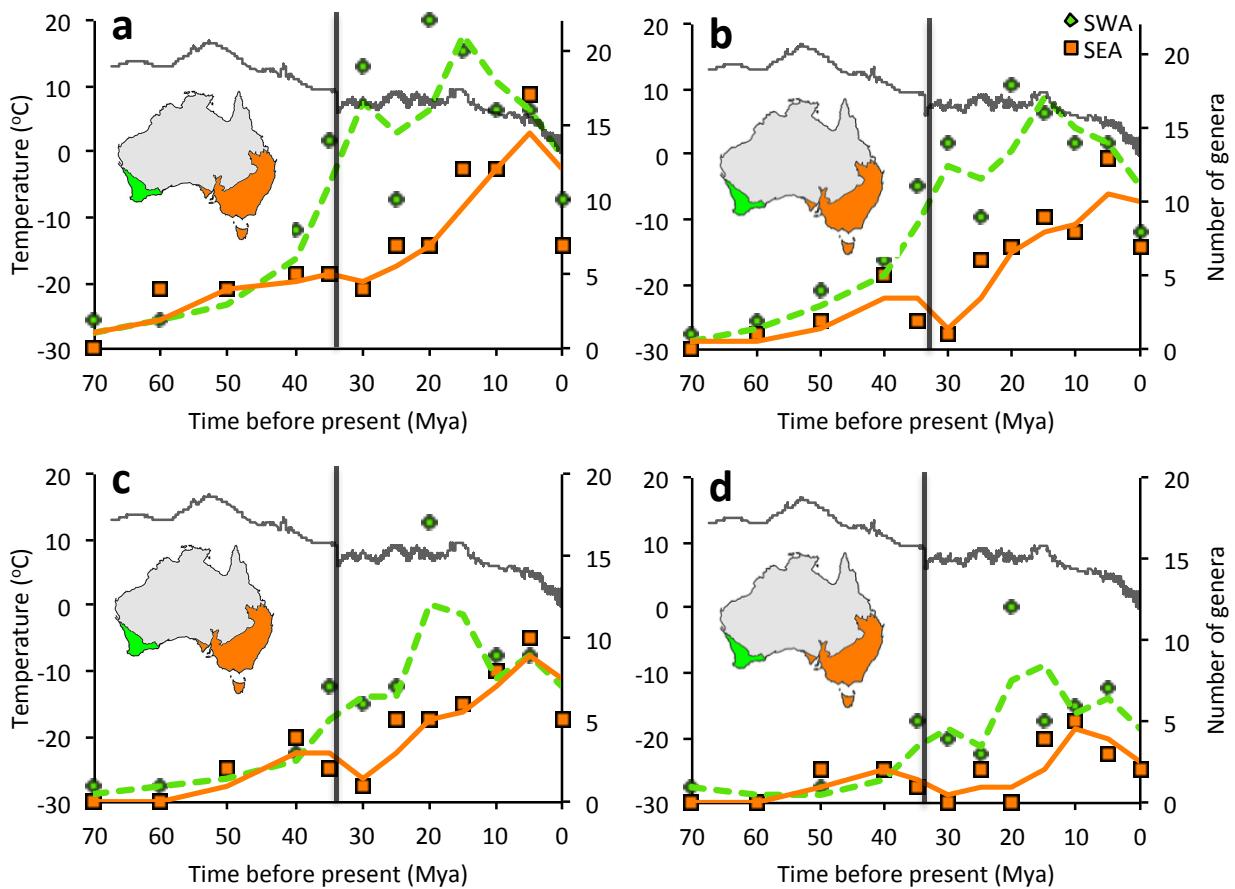


Fig. S3

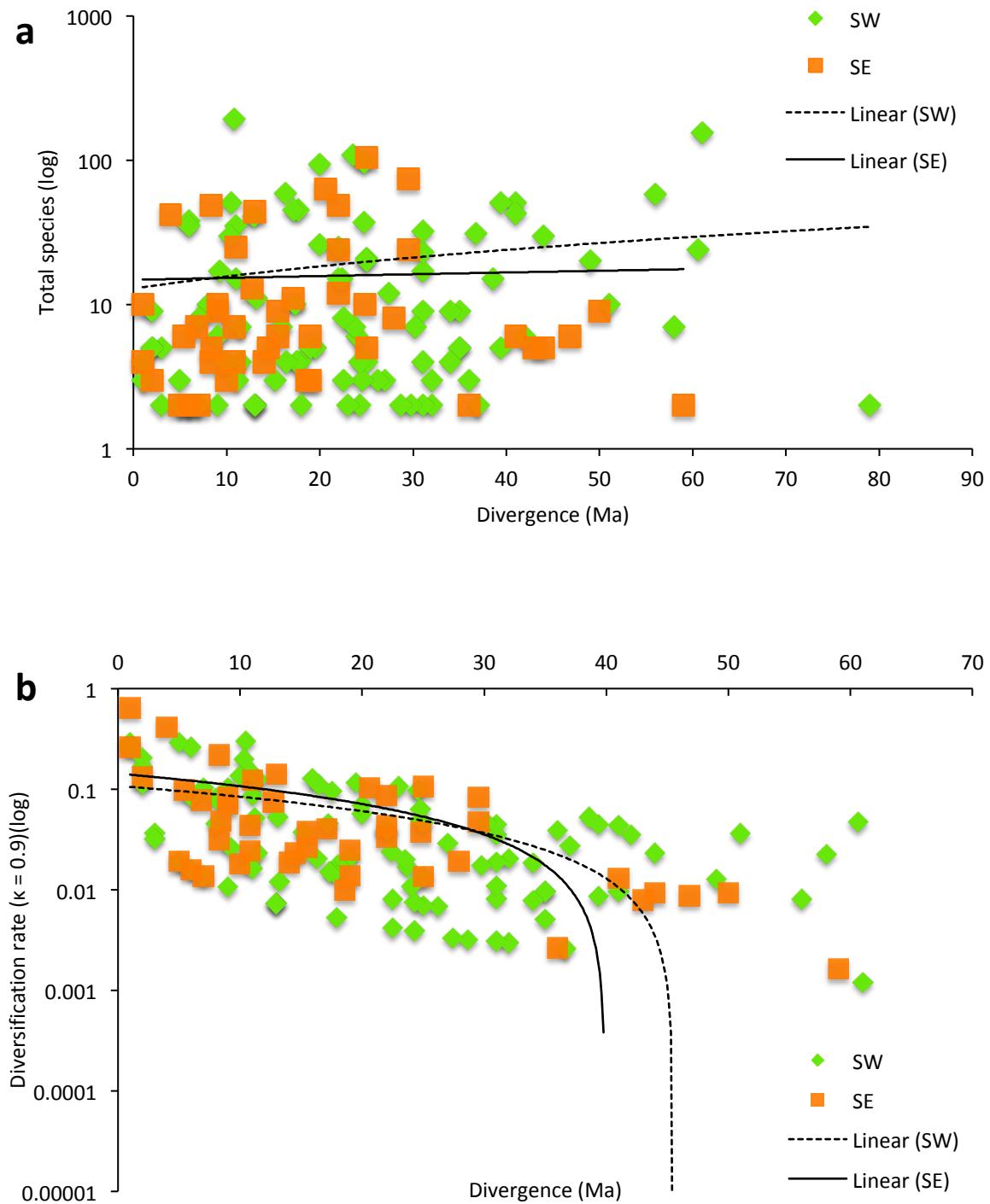


Fig. S3 continued.

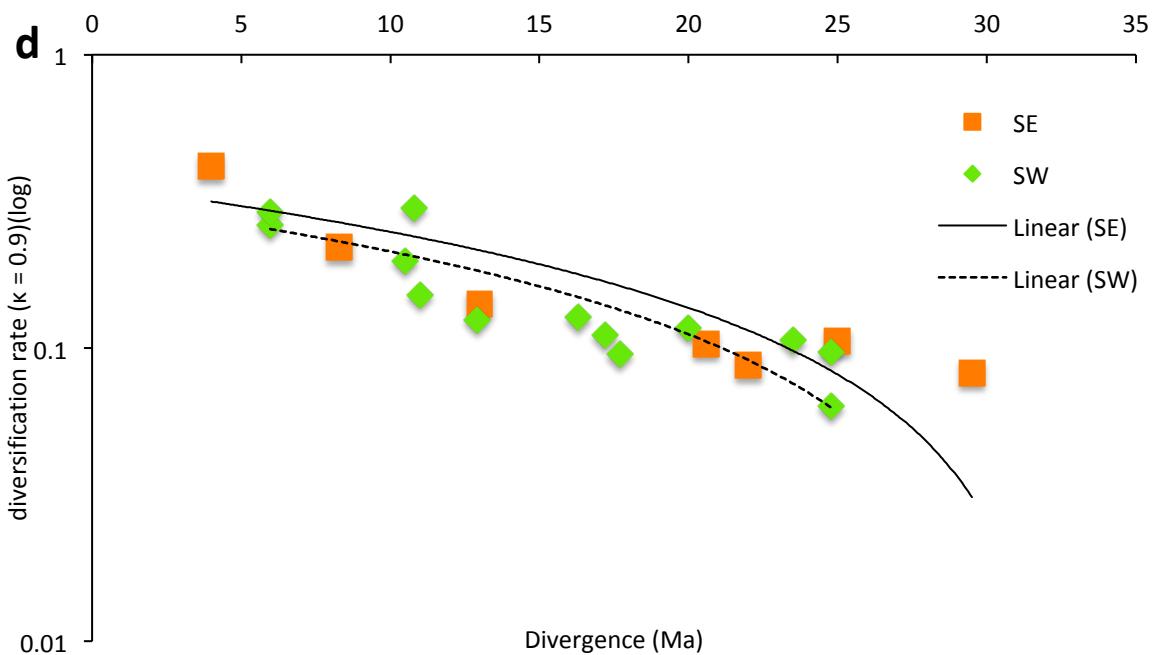
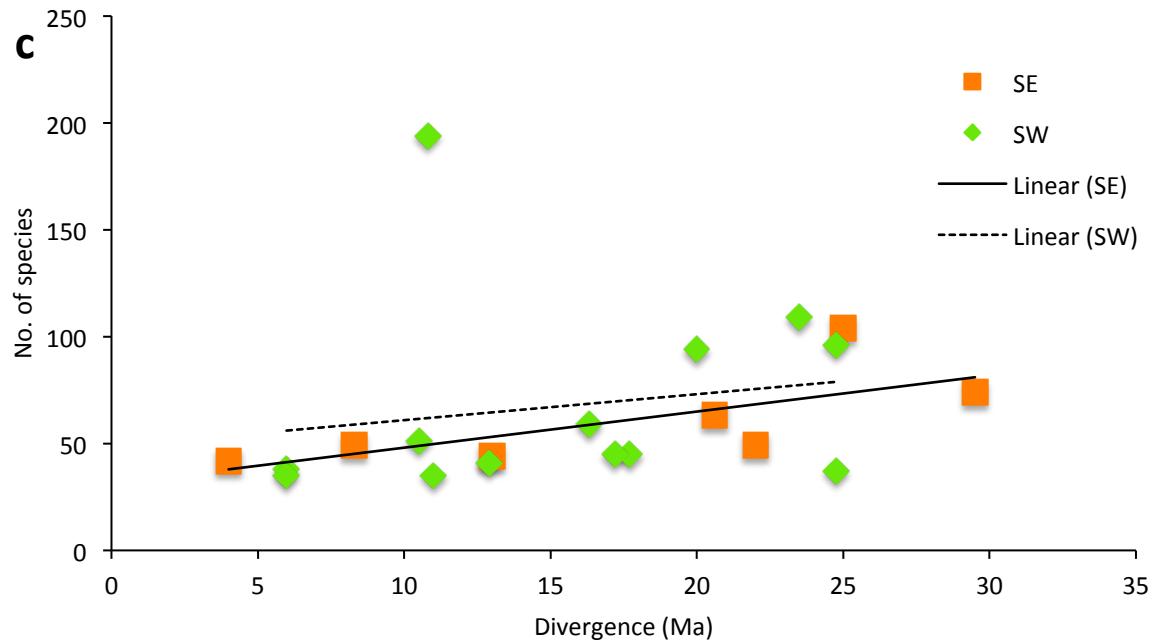


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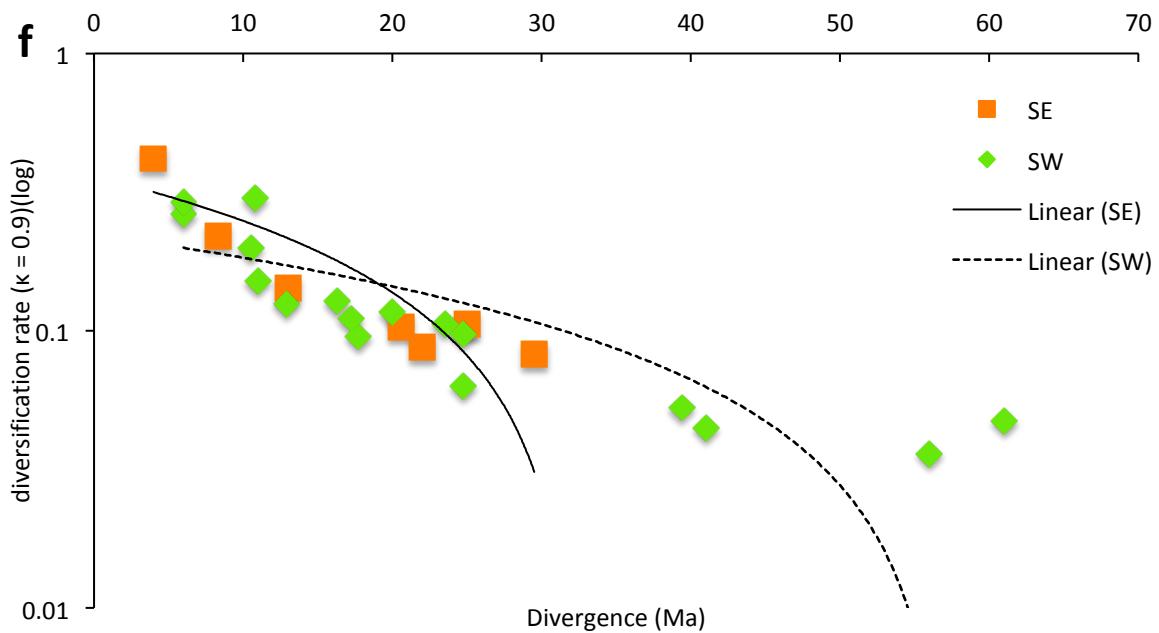
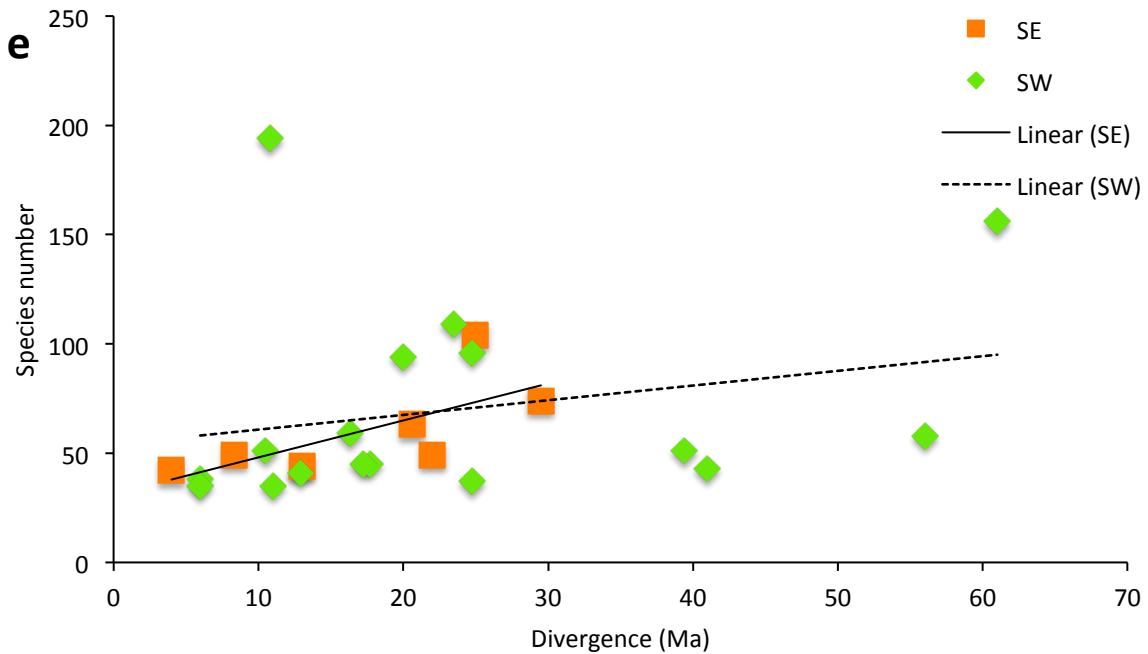


Fig. S4

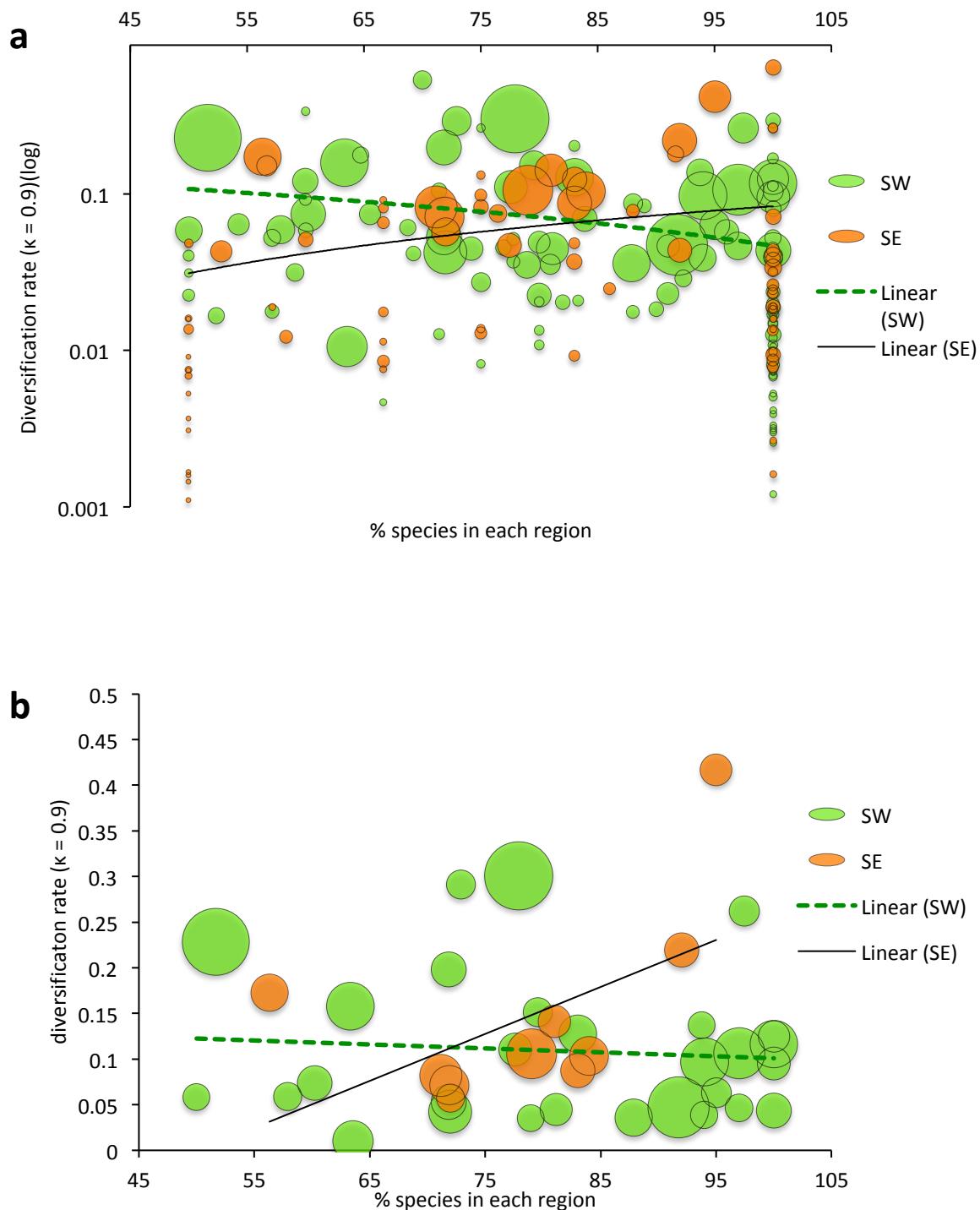


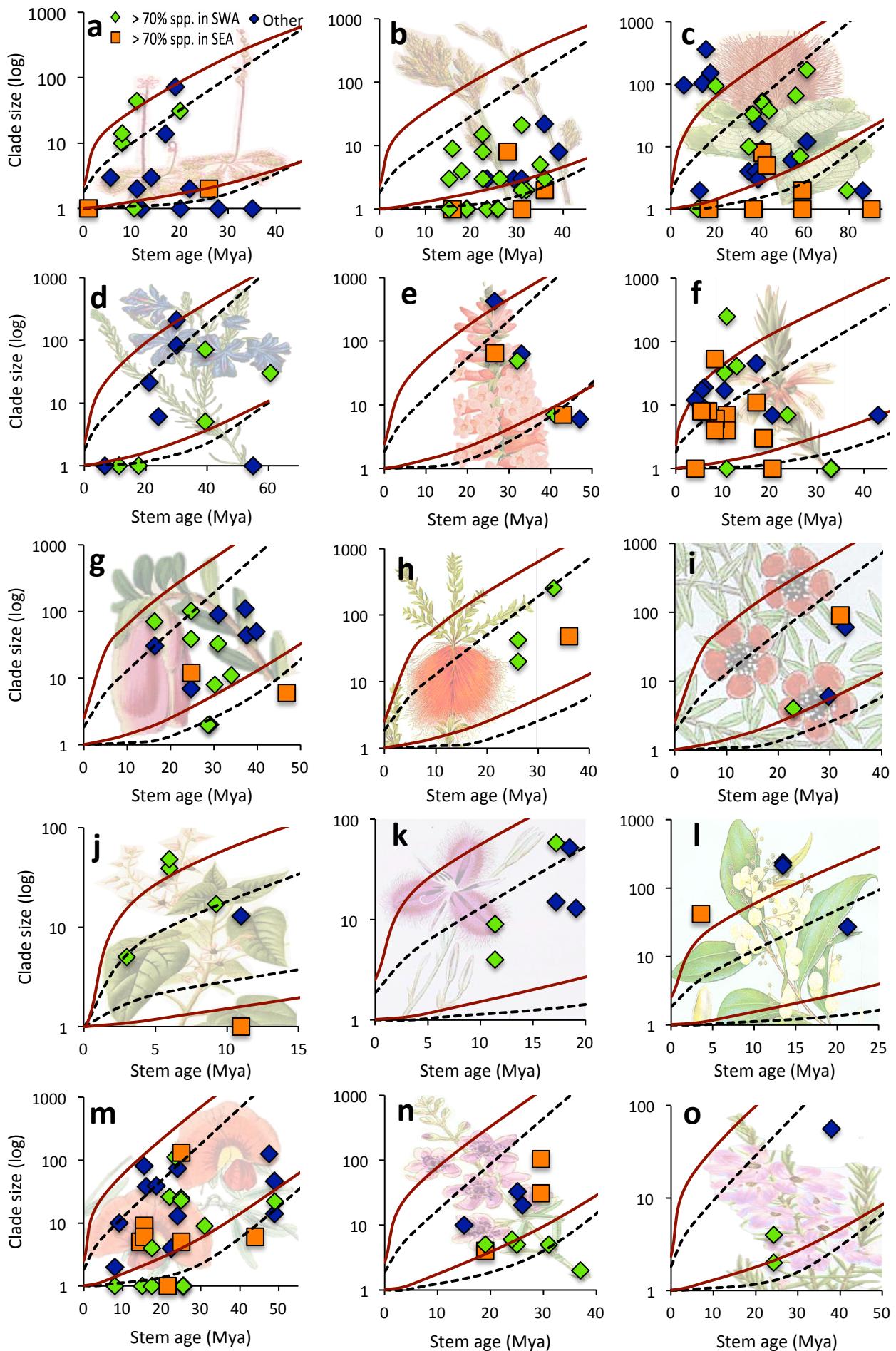
Fig. S5

Fig. S5 continued.

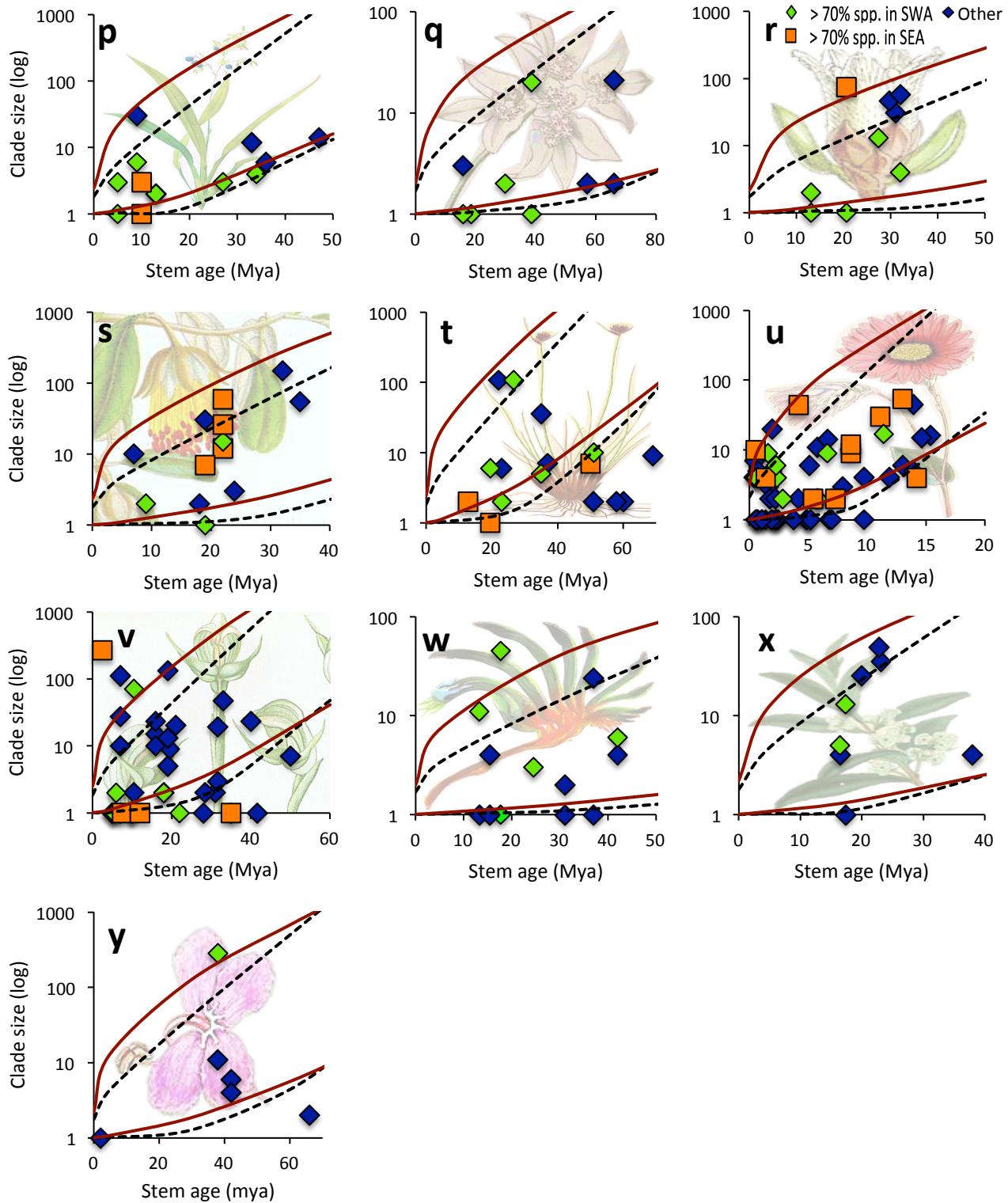


Fig. S6

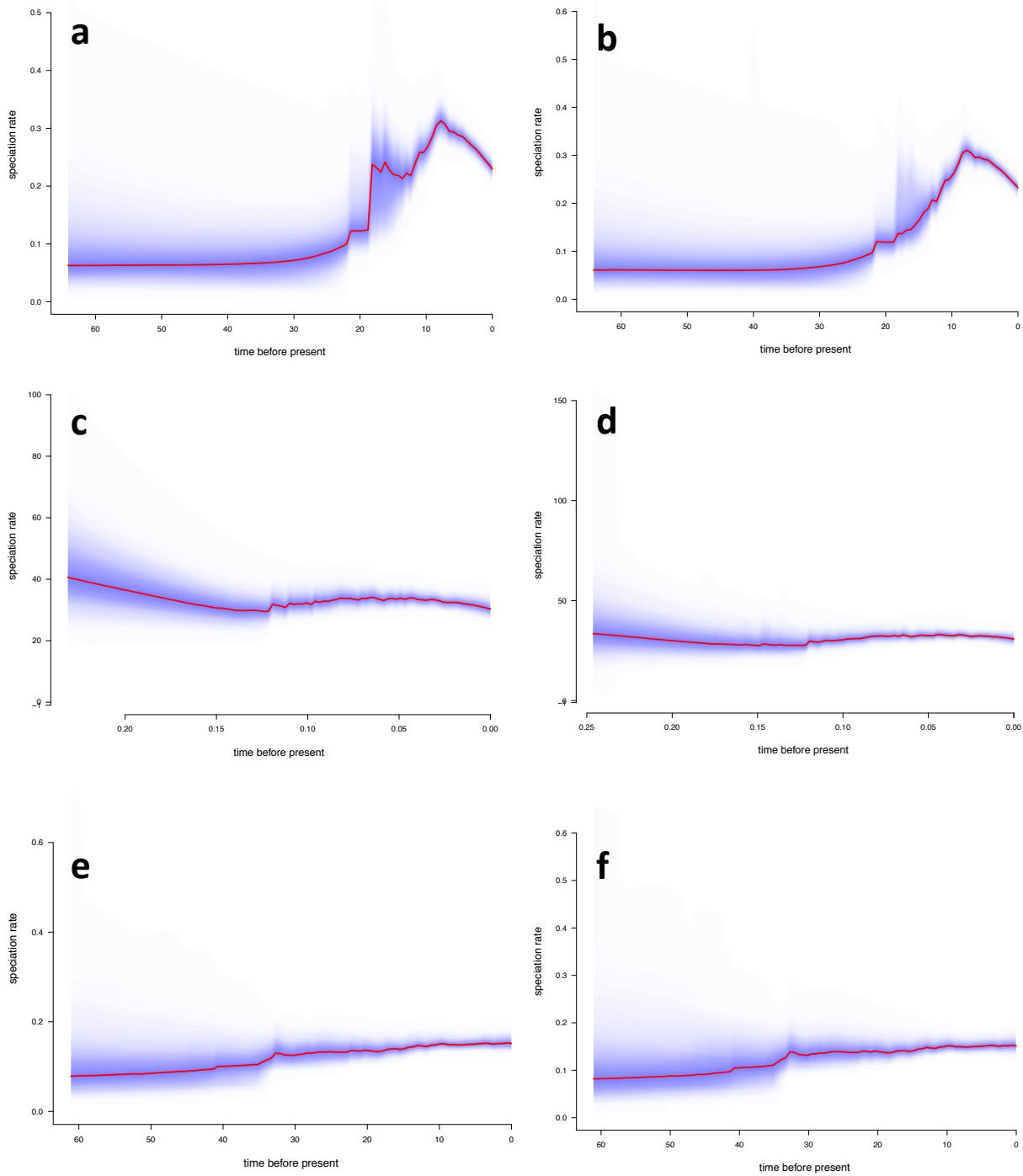


Fig. S7

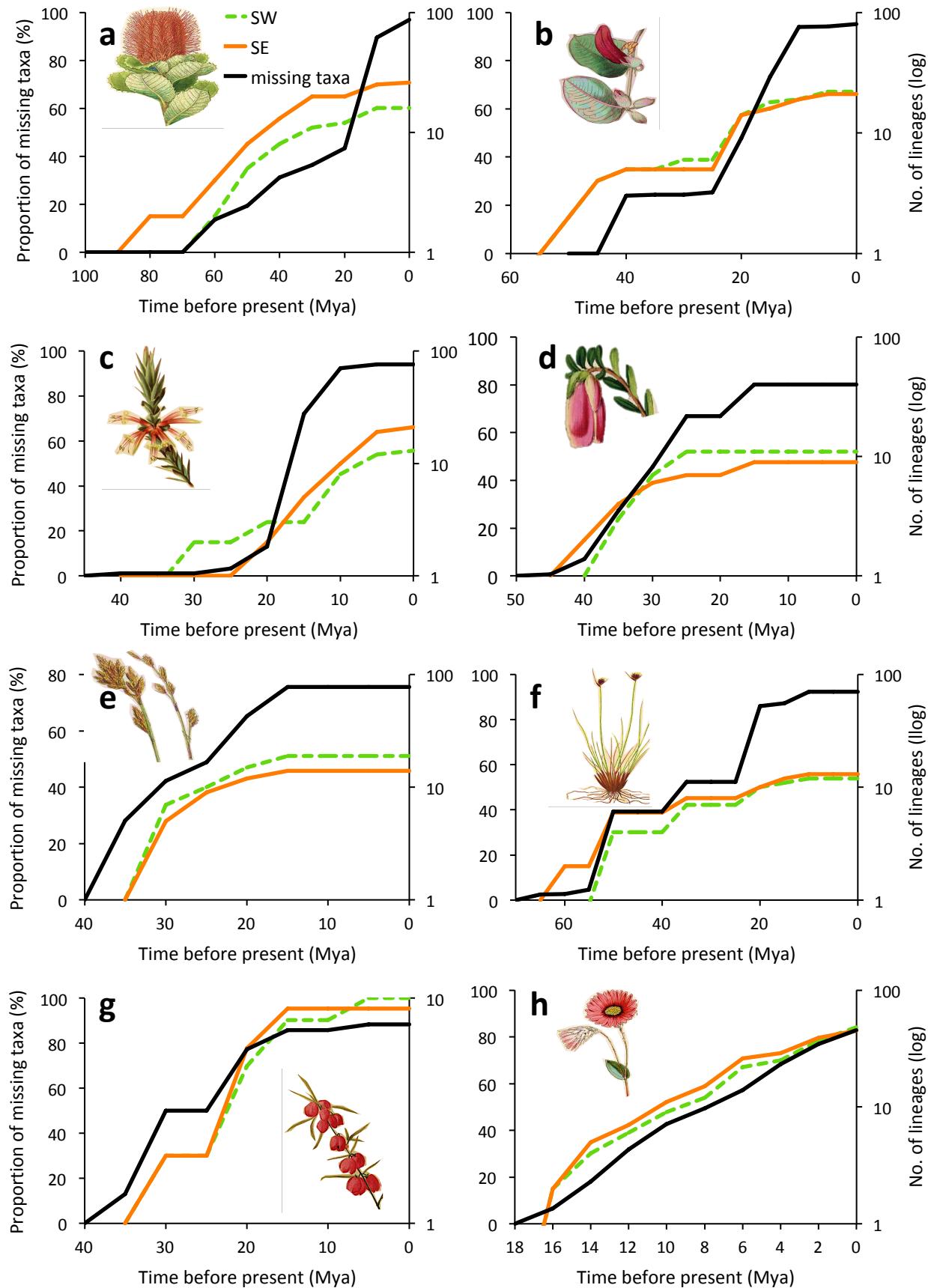


Fig. S8

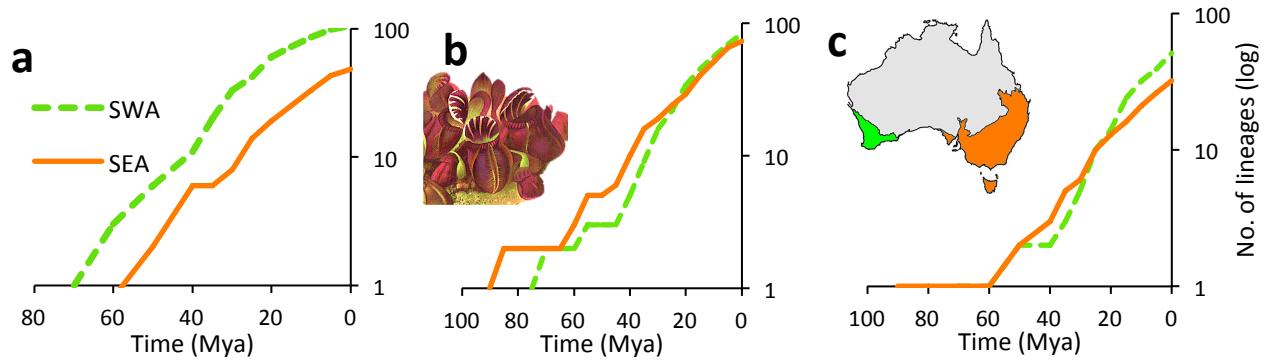


Fig. S9

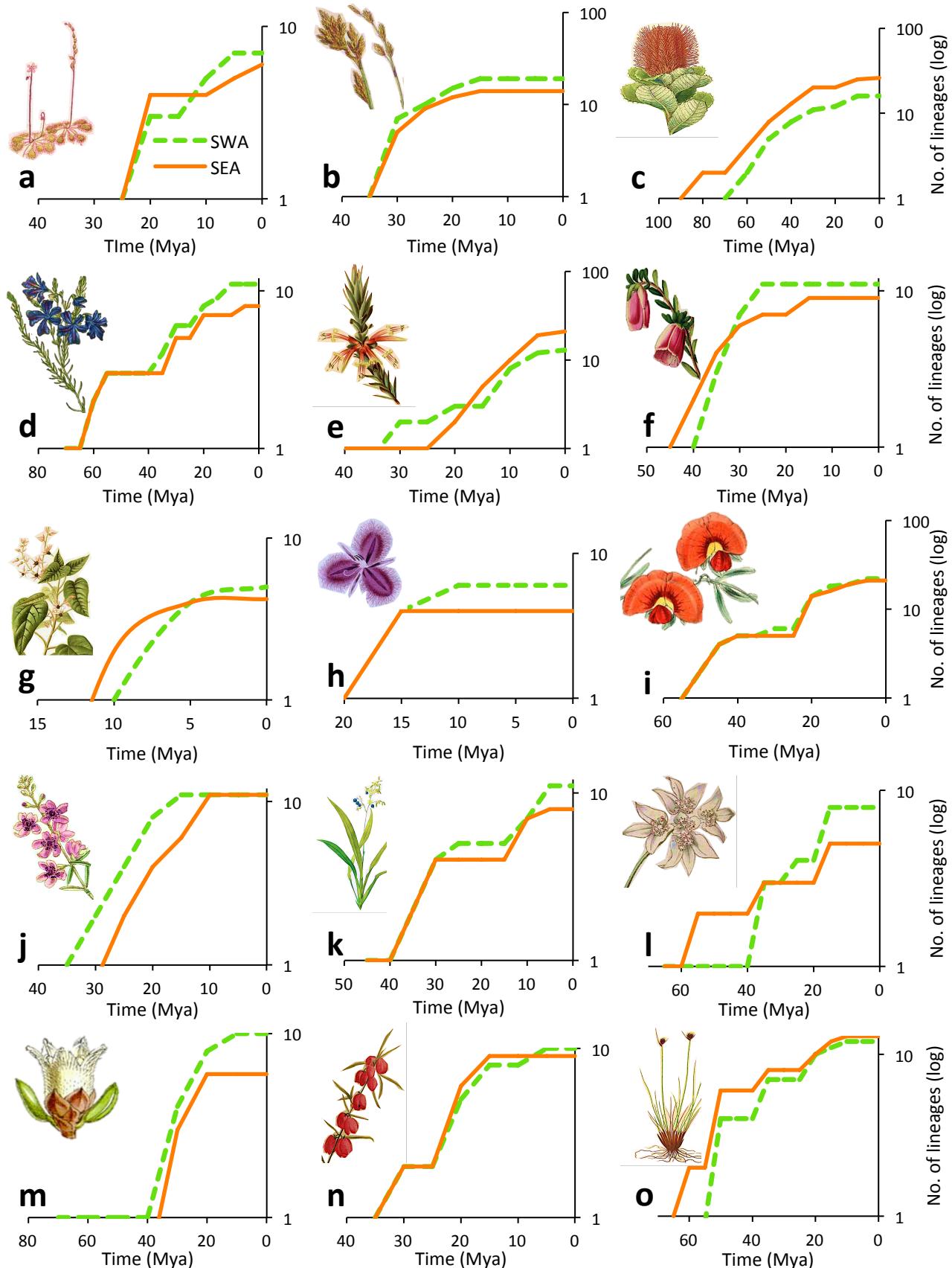
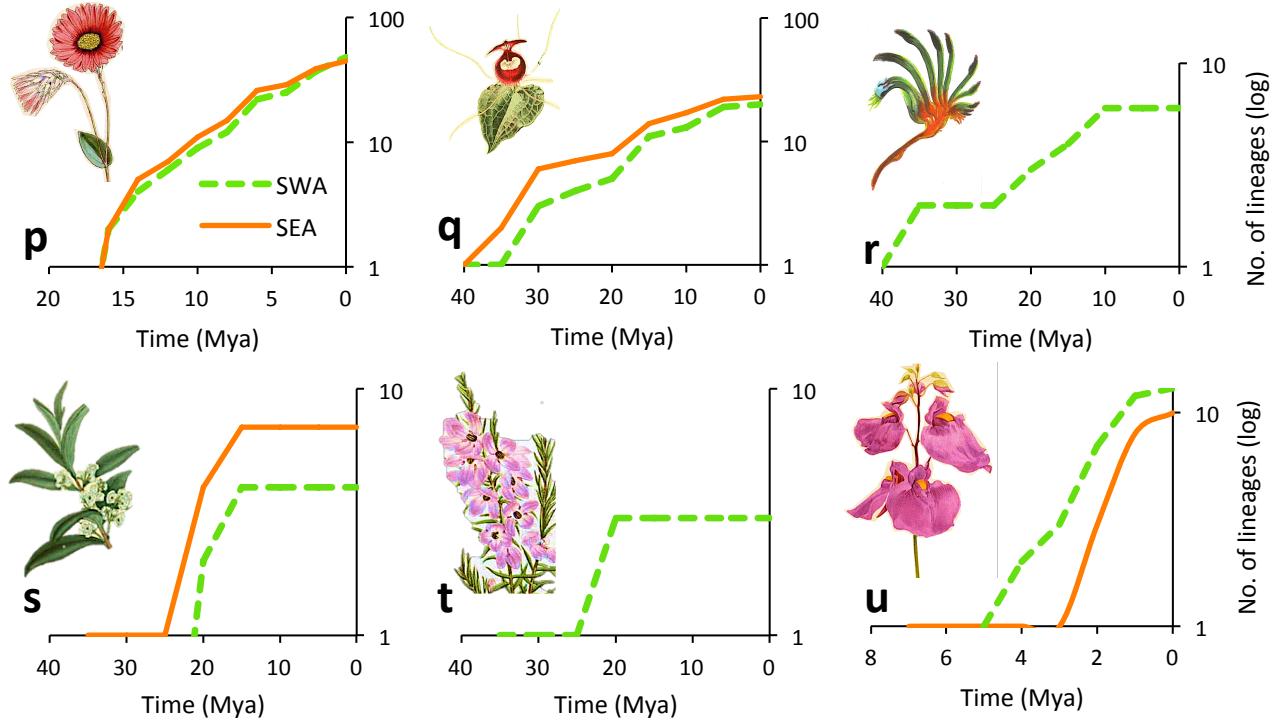


Fig. S9 continued.



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