

NON-RANDOM COEXTINCTIONS IN PHYLOGENETICALLY STRUCTURED MUTUALISTIC NETWORKS

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DATABASE

The compressed file **Rezende-SD.zip** contains an Excel file with the entire database listing (i) results from statistical analyses summarized in the main text and the supplementary material below, (ii) qualitative and quantitative pollination and frugivory interaction matrices employed in this study, (iii) species list with their taxonomic information and (iv) references.

METHODS

PHYLOGENETIC HYPOTHESES

We assembled and analysed one animal and one plant phylogeny per community. Phylogenies with less than 10 species and/or too many unresolved nodes were discarded due to the low statistical power to detect phylogenetic signal inherent in these phylogenetic trees (Blomberg et al. 2003). Although some communities present highly divergent groups interacting (e.g., birds and insects as pollinators), we excluded species belonging to distant taxonomic groups to avoid comparisons with multiple uncontrolled variables (Garland et al. 2005, p. 3024), as distant groups probably differ in many traits apart from the one being studied (i.e., in our study, species number of interactions and the identity of their interactors). For example, a phylogenetic analyses pooling birds and insects in a single phylogeny would assume that phenotypic resemblance between these species as pollinators stem from shared evolutionary history. However, birds and insects have diverged prior to the evolution of land plants, and most of the phenotypic variation between these two major groups probably reflect evolutionary histories absolutely independent of pollination. As a result, we obtained 105 phylogenies for the following groups: 35 insect phylogenies (Class Insecta; all pollinators), 18 bird phylogenies (Class Aves; all frugivores), and 52 angiosperm phylogenies (Infraphylum Angiospermae; 33 belonging to plant-pollinator and 19 to plant-frugivore networks).

Except for one small group of birds (see below), all original references depicted phylogenetic hypotheses based on DNA sequences (either nuclear or mitochondrial). Phylogenies in our study were assembled by hand, and conflicting branching patterns were resolved conservatively. To maximize statistical power, we included the maximum number of species possible without compromising the quality of the phylogeny: unresolved nodes were left as soft politomies, and several species were not included

given their uncertain phylogenetic position. Some species were included in the tree based on their taxonomic affiliation.

PLANTS

Plant phylogenies were built employing Phylomatic (Webb and Donoghue 2002), an online software that assembles phylogenetic trees for angiosperm families relying on taxonomic information, based primarily on the angiosperm phylogeny of Stevens (2001). Taxonomic information was obtained from the original studies, or from Index Nominum Genericorum Plantarum (<http://ravenel.si.edu/botany/ing/ingForm.cfm>) and Index Nominum Familiarum Plantarum Vascularium (Hoogland and Reveal 2005). To build our phylogenies, we employed the conservative tree available in Phylomatic, which leaves nodes with less than 80% support as soft politomies.

INSECTS

Phylogenetic hypotheses at the family level for insects were based on phylogenies available in Tree of Life (2002). We included families for four orders, which encompass the majority of insects in pollination networks: Hymenoptera, Lepidoptera, Diptera and Coleoptera (.txt files containing the complete phylogenetic information to the family level for these orders are available on request). Taxonomic affiliation for each species was determined from the original studies, or employing the following nomenclators on the web:

HYMENOPTERA

The database was developed as part of a PEET grant (Partnerships in Enhancing Expertise in Taxonomy) to Norman F. Johnson (Johnson.2@osu.edu). Supported by the National Science Foundation under grant DEB-9521648.

http://atbi.biosci.ohio-state.edu:210/hymenoptera/nomenclator.home_page
[accessed between February 23 and March 10, 2006]

LEPIDOPTERA

Beccaloni, G.W., Scoble, M.J., Robinson, G.S. & Pitkin, B. (eds). (2003). The Global Lepidoptera Names Index (LepIndex).

<http://internt.nhm.ac.uk/jdsml/perth/lepindex/index.dsml> [accessed between February 23 and March 10, 2006]

DIPTERA

Thompson, F. C. (ed.). (2005). Biosystematic Database of World Diptera, Version 7.5. 4 work records (not peer-reviewed material).

<http://www.diptera.org/names> [accessed between February 20 and March 10, 2006]

COLEOPTERA

Pitkin, B. (ed.). (2003). The Coleoptera Collection and Card Index. World Wide Web electronic publication. /research-curation/projects/coleoptera/
<http://intermt.nhm.ac.uk/jdsml/entomology/collections/beetles/index.dsml>
 [accessed between February 20 and March 10, 2006]

BIRDS

Bird phylogenies were built employing several sources of information, attempting to assemble our hypotheses according to the best information on avian relations currently available. Relations among major avian groups followed Fain and Houde (2004), whereas relationships within passerines were based on Barker et al. (2004) and Cibois and Cracraft (2004). Relations among a small group of new world tyrants (a total of 7 spp. in 3 different communities) followed Birdsley (2002), which was the only phylogeny not based on DNA sequence data (phylogenetic hypothesis based on morphological and behavioral characters). More detailed phylogenetic information for some groups was obtained from the following references:

PASSERINES

Oscine families (songbirds) – Spicer and Dunipace (2004)
 Fringillidae and Emberezidae – Burns et al. (2002, 2003), Yuri and Mindell (2002) and Ericson and Johansson (2003)
 Turdidae – Klicka et al. (2005)
 Trogonidae – Johansson and Ericson (2005)
 Tyrannids – Chesser (2004), Johansson et al. (2002) and Birdsley (2002)
 Corvids – Ericson et al. (2005) and Cicero and Johnson (2001)
 Paradisaea – Nunn and Cracraft (1996)
 Meliphagoidea – Driskell and Christidis (2004)
 Paridae – Gill et al. (2005)
 Sylviidae and Muscicapoidea – Bohning-Gaese et al. (2003)
Icterus genus – Omland et al. (1999)

NON-PASSERINES:

Columbiforms – Johnson (2004)
 Toucans – Barker and Lanyon (2000), Weckstein (2005) and Eberhard and Bermingham (2005)
 Woodpeckers – Webb and Moore (2005)

BRANCH LENGTH DIAGNOSTICS

We employed the diagnostic test proposed by Garland et al. (1992) to determine the statistical adequacy of different arbitrary branch lengths. This computes the correlation between the absolute value of each standardized contrast against its standard deviation

(i.e., the square root of the sum of its branch lengths). The absence of significant trends would suggest that contrasts are appropriately standardized (see also Diaz-Uriarte and Garland 1996). Three starter branch lengths were tested for the databases of species degree and strength: constant branch lengths (all branch lengths set equal to one), and arbitrary branch lengths following Grafen (1989) and Pagel (1992).

For phylogenies with species degree as tip data, none of the three arbitrary starter branch lengths were adequate for all 105 phylogenies according to the diagnostics. We opted to employ constant branch lengths for the majority of the database because the number of phylogenies violating diagnostics was considerably lower (whereas 62 phylogenies showed significant trends employing Grafen's, and 51 employing Pagel's, arbitrary branch lengths, only 28 phylogenies showed significant trends when all branch lengths were set equal to one; see Database). For the quantitative databases, violations occurred on 7 phylogenies with Grafen's branch lengths, 4 with Pagel's, and 5 with constant branch lengths, respectively. Therefore, we employed additional branch length transformations for the phylogenies that violated diagnostics strictly for statistical purposes. Arbitrary branch lengths according to Nee (cited in Purvis 1995, p. 416), or transforming Nee's branch lengths with Grafen's (1989) $\rho = 0.5$, proved to be adequate for these phylogenies.

PHYLOGENETIC SIGNAL

We tested for the presence of phylogenetic signal on species degree and strength with randomization and branch-length-transformation tests (Blomberg et al. 2003). The randomization test consists in comparing Mean Square Errors (MSE) of phylogenetic Generalized Least-Square regression, obtained from the studied phylogeny, against a distribution of MSE obtained when values of species degree or strength have been randomly permuted across the tips of the same tree. If the tested MSE is lower than MSE of 95% of the permuted datasets, then we conclude that phylogenetic signal is statistically significant at the 0.05 level. The amount of phylogenetic signal was quantified with the K statistic, which is roughly a fraction of the amount of signal present in the dataset over the amount of signal expected from Brownian motion for the same tree topology.

The branch-length-transformation test employs maximum likelihood to estimate, under some evolutionary models, the branch length transformation that would minimize MSE of the tip dataset, and tests whether the best fitting tree obtained under

different models of character evolution differs significantly from a star phylogeny (i.e., no hierarchical structure). Branch-length transformation tests were performed assuming the Ornstein-Uhlenbeck model of stabilizing selection (OU) and a model in which character evolution can accelerate or decelerate (ACDC). Because ACDC models did not converge in most cases, we discuss results from the OU model (all analyses are included in Supplementary Database for completeness). Although the randomization method and the branch-transformation method provide similar information about the presence of a phylogenetic signal, applying both techniques can be useful to determining how robust our results are and to overcoming limitations inherent to each statistical test (below).

COMPARING P-VALUES AND ESTIMATES OF PHYLOGENETIC SIGNAL

It is not straightforward to perform comparisons between different trees and/or tip data (Blomberg et al. 2003), hence we adopted two different strategies to perform our comparisons. First, when we addressed whether the presence of phylogenetic signal was statistically significant, we employed phylogenies with branch lengths that were adequate according to diagnostics (in other words, branch lengths varied depending on the phylogeny and tip data; i.e., degree or species strength). Although the relationship between diagnostics and the randomization test is not clear, results from our database suggest that violations of traditional diagnostics can decrease the statistical power to detect phylogenetic signal (see also Table 1 in Rezende et al. 2004, and power analyses below). For instance, P-values obtained from randomization tests on 28 phylogenies, employing branch lengths which were adequate according to diagnostics, were significantly lower (paired t-test, $t_{27} = 3.075$, $P = 0.005$) than values obtained for the same phylogenies when all branch lengths were set equal to one (which violated diagnostics, see above). Accordingly, phylogenetic signal was significant ($P < 0.05$) in 10 phylogenies, instead of 4, after branch lengths were appropriately transformed.

Second, we compared K estimates (roughly the fraction of the amount of signal of the real data respect to the expectation assuming Brownian motion) obtained with species degree and strength employing the same phylogeny, with branch lengths set equal to one for all trees. Because our goal was to perform a pairwise comparison between K obtained with these different surrogates for species propensity to interact, we opted to employ the same branch lengths for species degree and strength to avoid confounding effects associated with different degrees of hierarchy on the starter

phylogenies (e.g., see eq. 4 in Blomberg et al. 2003). This test would indicate whether a more hierarchical phylogeny would consistently fit better one trait than the other, which provides insights on which surrogate might be more dependent on evolutionary history.

POWER ANALYSIS

How pervasive is the presence of phylogenetic signal across taxa and communities?

Lack of statistically significant phylogenetic signal may result from (i) the absence of any real effect of phylogeny on species propensity to interact, or from (ii) low statistical power ($1 - \text{Type II error rate}$) to detect signal if it is present. For this reason, results must be interpreted with caution. Although it is possible that phylogenetic signal is not present in some communities, statistical power of the randomisation test and branch-length-transformation test may be considerably low in some cases, for several reasons.

First, measurement errors can reduce dramatically the power to detect phylogenetic signal, and error is unavoidable in such a large scale study, despite the efforts to minimize it. Measurement errors in this study may have occurred at several different levels: during the estimation of species interactions, during species identification, taxonomic classification and/or the phylogenetic position of particular species or clades may be inaccurate, arbitrary branch lengths, etc. In addition, estimates of species degree and strength may be biased (e.g., researchers exclude species without interactions from their networks, although their close relatives may present several interactions), and this might affect the power to detect signal.

Second, not surprisingly, the power to detect signal is lower for phylogenies with low number of species. Statistical power to detect phylogenetic signal with the randomisation test decreases from 0.8 for sample sizes of 20 species to less than 0.4 for 10 species (see Fig. 2 in Blomberg et al. 2003). There is some evidence that we might be underestimating the presence of phylogenetic signal because of decreased power at lower sample sizes. For instance, the proportion of phylogenies with significant signal is substantially higher in the subset of phylogenies with larger sample sizes ($N > 50$) than in the database as a whole (50 % versus 32%). In addition, the slopes of linear regressions of K versus sample size differ significantly between phylogenies where significant phylogenetic signal has been detected versus those without significant signal (Fig. S1), and suggest that K should be disproportionately larger at lower sample sizes in order to attain significance (results remain qualitatively identical after removing the potentially influential point with $K = 2.14$). Accordingly, a multiple regression of log

(P -value + 1) on $\log$ (number of species N) and $\log K$, reproducing the analyses of Blomberg et al. (2003) with our data, supports that N and K are significant negative predictors of the probability of rejecting absence of signal as the null hypothesis ($\log N$: $F = 86.9$, $P < 0.001$; $\log K$: $F = 74.1$, $P > 0.001$).

Third, the nature of the data itself. Species degree and strength are discrete data, and neither are normally distributed (for several of the matrices analysed here, the distribution of species degree and species strength are highly skewed; Jordano et al. 2003, Bascompte et al. 2006). Consequently, the statistical power of the randomisation test should be lower simply because several species share the same tip data (e.g., Database). To test this hypothesis, we first simulated 100 datasets under Brownian motion on eight phylogenies of our database and estimated the statistical power to detect phylogenetic signal as described in Blomberg et al. (2003). We then sorted the tip data of each simulated dataset, replaced these value by the sorted degree values of the real set of species (obtaining 100 datasets with phylogenetic signal and the same degree distribution of the tested phylogeny), and estimated statistical power again. As expected, departures from normality and the discrete nature of the data decreased statistical power in most cases, and the magnitude of this effect varied considerably between datasets (from no effect up to a 46 % decrease in power, Fig. S2).

Differences in statistical power between datasets probably stem from the interaction of several factors, such as the phylogeny size, topology (e.g. degree of hierarchy and number of unresolved nodes) and the frequency distribution of tip data. Controlling for the effects of these factors can be cumbersome and possibly misleading, hence we opted for a conservative strategy of employing a critical significance level of $\alpha = 0.05$. Nevertheless, because the Type II error rates for the randomisation rates are considerably higher than Type I error rates, and the amount of signal estimated as K , d or g (see original paper) is considerably low in most cases, we are confident that results reported in our study are conservative.

MANTEL TEST

We used Mantel tests to compare phylogenetic distance matrices with matrices of ecological distances between species. Phylogenetic distance between pairs of plants (or animals) was estimated as the expected covariance of the trait between the two species (Blomberg et al. 2003; Garland et al. 2005). Ecological distance was calculated as $1-S$, where S is the Jaccard index of similarity obtained from qualitative interaction matrices

(Lengendre and Legendre 1998). The similarity between two species, i and j , is defined as $S(i, j) = a / (a + b + c)$, where a , b , and c represent the number of shared interacting species, the number of interactions specific to species i , and the number of interactions exclusive to species j , respectively.

Because differences in degree affect Jaccard estimates, we also performed partial Mantel tests controlling for degree (the pairwise distance in degree was calculated as the absolute difference in degree between two species). Hence, this partial test can discern whether phylogeny affects strictly with whom species interact, independently of the total number of interactions of each species. Because partial Mantel test can inflate Type I error rates (e.g., Raufaste and Rousset 2001, Castellano and Balleto 2002), employing different null models may be more appropriate depending on the characteristics of the data (Legendre 2000). We performed permutations of the residuals and of the raw data for all phylogenies (the second method was suggested by Legendre [2000] to avoid increased Type I error rates associated with data skewness), employing the software developed by Bonnet and Van de Peer (2002). Because all results were qualitatively identical, we report values obtained with permutation of residuals.

TAXONOMIC DIVERSITY AND COEXTINCTION SIMULATIONS

As a surrogate for phylogenetic diversity, we estimated taxonomic diversity of plants and animals in the largest available phylogenies (23 plant and 27 pollinator phylogenies with more than 30 species, and 15 bird phylogenies with more than 15 species; see Supplementary Methods). Briefly, path length weights between species increase as they are more distantly related taxonomically (i.e., species of the same genus have a distance of 1 whereas species from different genera within the same family have a distance of 2, and so on), generating a matrix of pairwise taxonomic distances. The mean taxonomic distance between all species was employed as an index of taxonomic diversity in subsequent regressions (Clarke and Warwick 1998).

Extinction cascades were simulated for the 10 largest communities (all having more than 40 animal and plant species) with available taxonomic affiliation, following Memmott et al. (2004). After one species is removed, species left without any interaction go coextinct. Species removal started from the most specialized (least-linked) to the most generalized (most-linked) species, which was proposed as a more plausible extinction sequence because specialist species tend to be less abundant than generalists (Jordano et al. 2003; Memmott et al. 2004; Vázquez and Aizen 2004).

After an extinction cascade, we calculated the decrease of taxonomic diversity of the real community respect to the expected decrease in the absence of phylogenetic signal. This was done by replicating the coextinction cascade after randomizing the taxonomic affiliation of species going coextinct (i.e., nodes remain unchanged but their “name tags” are shuffled). This null model removes effects of phylogenetic relatedness (Blomberg et al. 2003) controlling for network structure and species number. The relative taxonomic diversity is the ratio between real and null values, and the average rate of taxonomic loss per community is the slope of a linear regression with an intercept forced through 1 (i.e., real values and the null expectation are equal when no species are removed).

REFERENCES

- Barker F.K., A. Cibois, P. Schikler, J. Feinstein and J. Cracraft (2004). Phylogeny and diversification of the largest avian radiation. *Proc. Nat. Acad. Sci.* 101: 11040–11045.
- Barker, F.K. and S.M. Lanyon (2000). The impact of parsimony weighting schemes on inferred relationships among toucans and Neotropical barbets (Aves: Piciformes). *Mol. Phyl. Evol.* 15: 215–234.
- Bascompte, J., P. Jordano, C. J. Melian, and J. M. Olesen. (2003). The nested assembly of plant-animal mutualistic networks. *PNAS* 100:9383–9387.
- Bascompte, J.P., Jordano and J.M. Olesen. (2006). Asymmetric coevolutionary networks facilitate biodiversity maintenance. *Science* 312: 431–433.
- Birdsley, J.S. (2002). Phylogeny of the tyrant flycatchers (Tyrannidae) based on morphology and behavior. *Auk* 119:715–734.
- Blomberg, S.P., T. Garland, Jr., and A.R. Ives (2003). Testing for phylogenetic signal in comparative data: behavioral traits are more labile. *Evolution* 57:717–745.
- Bohning-Gaese, K., M.D. Schuda and A.J. Helbig (2003). Weak phylogenetic effects on ecological niches of *Sylvia* warblers. *J. Evol. Biol.* 16: 956–965.
- Bonnet, E. and Y. Van de Peer. (2002). ZT: a software tool for simple and partial Mantel tests. *J. Statist. Software* 7(10): 1–12.
- Burns, K.J., S.J. Hackett and N.K. Klein (2002). Phylogenetic relationships and morphological diversity in Darwin’s finches and their relatives. *Evolution* 56: 1240–1252.
- Burns, K.J., S.J. Hackett and N.K. Klein (2003). Phylogenetic relationships of Neotropical honeycreepers and the evolution of feeding morphology. *J. Avian. Biol.* 34:360–370
- Castellano S., E. Balletto. 2002. Is the partial Mantel test inadequate? *Evolution.* 56:1871–1873.
- Chesser, R.T. (2004). Molecular systematics of New World suboscine birds. *Mol. Phyl. Evol.* 32:11–24.
- Cibois, A. and J. Cracraft (2004). Assessing the passerine “Tapestry”: phylogenetic relationships of the Muscicapoidea inferred from nuclear DNA sequences. *Mol. Phyl. Evol.* 32: 264–273.
- Cicero, C. and N.K. Johnson (2001). Higher-level phylogeny of new world vireos (Aves: Vireonidae) based on sequences of multiple Mitochondrial DNA genes. *Mol. Phyl. Evol.* 20:27–40.
- Clarke, K.R. and R.M. Warwick (1998). A taxonomic distinctness index and its statistical properties. *J. App. Ecol.* 35: 523–531.
- Diaz-Uriarte, R. and T. Garland, Jr. (1996) Testing hypotheses of correlated evolution using phylogenetically independent contrasts: sensitivity to deviations from Brownian motion. *Syst. Biol.* 45: 27–47.
- Driskell, A.C. and L. Christidis (2004). Phylogeny and evolution of the Australo-Papuan honeyeaters (Passeriformes, Meliphagidae). *Mol. Phyl. Evol.* 31:943–960.
- Eberhard, J.R. and E. Bermingham (2005). Phylogeny and comparative biogeography of *Pionopsitta* parrots and *Pteroglossus* toucans. *Mol. Phyl. Evol.* 36: 288–304.
- Ericson, P.G.P. and U.S. Johansson (2003). Phylogeny of Passerida (Aves: Passeriformes) based on nuclear and mitochondrial sequence data. *Mol. Phyl. Evol.* 29: 126–138.

- Ericson, P.G.P., A.-L. Jansén, U.S. Johansson and J. Ekman (2005). Inter-generic relationships of the crows, jays, magpies and allied groups (Aves: Corvidae) based on nucleotide sequence data. *J. Avian. Biol.* 36:222-234.
- Fain, M.G. and P. Houde (2004). Parallel radiations in the primary clades of birds. *Evolution* 58: 2558-2573.
- Garland, T., Jr., and A.R. Ives. (2000). Using the past to predict the present: confidence intervals for regression equations in phylogenetic comparative methods. *Am. Nat.* 155:346-364.
- Garland, T., Jr, P.H. Harvey and A.R. Ives (1992). Procedures for the analysis of comparative data using phylogenetically independent contrasts. *Syst. Biol.* 41: 18-32.
- Garland, T., A. F. Bennett and E.L. Rezende (2005). Phylogenetic approaches in comparative physiology. *J. Exp. Biol.* 208: 3015-3035.
- Gill, F.B., B. Slikas and F.H. Sheldon (2005). Phylogeny of Titmice (Paridae): ii. species relationships based on sequences of the Mitochondrial Cytochrome-b gene. *Auk* 122: 121-143.
- Grafen, A. (1989). The phylogenetic regression. *Phil. Trans. R. Soc. Lond. B* 326: 119-157.
- Hoogland, R.D. and J.L. Reveal (2005). Index Nominum Familiarum Plantarum Vascularium. *The Botanical Review* 71 (1/2): 1–291.
- Jordano, P., J. Bascompte and J.M. Olesen. (2003). Invariant properties in coevolutionary networks of plant–animal interactions. *Ecol. Lett.* 6: 69–81.
- Johansson, U.S. and P.G.P. Ericson (2005). A re-evaluation of basal phylogenetic relationships within trogons (Aves: Trogonidae) based on nuclear DNA sequences. *J. Zool. Syst. Evol. Res.* 43: 166-173.
- Johansson, U.S., M. Irestedt, T.L. Parsons and P.G.P. Ericson (2002). Basal phylogeny of the Tyrannoidea based on comparisons of Cytochrome b and exons of nuclear c-myc and RAG-1 genes. *Auk* 119: 984-995.
- Johnson, K.P. (2004). Deletion bias in avian introns over evolutionary timescales. *Mol. Biol. Evol.* 21:599–602.
- Legendre, P. (2000) Comparison of permutation methods for the partial correlation and partial Mantel tests. *J. Statist. Comput. Simul.* 67: 37 – 73.
- Legendre, P. and L. Legendre (1998). *Numerical Ecology*. 2nd English edition. Elsevier Scientific Publishing Company, Amsterdam.
- Lewinsohn, T.M., P.I. Prado, P. Jordano, J. Bascompte and J.M. Olesen (2006). Structure in plant-animal interaction assemblages. *Oikos* 113: 174-184.
- Memmott, J., N. M. Waser and M.V. Price (2004). Tolerance of pollination networks to species extinctions. *Proc. R. Soc. London B* 271, 2605-2611.
- Nunn, G.B. and J. Cracraft (1996). Phylogenetic relationships among the major lineages of the birds-of-paradise (Paradisaeidae) using Mitochondrial DNA gene sequences. *Mol. Phyl. Evol.* 5: 445-459.
- Omland, K.E., S.M. Lanyon and S.J. Fritz (1999). A molecular phylogeny of the NewWorld orioles (*Icterus*): the importance of dense taxon sampling. *Mol. Phyl. Evol.* 12:224-239.
- Pagel, M. D. (1992). A method for the analysis of comparative data. *J. Theor. Biol.* 156: 431-442.
- Purvis, A. (1995). A composite estimate of primate phylogeny. *Phil. Trans. Royal Soc. Lond. B* 348:405-421.
- Raufaste N., F. Rousset. 2001. Are partial Mantel tests adequate? *Evolution*. 55:1703–1705.

- Spicer, G.S and L. Dunipace (2004). Molecular phylogeny of songbirds (Passeriformes) inferred from mitochondrial 16S ribosomal RNA gene sequences. *Mol. Phyl. Evol.* 30: 325-335.
- Stevens, P. F. (2001). Angiosperm Phylogeny Website. Version 6, May 2005 [and more or less continuously updated since].
<http://www.mobot.org/MOBOT/research/APweb/>
- Tree of Life Web Project. (2002). Insecta. Insects. Version 01 January 2002 (under construction). <http://tolweb.org/Insecta/8205/2002.01.01> in The Tree of Life Web Project, <http://tolweb.org/> [accessed on February 27, 2006]
- Vásquez, D.P. and M.A. Aizen (2004). Asymmetric specialization: a pervasive feature of plant-pollinator interactions. *Ecology* 85: 1251-1257.
- Webb, C.O. and M.J. Donoghue (2002). *Phylomatic: A Database for Applied Phylogenetics*. <http://www.phylodiversity.net/phylomatic> [accessed between February 2 and February 23, 2006].
- Webb, D.M. and W.S. Moore (2005). A phylogenetic analysis of woodpeckers and their allies using 12S, Cyt b, and COI nucleotide sequences (class Aves; order Piciformes). *Mol. Phyl. Evol.* 36:233-248.
- Weckstein, J.D. (2005). Molecular phylogenetics of the ramphastos toucans: implications for the evolution of morphology, vocalizations, and coloration. *Auk* 122: 1191-1209.
- Yuri, T. and D.P. Mindell (2002). Molecular phylogenetic analysis of Fringillidae, “New World nine-primaried oscines” (Aves: Passeriformes). *Mol. Phyl. Evol.* 23: 229–243.

TABLE S1

Summary for the 59 communities studied, listing results of randomisation analyses (K), regular Mantel (Z) and partial Mantel tests (Z_{partial}) performed separately for plants and animals (105 phylogenies total). P-values of zero actually indicate $P < 0.001$.

CODE	Pol/Frug	PLANTS								ANIMALS								Pl_An ^b
		N sp. Plants ^a	N sp. Animals ^a	K	P _K	Z	P _Z	Z _{partial}	P _{Zpartial}	K	P _K	Z	P _Z	Z _{partial}	P _{Zpartial}			
ARR1	P	84 / 84	101 / 97	0.307	0.084	0.035	0.068	0.08	0.001	0.224	0.168	0.152	0.001	0.145	0.001	A		
ARR2	P	43 / 43	64 / 60	0.358	0.246	0.076	0.046	0.116	0.005	0.24	0.12	0.192	0.001	0.194	0.001	PA		
ARR3	P	36 / 36	25 / 23	0.43	0.116	-0.05	0.147	-0.01	0.572	0.242	0.793	0.247	0.001	0.225	0.001	A		
BAHE	P	12 / 12	102 / 91	0.479	0.484	-0.12	0.802	-0.12	0.785	0.307	0.015	-0.02	0.784	-0.01	0.611			
BAIR	F	7 / -	21 / 21	-	-	-	-	-	-	0.283	0.463	0.084	0.13	0.185	0.006			
BEEH	F	31 / 31	9 / -	0.268	0.982	0.053	0.137	0.055	0.163	-	-	-	-	-	-			
CACG	F	25 / 23	16 / 15	0.45	0.494	0.055	0.197	0.155	0.021	0.279	0.981	0.11	0.154	0.195	0.004			
CACI	F	34 / 33	20 / 20	0.389	0.4	0.06	0.078	0.12	0.006	0.475	0.114	-0.04	0.666	0.078	0.206			
CACO	F	25 / 23	13 / 13	0.466	0.162	0.101	0.07	0.124	0.046	0.541	0.154	0.129	0.125	-0.15	0.903			
CAFR	F	21 / 21	15 / 15	0.424	0.455	-0.12	0.959	0	0.505	0.32	0.753	0.148	0.093	0.233	0.003			
CLLO	P	96 / 96	275 / 246	0.255	0.067	0.018	0.196	0.015	0.214	0.228	0	0.095	0.001	0.13	0.001	A		
CROM	F	72 / 71	7 / -	0.3	0.014	0	0.569	-0.12	0.99	-	-	-	-	-	-			
DIHI	P	17 / 17	61 / 58	0.349	0.894	0.117	0.118	0.115	0.129	0.322	0.088	0.116	0.002	0.031	0.239	A		
DISH	P	16 / 16	36 / 34	0.317	0.397	0.077	0.185	0.112	0.113	0.4	0.232	0.166	0.002	0.134	0.003	A		
DUPO	P	11 / 11	38 / 36	0.57	0.322	0.04	0.394	0.069	0.301	0.315	0.792	0.099	0.011	0.086	0.041	A		
EOL	P	24 / 24	118 / 112	0.433	0.079	0.054	0.192	0.054	0.18	0.197	0.24	0.019	0.117	0.007	0.386			
EOLZ	P	31 / 31	76 / 74	0.499	0.02	0.092	0.052	0.089	0.055	0.222	0.01	0.082	0.001	0.085	0.001	A		
ESKI	P	14 / 14	13 / 12	0.422	0.732	0.065	0.276	0.115	0.146	0.448	0.518	0.062	0.314	-0.07	0.657			
FROS	F	16 / 16	10 / -	2.14	0.016	0.5	0.001	0.334	0.001	-	-	-	-	-	-			
GEN1	F	7 / -	18 / 17	-	-	-	-	-	-	0.911	0.021	0.344	0.002	0.113	0.109			
GEN2	F	35 / 34	29 / 28	0.412	0.128	0.088	0.028	0.105	0.013	0.525	0.041	0.269	0.001	0.269	0.001	PA		
HAMM	F	45 / 43	19 / 16	0.281	0.087	0.328	0.001	0.361	0.001	0.502	0.189	0.534	0.001	0.293	0.002	PA		
HERR	P	26 / 26	179 / 164	0.435	0.183	0.094	0.06	0.098	0.073	0.227	0.047	0.173	0.001	0.159	0.001	A		
HOCK	P	29 / 29	81 / 72	0.532	0.011	0.133	0.008	0.151	0.003	0.257	0.129	0.11	0.002	0.049	0.039	PA		
HRAT	F	16 / 16	16 / 16	0.531	0.394	0.033	0.347	0.208	0.013	0.396	0.259	0.116	0.106	-0.01	0.523			
INPK	P	42 / 42	85 / 80	0.363	0.666	0.091	0.067	0.063	0.106	0.178	0.752	0.068	0.002	0.066	0.003	A		
KANT	F	5 / -	27 / 27	-	-	-	-	-	-	0.346	0.281	0.05	0.194	-0.11	0.971			
KEVN	P	20 / 20	91 / 75	0.525	0.072	0	0.489	0.006	0.394	0.21	0.126	0.122	0.001	0.055	0.036	A		
KT90 [#]	P	91 / 91	679 / 101	0.261	0.155	-0.03	0.926	-0.02	0.846	0.252	0.267	-	-	-	-			
LAMB	F	25 / -	61 / 61	-	-	-	-	-	-	0.303	0.001	0.083	0.002	0.05	0.042			
LOPE	F	19 / 17	8 / -	0.337	0.51	-0.13	0.93	-0.19	0.924	-	-	-	-	-	-			
MACK	F	32 / 32	32 / 32	0.292	0.382	-0.09	0.957	-0.05	0.811	0.3	0.181	0.147	0.002	0.215	0.001	A		

MED1	P	21 / 21	45 / 43	0.386	0.253	-0.02	0.604	-0.01	0.557	0.332	0.014	0.136	0.014	0.098	0.048	A
MED2	P	23 / 23	72 / 68	0.435	0.64	0.012	0.394	0.031	0.286	0.252	0.313	0.049	0.049	0.061	0.032	A
MEMM	P	25 / 25	79 / 42	0.454	0.124	0.147	0.028	0.159	0.021	0.31	0.313	0.174	0.001	0.21	0.001	PA
MOMA	P	11 / 11	18 / 17	0.466	0.67	-0.17	0.893	-0.13	0.758	0.28	0.607	0.321	0.001	0.355	0.001	A
MONT	F	170 / 168	40 / 39	0.175	0.842	-0.02	0.947	0.004	0.401	0.231	0.265	0.069	0.037	0	0.536	A
MOTT	P	13 / 13	44 / 42	0.537	0.212	-0.02	0.579	0.018	0.428	0.398	0.477	0.011	0.376	0.027	0.212	
MULL	P	105 / 105	54 / 39	0.246	0.392	-0.02	0.7	0.025	0.173	0.316	0.175	-0.06	0.936	-0.04	0.859	
NCOR	F	25 / 25	33 / 33	0.243	0.66	-0.02	0.653	0.047	0.223	0.301	0.018	0.053	0.13	0.135	0.001	
NNOG	F	18 / 18	28 / 28	0.335	0.486	-0.1	0.865	-0.05	0.739	0.28	0.077	0.042	0.212	0.176	0.001	
OFLO	P	10 / 10	12 / -	0.632	0.231	0.272	0.023	0.379	0.007	-	-	-	-	-	-	
OFST	P	7 / -	42 / 39	-	-	-	-	-	-	0.302	0.237	-0.05	0.946	-0.07	0.912	
OLAU	P	29 / 29	55 / 54	0.251	0.65	-0.08	0.929	-0.04	0.249	0.311	0.12	0.137	0.001	0.099	0.004	A
OLLE	P	9 / -	56 / 39	-	-	-	-	-	-	0.257	0.677	0.053	0.16	-0.07	0.856	
PERC	P	61 / 61	36 / 31	0.342	0.046	-0.06	0.99	-0.02	0.728	0.337	0.122	0.359	0.001	0.328	0.001	A
PRAP	P	18 / 18	60 / 53	0.876	0.007	0.147	0.021	0.21	0.008	0.21	0.327	0.045	0.076	0.052	0.077	P
PRCA	P	41 / 41	139 / 131	0.323	0.18	0.134	0.022	0.133	0.009	0.239	0.004	0.115	0.001	0.133	0.001	PA
PRCG	P	49 / 49	118 / 111	0.243	0.477	-0.02	0.66	-0.04	0.816	0.246	0.016	0.073	0.002	0.1	0.001	A
PTND [#]	P	131 / 131	666 / 68	0.268	0.01	0.074	0.001	0.094	0.001	0.245	0.114	-	-	-	-	
RABR	P	33 / 33	53 / 46	0.498	0.043	0.056	0.153	0.103	0.046	0.3	0.311	0.055	0.045	0.056	0.043	A
RMRZ	P	48 / 48	49 / 46	0.408	0.024	0.022	0.272	0.01	0.4	0.437	0.031	0.103	0.001	0.176	0.001	A
SAPF	F	27 / 27	8 / -	0.416	0.275	-0.09	0.789	0.075	0.209	-	-	-	-	-	-	
SCHM	P	7 / -	33 / 32	-	-	-	-	-	-	0.539	0.069	0.131	0.004	-0.01	0.559	
SMAL	P	13 / 13	34 / 32	0.712	0.148	0.566	0.002	0.519	0.001	0.417	0.022	0.015	0.389	-0.03	0.651	P
SMRA	P	26 / 26	130 / 122	0.483	0.02	0	0.496	0.131	0.01	0.342	0.001	0.051	0.001	0.026	0.116	A
SNOW	F	50 / 48	14 / 14	0.466	0.086	0.163	0.001	0.233	0.001	0.948	0.008	0.118	0.126	0.223	0.016	P
WES	F	207 / 206	110 / 80	0.277	0.006	0.085	0.001	0.094	0.001	0.178	0.486	0.164	0.001	0.162	0.001	PA
WYTH	F	11 / 11	14 / 14	0.552	0.689	0.152	0.122	0.224	0.046	0.306	0.824	0.091	0.176	0.034	0.381	

^a Listed as number of species on the original matrix / number of species included in the phylogeny.

^b List of which phylogenies (P = plants, A = animals, PA = both) were significantly correlated with ecological distances, according to regular Mantel tests (main text, Fig. 4).

[#] Randomisation tests for animal phylogenies were performed on families averages because the original number of species was extremely large, Mantel tests were not performed.

FIGURES

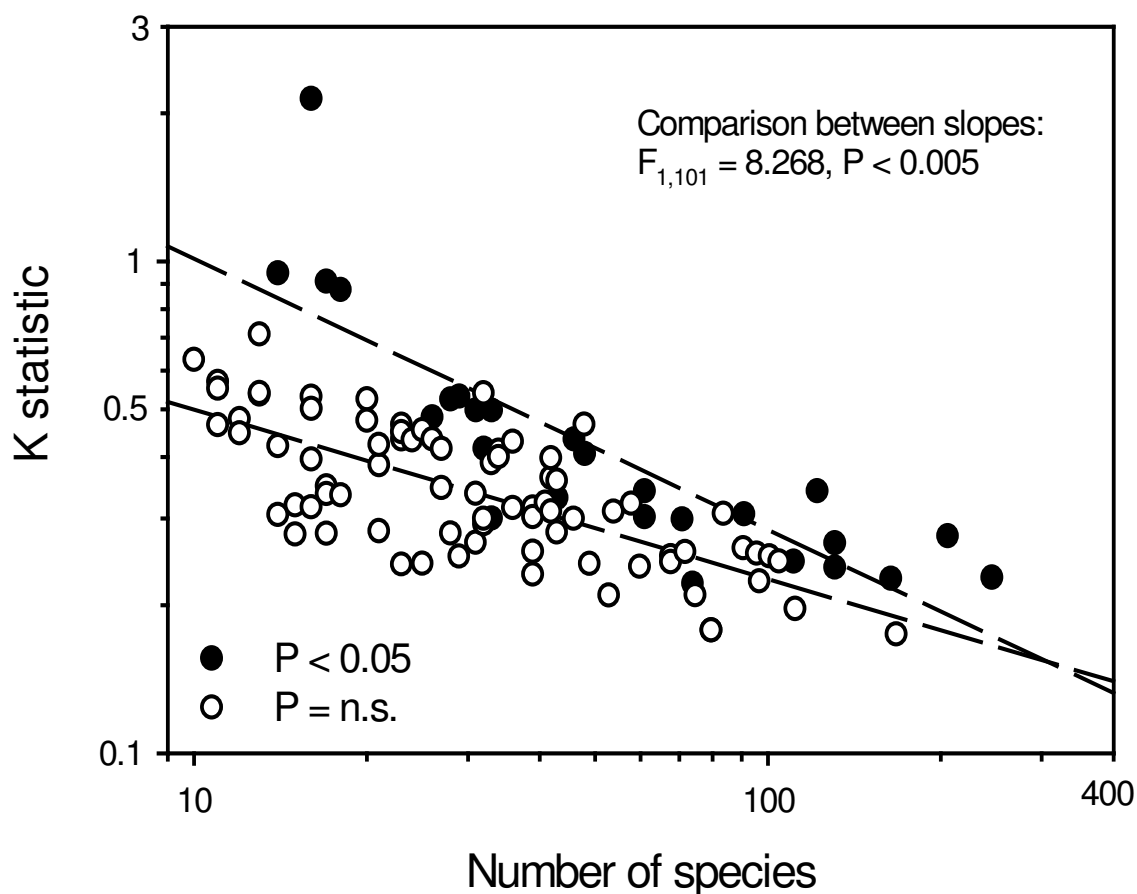


Figure S1. Relationship between *K* statistics and number of species per phylogeny, comparing the slopes of linear regressions (in a log-log scale) between phylogenies where significant phylogenetic signal was detected ($P < 0.05$) versus those where signal was not significant.

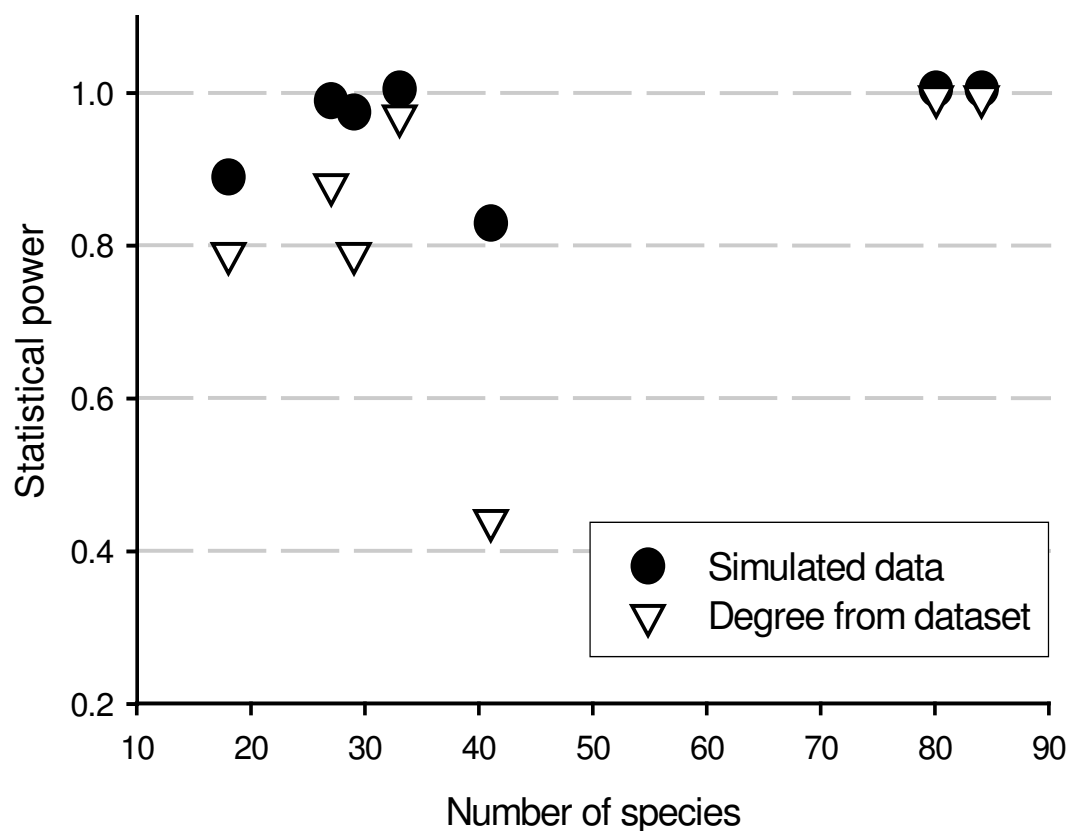
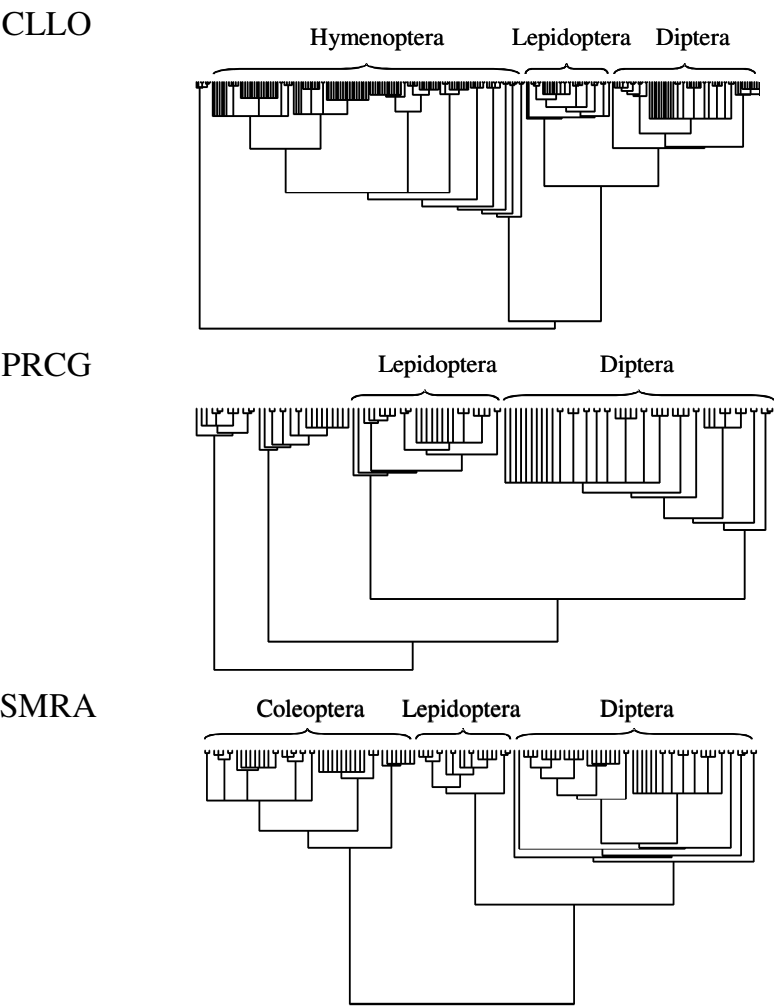


Figure S2. Estimates of statistical power of the randomization test, employing continuous simulated data and the degree distribution of the real dataset (see text for details). Phylogenies employed here were, in increasing order of size: PRAP (plant), SAPF (plant), OLAU (plant), NCOR (animal), PRCA (plant), WES (animal) and ARR1 (plant).

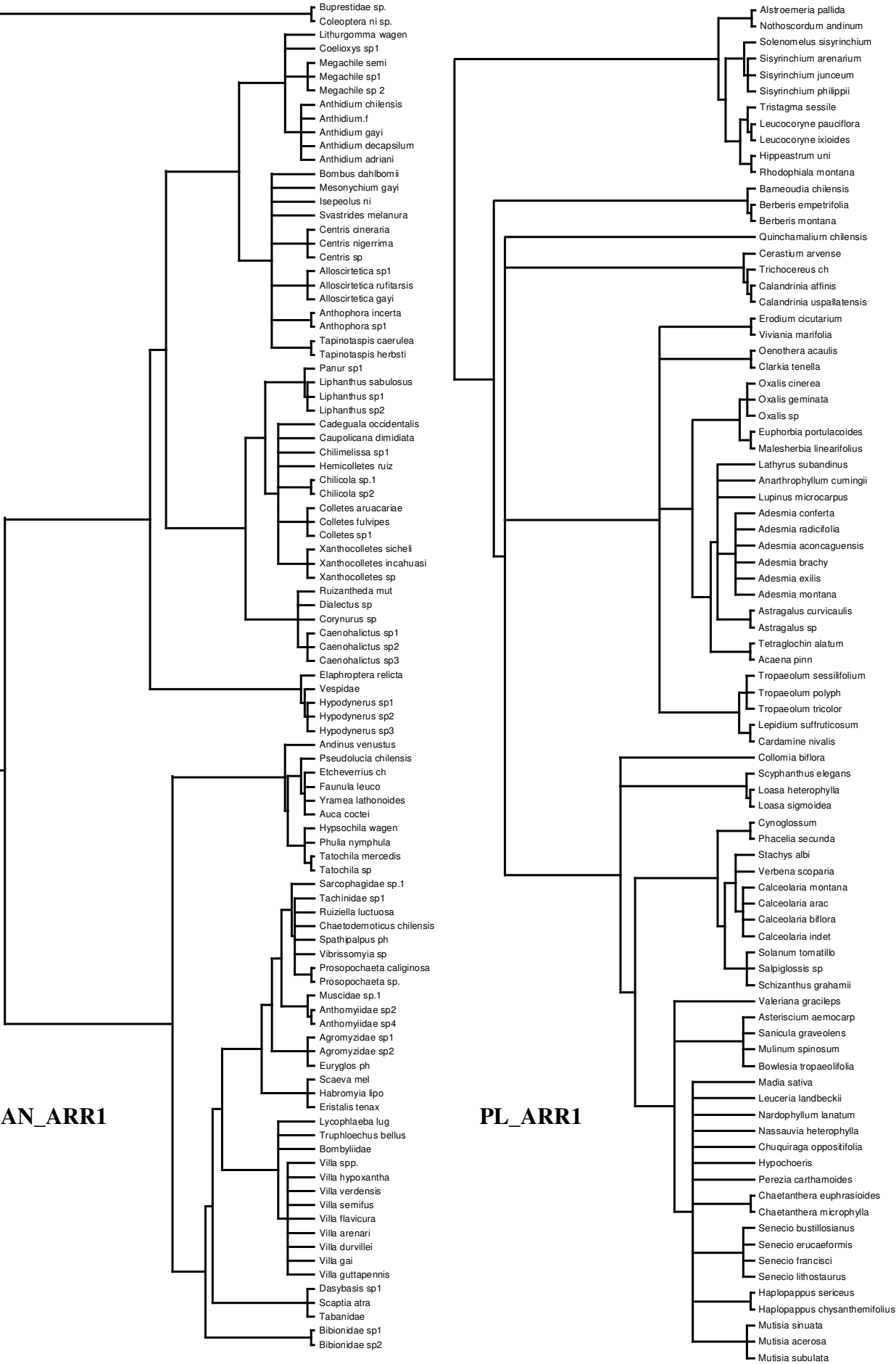


Community	Taxonomic group	Number of species	Randomization		Mantel	
			<i>K</i>	<i>P</i>	<i>Z</i>	<i>P</i>
CLLO	Hymenoptera	135	0.258	0.002	0.060	0.011
	Lepidoptera	37	0.352	0.177	0.110	0.007
	Diptera	67	0.302	0.462	0.049	0.075
PRCG	Lepidoptera	29	0.703	< 0.001	0.171	0.081
	Diptera	52	0.325	0.037	-0.006	0.508
SMRA	Coleoptera	47	0.371	0.248	-0.013	0.565
	Lepidoptera	21	0.797	0.008	0.133	0.044
	Diptera	52	0.254	0.138	0.031	0.268

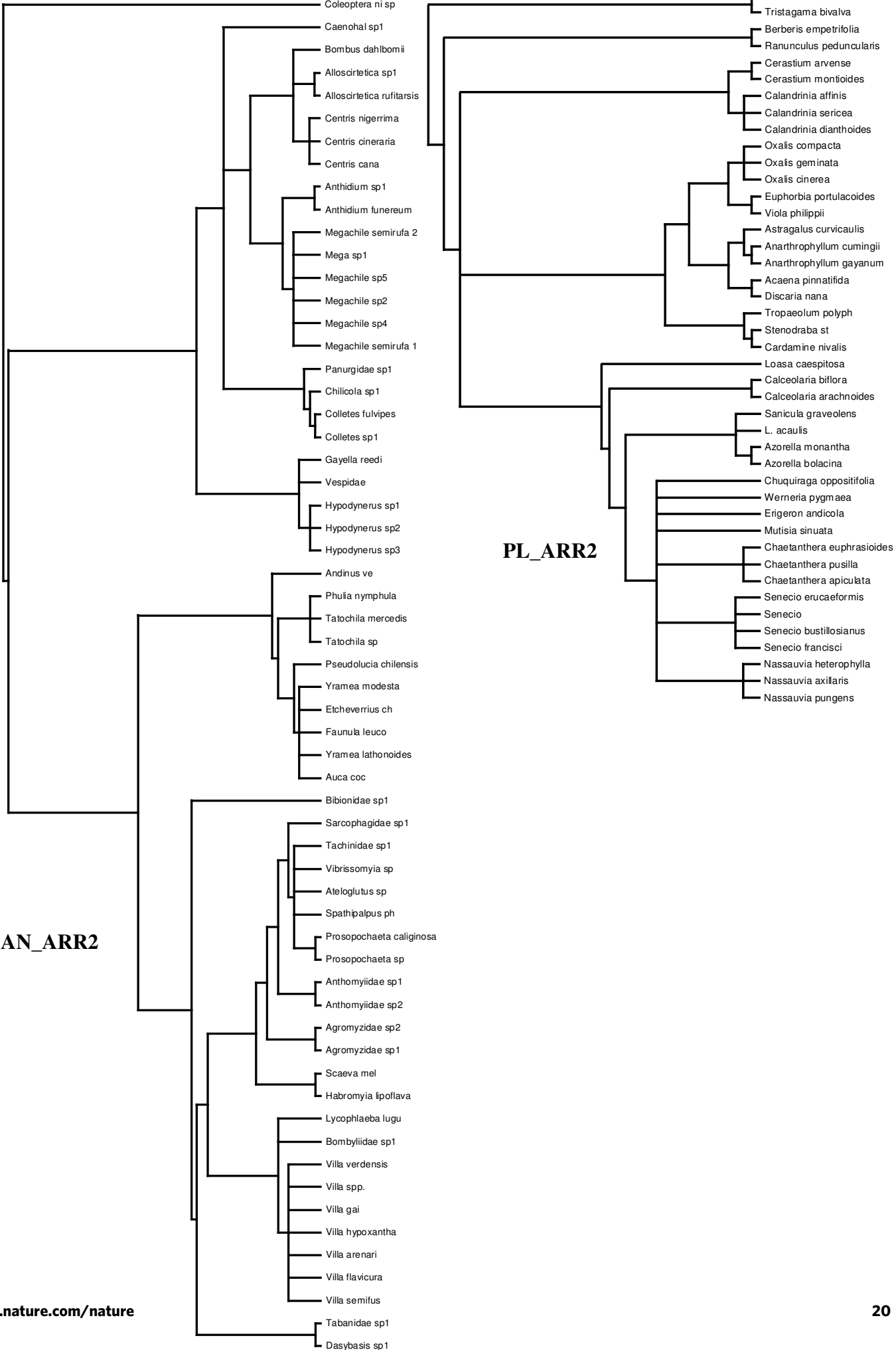
Figure S3. Assessing the magnitude and significance of phylogenetic effects within major taxonomic groups in three insect (pollinator) species. Only groups with more than 20 spp. were analyzed. Results from randomization and Mantel tests are listed on the table at the bottom (results for the entire communities are listed in Table S1).

PHYLOGENIES

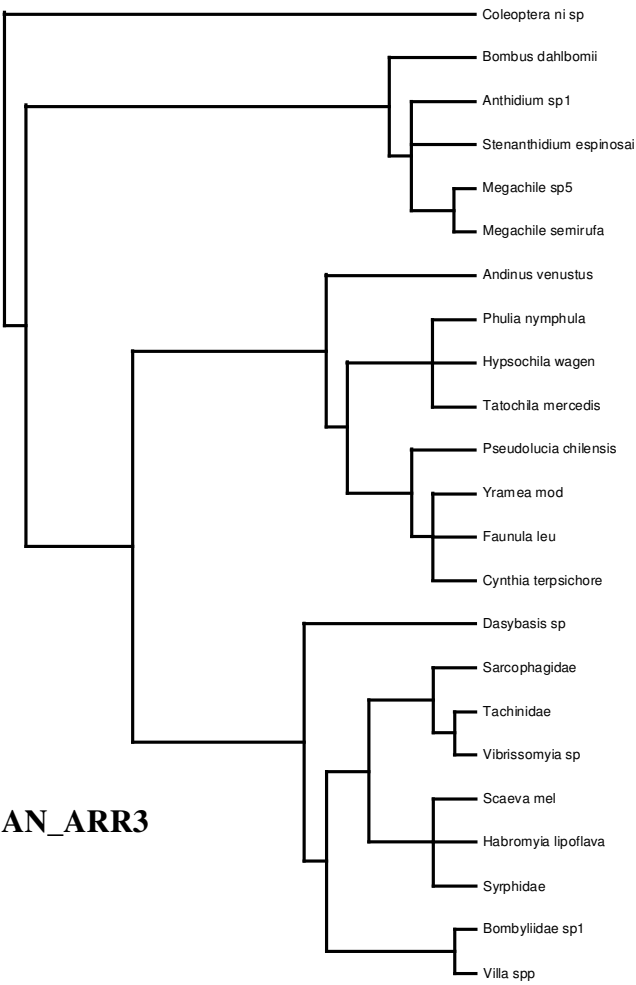
COMMUNITY ARR1 – Pollination



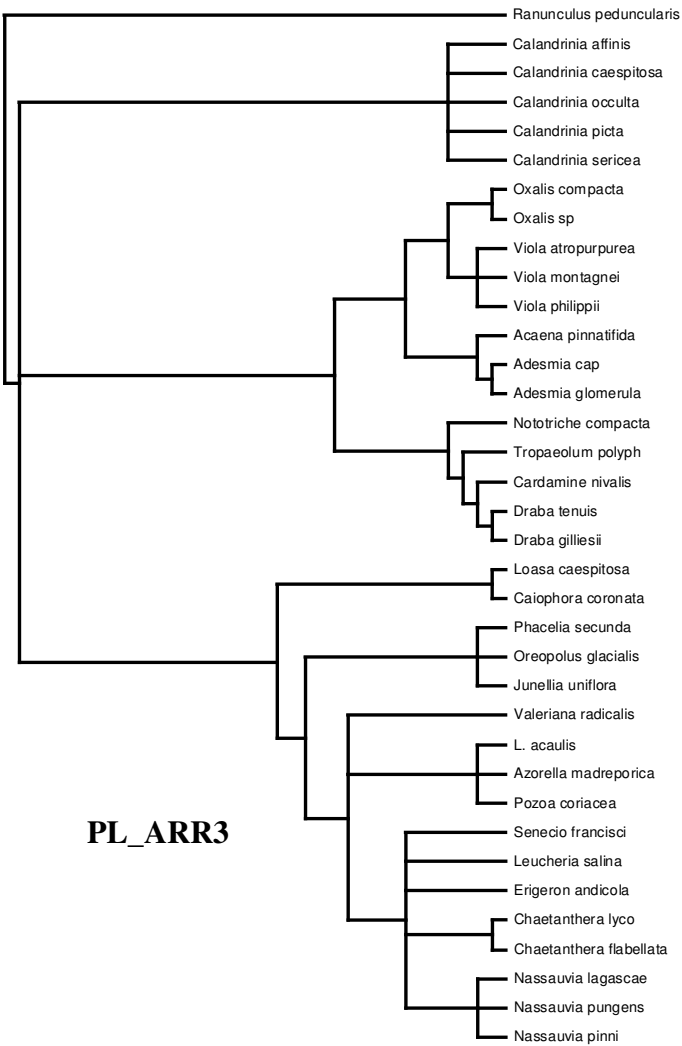
COMMUNITY ARR2 – Pollination



COMMUNITY ARR3 – Pollination

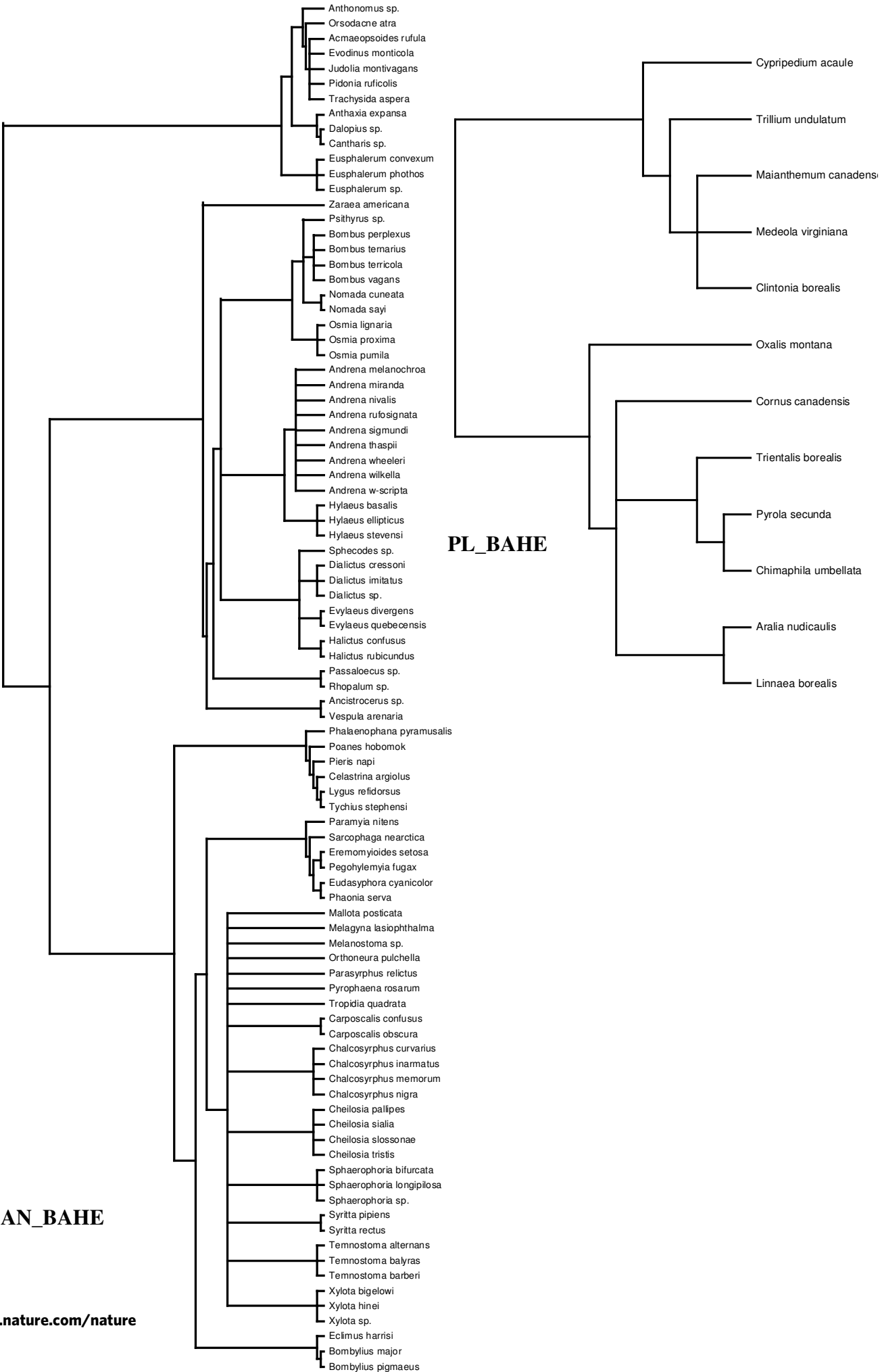


AN_ARR3

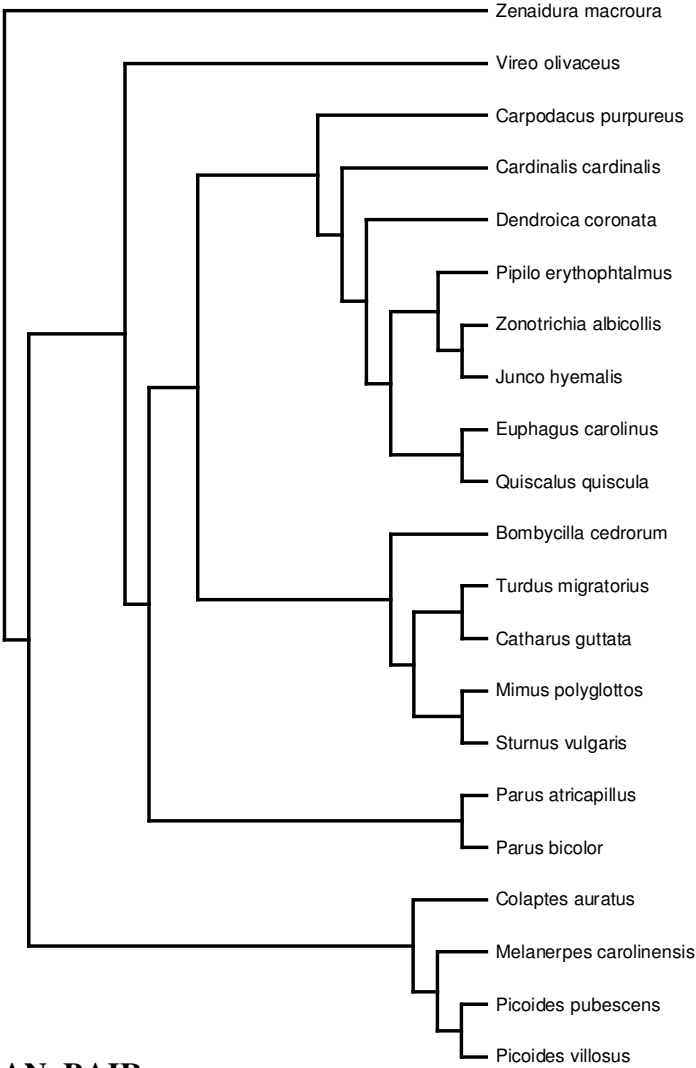


PL_ARR3

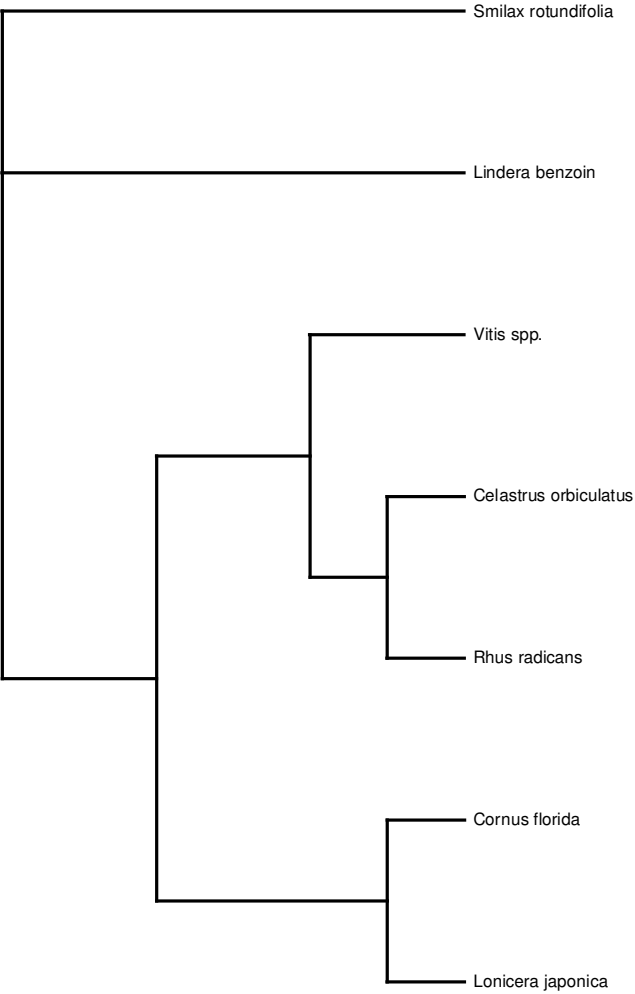
COMMUNITY BAHE – Pollination



COMMUNITY BAIR – Frugivory

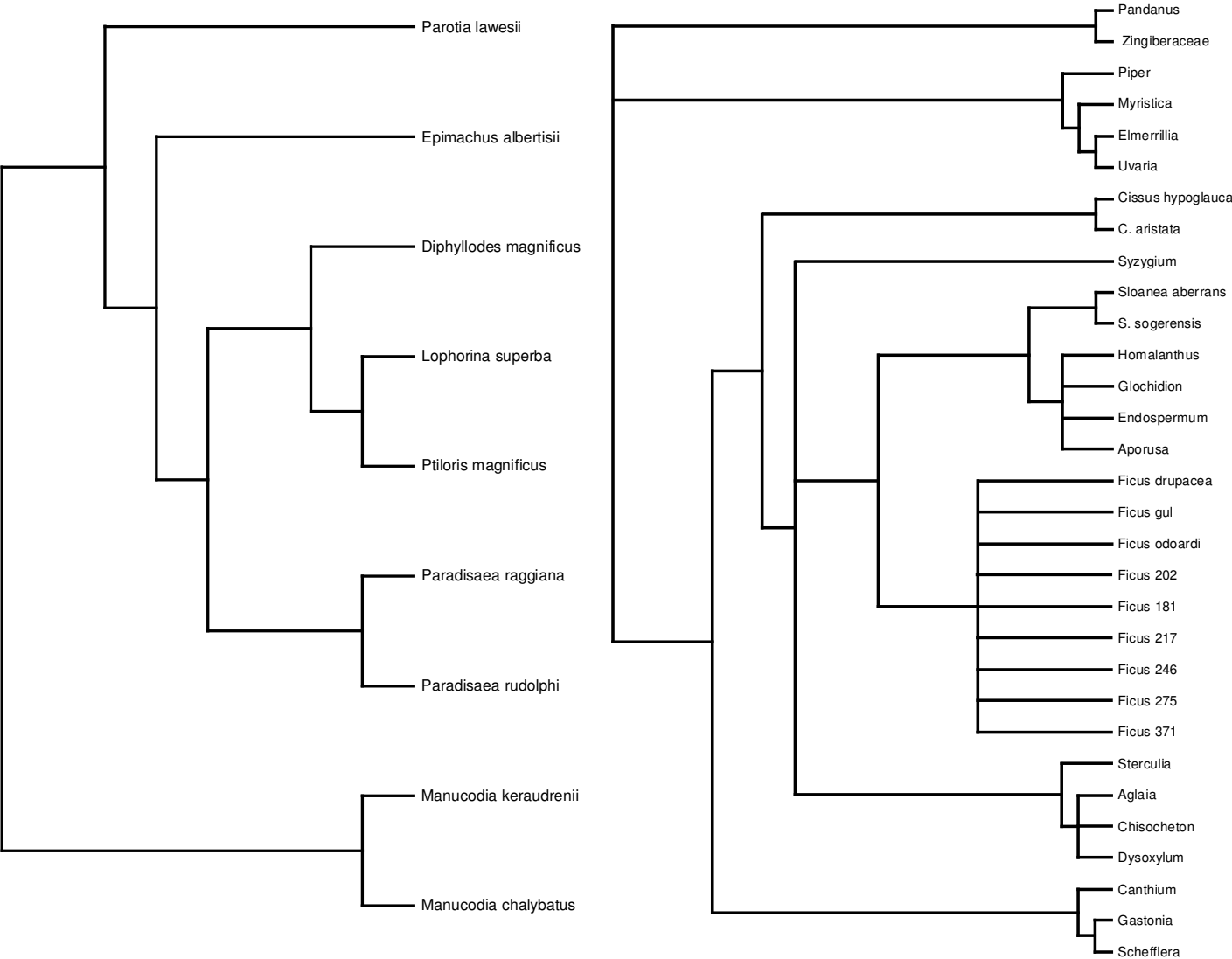


AN_BAIR



PL_BAIR
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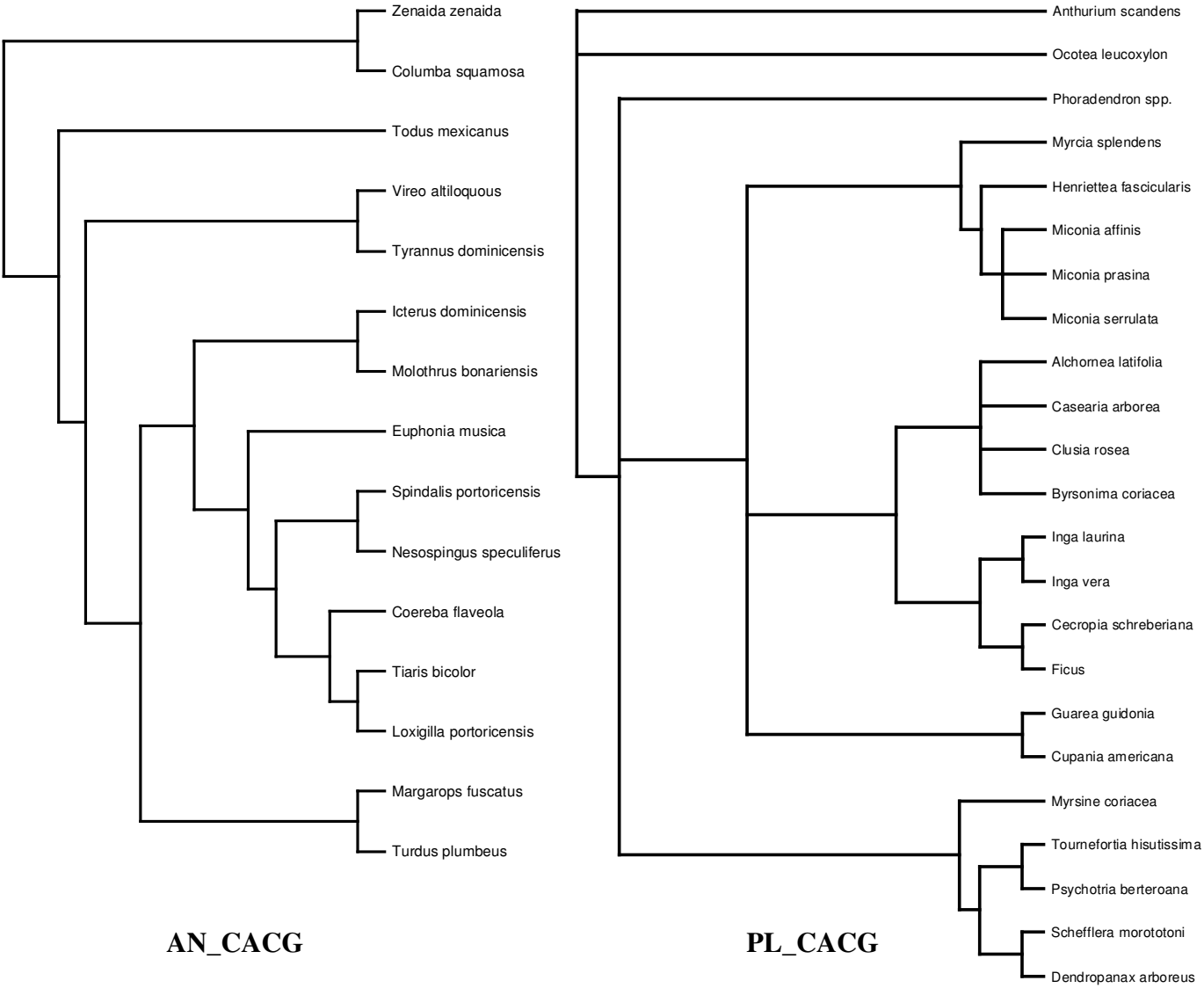
COMMUNITY BEEH – Frugivory



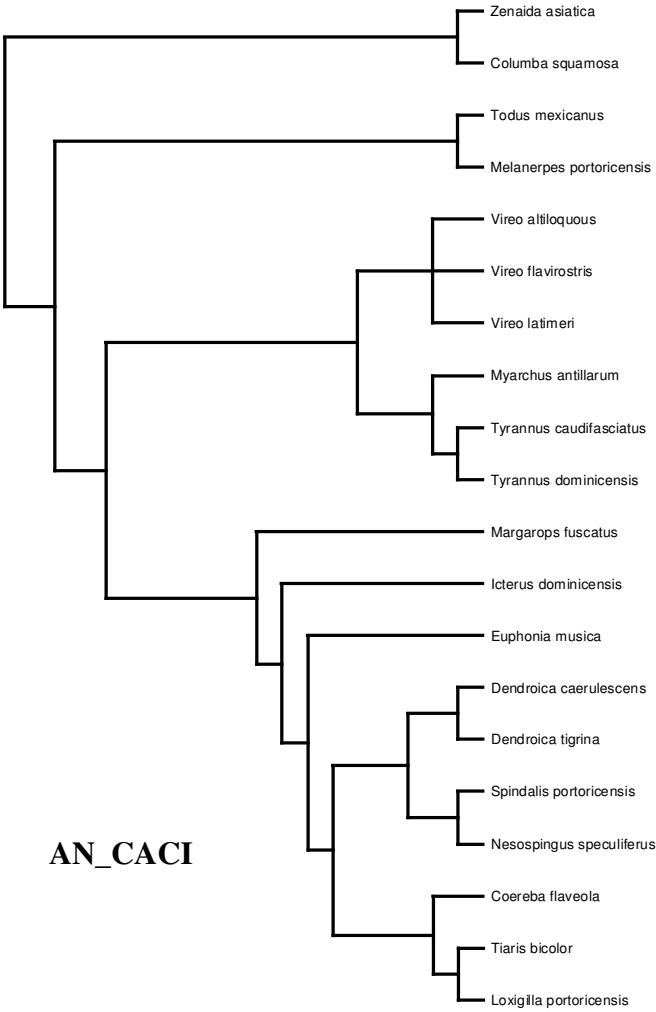
AN_BEEH
(not included in analysis)

PL_BEEH

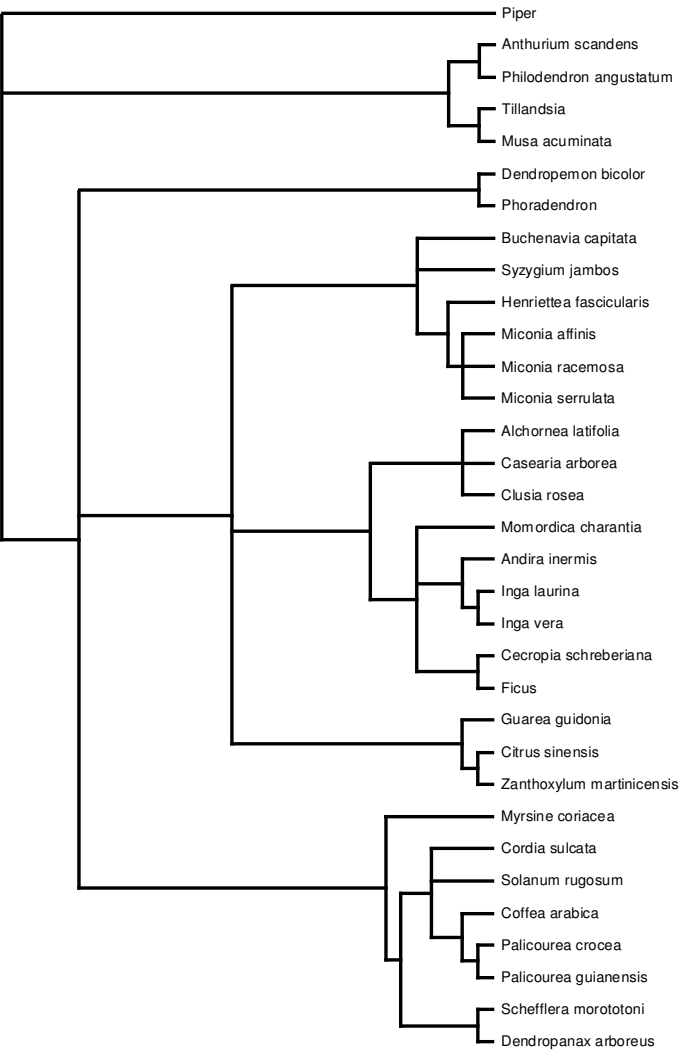
COMMUNITY CACG – Frugivory



COMMUNITY CACI – Frugivory

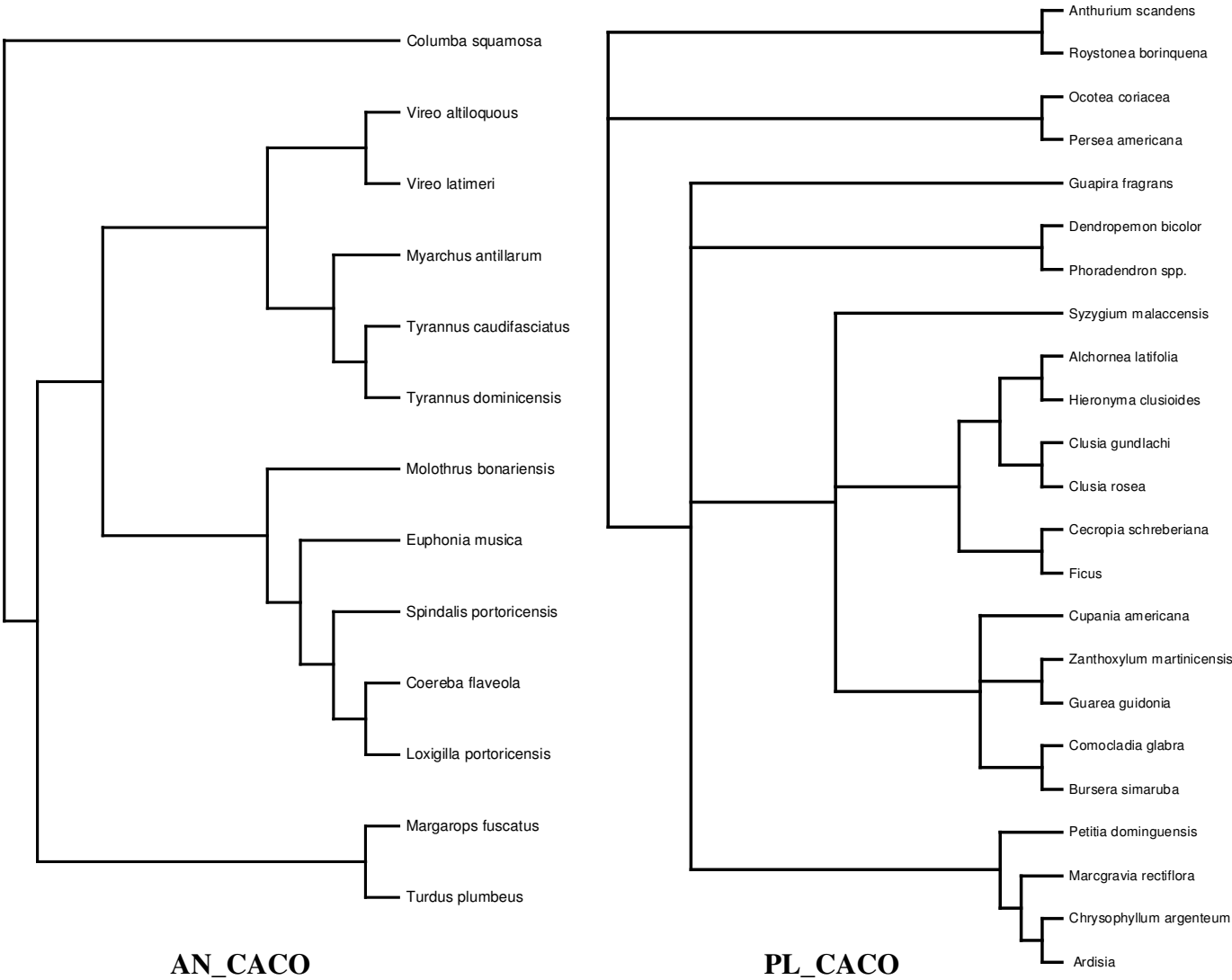


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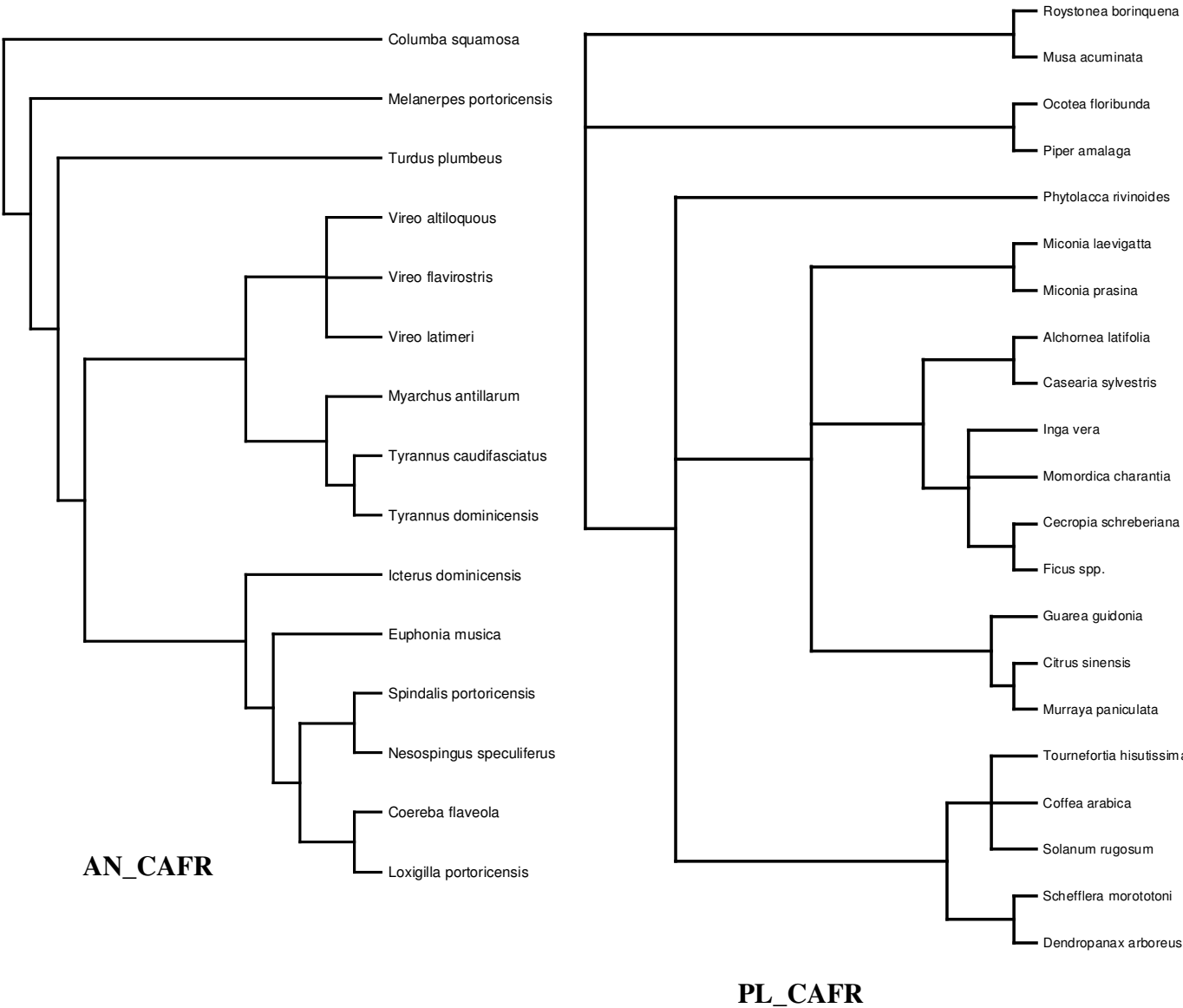


PL_CACI

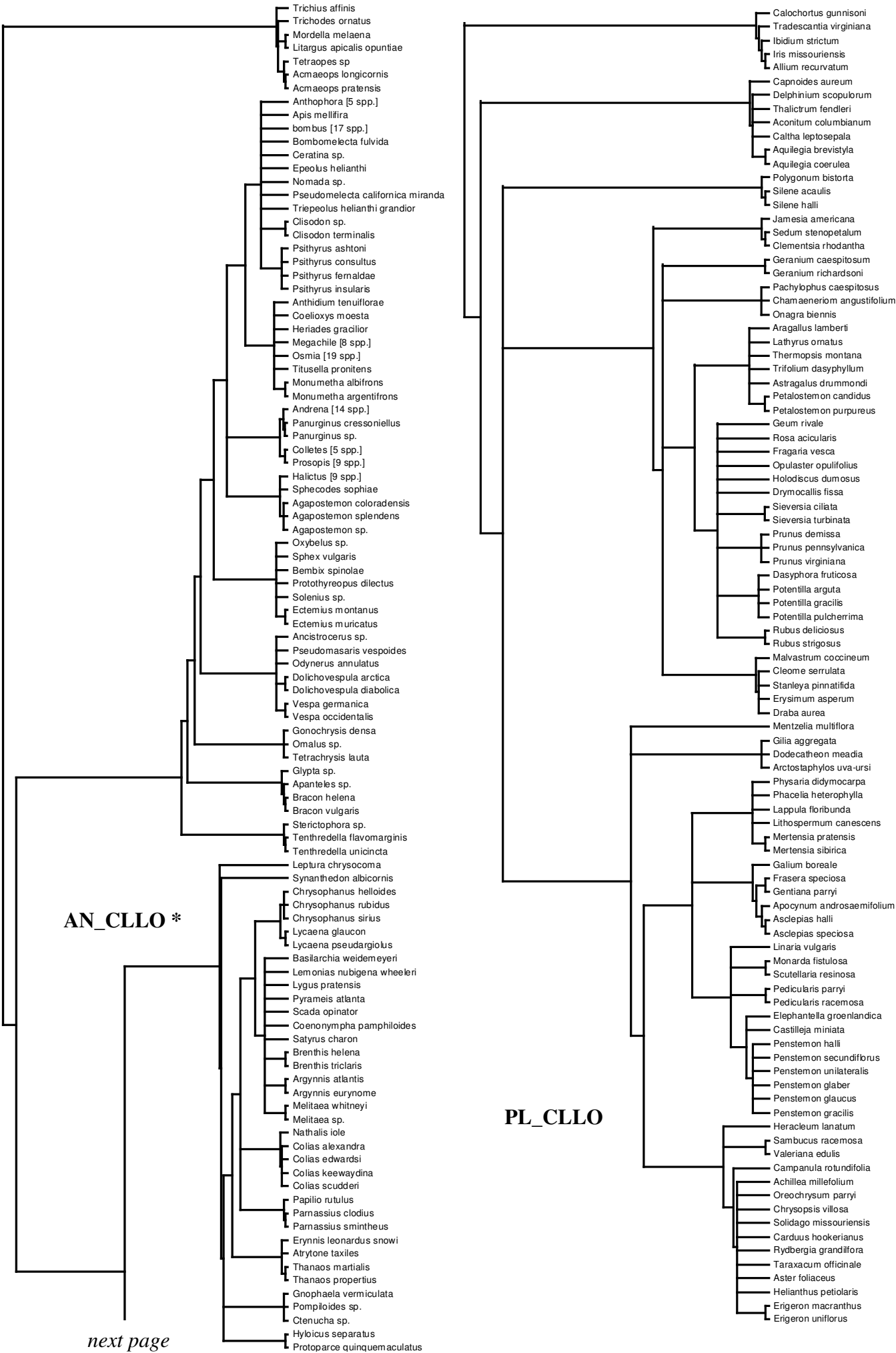
COMMUNITY CACO – Frugivory



COMMUNITY CAFR – Frugivory

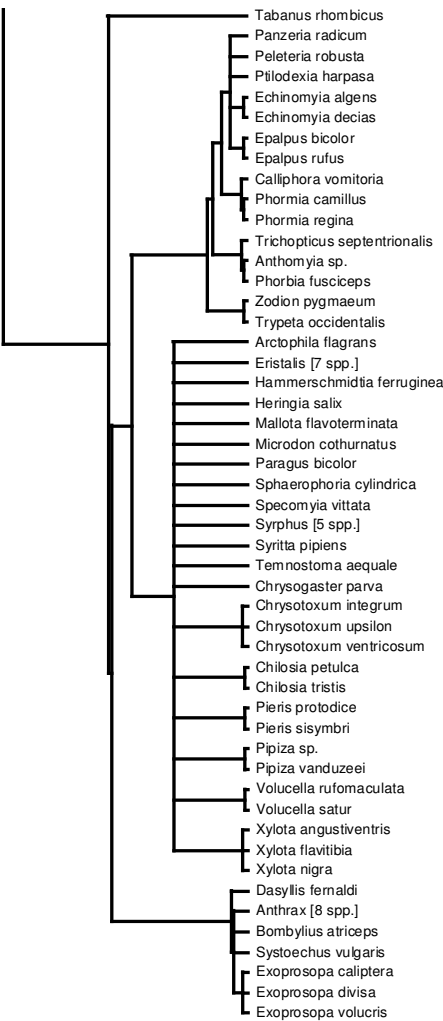


COMMUNITY CLLO– Pollination



next page

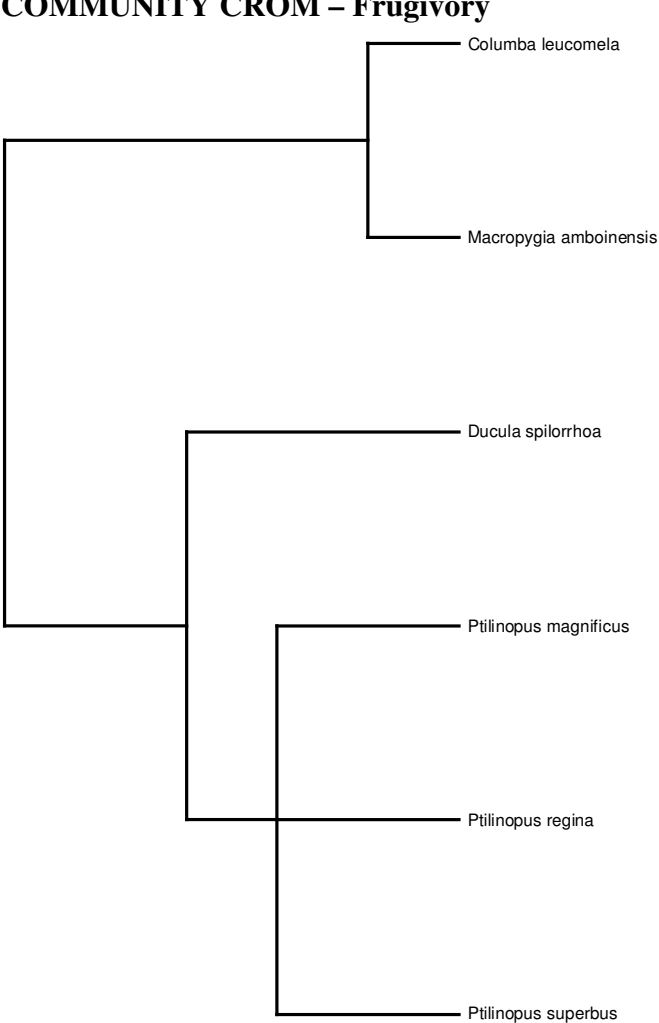
Community CLLO (continued)



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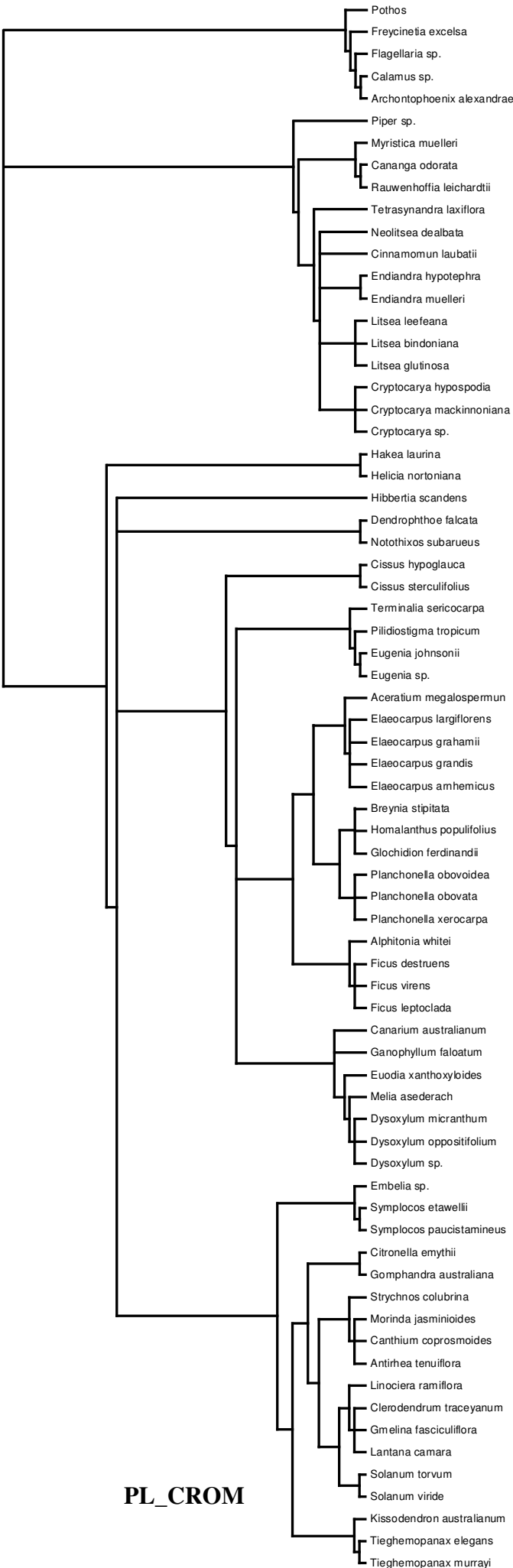
* Obs: large politomies within genera were removed for clarity (but were included in analyses).
Number of congeneric species included as soft politomies are shown within brackets.

COMMUNITY CROM – Frugivory

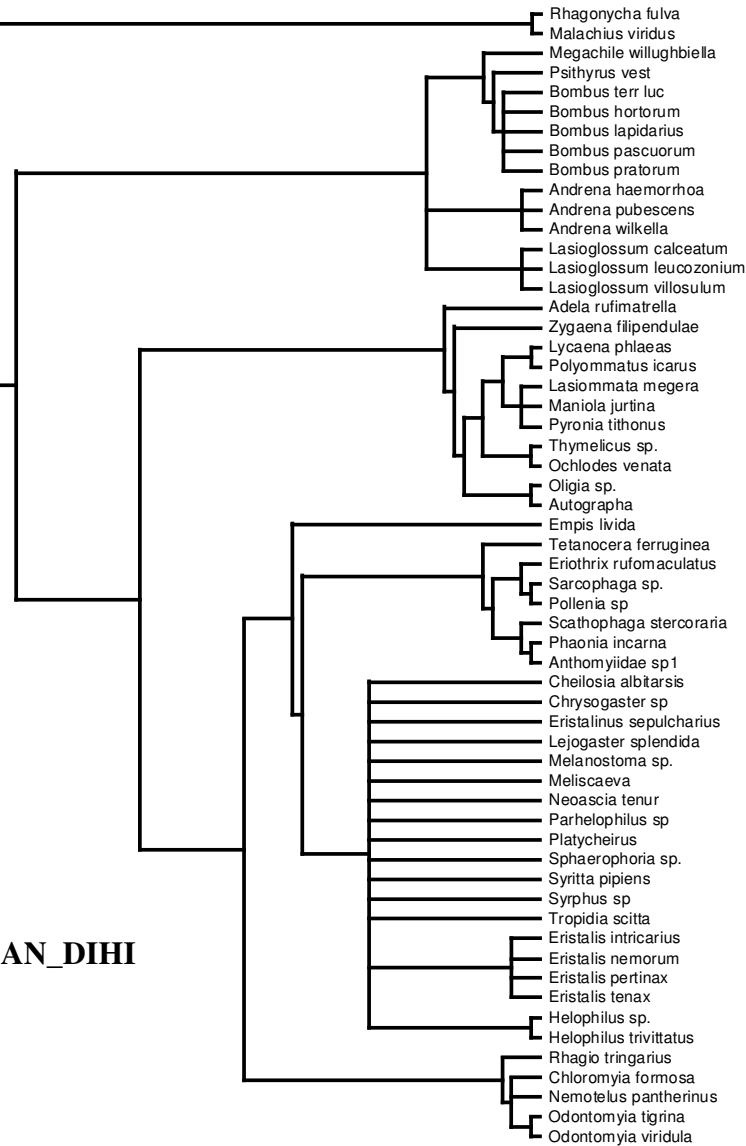


AN_CROM
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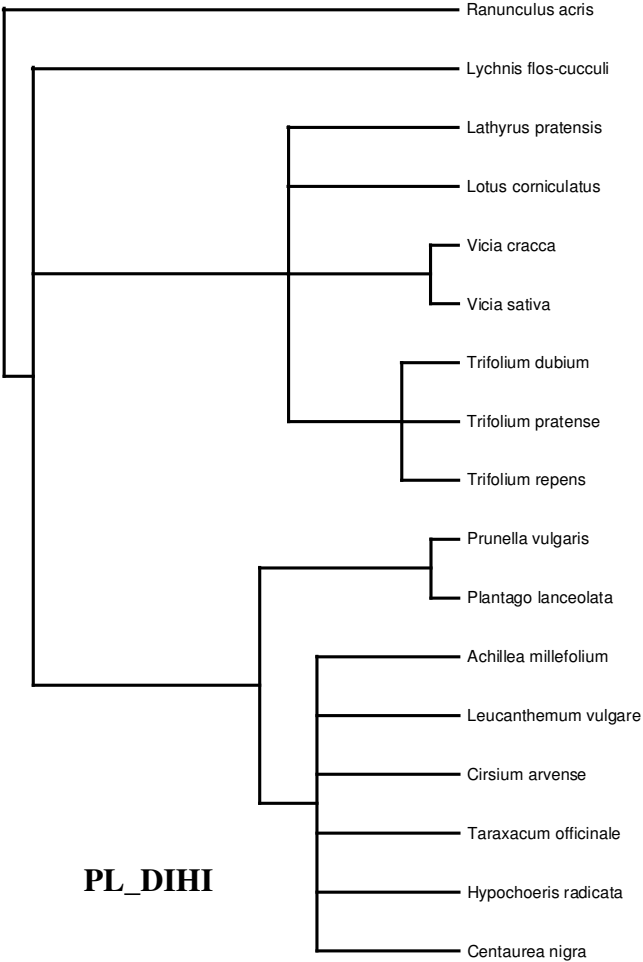
PL_CROM



COMMUNITY DIHI – Pollination

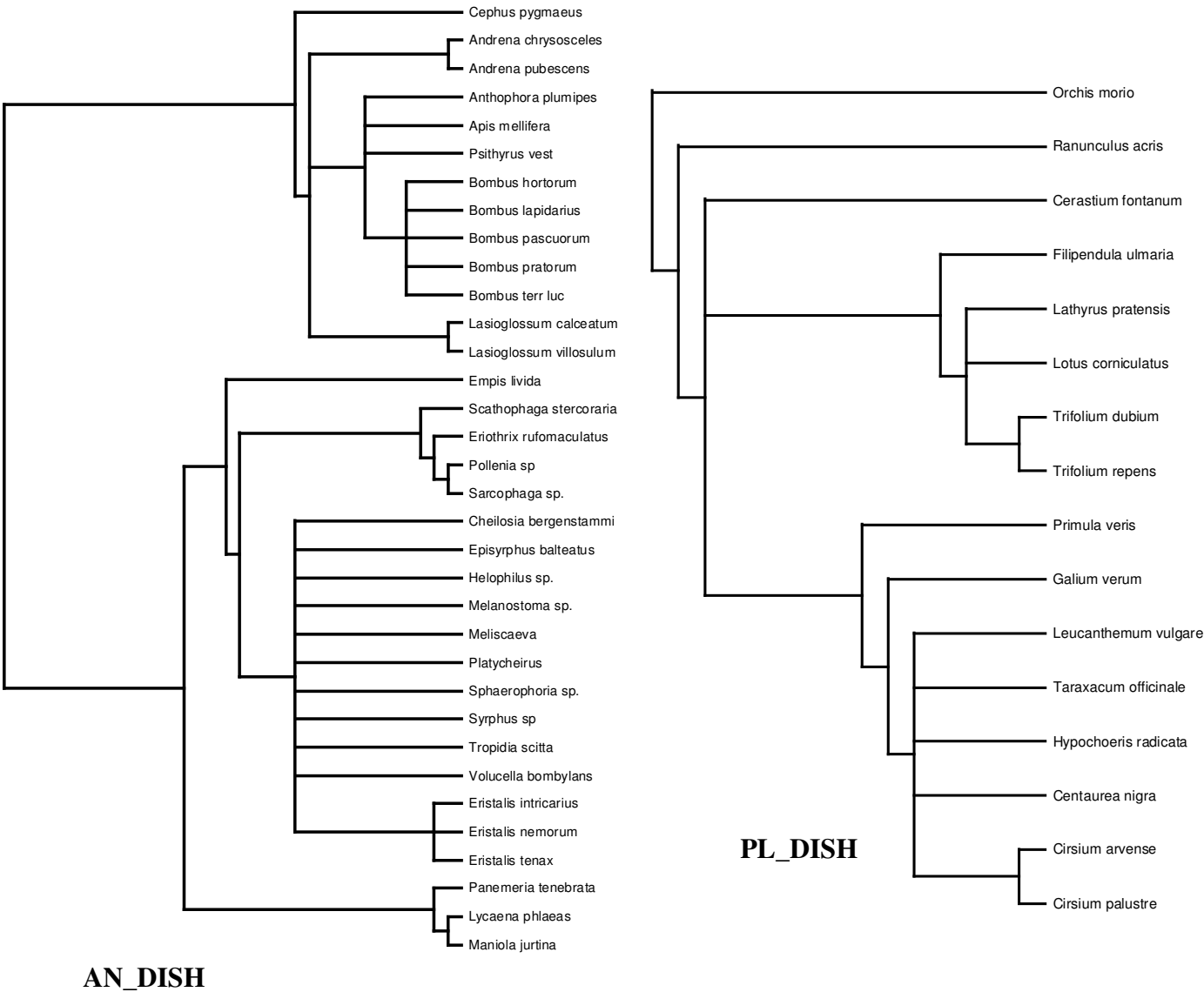


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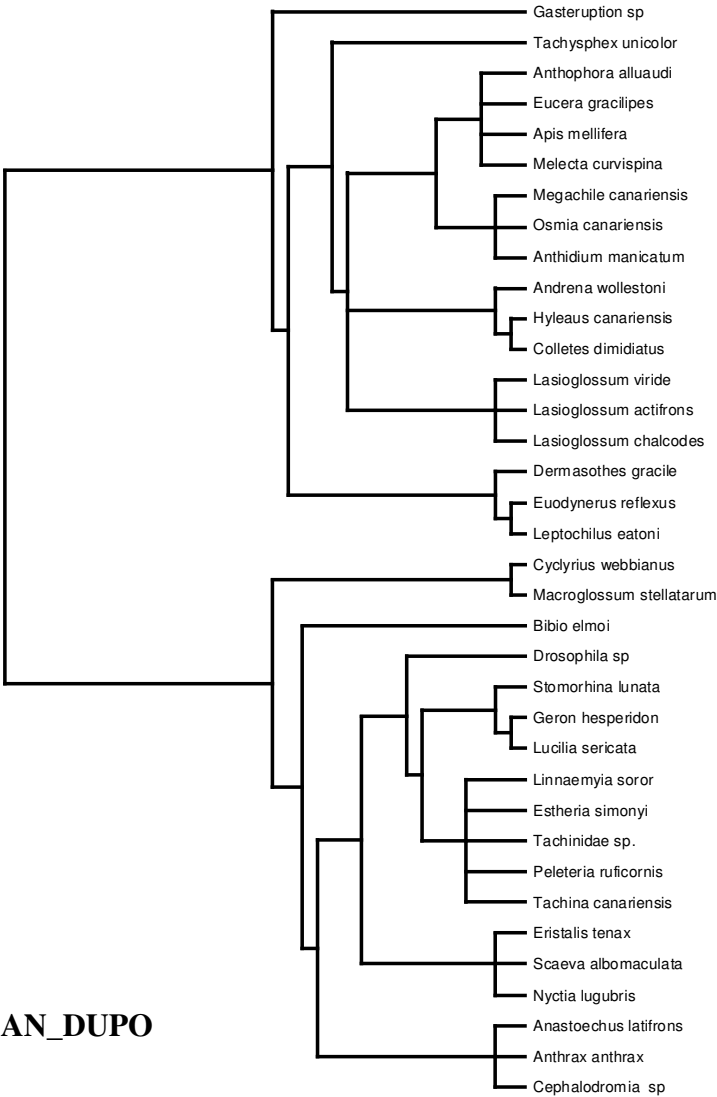


PL_DIHI

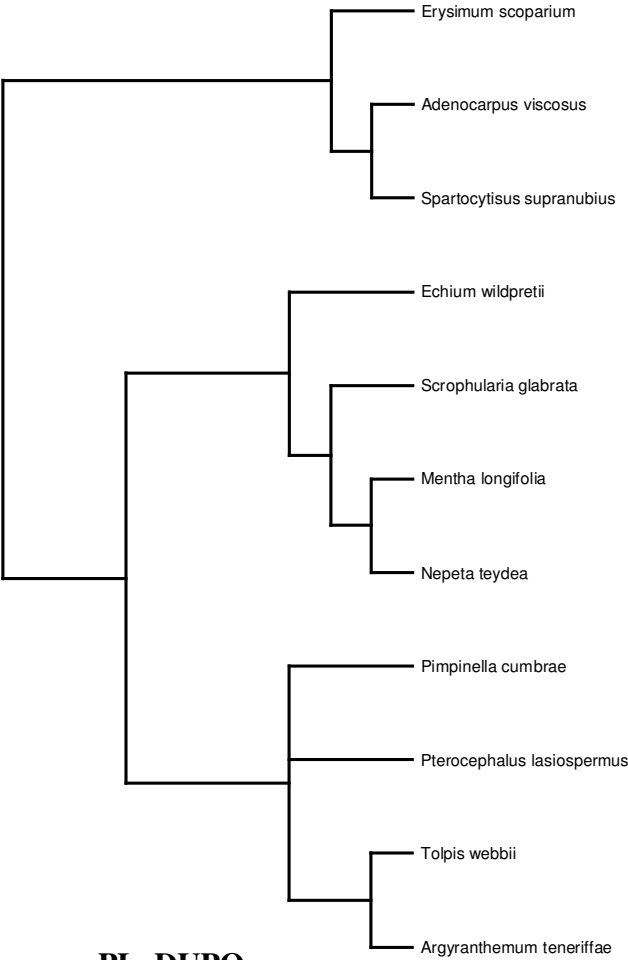
COMMUNITY DISH – Pollination



COMMUNITY DUPO – Pollination

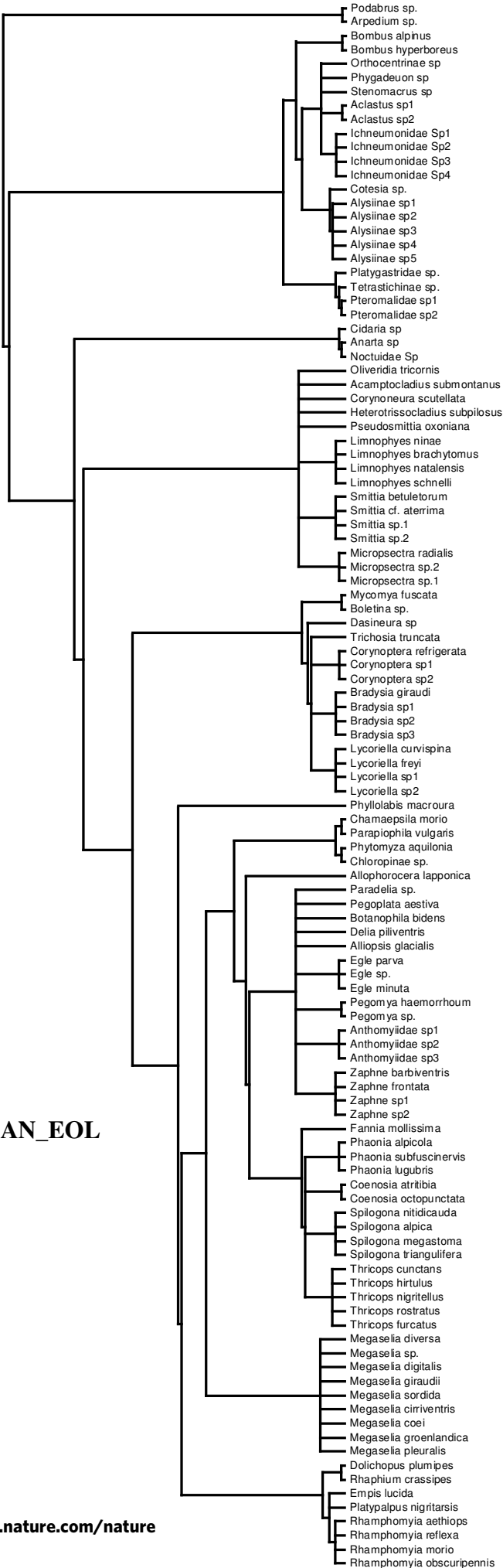


AN_DUPO

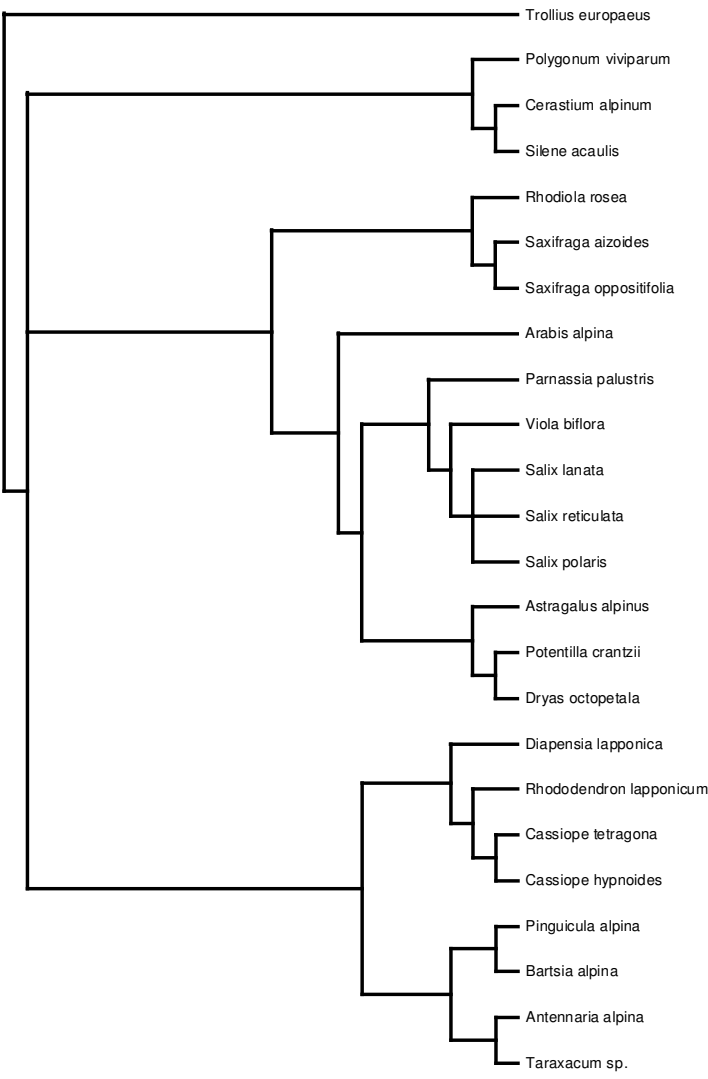


PL_DUPO

COMMUNITY EOL – Pollination

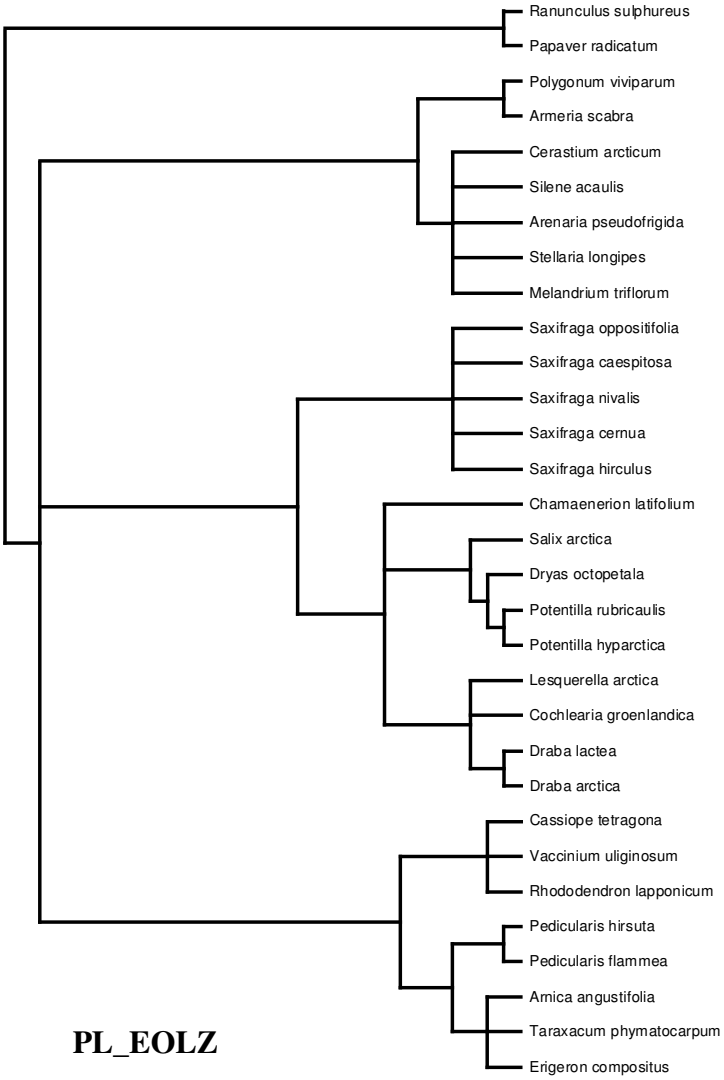
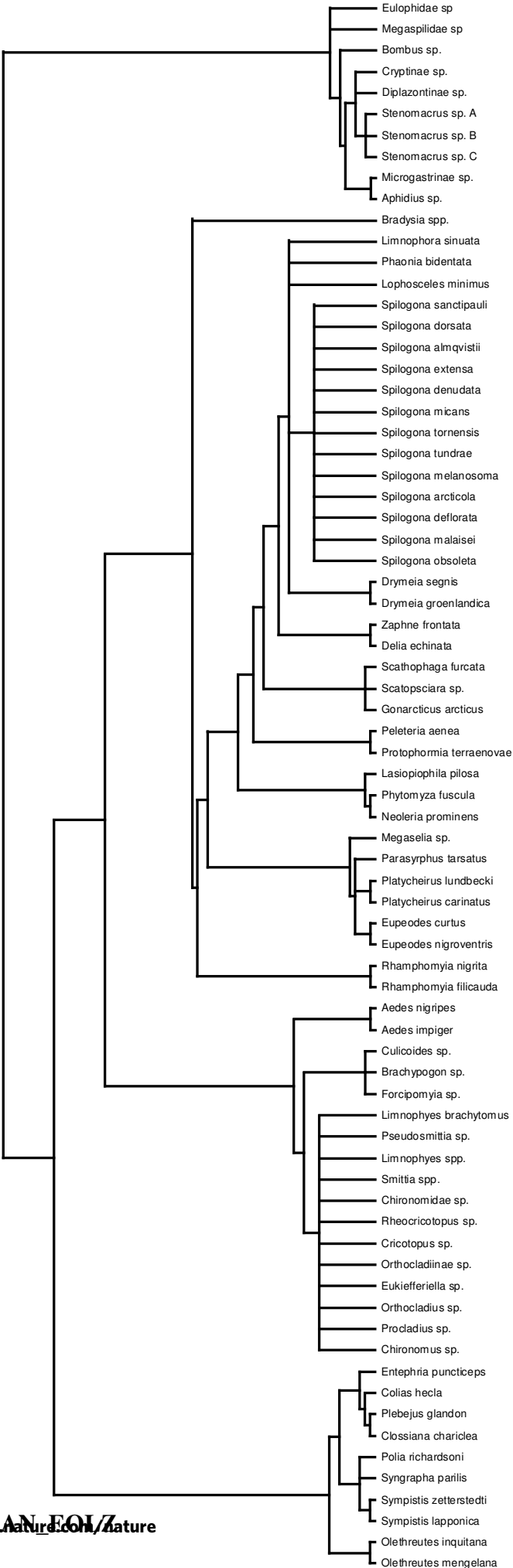


AN_EOL



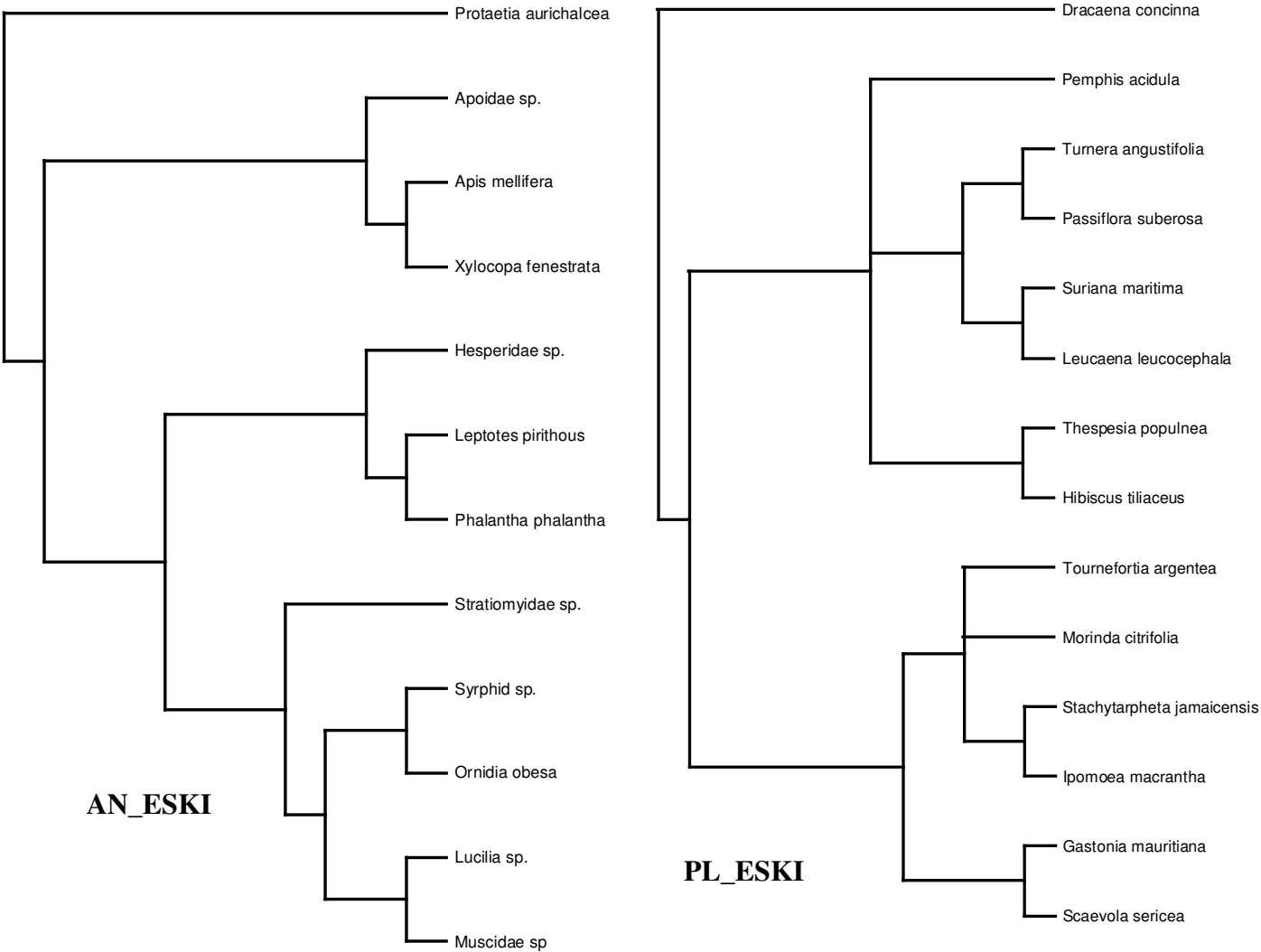
PL_EOL

COMMUNITY EOLZ – Pollination

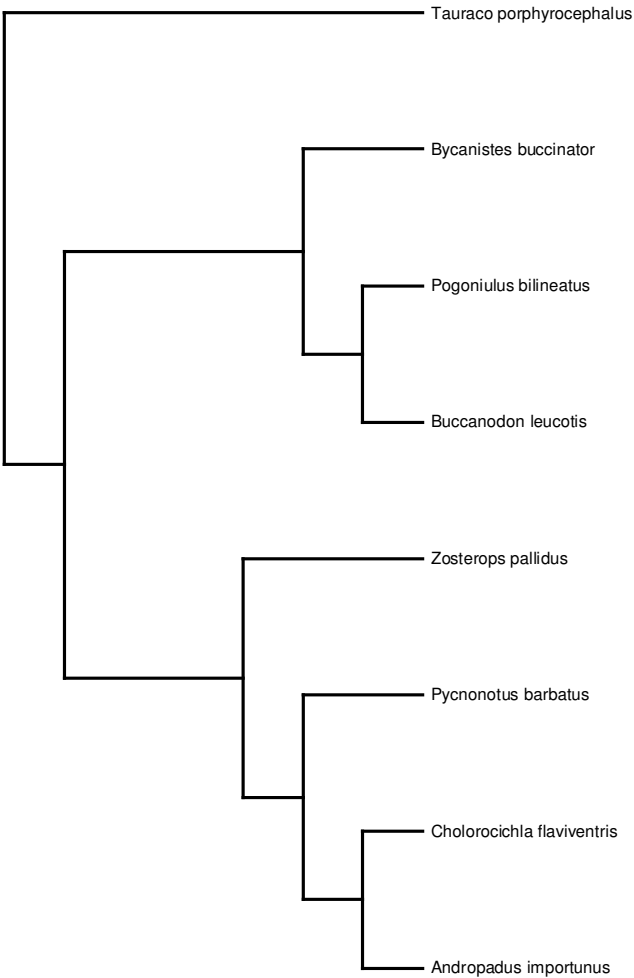


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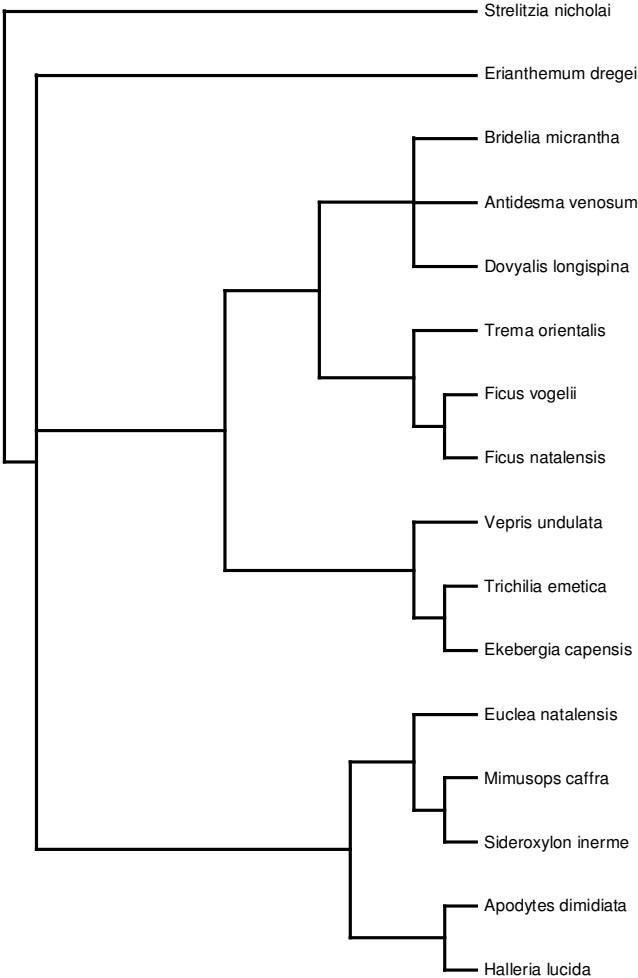
COMMUNITY ESKI – Pollination



COMMUNITY FROS – Frugivory

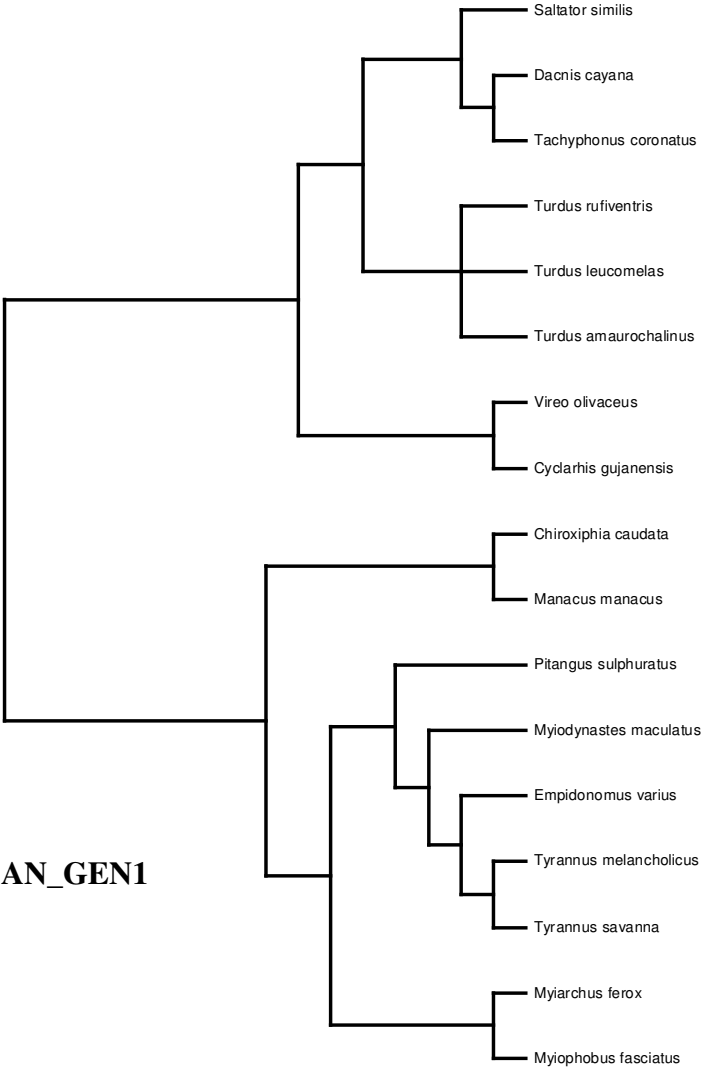


AN_FROS
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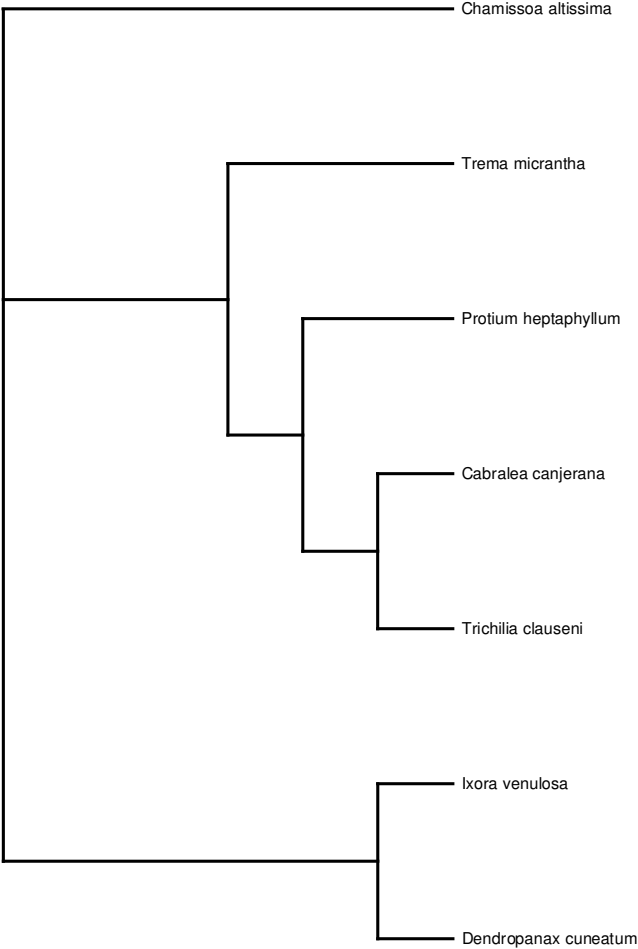


PL_FROS

COMMUNITY GEN1 – Frugivory

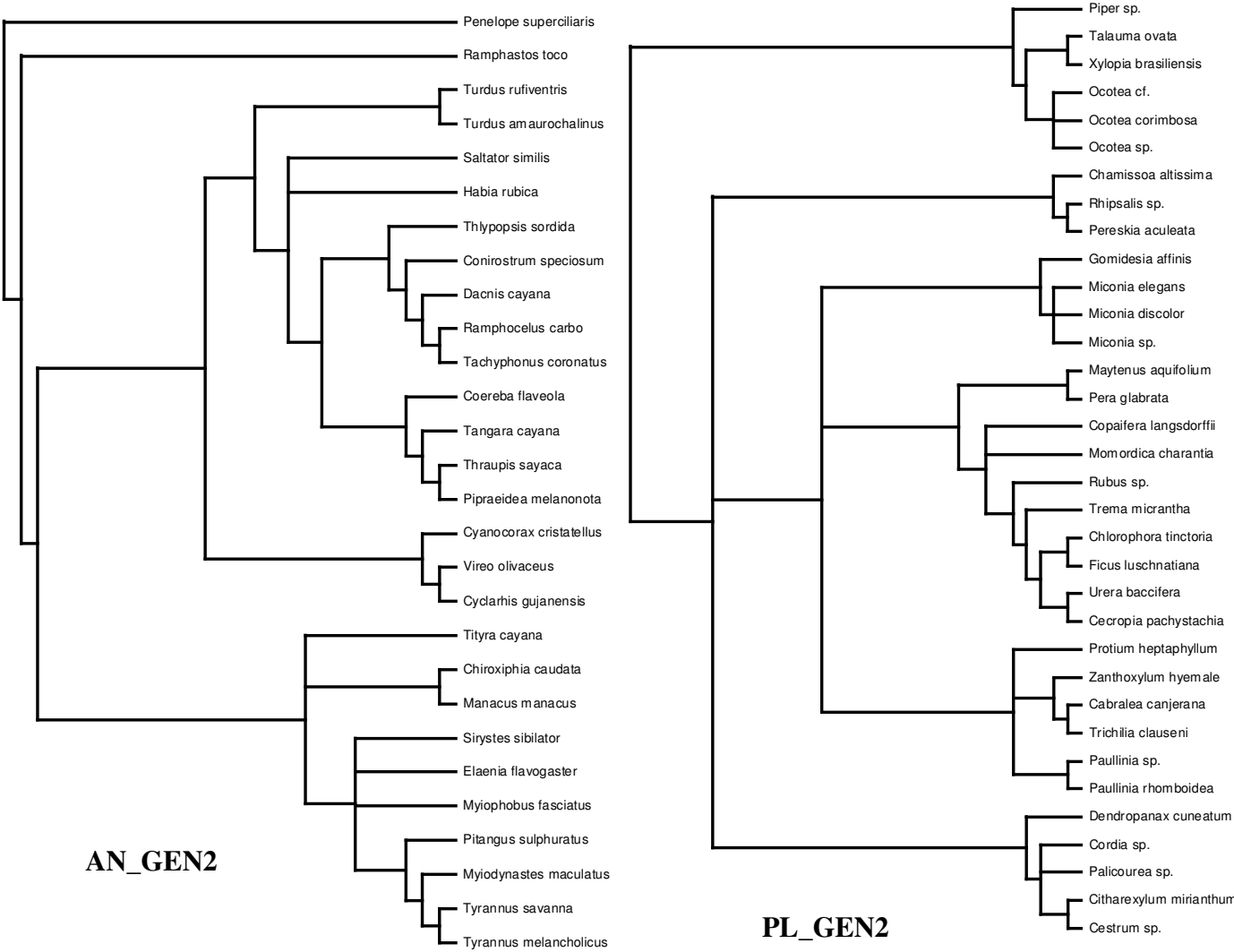


AN_GEN1

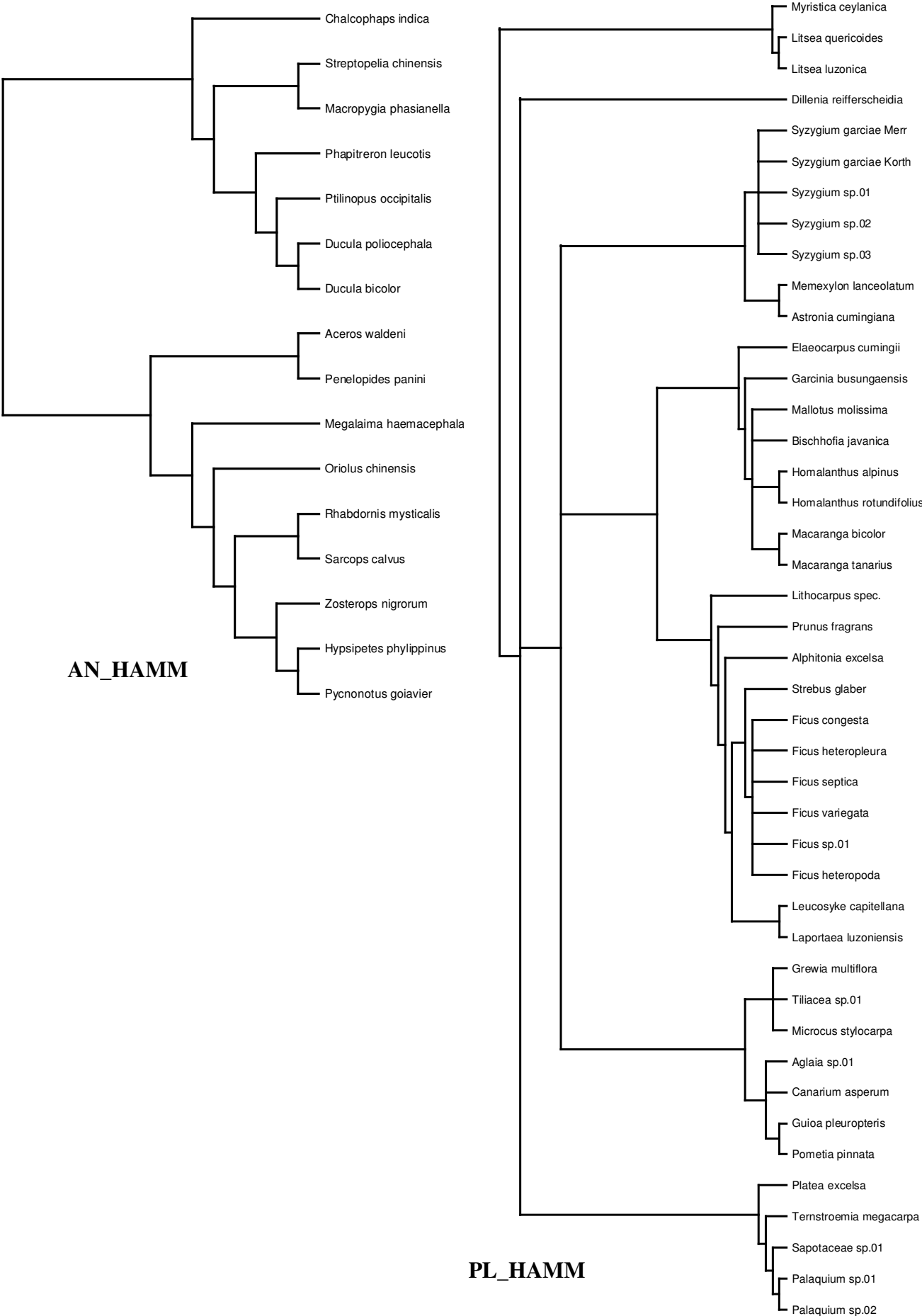


PL_GEN1
(not included in analyses)

COMMUNITY GEN2 – Frugivory

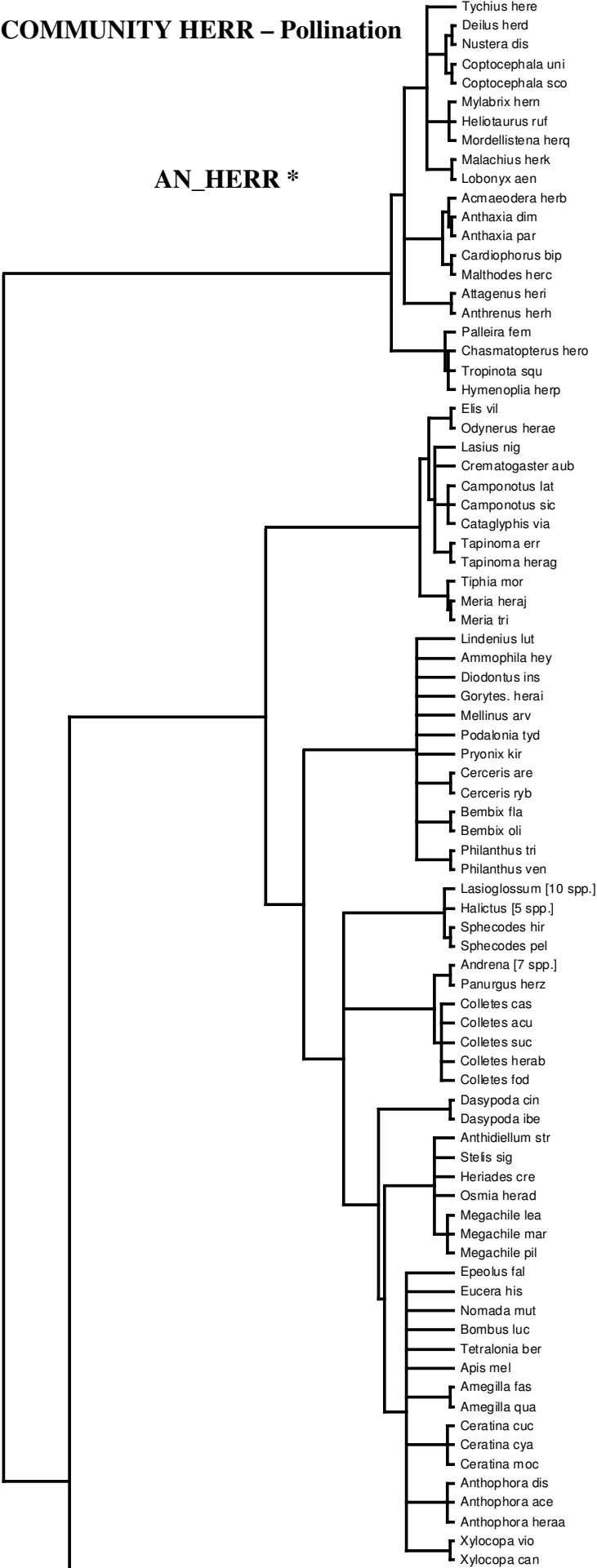


COMMUNITY HAMM – Frugivory

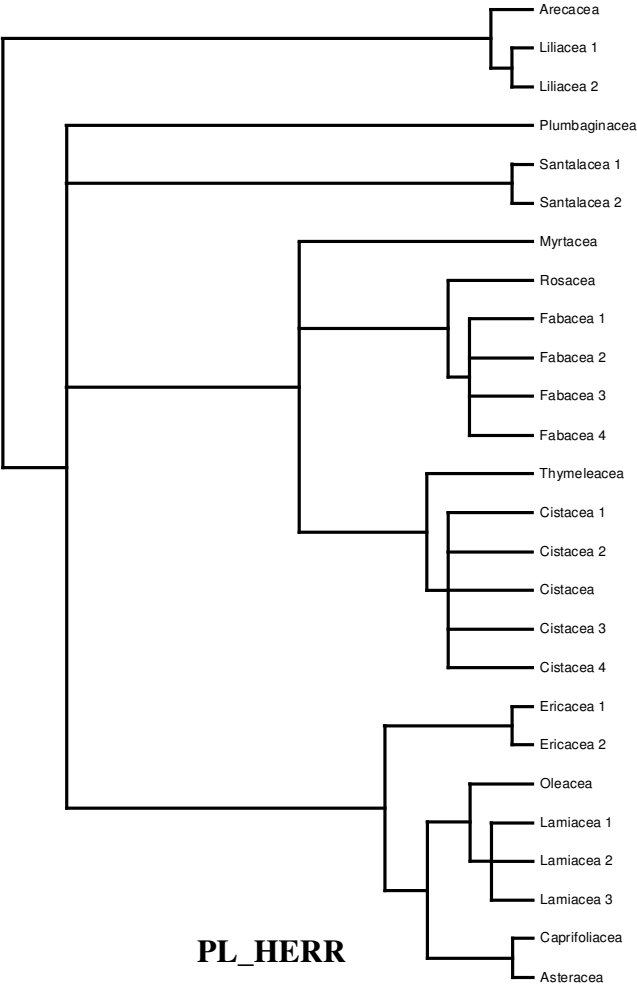


COMMUNITY HERR – Pollination

AN_HERR *

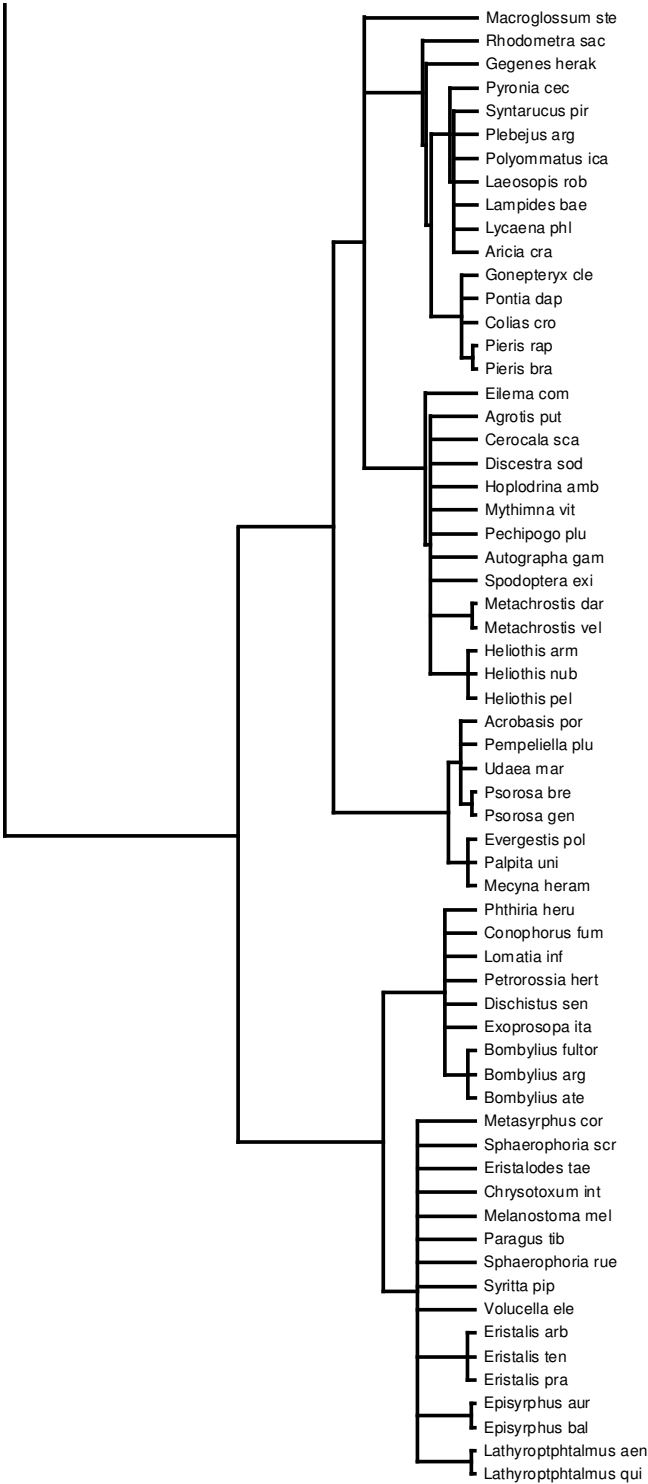


PL_HERR



next page

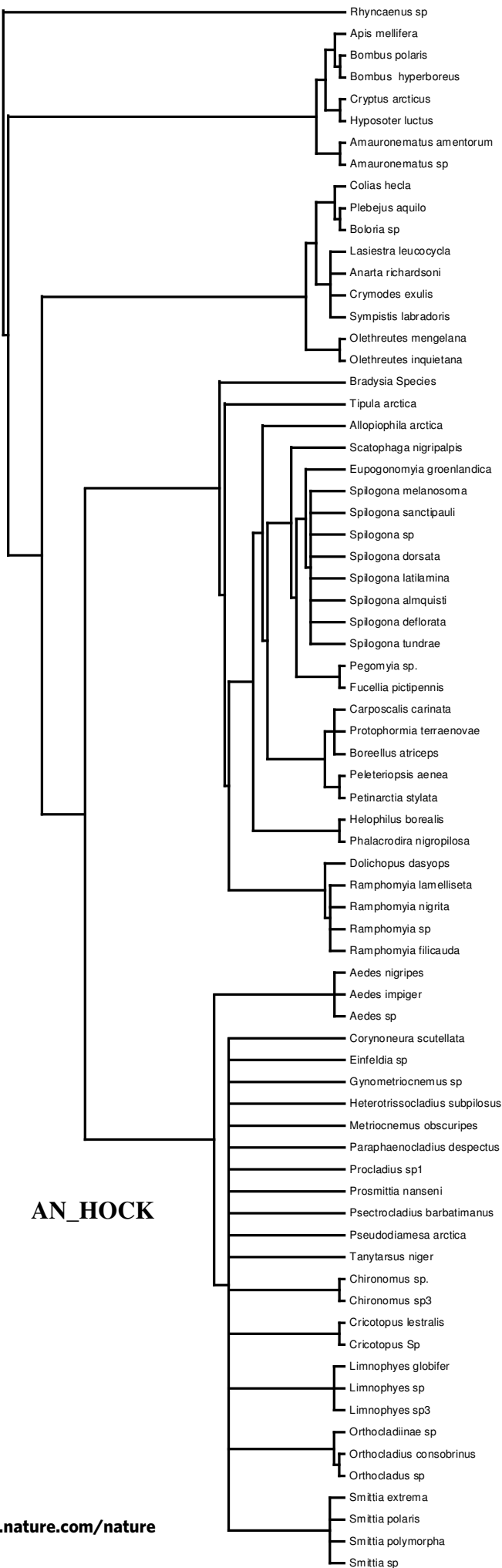
Community HERR (continued)



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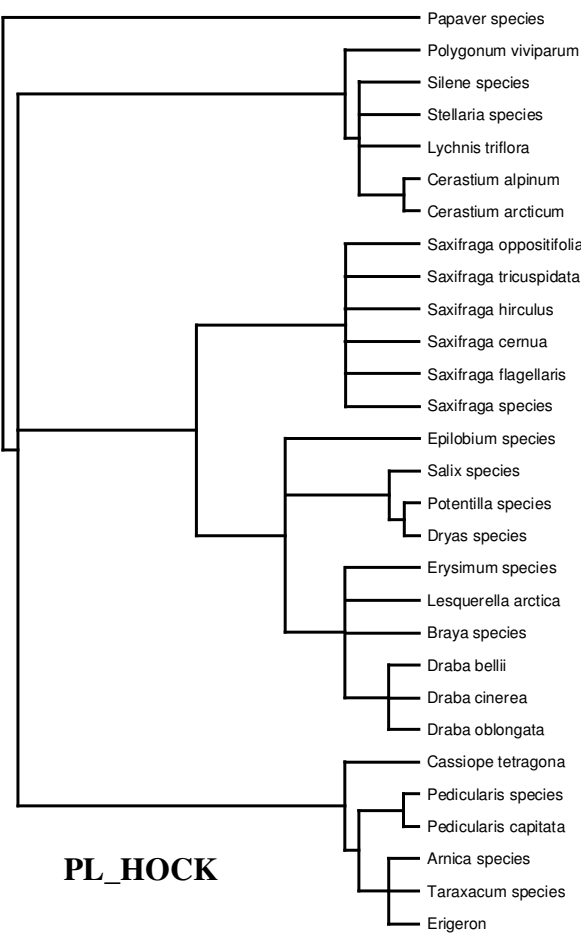
* Obs: large politomies within genera were removed for clarity (but were included in analyses).
Number of congeneric species included as soft politomies are shown within brackets.

COMMUNITY HOCK – Pollination

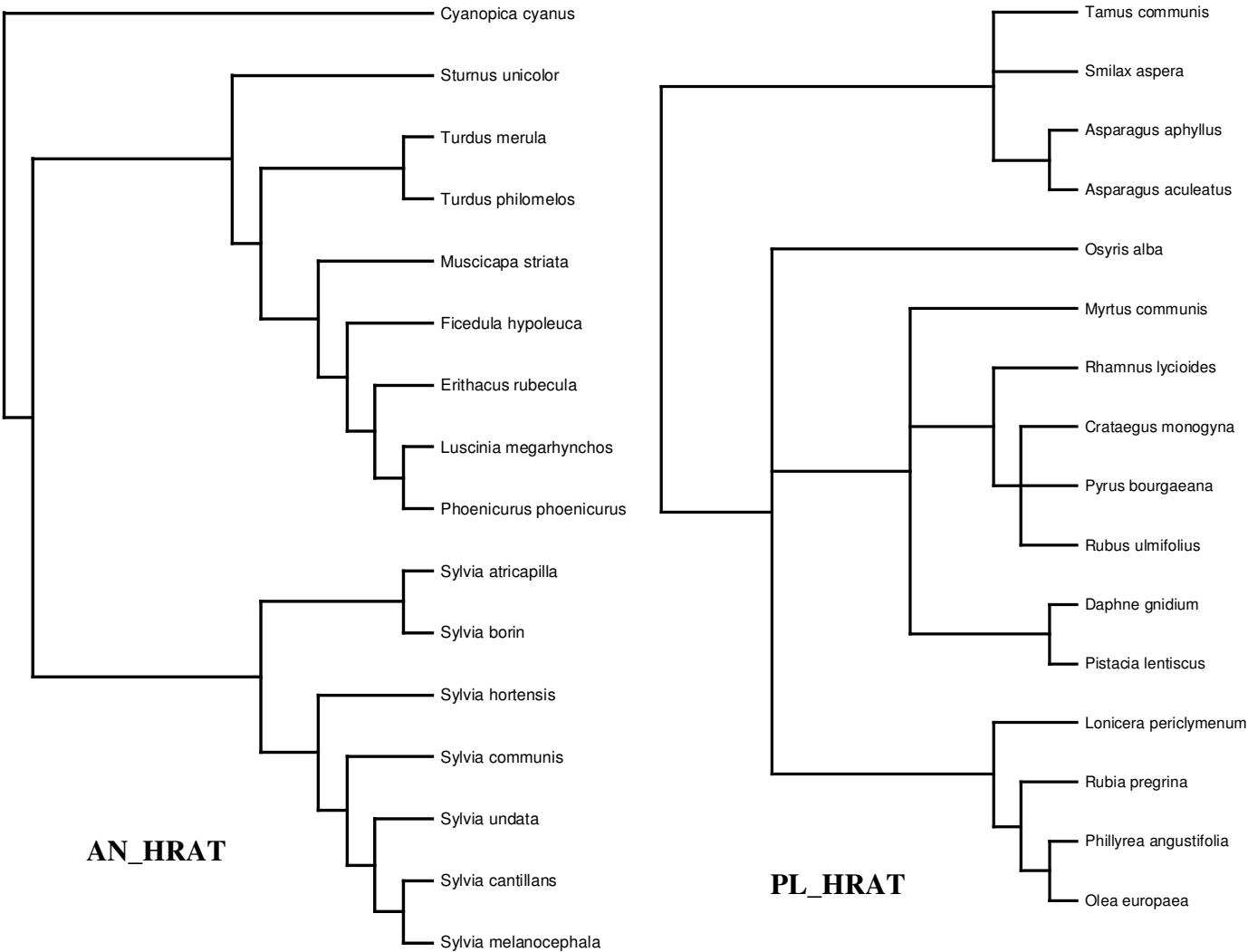


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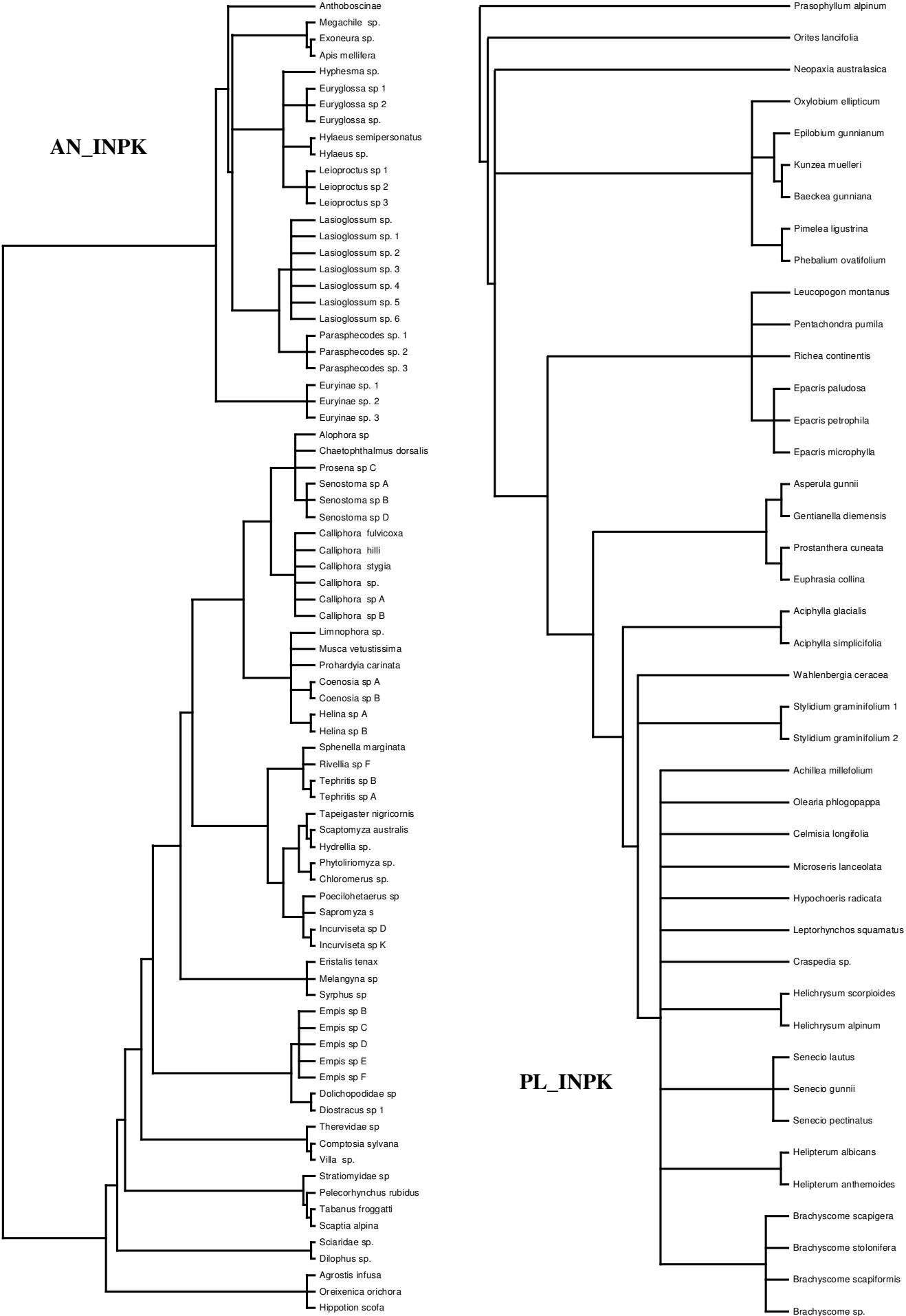
PL_HOCK



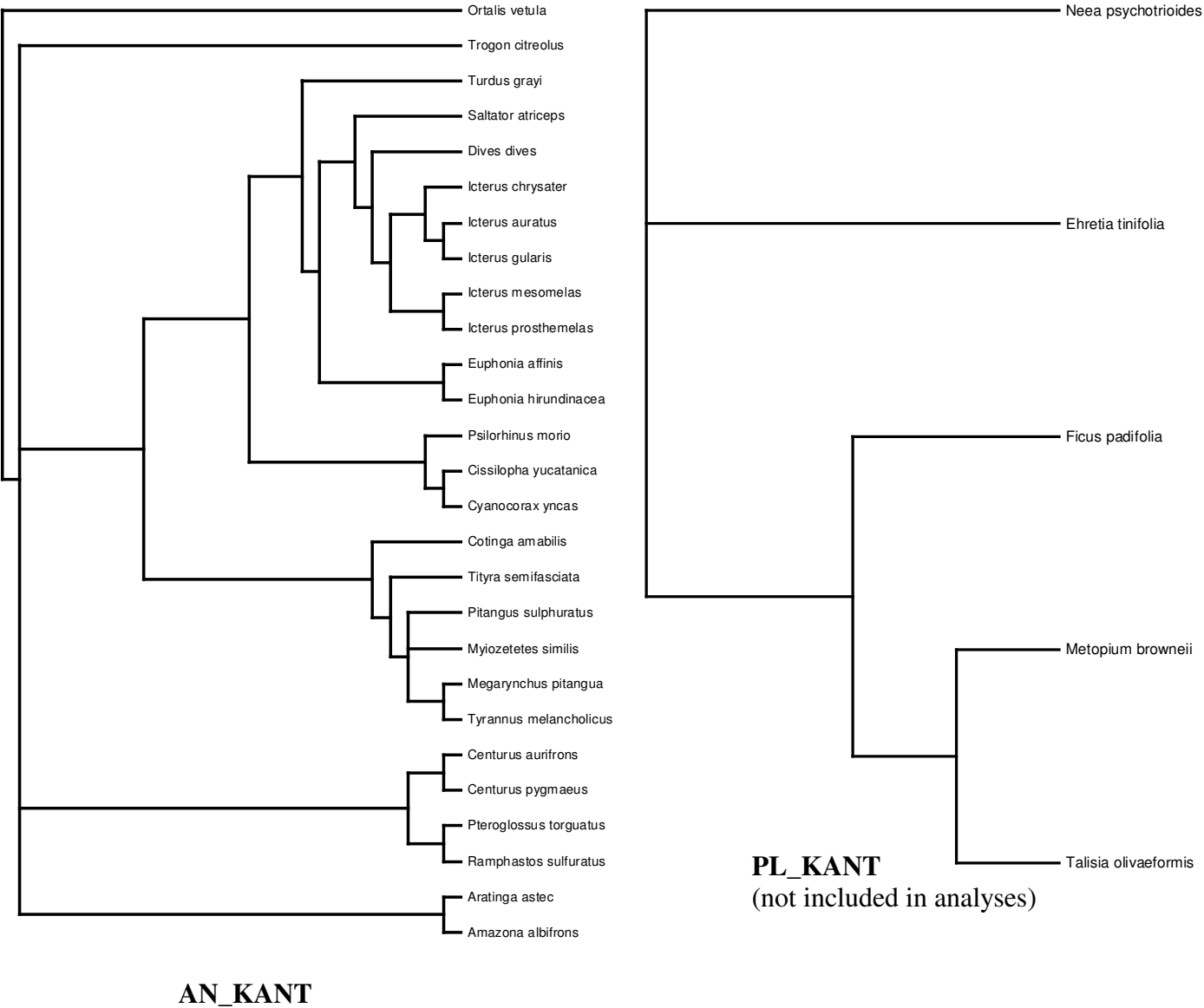
COMMUNITY HRAT – Frugivory



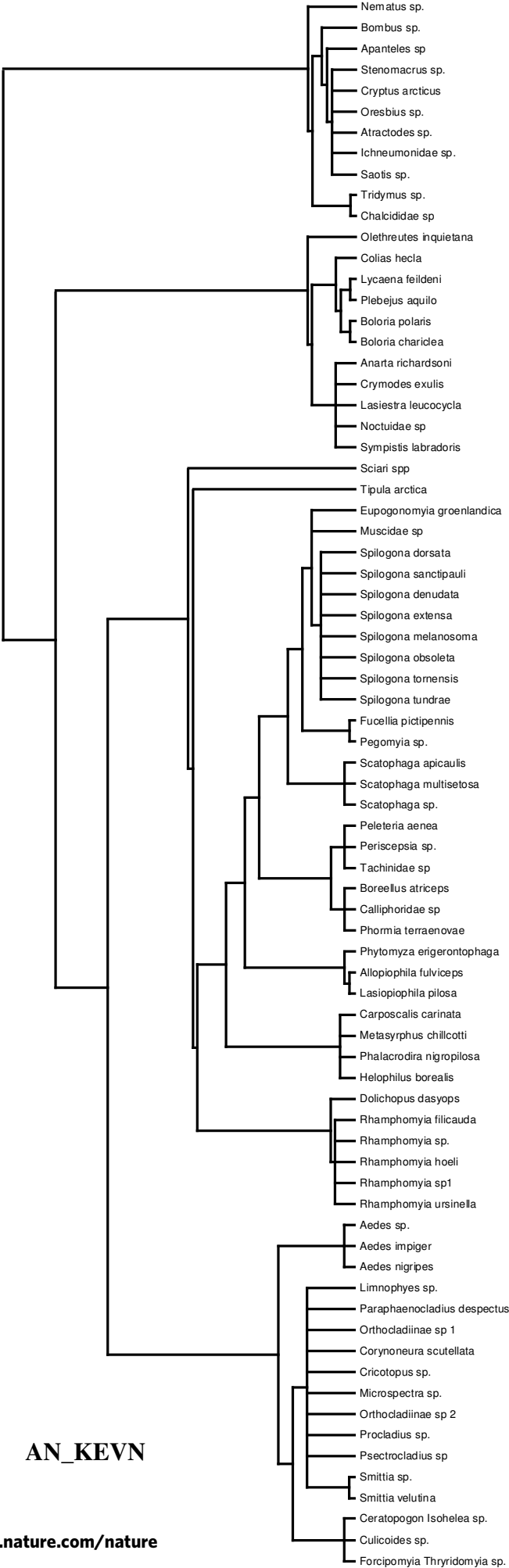
COMMUNITY INPK – Pollination



COMMUNITY KANT – Frugivory



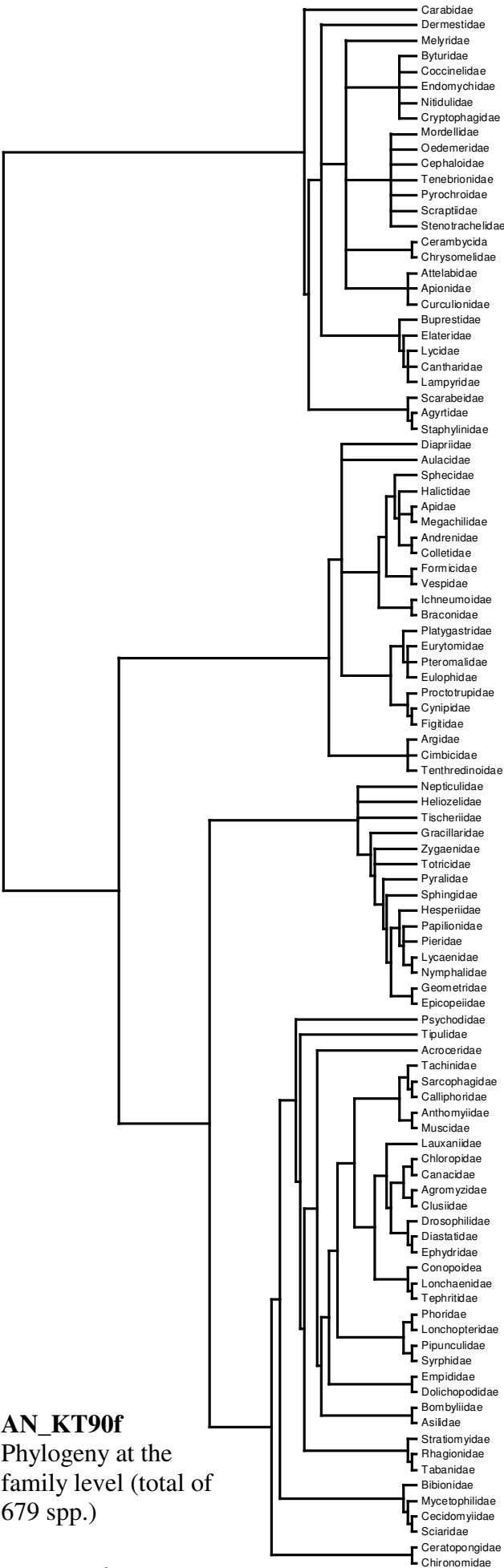
COMMUNITY KEVN – Pollination



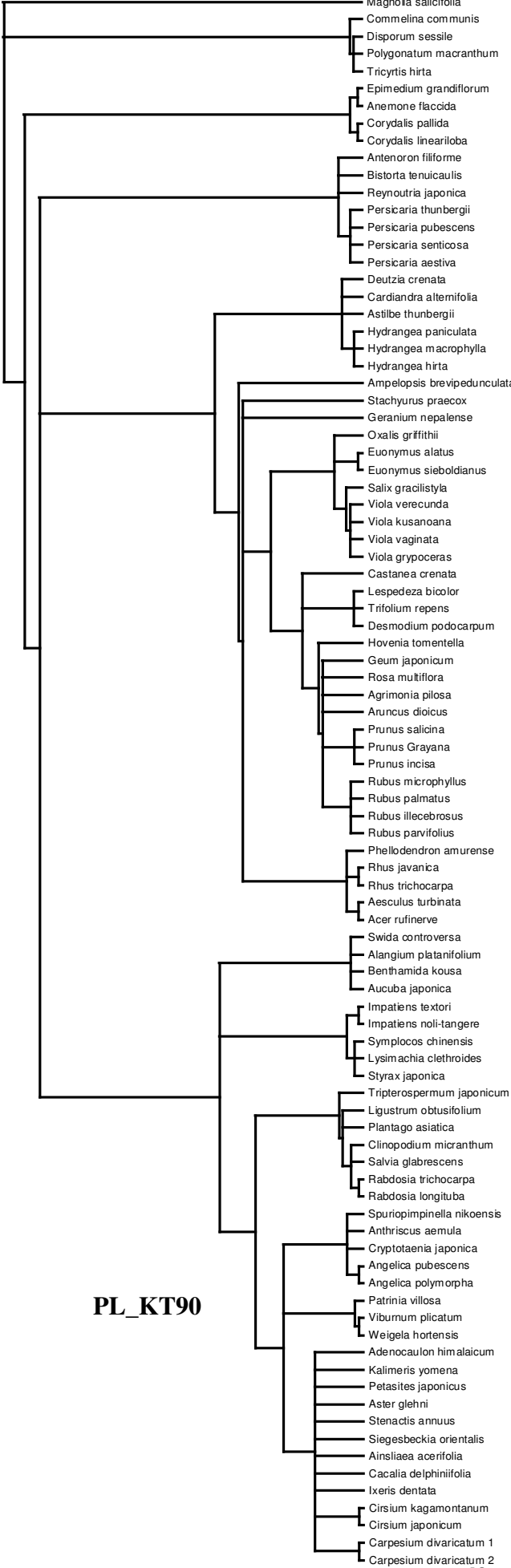
AN_KEVN

PL_KEVN

COMMUNITY KT90 – Pollination

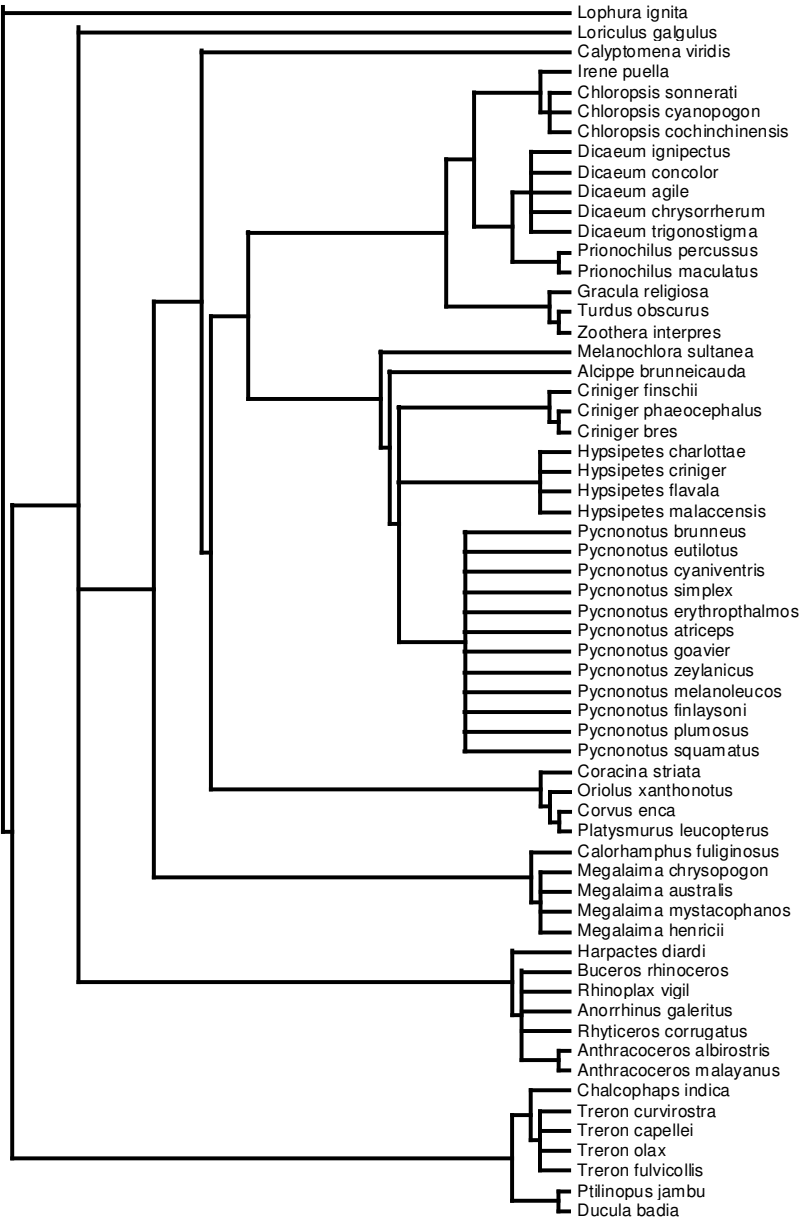


AN_KT90f
Phylogeny at the
family level (total of
679 spp.)



PL_KT90

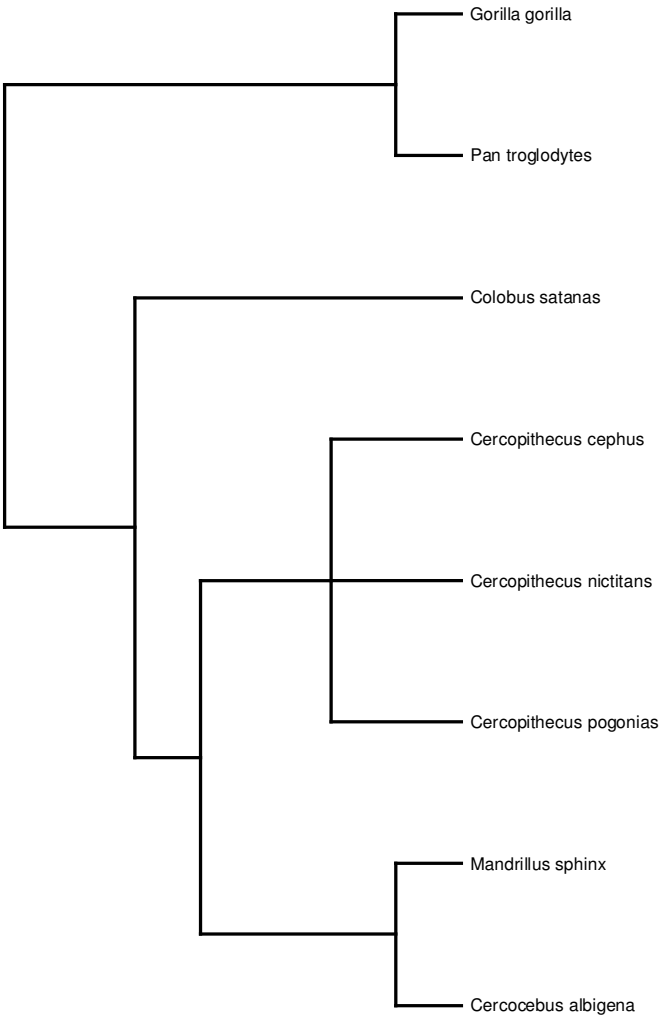
COMMUNITY LAMB – Frugivory



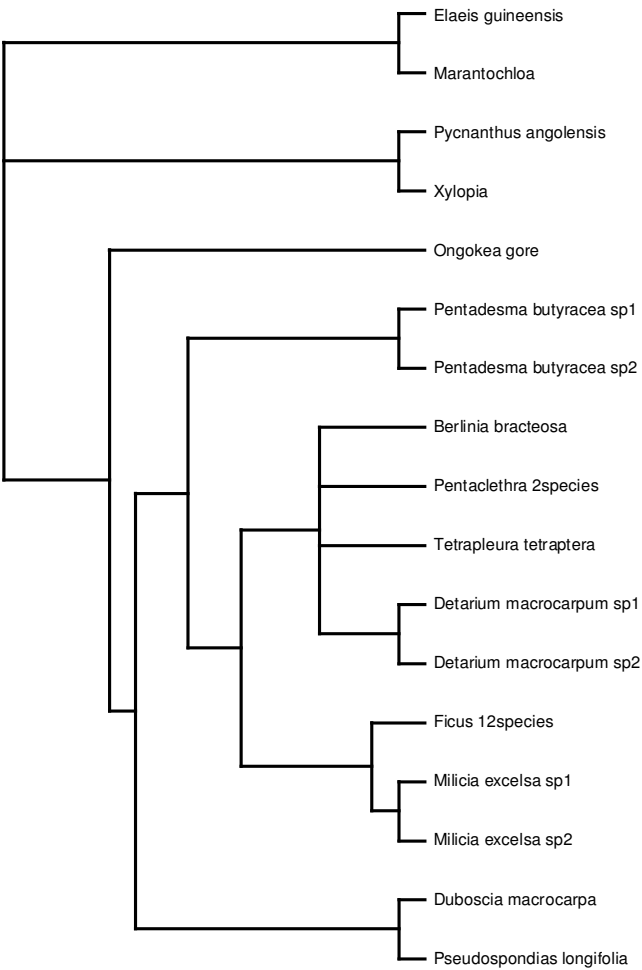
PL_LAMB not available
(not included in analyses)

AN_LAMB

COMMUNITY LOPE – Frugivory

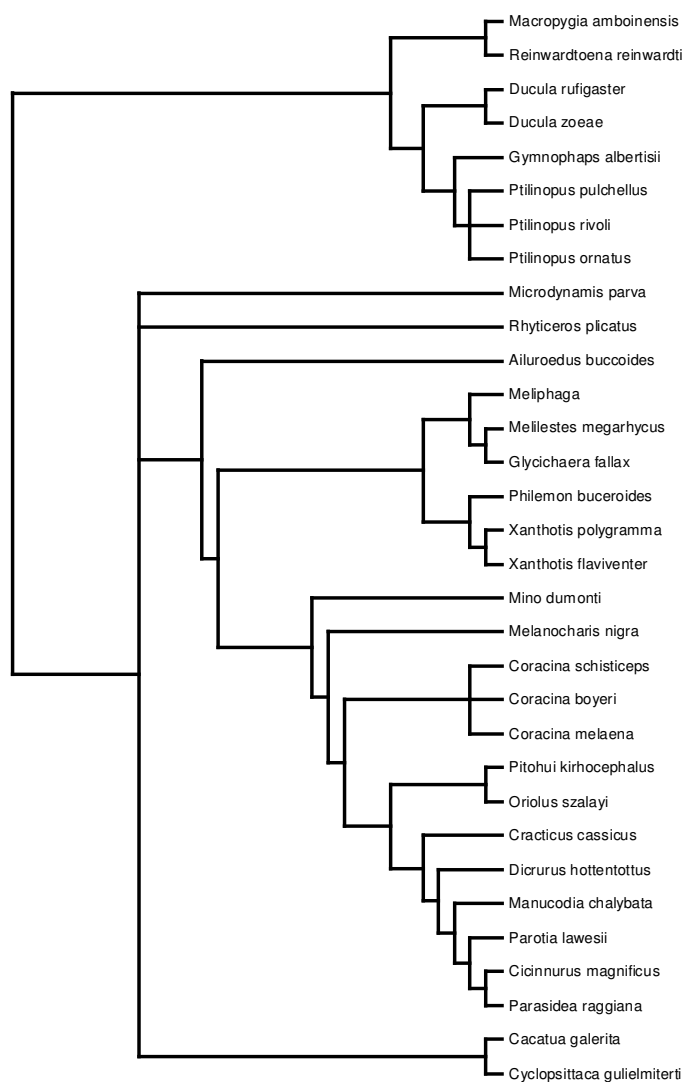


AN_LOPE
(Primate phylogeny, not included in analyses)

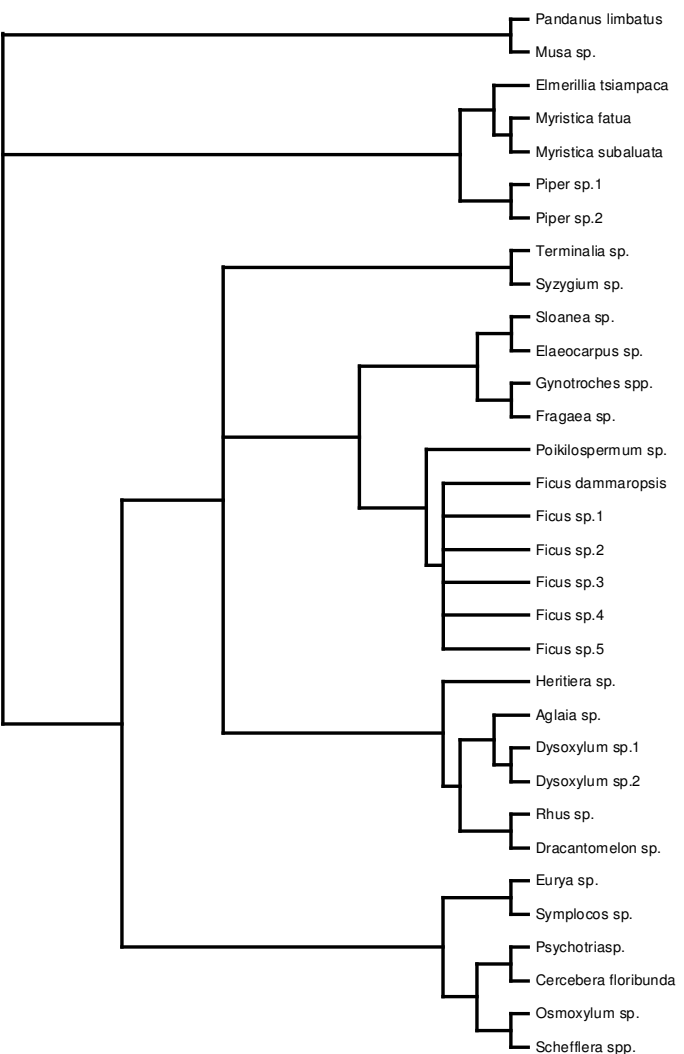


PL_LOPE

COMMUNITY MACK – Frugivory

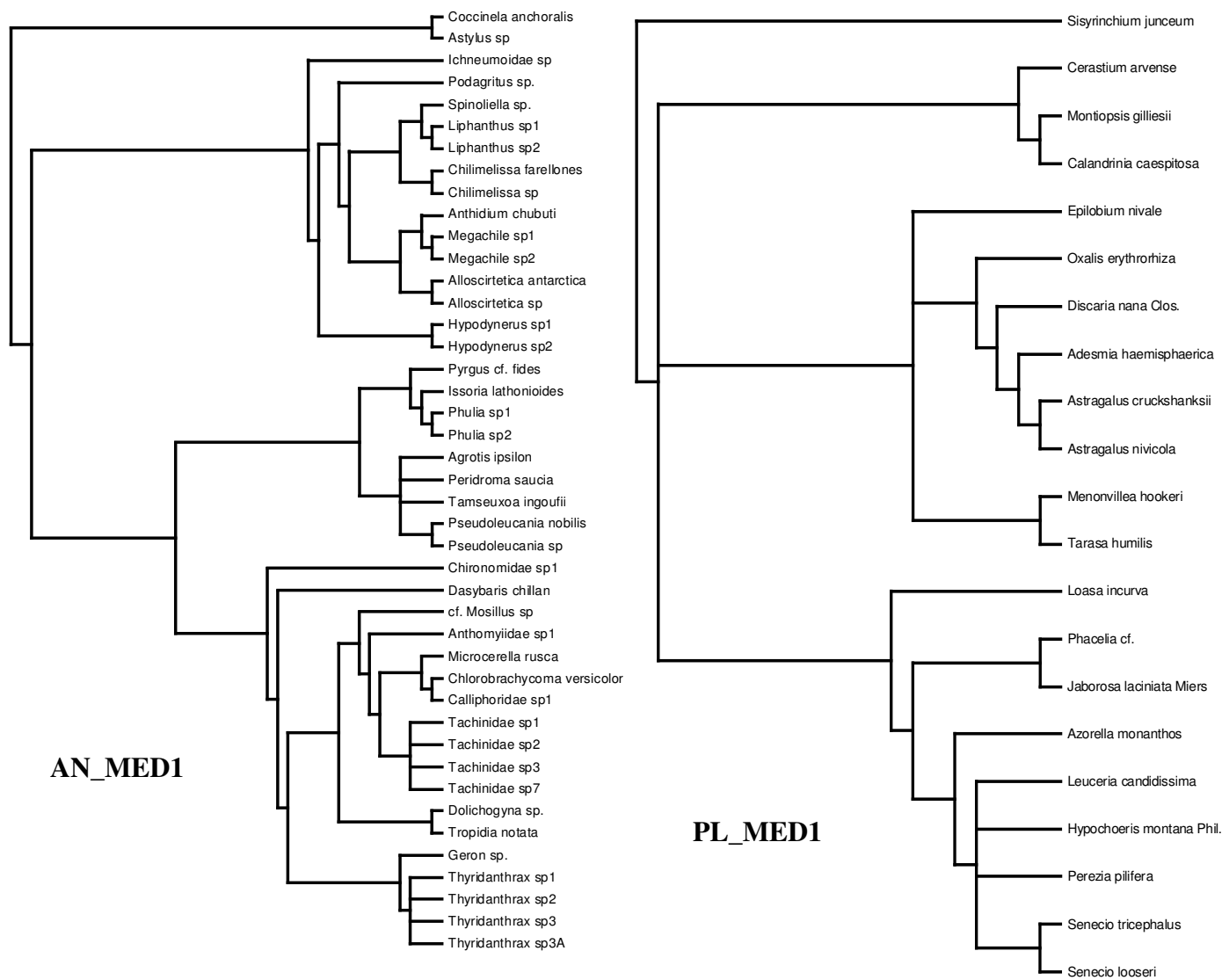


AN_MACK

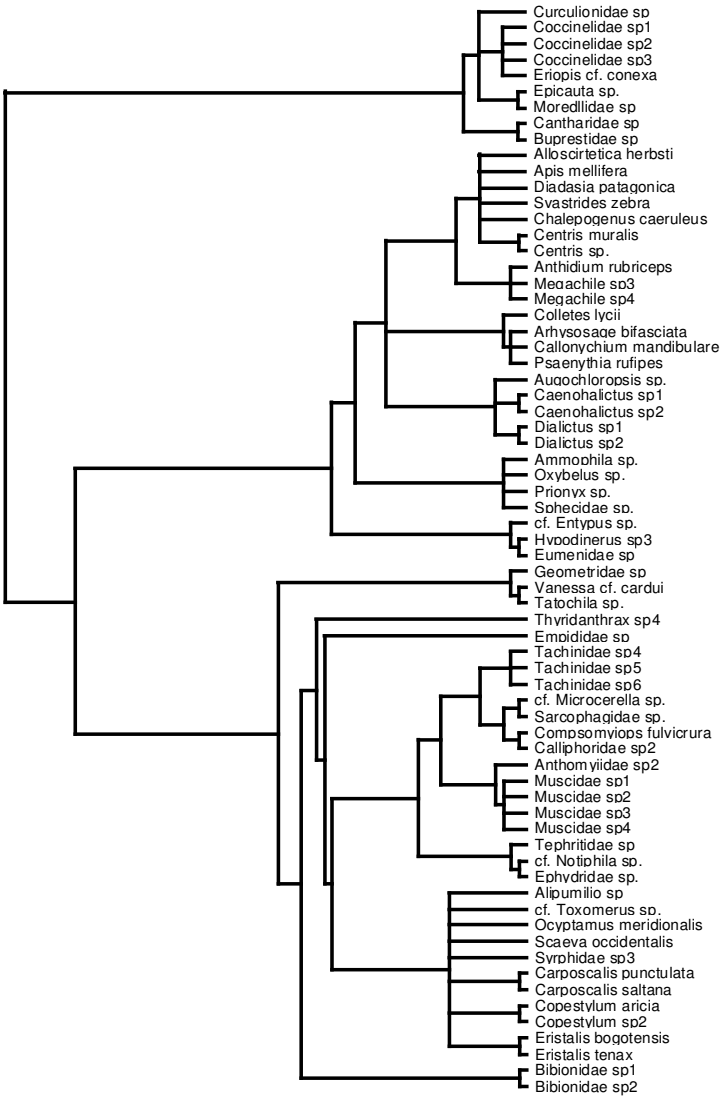


PL_MACK

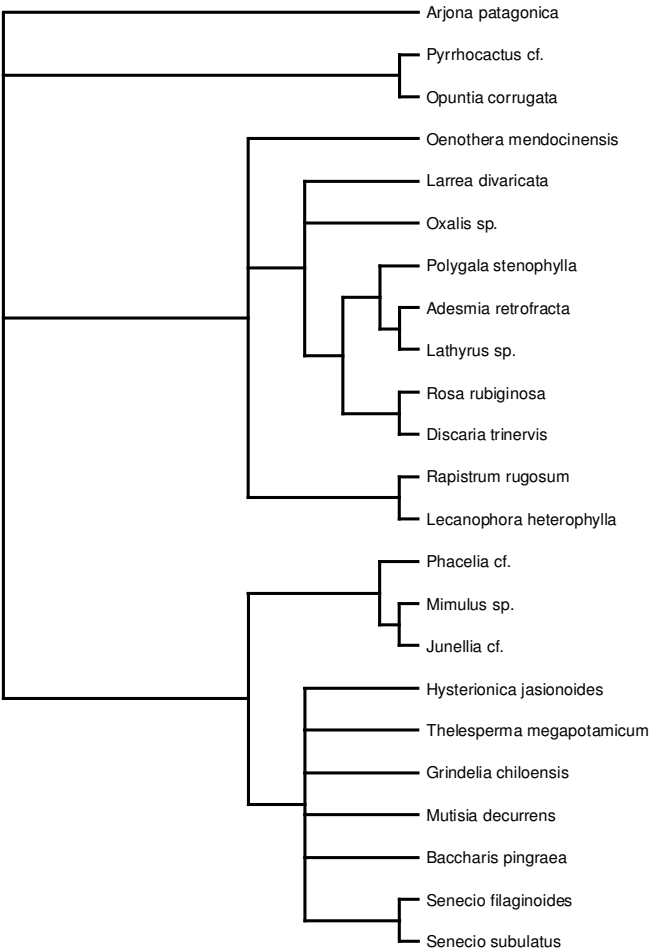
COMMUNITY MED1 – Pollination



COMMUNITY MED2 – Pollination

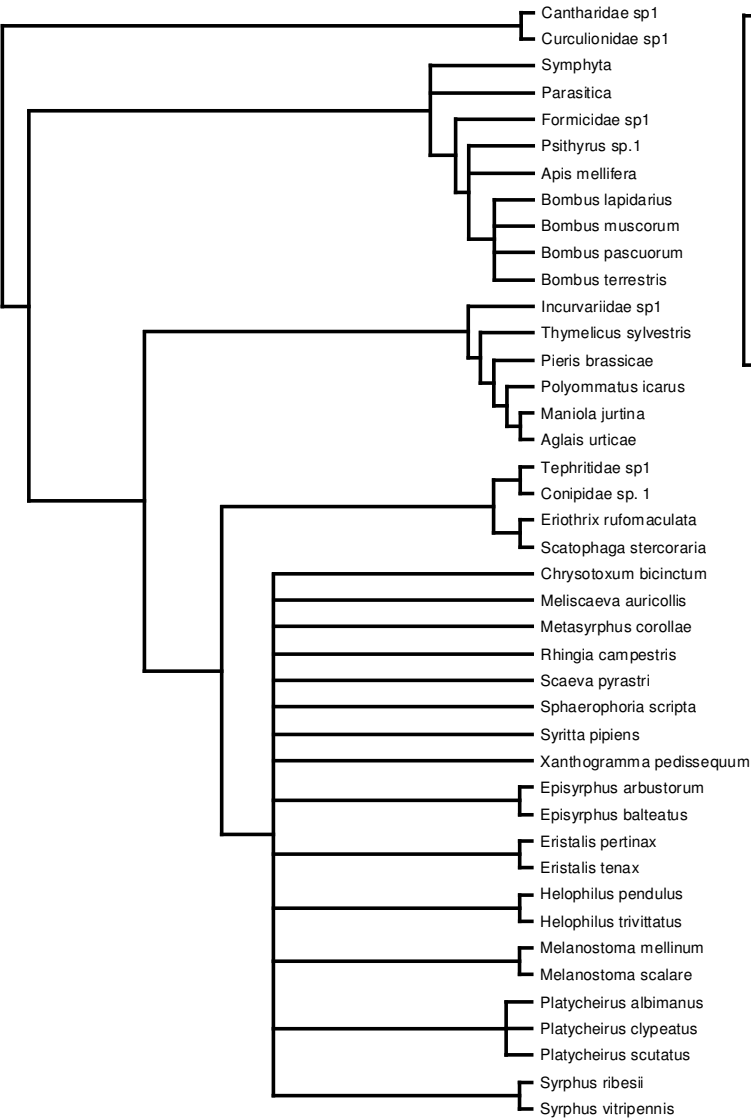


AN_MED2

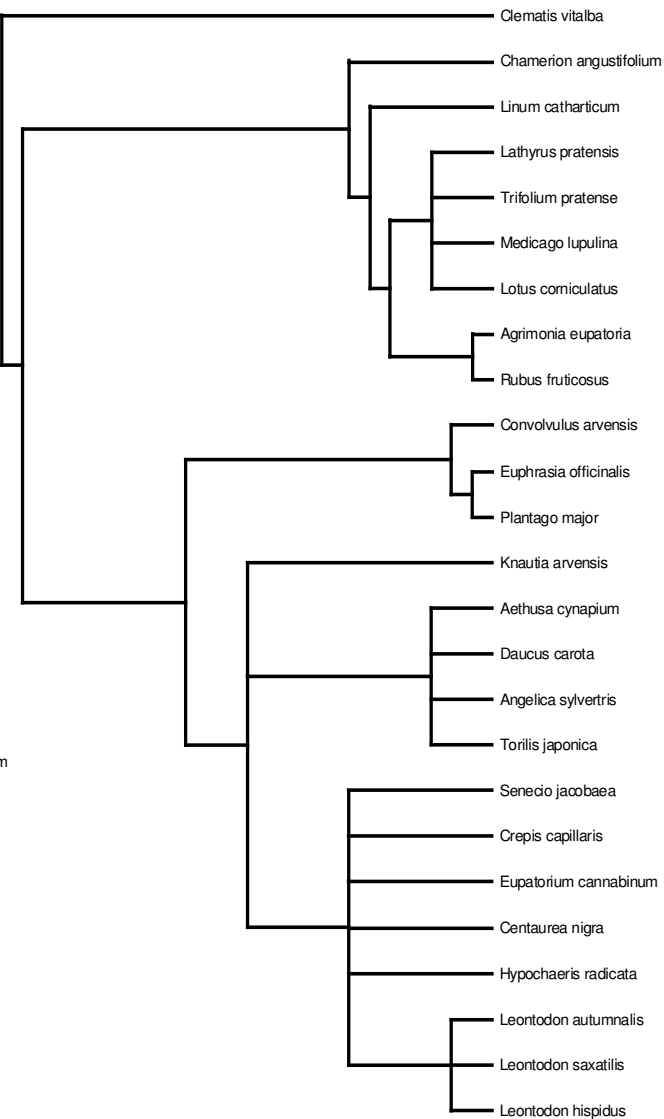


PL_MED2

COMMUNITY MEMM – Pollination

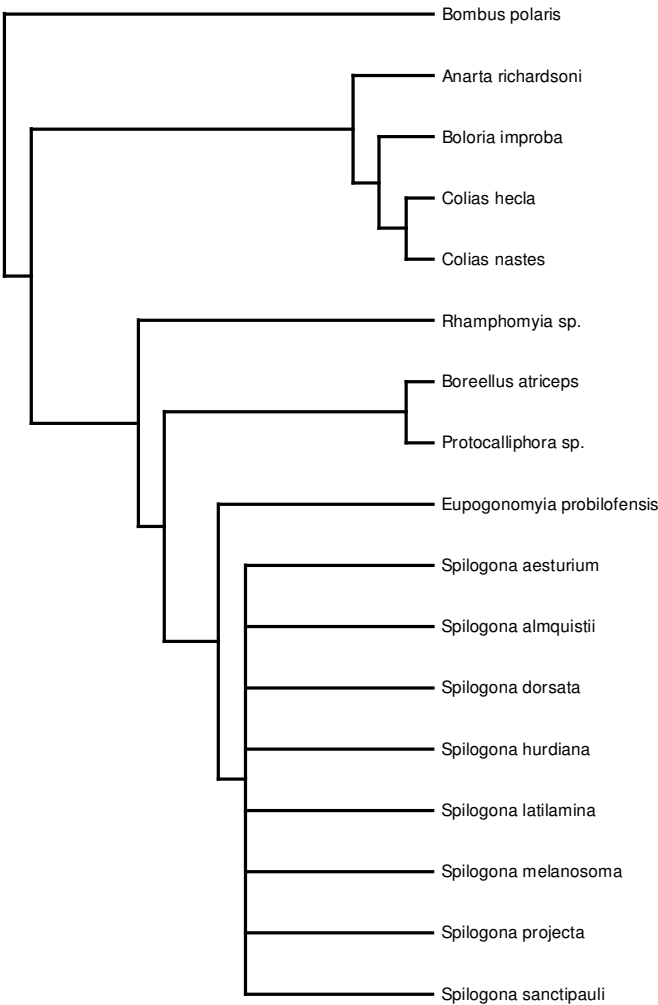


AN_MEMM

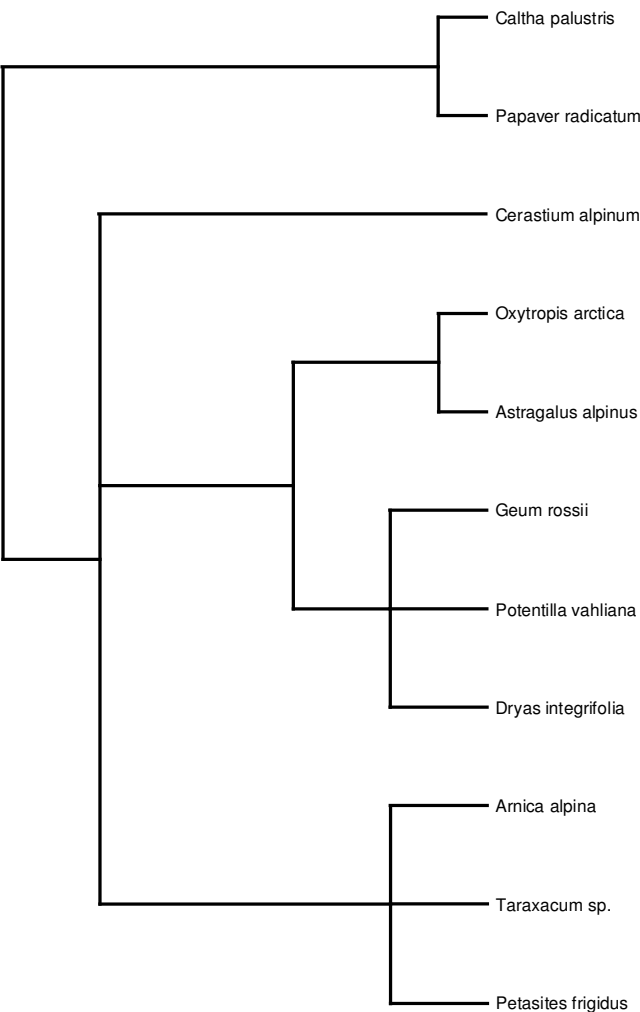


PL_MEMM

COMMUNITY MOMA – Pollination

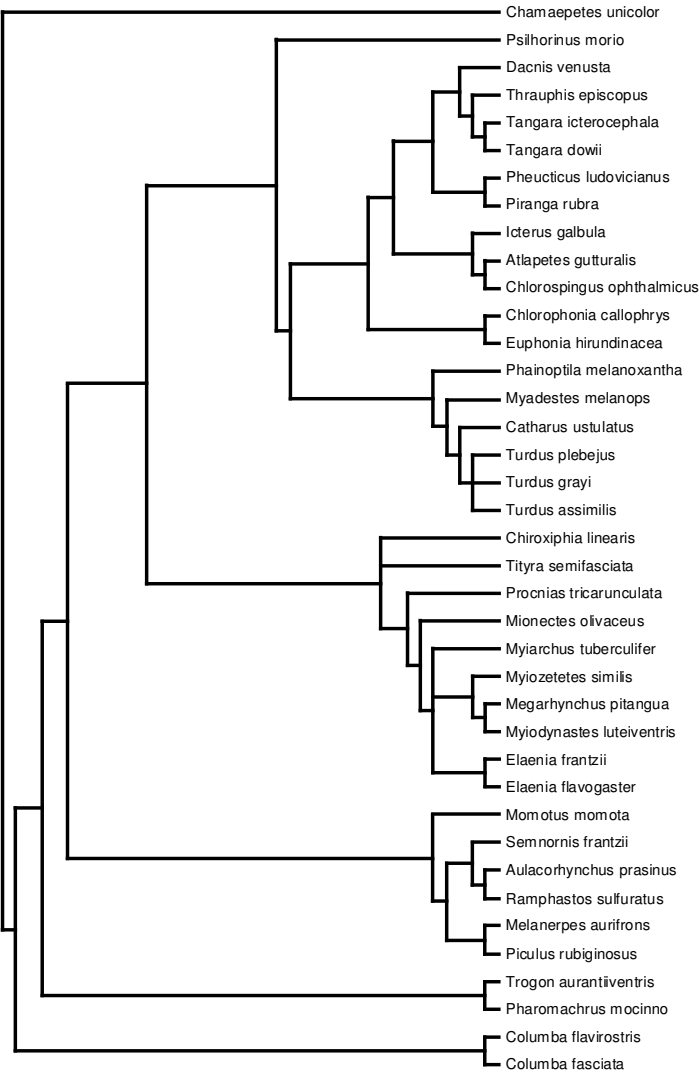


AN_MOMA

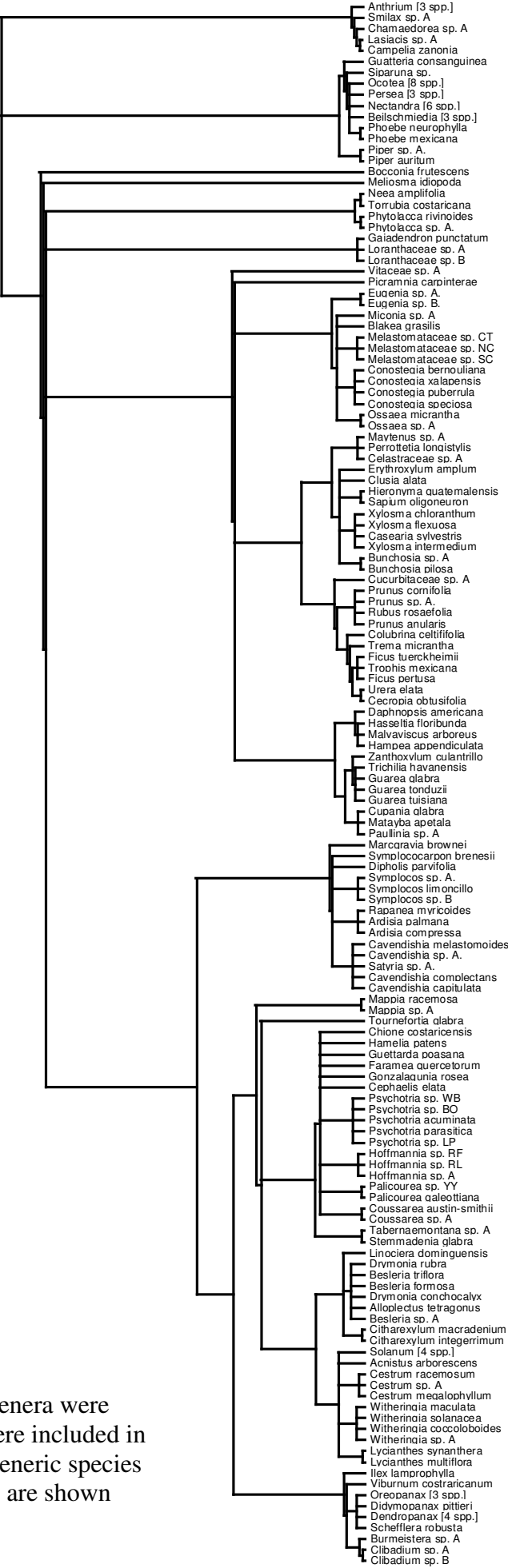


PL_MOMA

COMMUNITY MONT – Frugivory



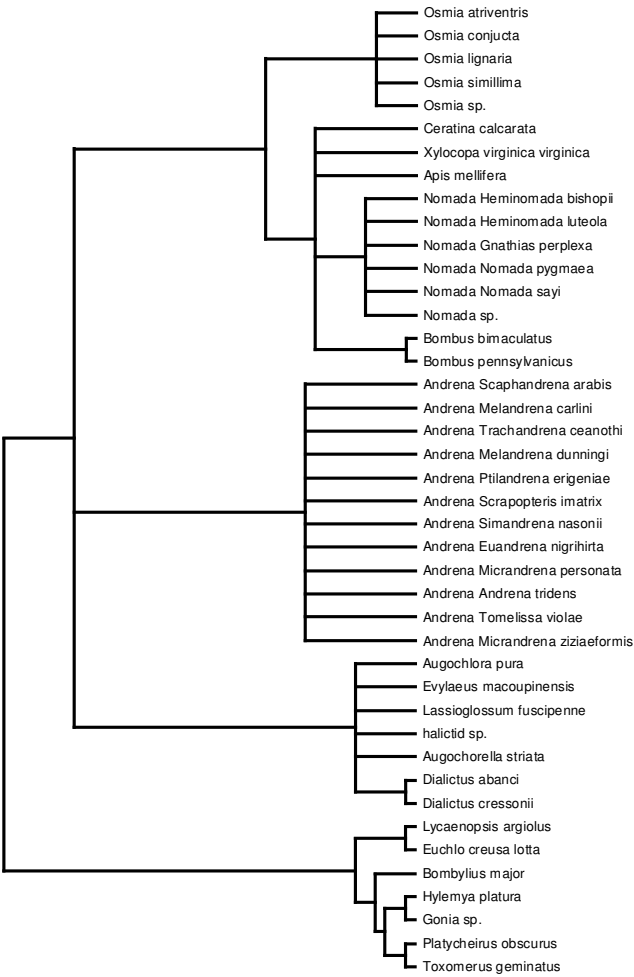
AN_MONT



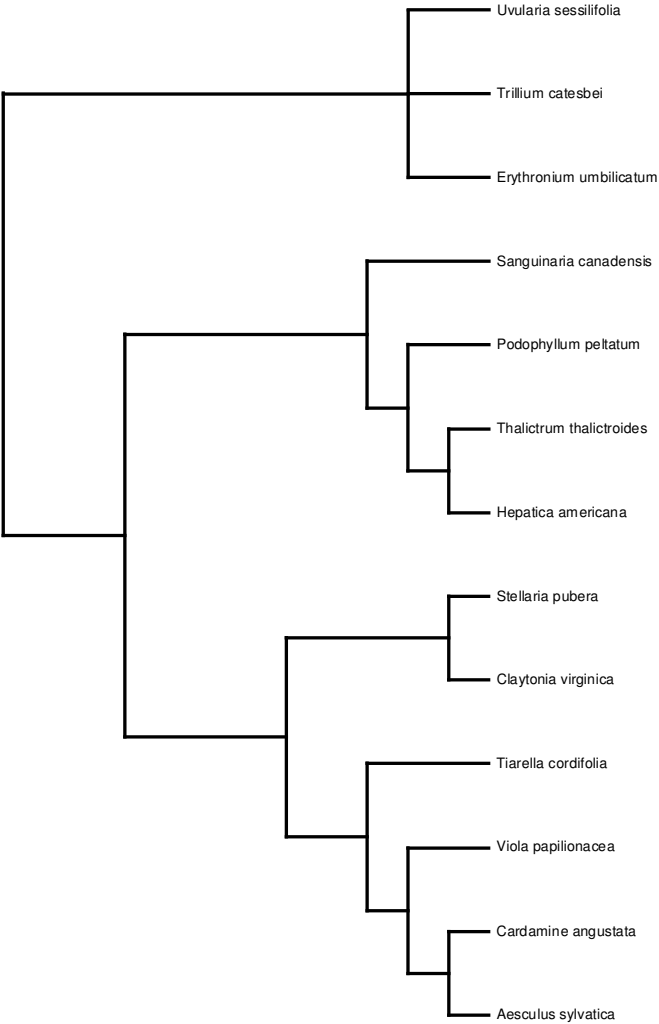
PL_MONT *

* Obs: politomies within genera were removed for clarity (but were included in analyses). Number of congeneric species included as soft politomies are shown within brackets.

COMMUNITY MOTT – Pollination

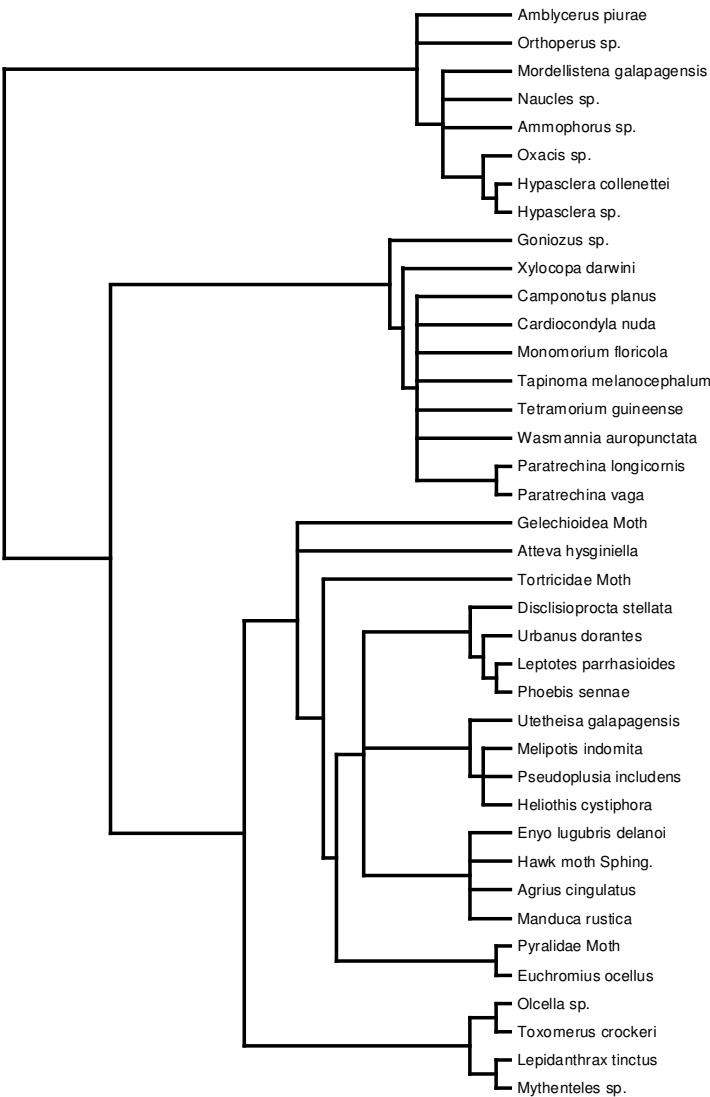


AN_MOTT

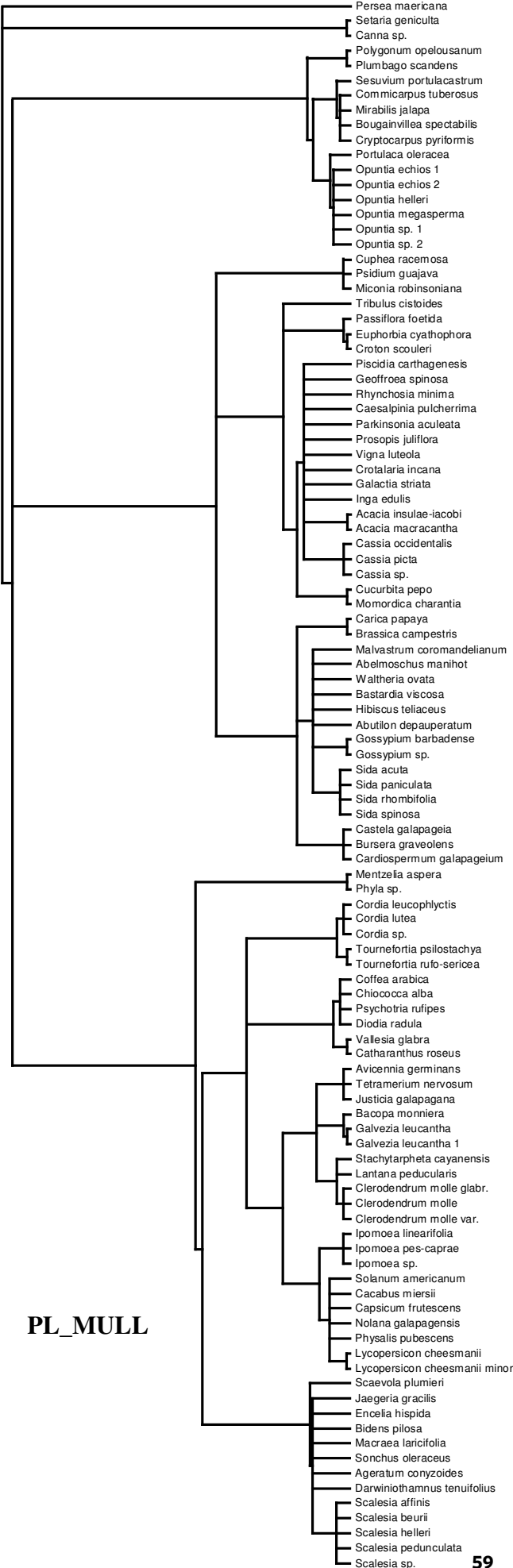


PL_MOTT

COMMUNITY MULL – Pollination

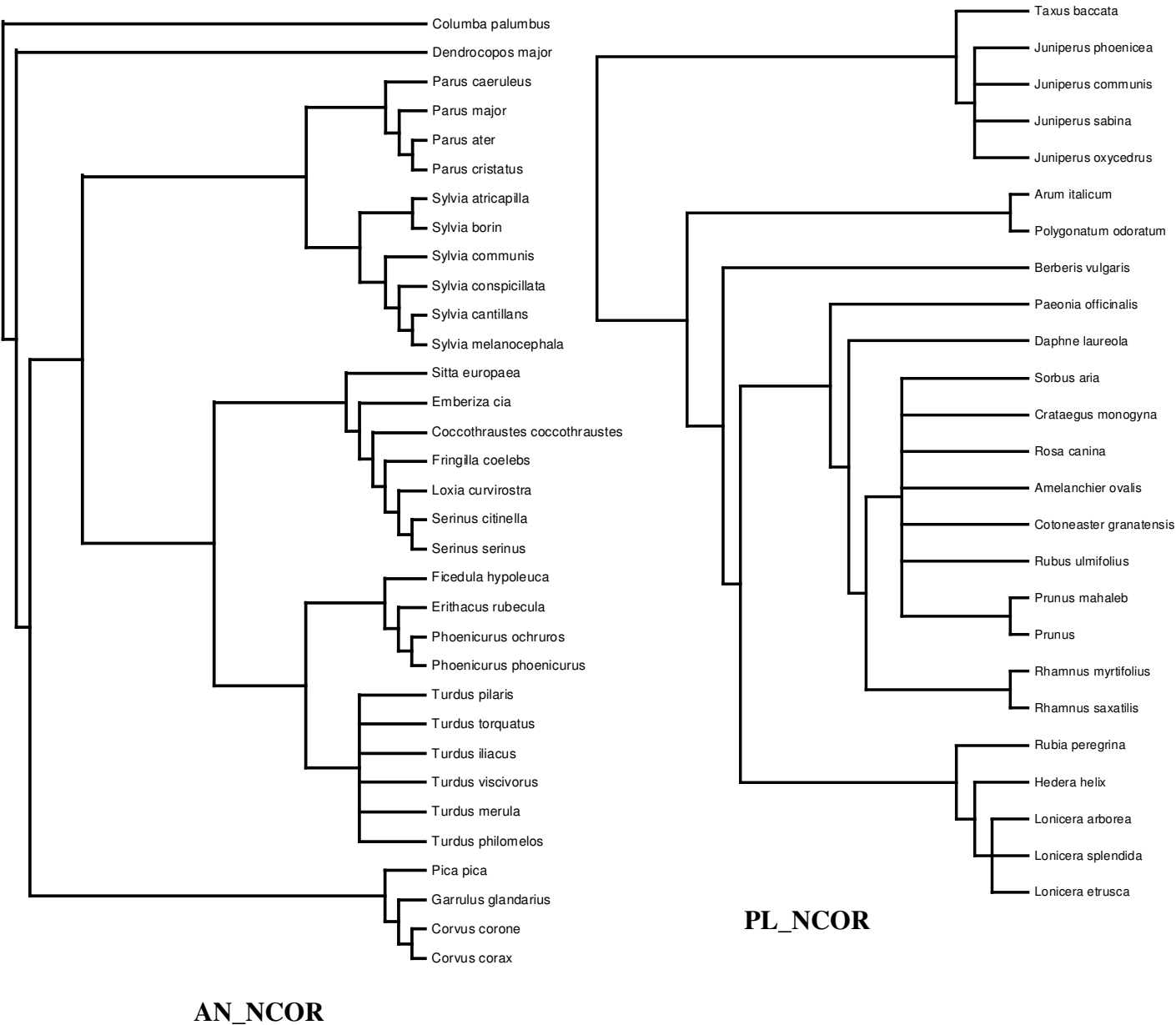


AN_MULL

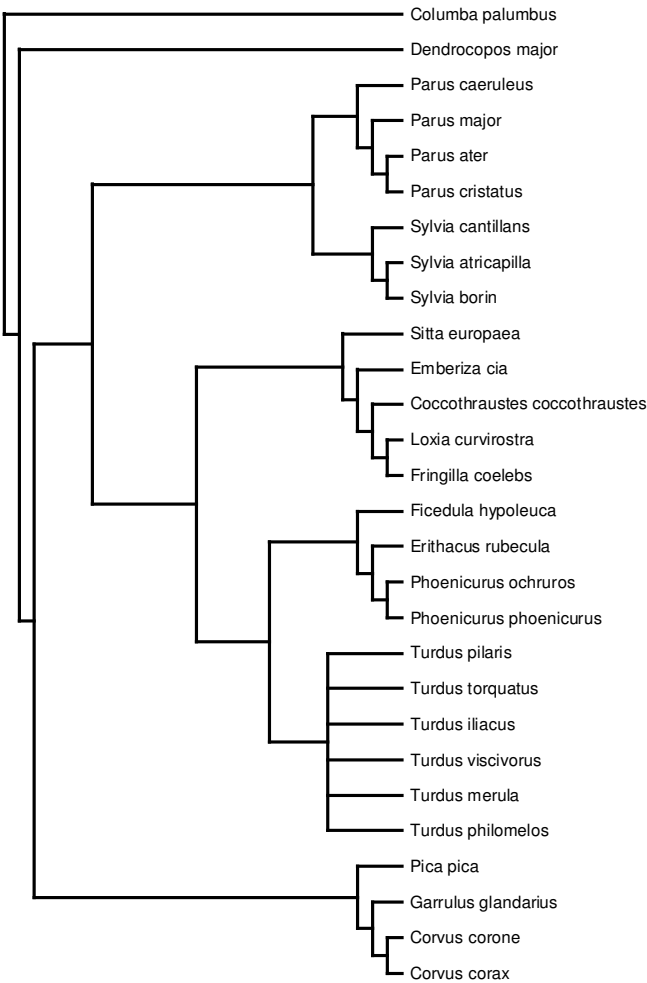


PL_MULL

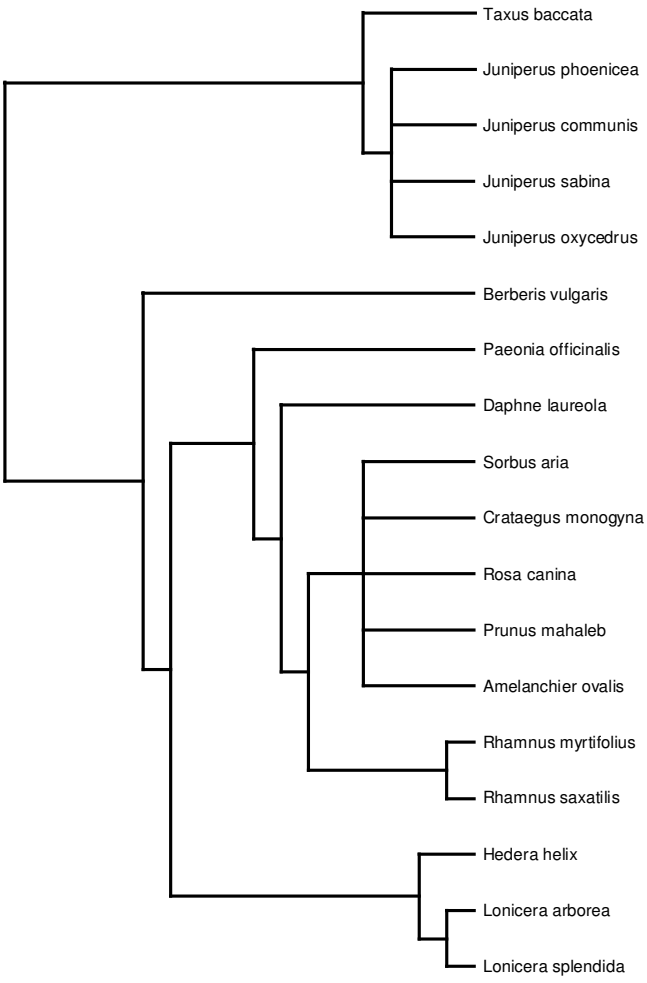
COMMUNITY NCOR – Frugivory



COMMUNITY NNOG – Frugivory



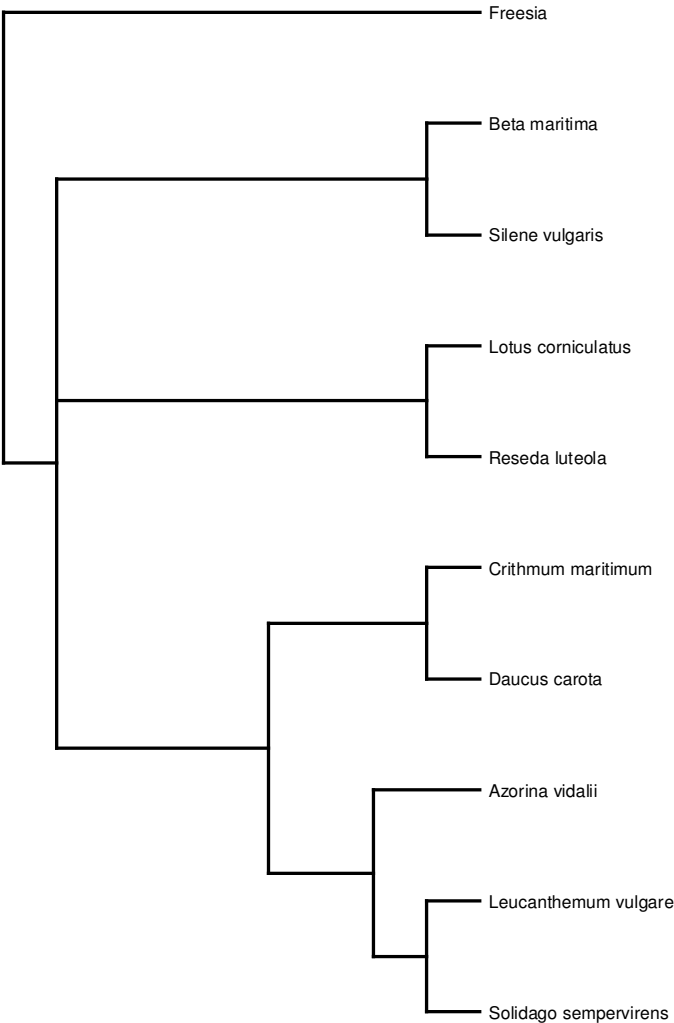
AN_NNOG



PL_NNOG

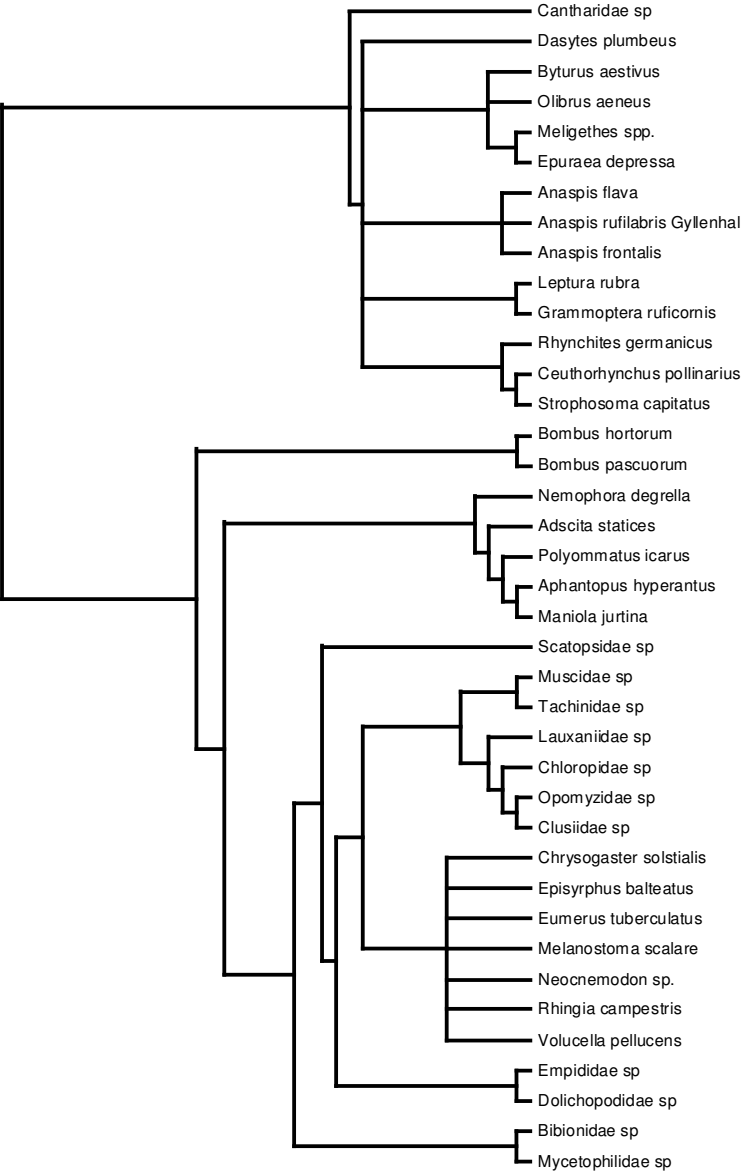
COMMUNITY OFLO – Pollination

AN_OFLO not available
(not included in analyses)



PL_OFLO

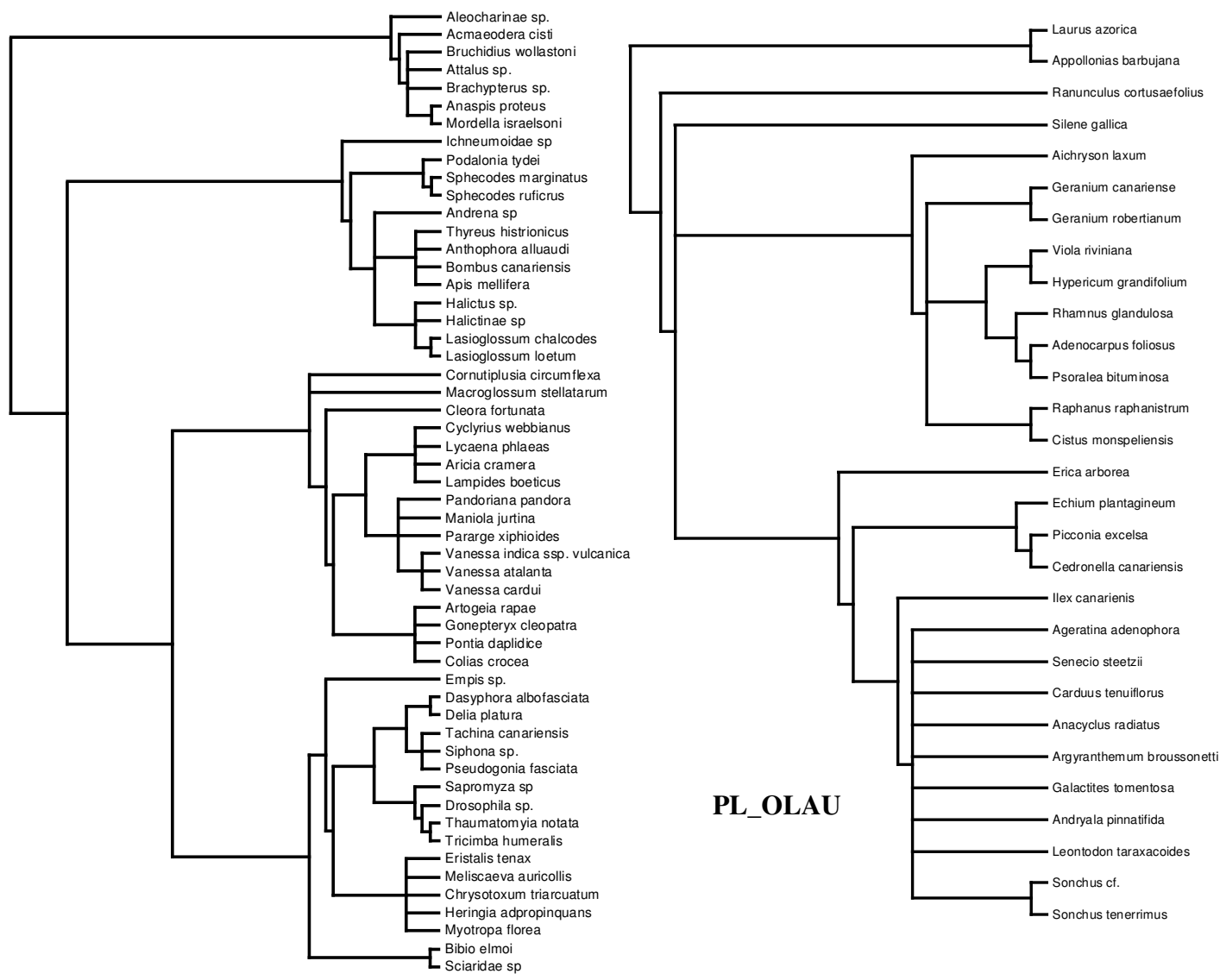
COMMUNITY OFST – Pollination



PL_OFST not available
(not included in analyses)

AN_OFST

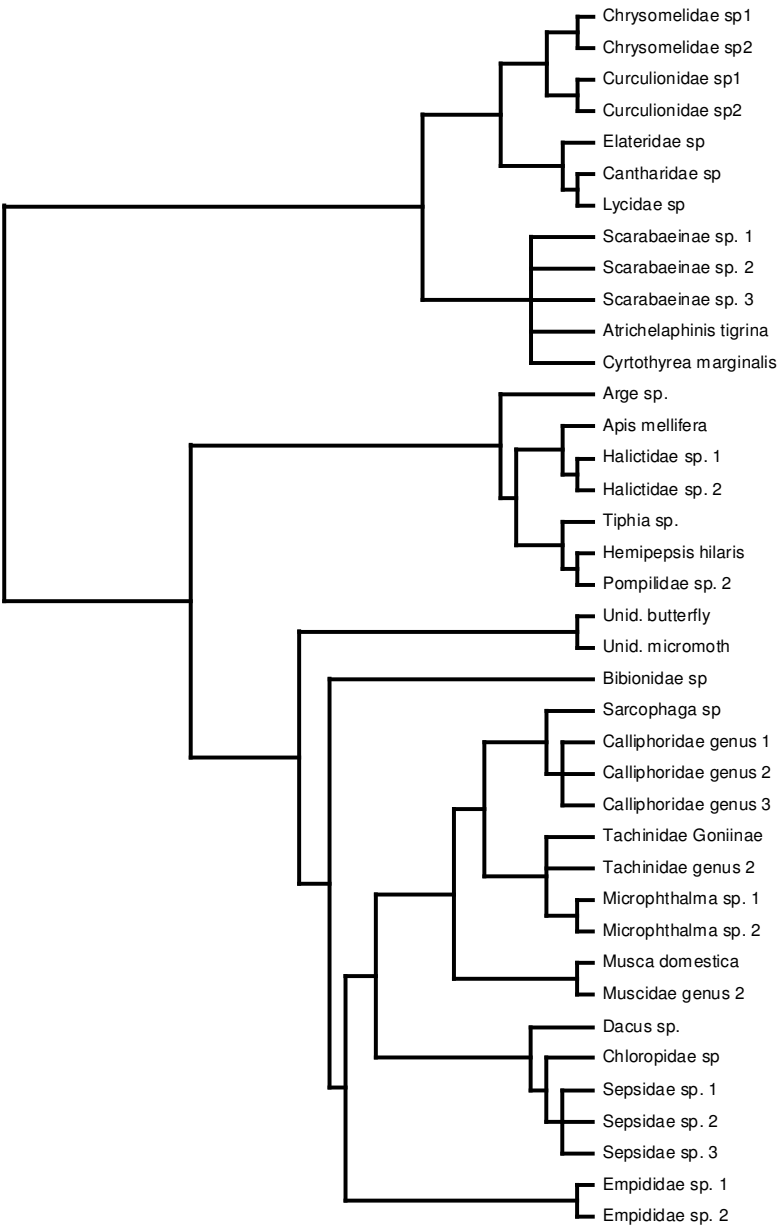
COMMUNITY OLAU – Pollination



AN_OLAU

PL_OLAU

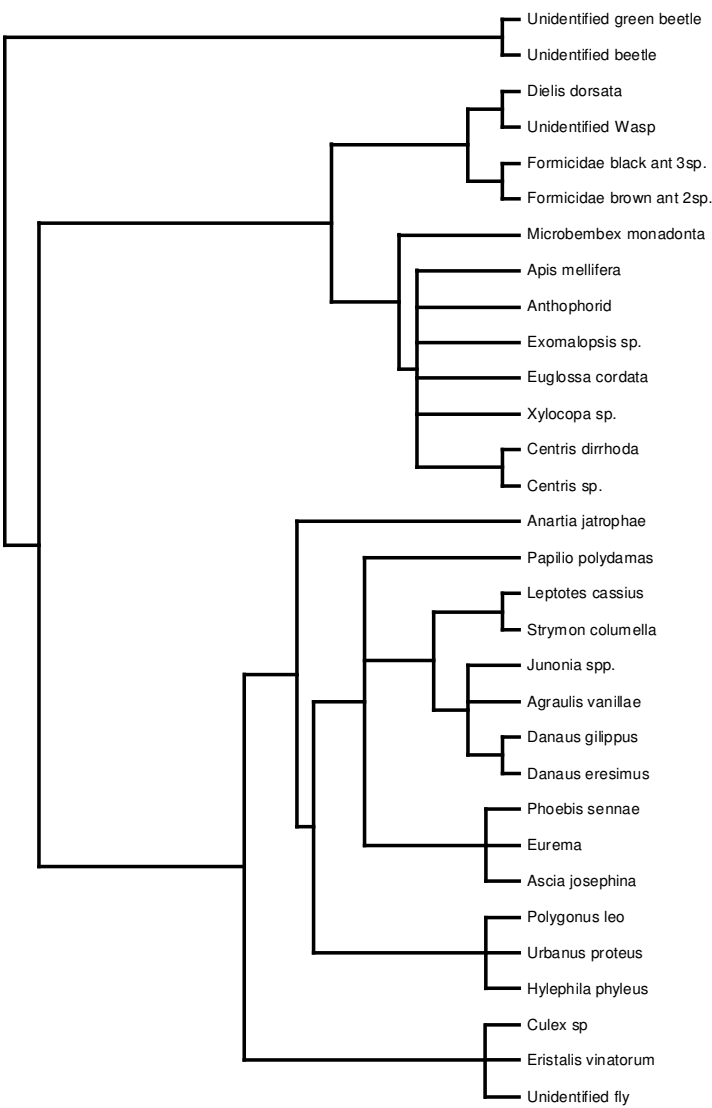
COMMUNITY OLLE – Pollination



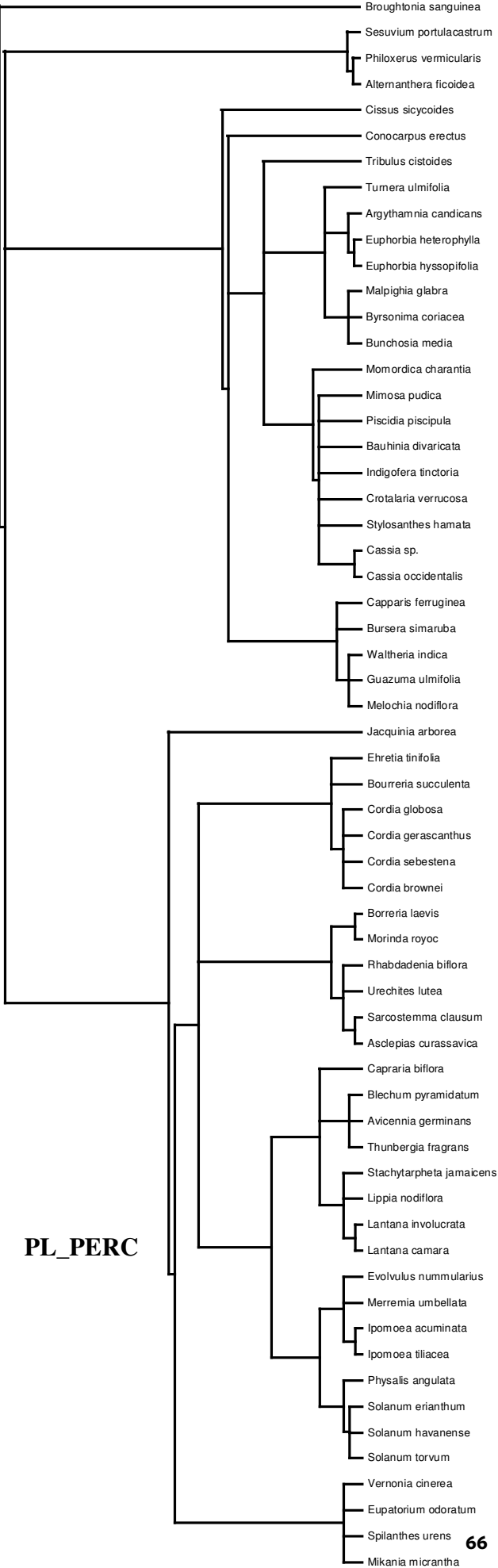
PL_OLLE not available
(not included in analyses)

AN_OLLE

COMMUNITY PERC – Pollination

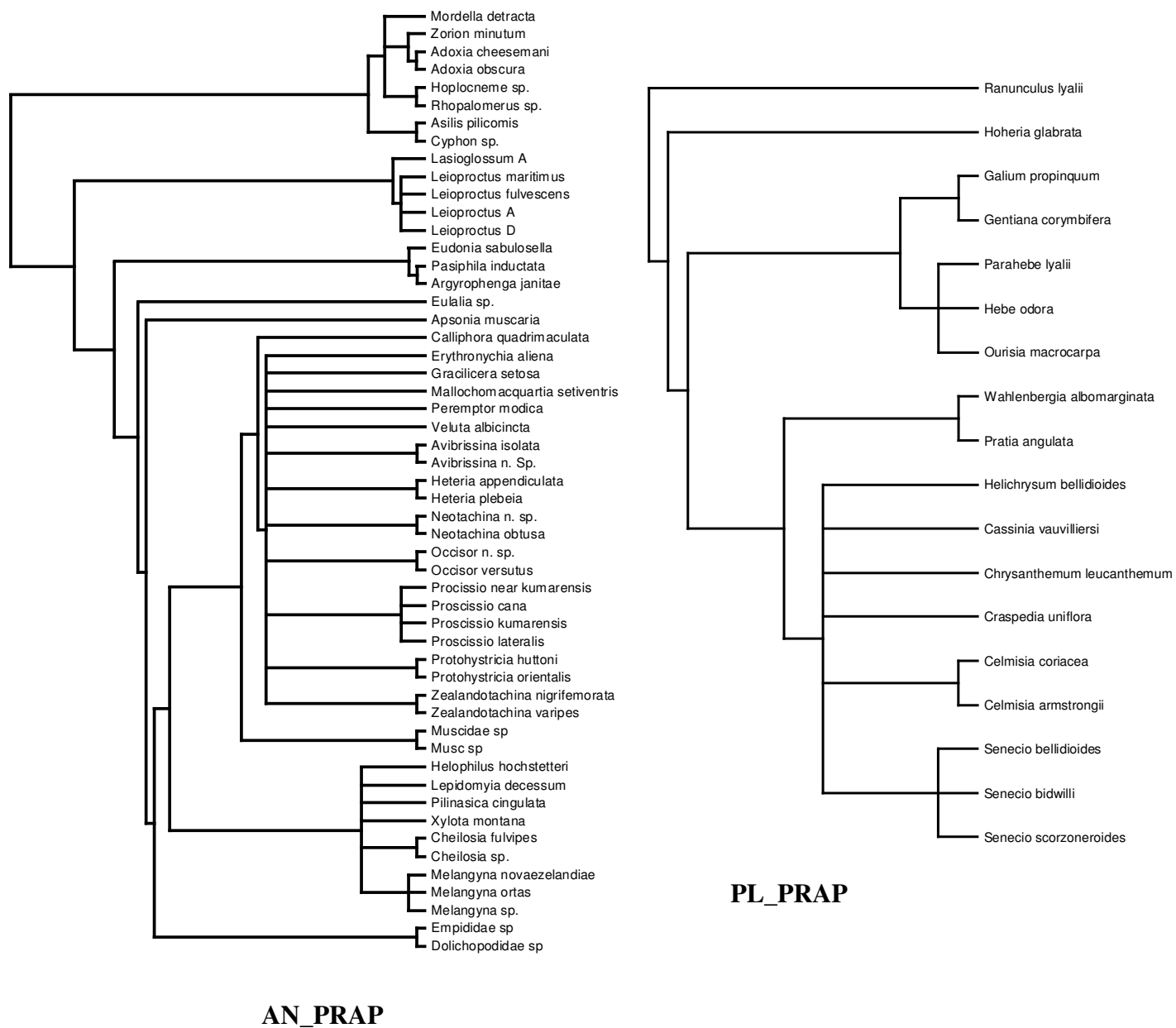


AN_PERC

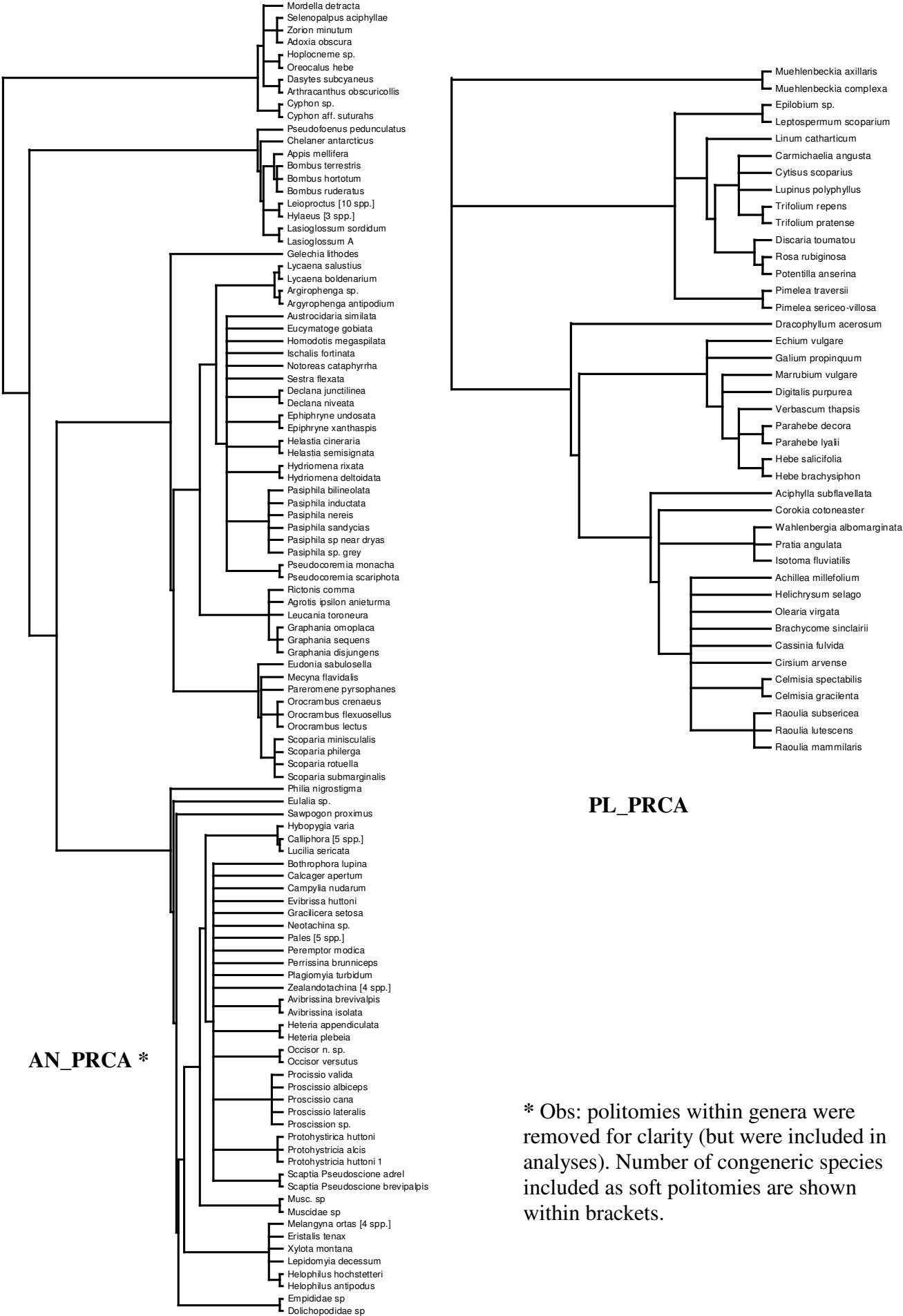


PL_PERC

COMMUNITY PRAP – Pollination

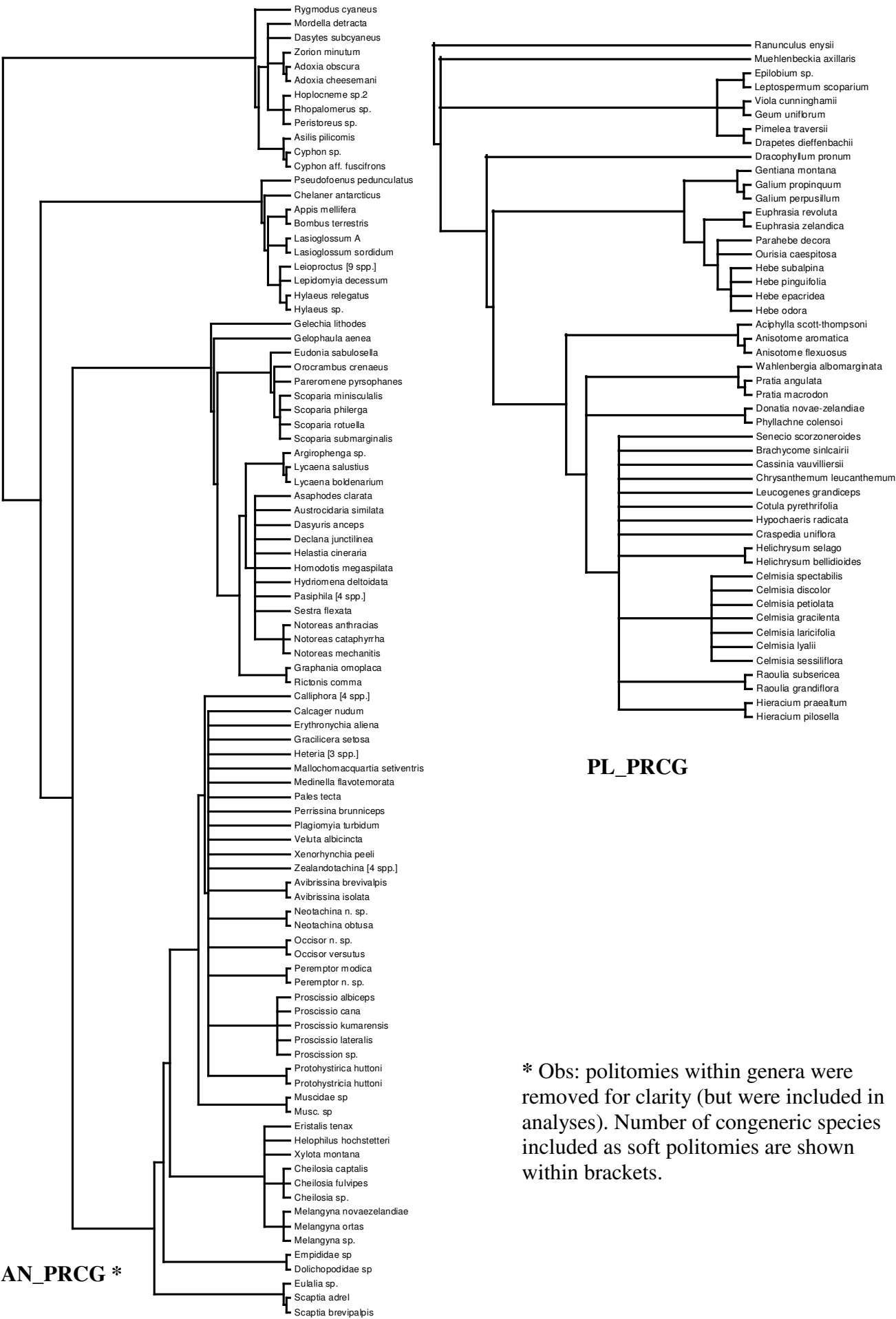


COMMUNITY PRCA – Pollination

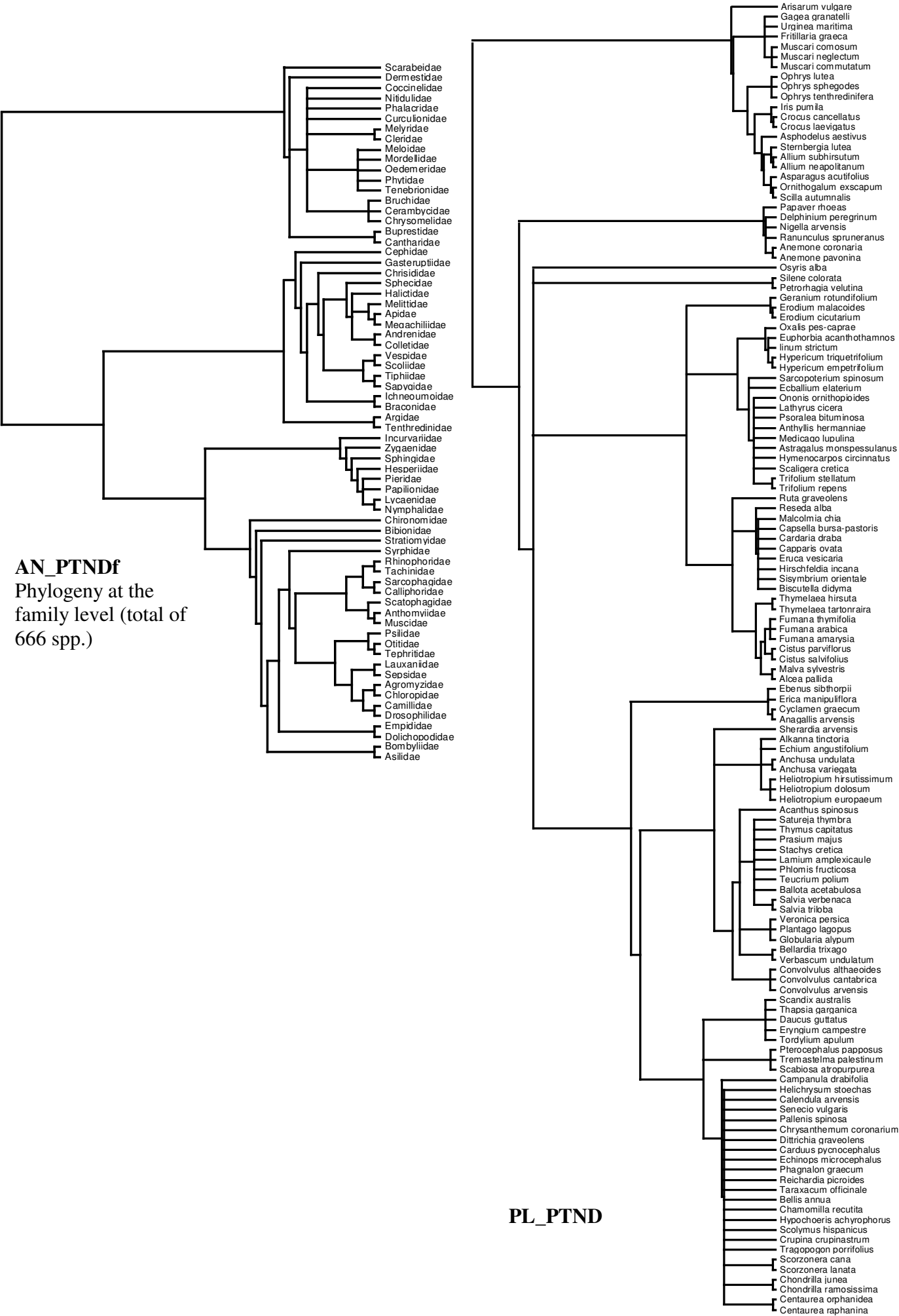


* Obs: politomies within genera were removed for clarity (but were included in analyses). Number of congeneric species included as soft politomies are shown within brackets.

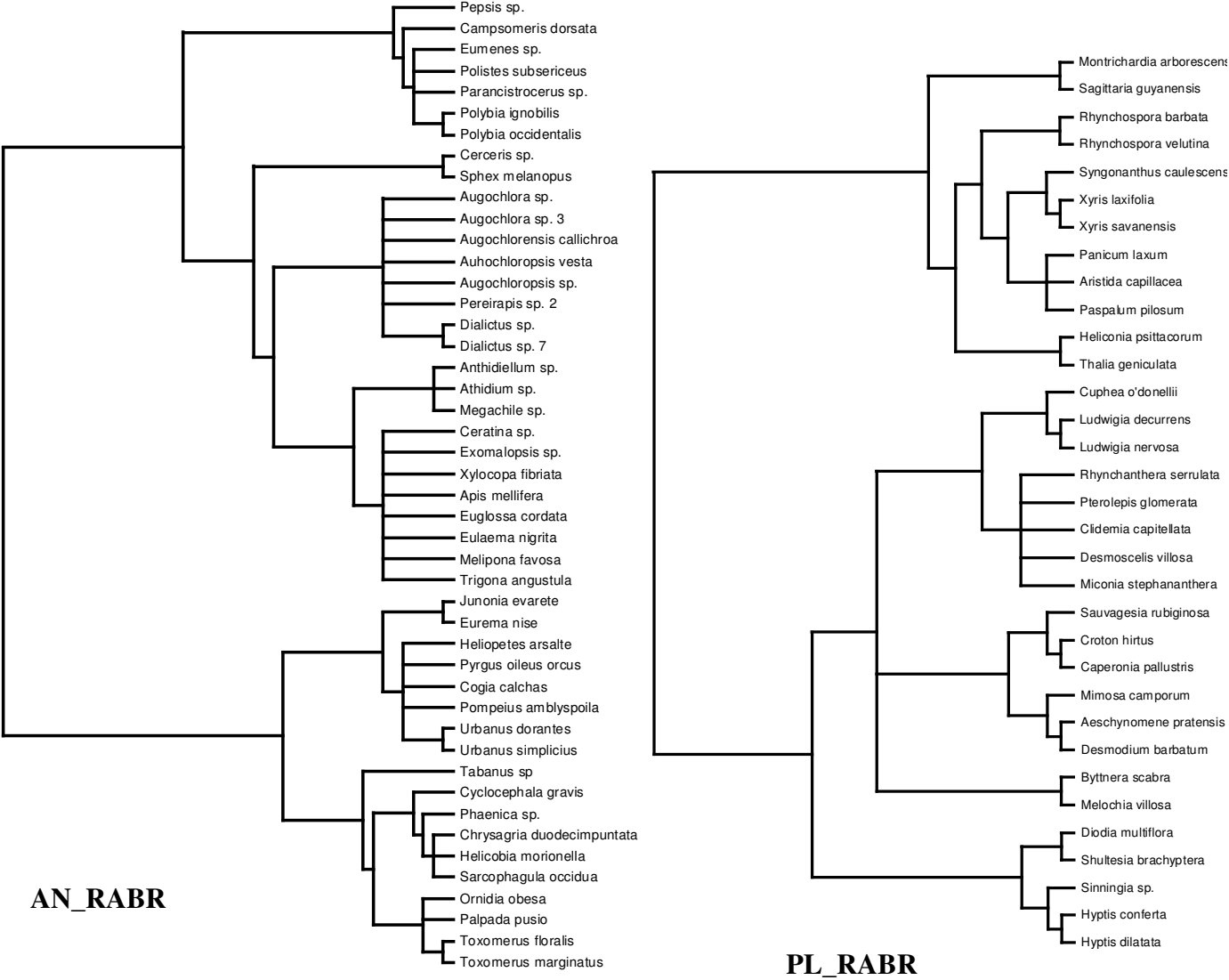
COMMUNITY PRCG – Pollination



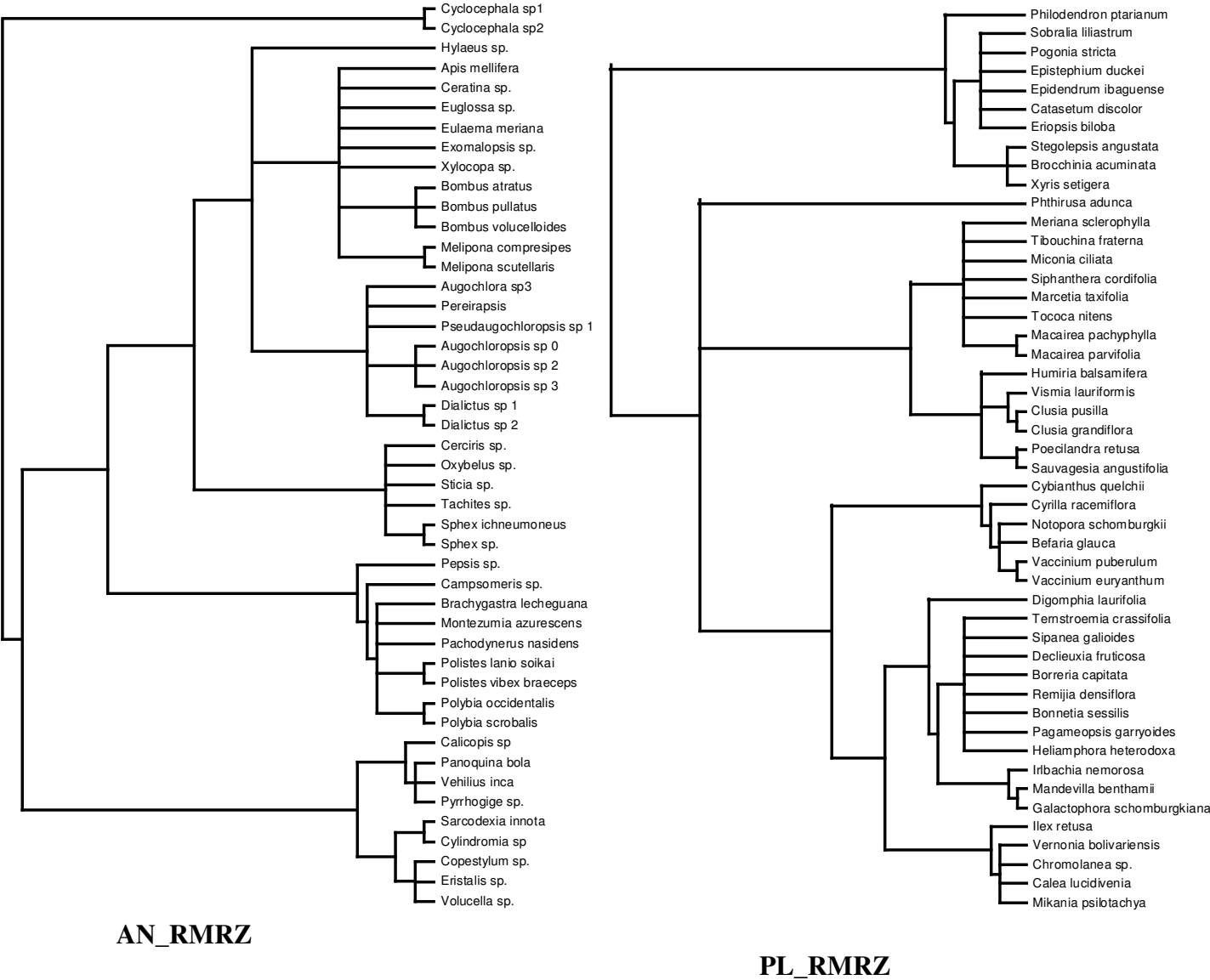
COMMUNITY PTND – Pollination



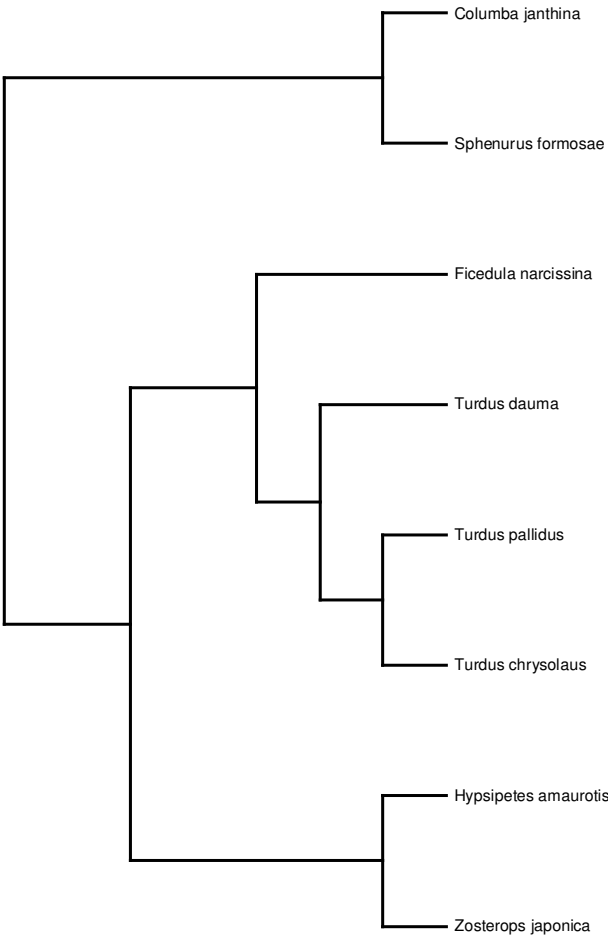
COMMUNITY RABR – Pollination



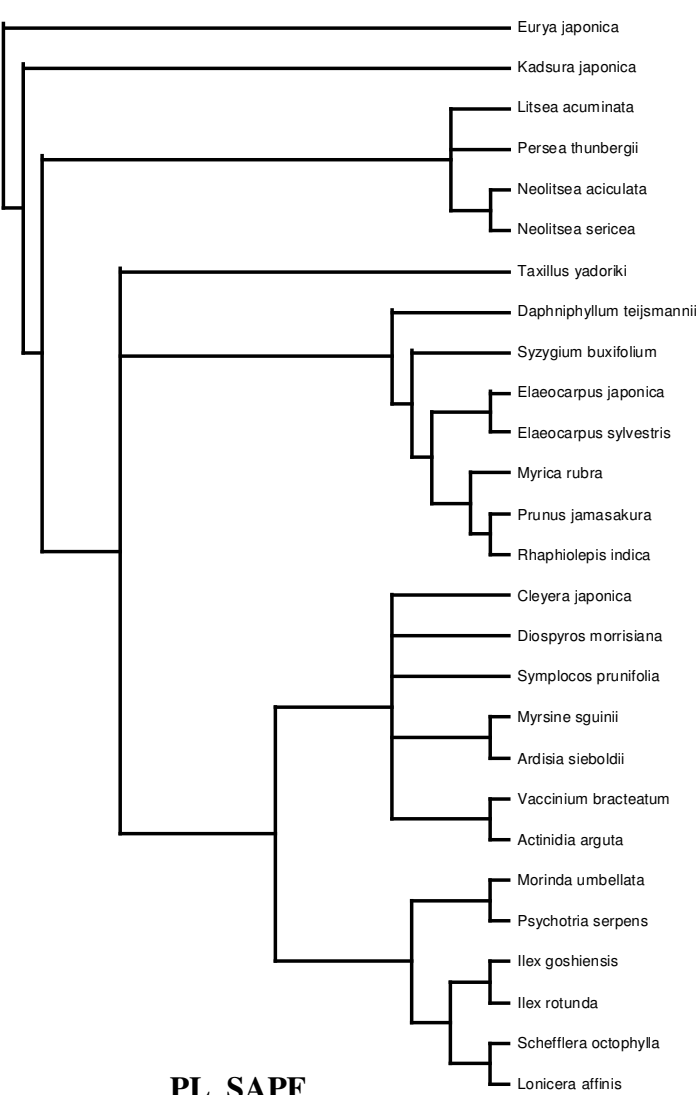
COMMUNITY RMRZ – Pollination



COMMUNITY SAPF – Frugivory

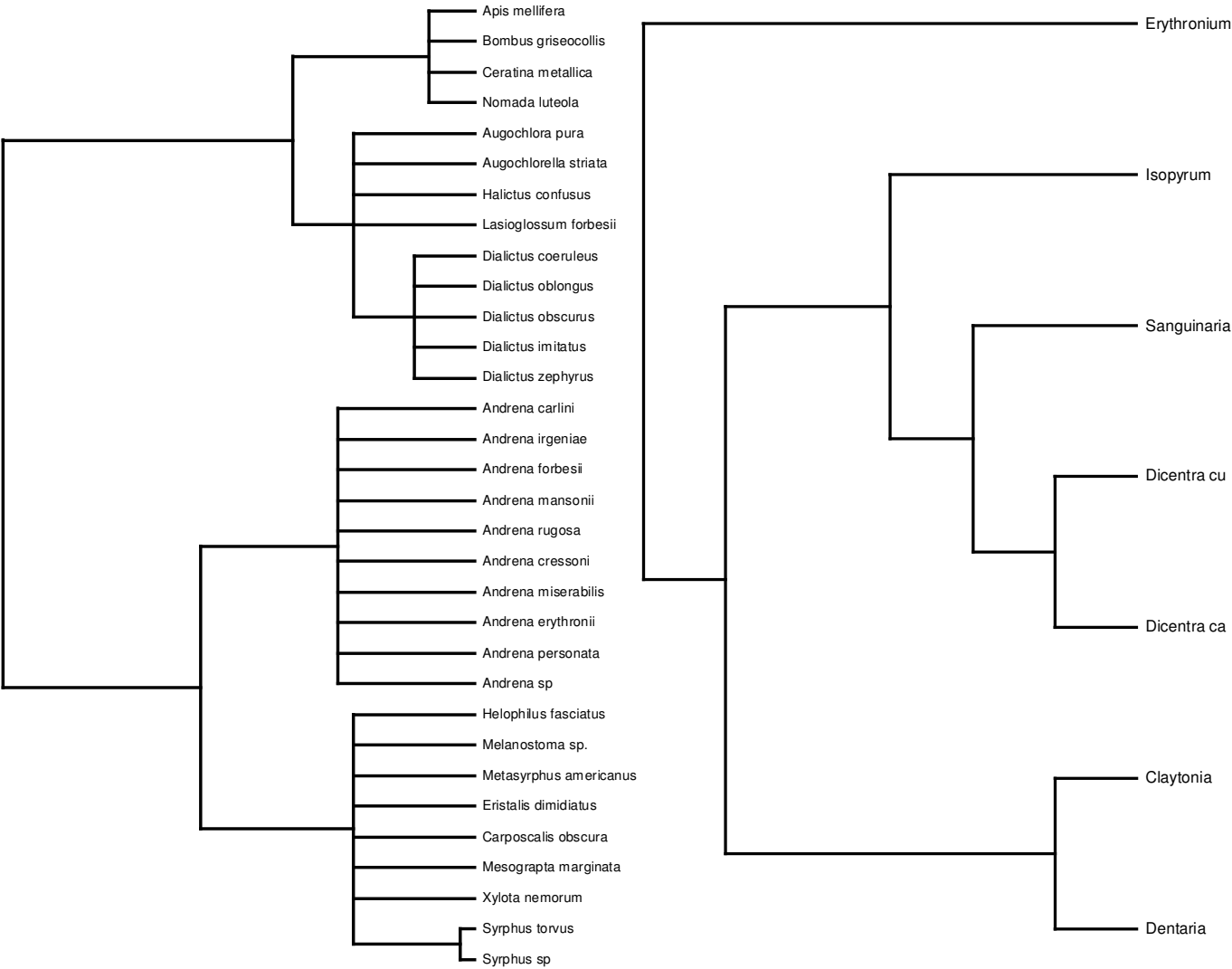


AN_SAPF
(not included in analyses)



PL_SAPF

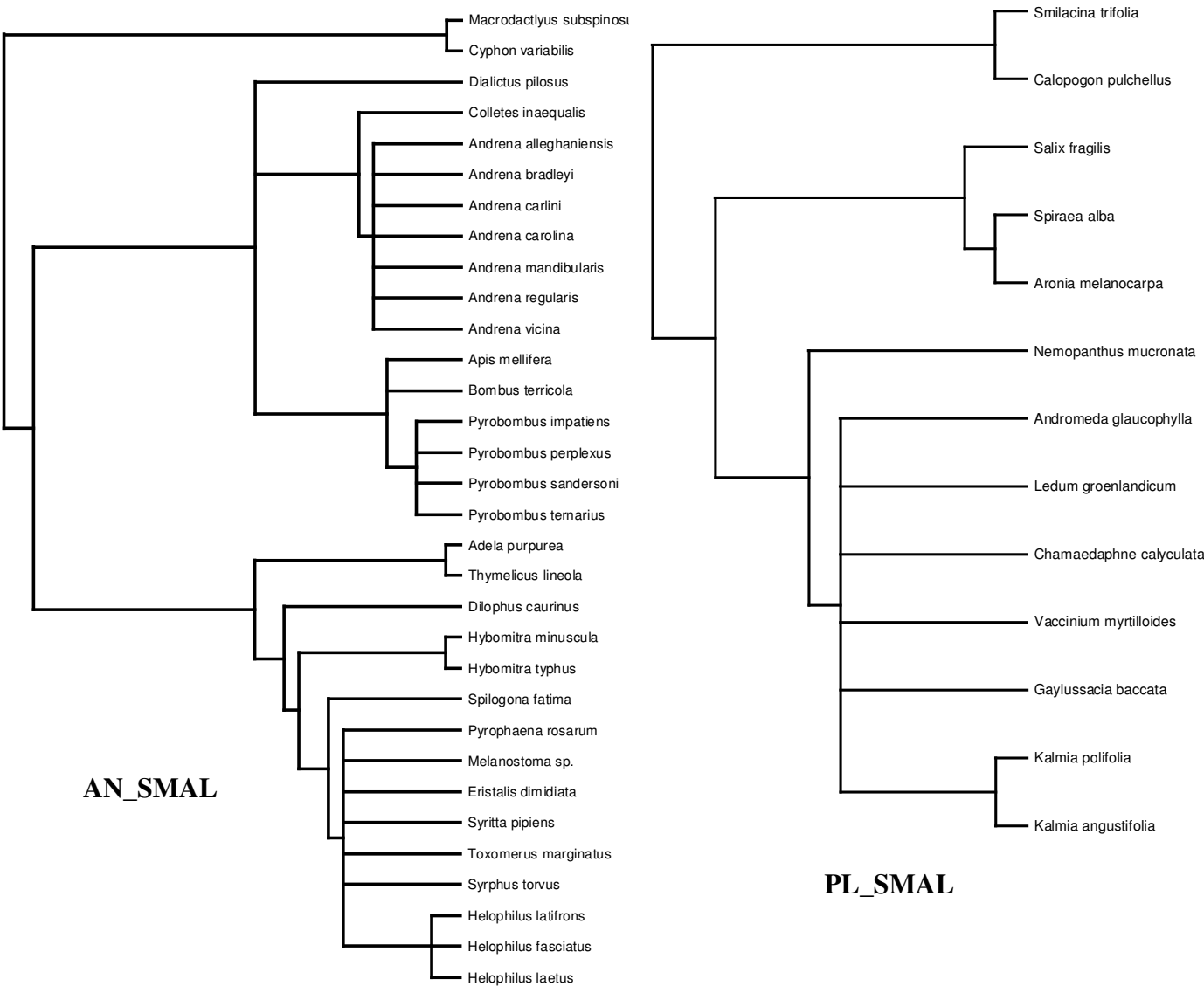
COMMUNITY SCHM – Pollination



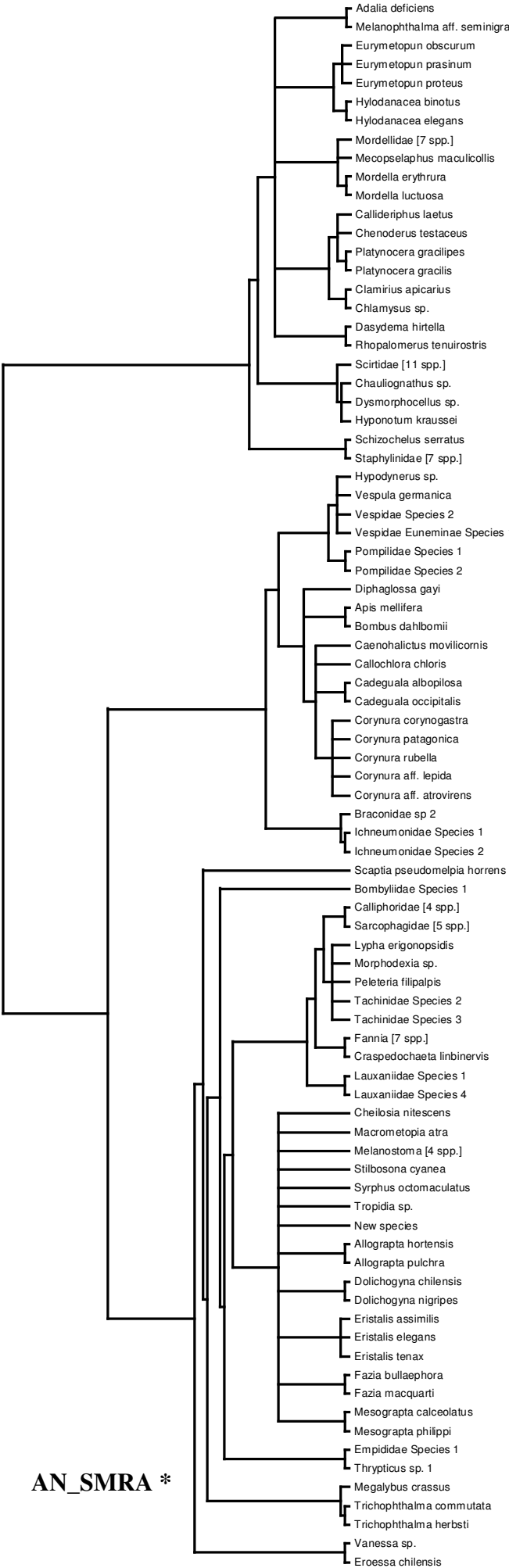
AN_SCHM

PL_SCHM
(not included in analyses)

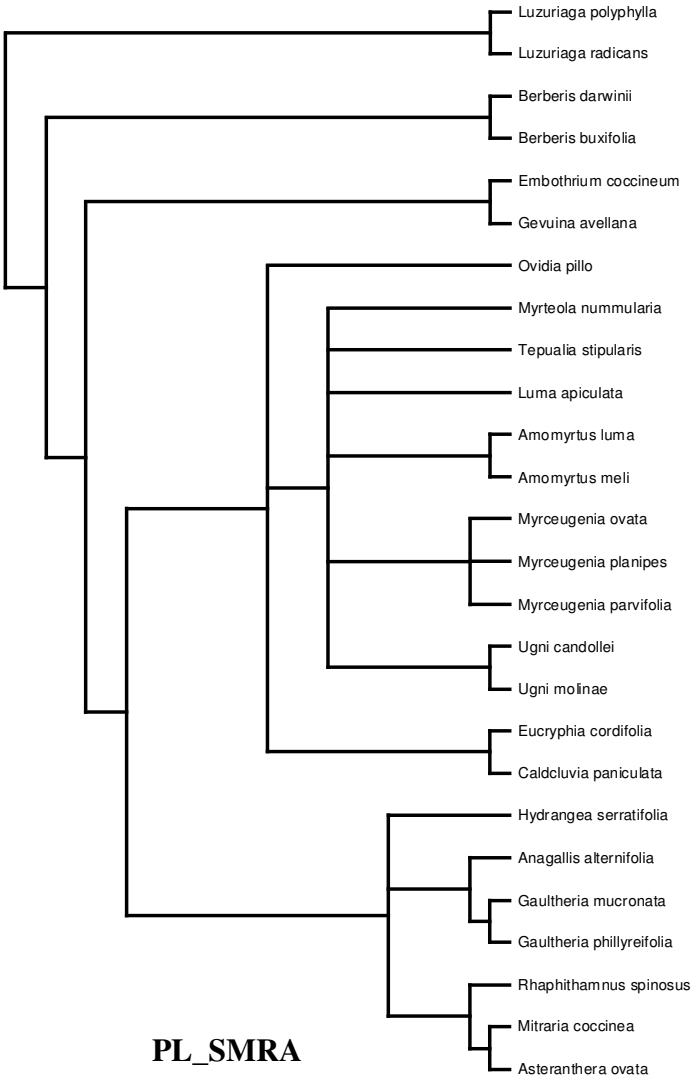
COMMUNITY SMAL – Pollination



COMMUNITY SMRA – Pollination



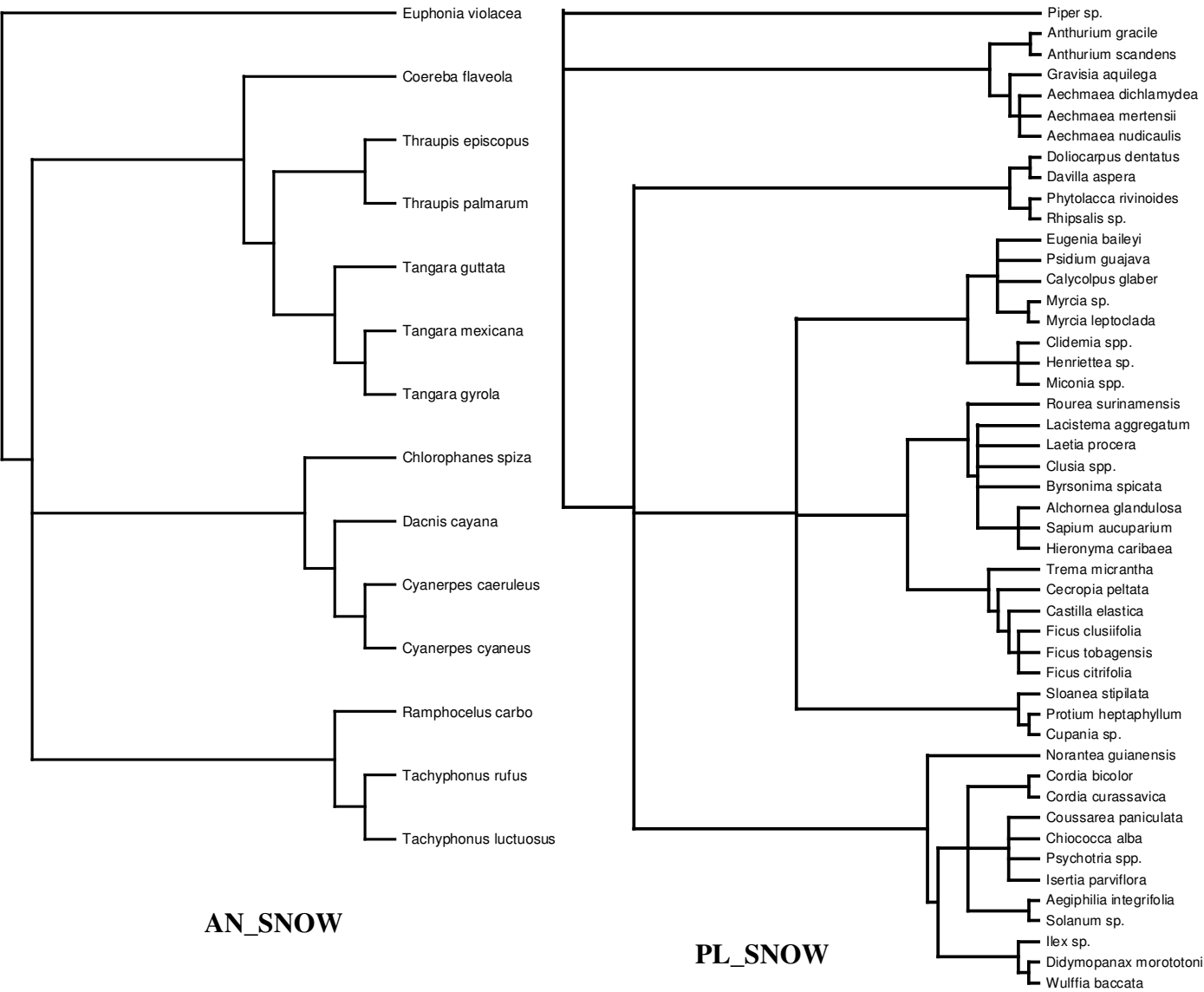
AN_SMRA *

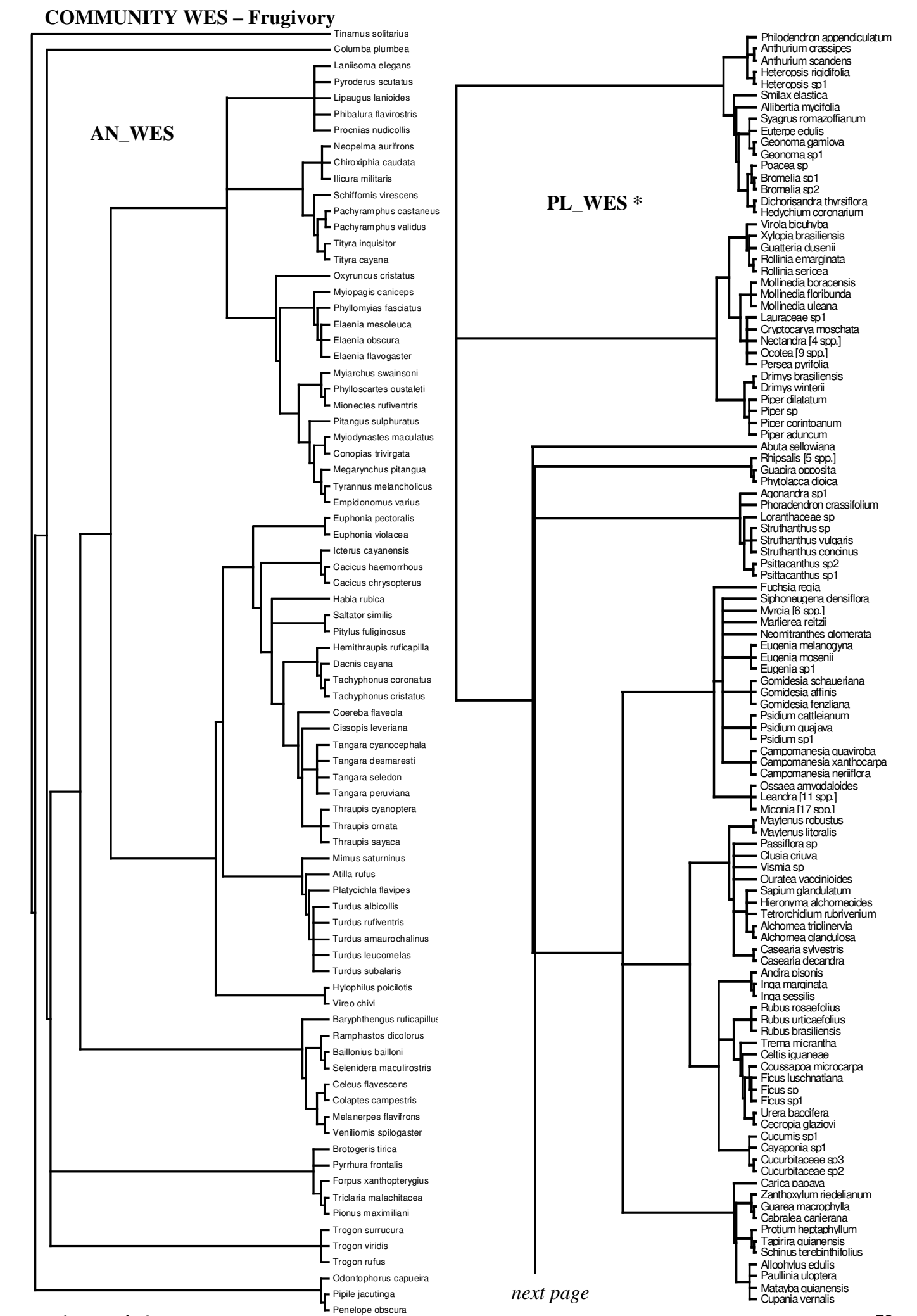


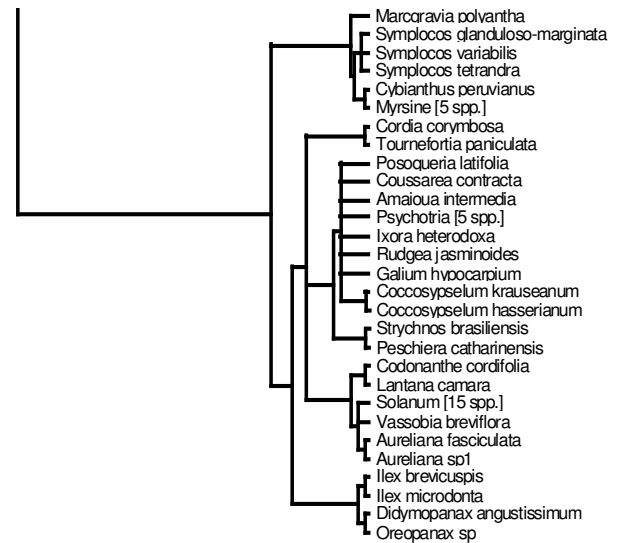
PL_SMRA

* Obs: politomies within genera or families were removed for clarity (but were included in analyses). Number of species included as soft politomies within each group are shown in brackets.

COMMUNITY SNOW – Frugivory





Community WES (*continued*)**PL_WES ***

* Obs: politomies within genera were removed for clarity (but were included in analyses). Number of congeneric species included as soft politomies are shown within brackets.

COMMUNITY WYTH – Frugivory

