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# 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://internt.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 – 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 wihtout 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 disproportionally 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).

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# 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.

| | | PLANTS | | | | | | | | ANIMALS | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CODE** | **Pol/Frug** | **N sp. Plants** [a] | **N sp. Animals** [a] | **K** | **$P_K$** | **Z** | **$P_Z$** | **$Z_{partial}$** | **$P_{Zpartial}$** | **K** | **$P_K$** | **Z** | **$P_Z$** | **$Z_{partial}$** | **$P_{Zpartial}$** | **Pl_An** [b] |
| 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

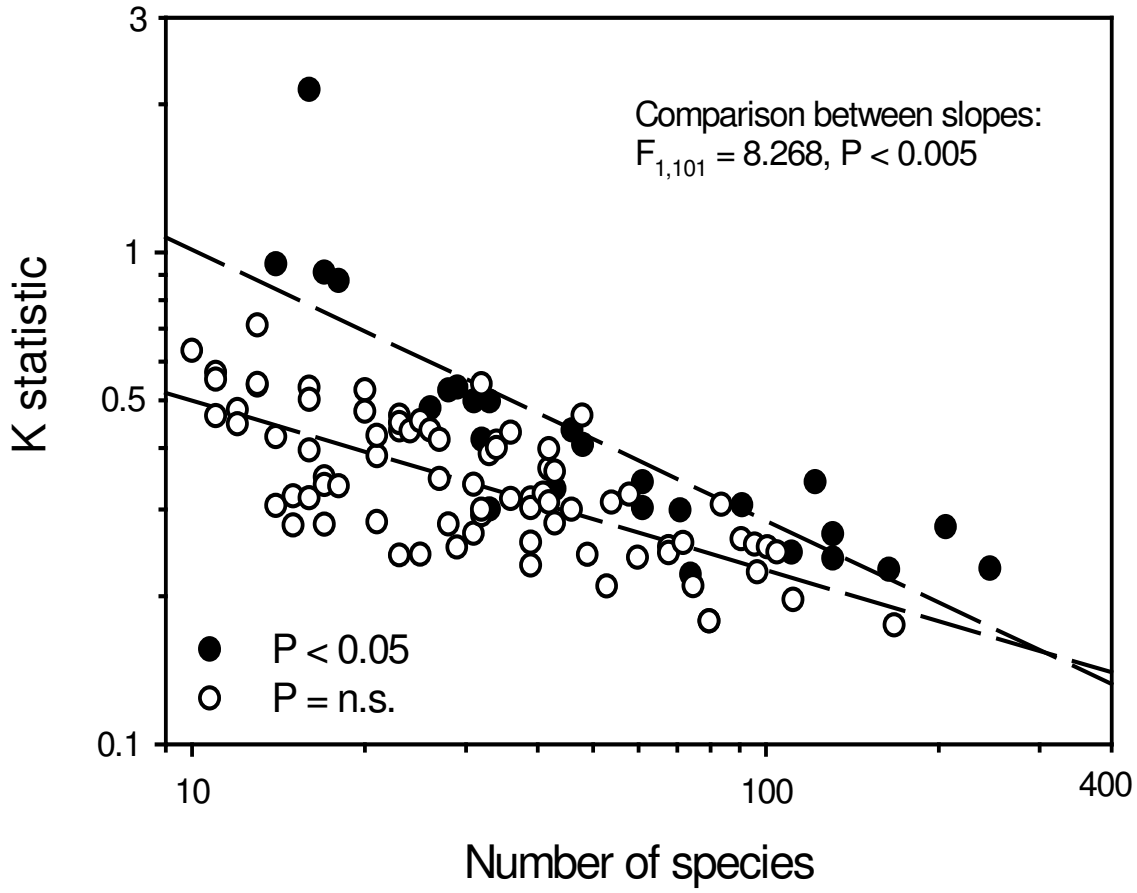



Figure S1. Relationship between *K* statistics and number of species per phylogeny, comparing the slopes of linear regressions (in a log-log scale) between phylogenies where significant phylogenetic signal was detected ($P < 0.05$) versus those where signal was not significant.

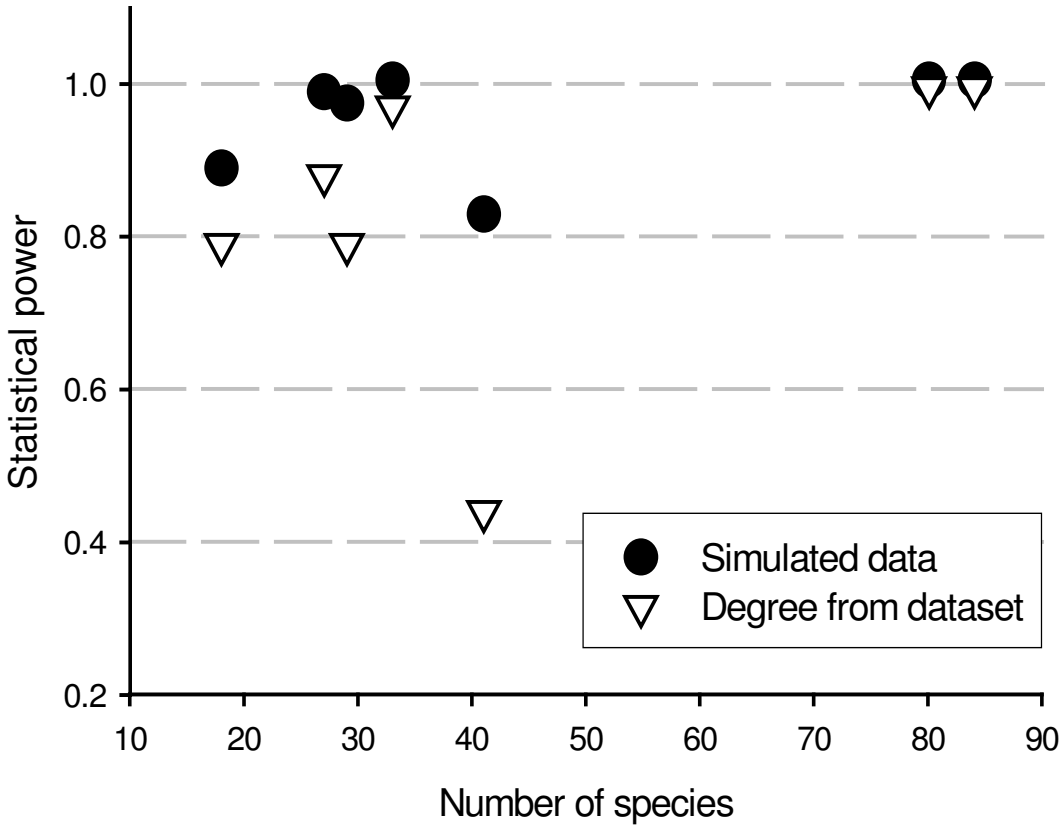
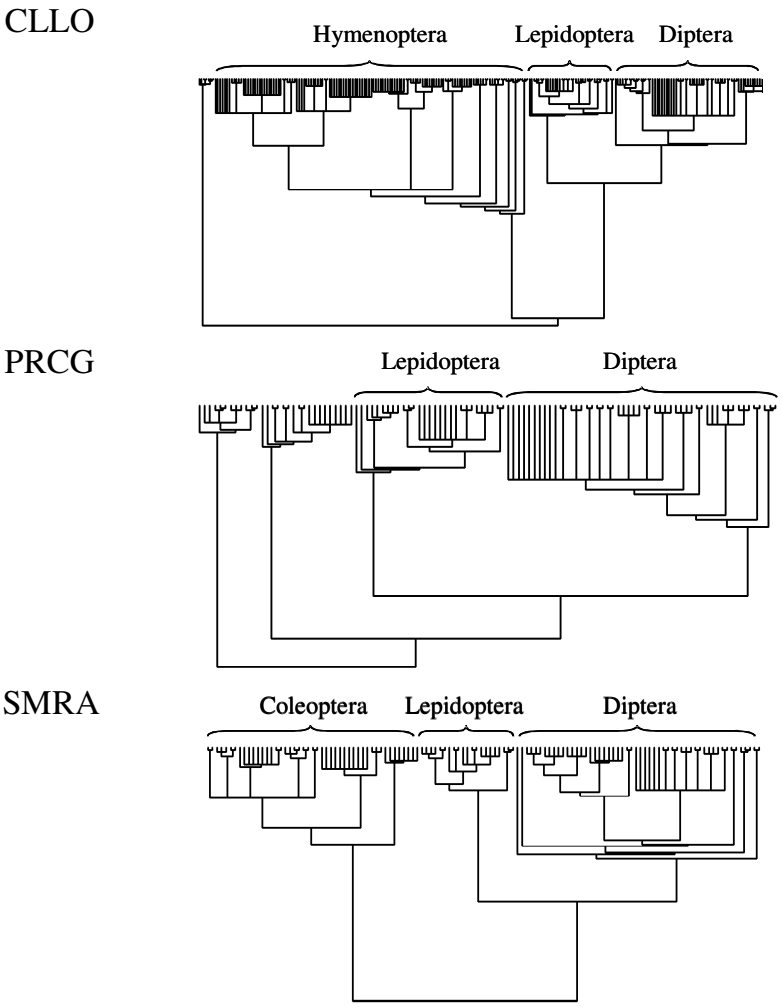



Figure S2. Estimates of statistical power of the randomization test, employing continuous simulated data and the degree distribution of the real dataset (see text for details). Phylogenies employed here were, in increasing order of size: PRAP (plant), SAPF (plant), OLAU (plant), NCOR (animal), PRCA (plant),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

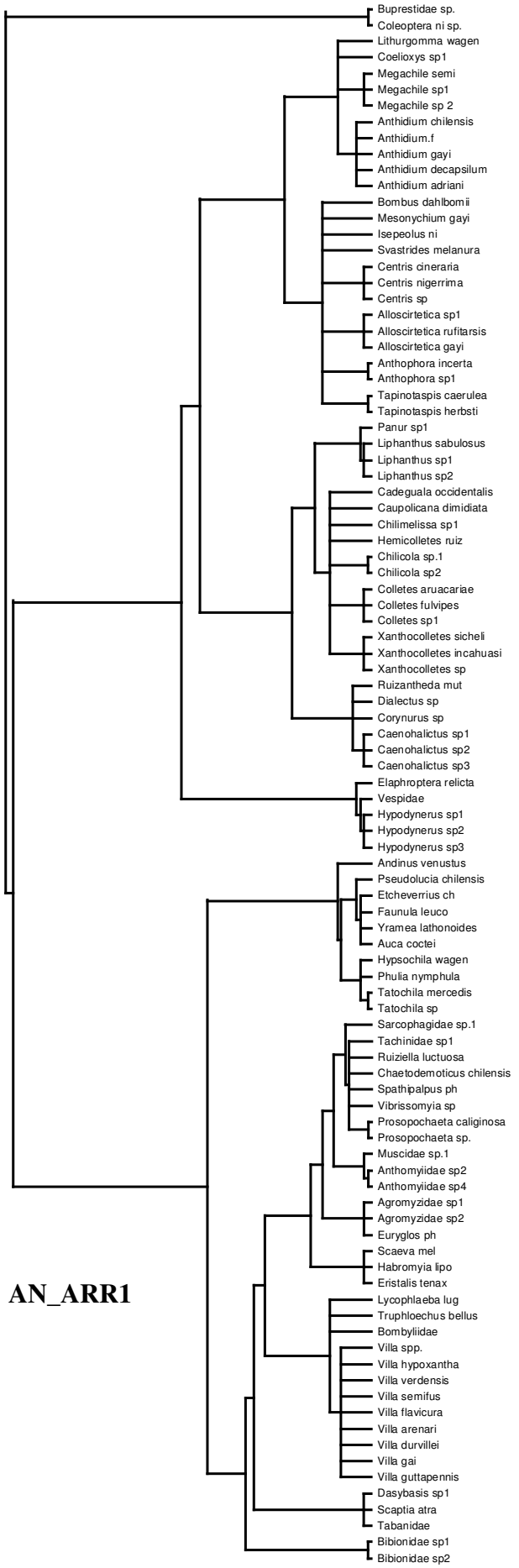



| Community | Taxonomic group | Number of species | Randomization *K* | Randomization *P* | Mantel *Z* | Mantel *P* |
|---|---|---|---|---|---|---|
| CLLO | Hymenoptera | 135 | 0.258 | 0.002 | 0.060 | 0.011 |
| | Lepidoptera | 37 | 0.352 | 0.177 | 0.110 | 0.007 |
| | Diptera | 67 | 0.302 | 0.462 | 0.049 | 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 |

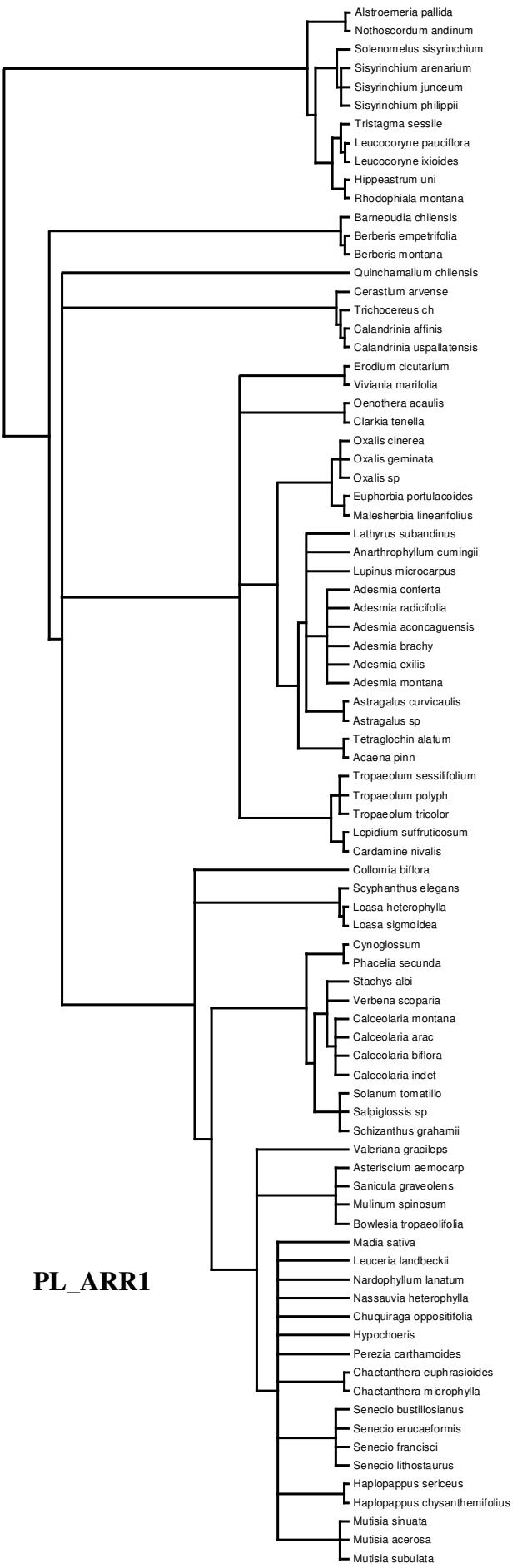
Figure S3. Assessing the magnitude and significance of phylogenetic effects within major taxonomic groups in three insect (pollinator) species. Only groups with more than 20 spp. were analyzed. Results from randomization and Mantel tests are listed on the table at the bottom (results for the entire communities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

# PHYLOGENIES

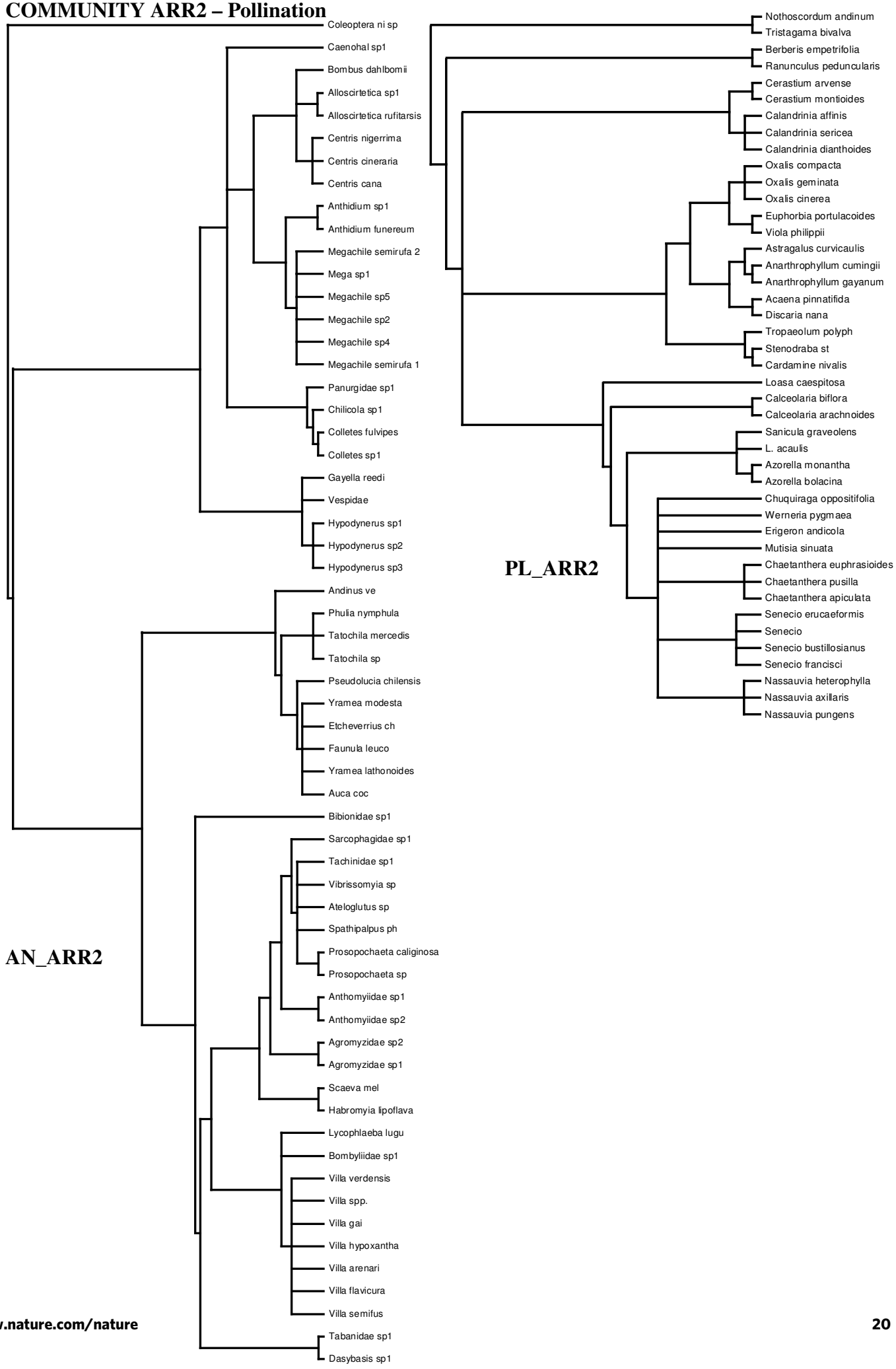
## COMMUNITY ARR1 – Pollination



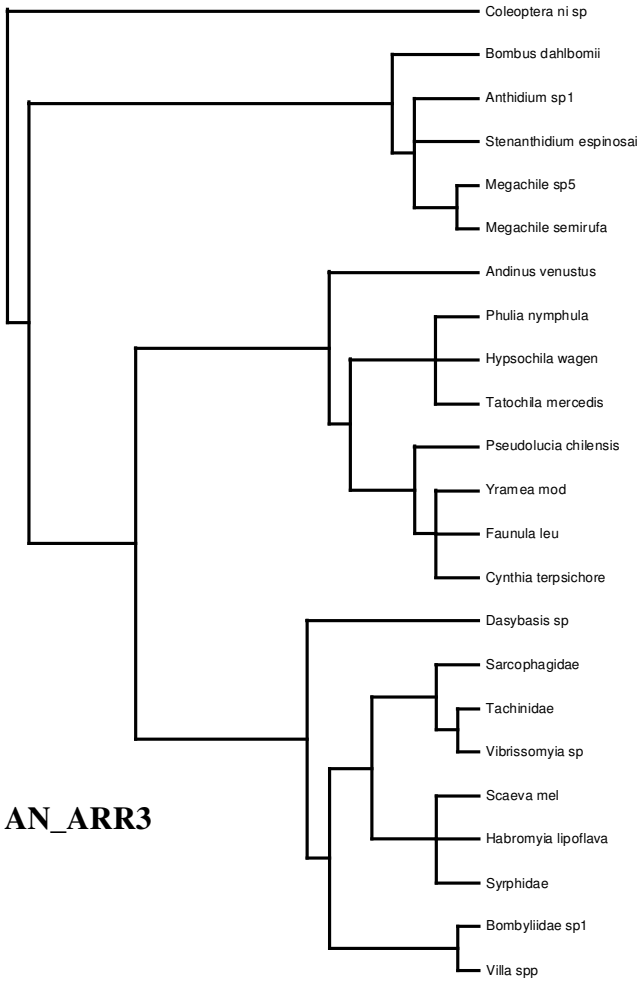

**AN_ARR1**



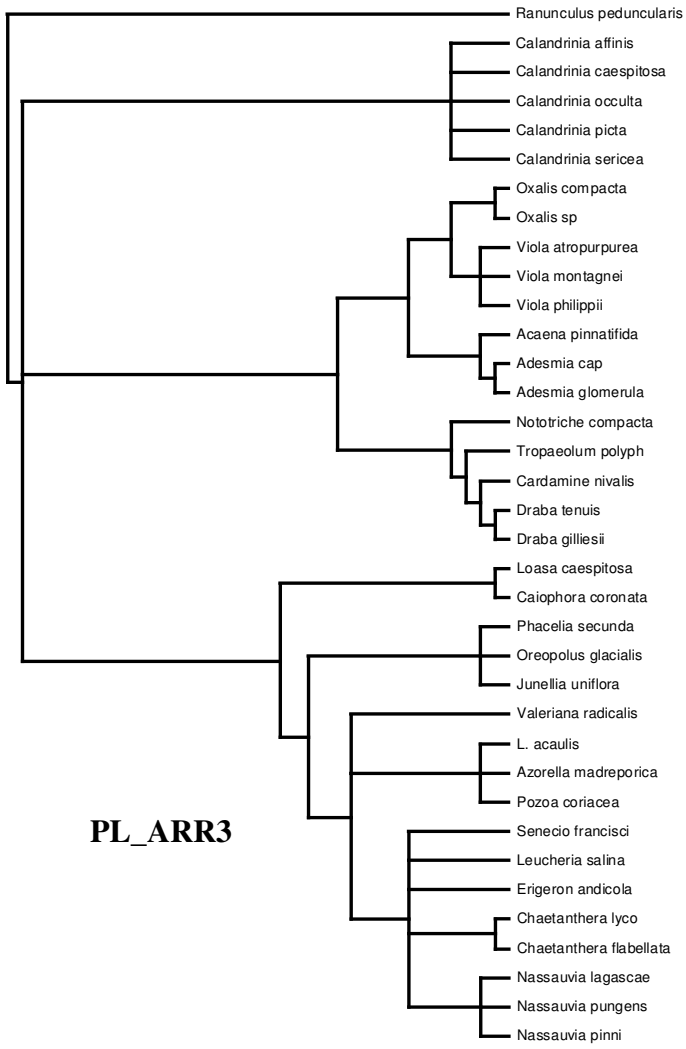

**PL_ARR1**


COMMUNITY ARR2 – Pollination
Coleoptera ni sp
Caenohal sp1
Bombus dahlbomii
Alloscirtetica sp1
Alloscirtetica rufitarsis
Centris nigerrima
Centris cineraria
Centris cana
Anthidium sp1
Anthidium funereum
Megachile semirufa 2
Mega sp1
Megachile sp5
Megachile sp2
Megachile sp4
Megachile semirufa 1
Panurgidae sp1
Chilicola sp1
Colletes fulvipes
Colletes sp1
Gayella reedi
Vespidae
Hypodynerus sp1
Hypodynerus sp2
Hypodynerus sp3
Andinus ve
Phulia nymphula
Tatochila mercedis
Tatochila sp
Pseudolucia chilensis
Yramea modesta
Etcheverrius ch
Faunula leuco
Yramea lathonoides
Auca coc
Bibionidae sp1
Sarcophagidae sp1
Tachinidae sp1
Vibrissomyia sp
Ateloglutus sp
Spathipalpus ph
Prosopochaeta caliginosa
Prosopochaeta sp
Anthomyiidae sp1
Anthomyiidae sp2
Agromyzidae sp2
Agromyzidae sp1
Scaeva mel
Habromyia lipoflava
Lycophlaeba lugu
Bombyliidae sp1
Villa verdensis
Villa spp.
Villa gai
Villa hypoxantha
Villa arenari
Villa flavicura
Villa semifus
Tabanidae sp1
Dasybasis sp1
AN_ARR2
Nothoscordum andinum
Tristagama bivalva
Berberis empetrifolia
Ranunculus peduncularis
Cerastium arvense
Cerastium montioides
Calandrinia affinis
Calandrinia sericea
Calandrinia dianthoides
Oxalis compacta
Oxalis geminata
Oxalis cinerea
Euphorbia portulacoides
Viola philippii
Astragalus curvicaulis
Anarthrophyllum cumingii
Anarthrophyllum gayanum
Acaena pinnatifida
Discaria nana
Tropaeolum polyph
Stenodraba st
Cardamine nivalis
Loasa caespitosa
Calceolaria biflora
Calceolaria arachnoides
Sanicula graveolens
L. acaulis
Azorella monantha
Azorella bolacina
Chuquiraga oppositifolia
Werneria pygmaea
Erigeron andicola
Mutisia sinuata
Chaetanthera euphrasioides
Chaetanthera pusilla
Chaetanthera apiculata
Senecio erucaeformis
Senecio
Senecio bustillosianus
Senecio francisci
Nassauvia heterophylla
Nassauvia axillaris
Nassauvia pungens
PL_ARR2

## COMMUNITY ARR3 – Pollination

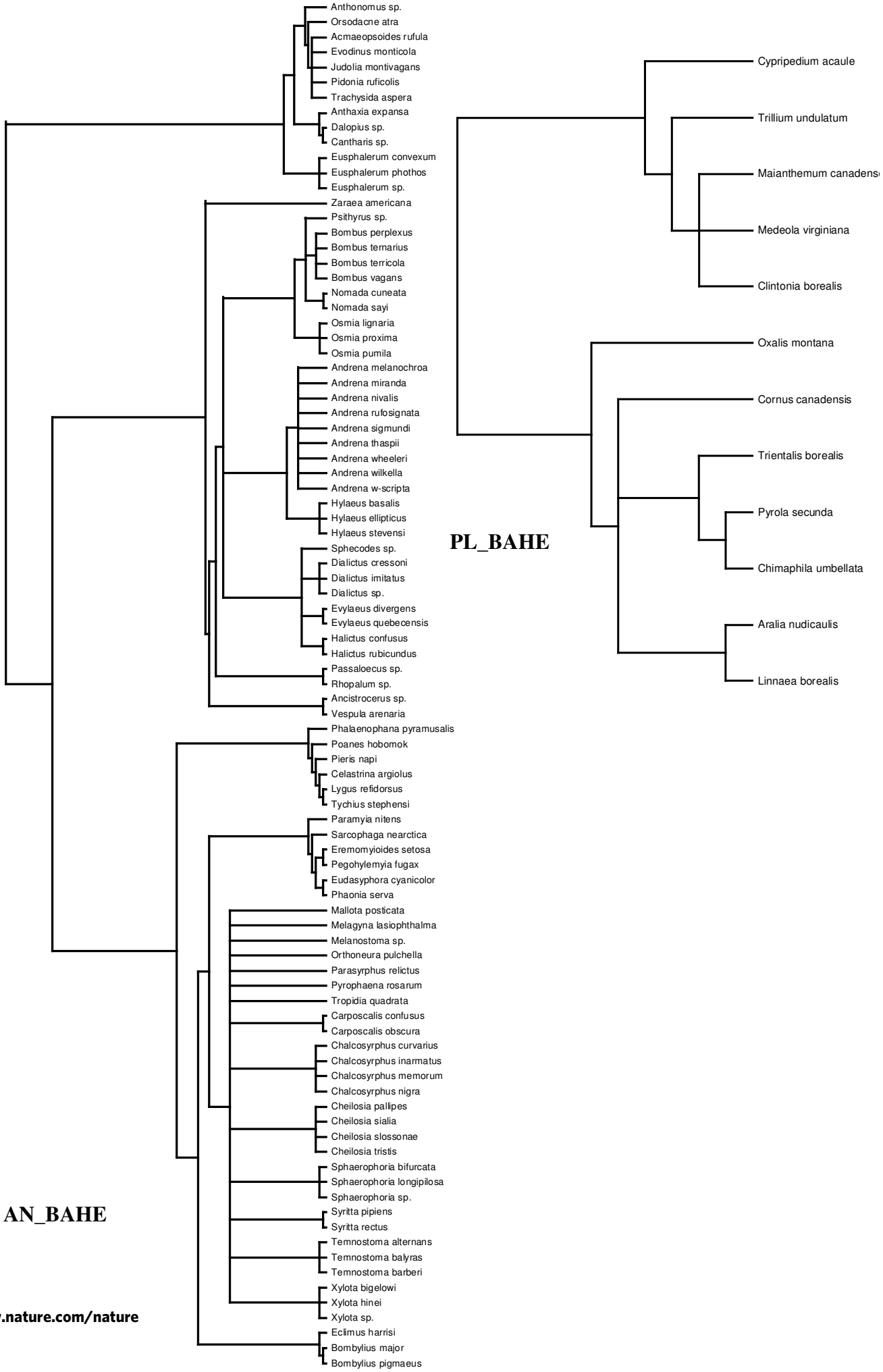



**AN_ARR3**

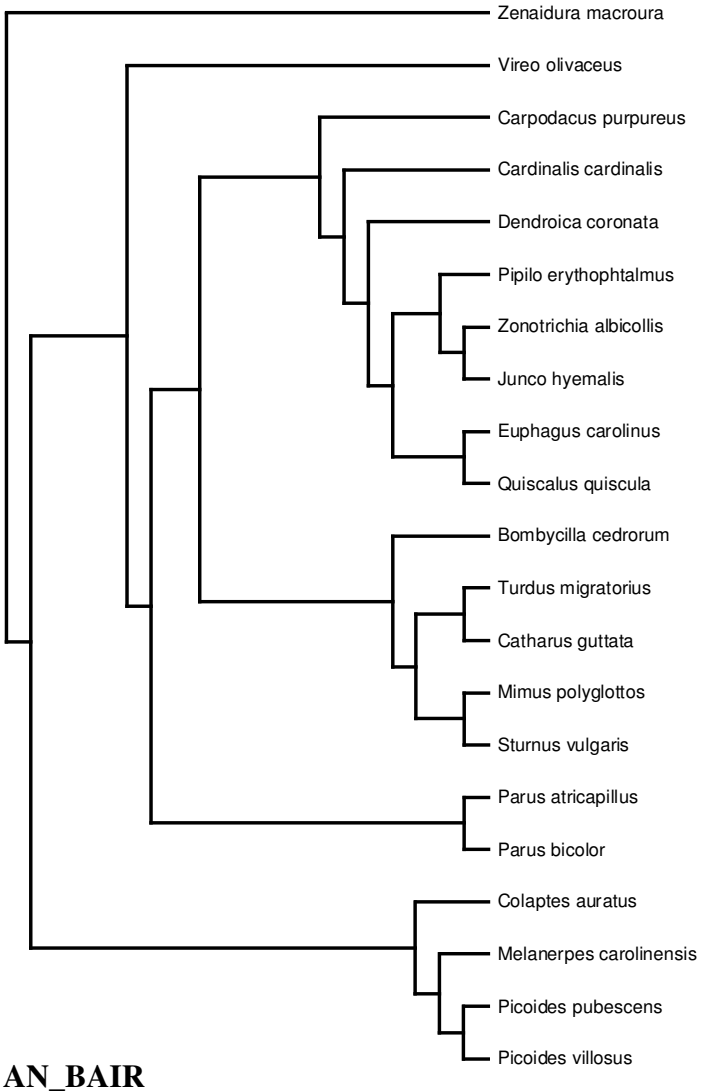



**PL_ARR3**

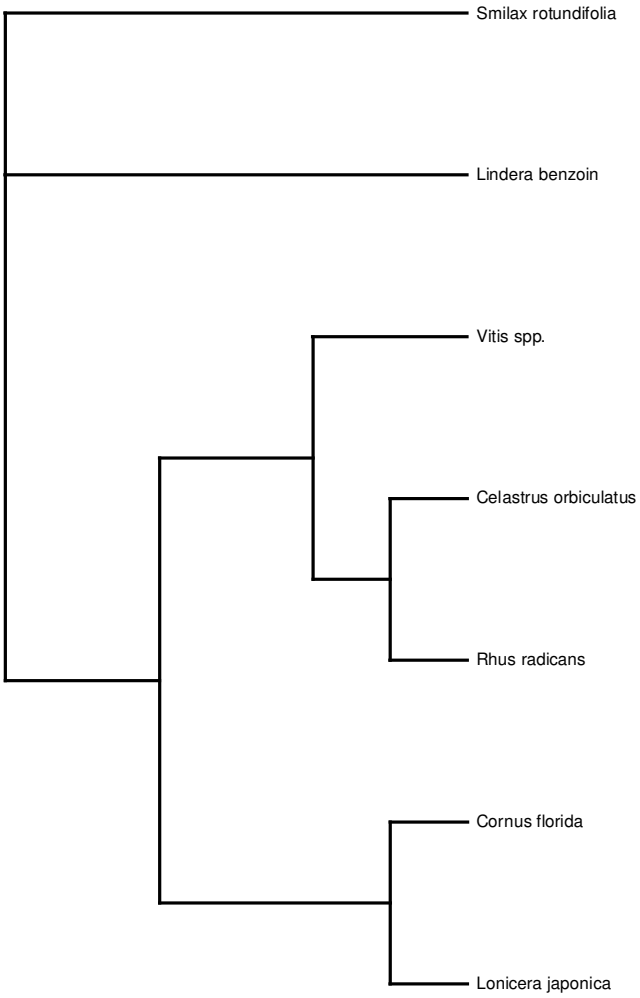
## COMMUNITY BAHE – Pollination



**COMMUNITY BAIR – Frugivory**

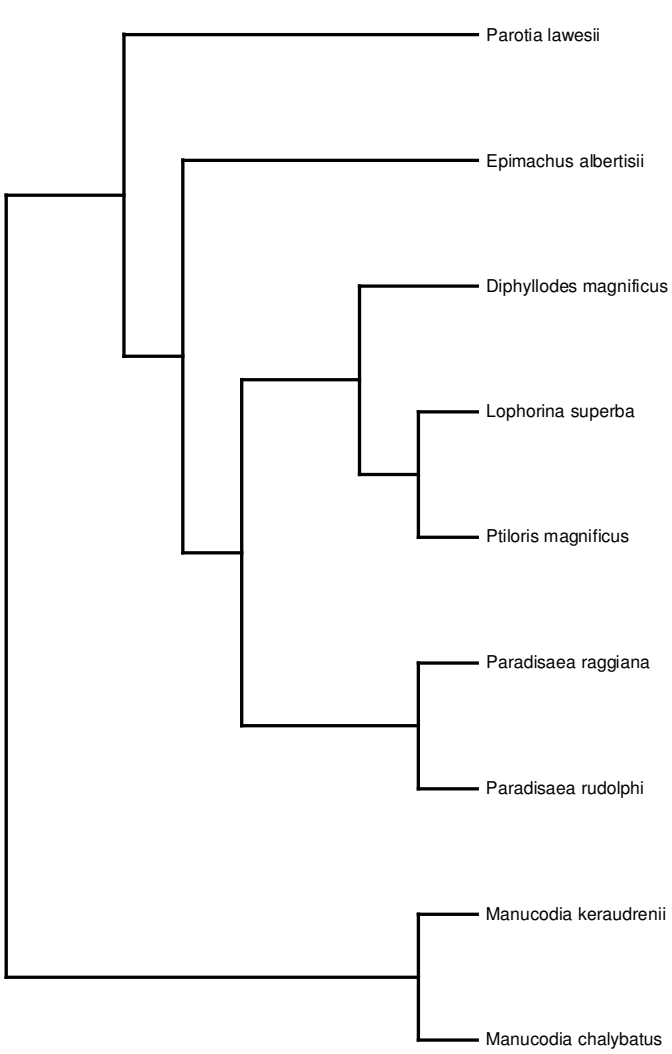



**AN_BAIR**

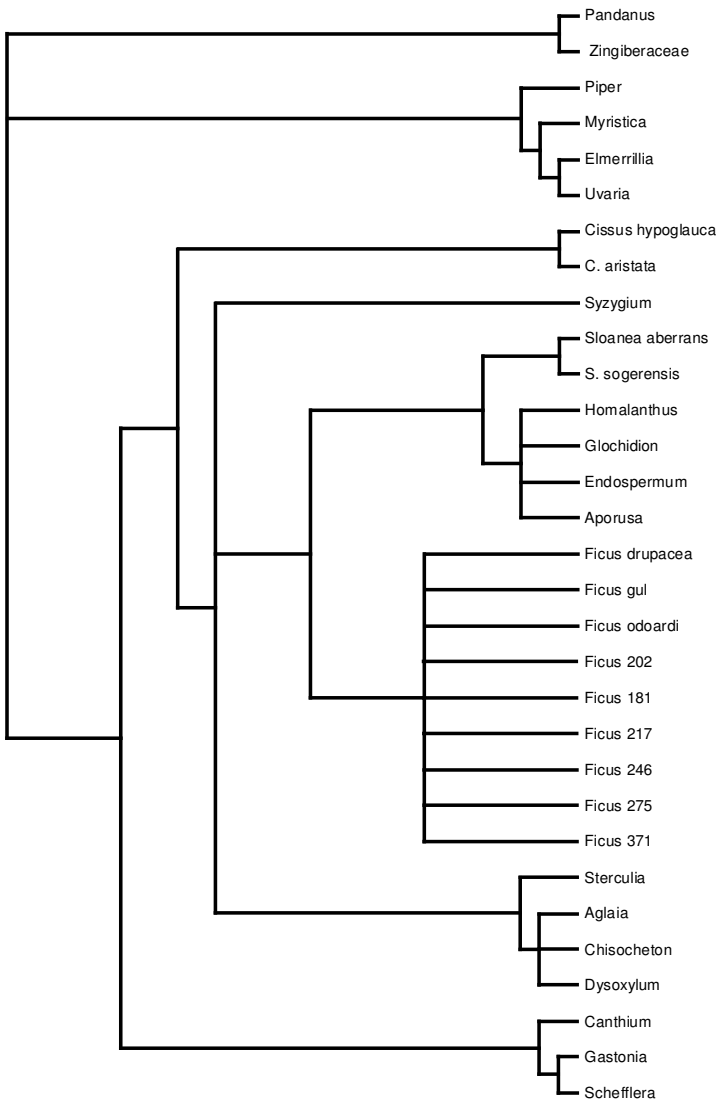



**PL_BAIR**
(not included in analyses)

**COMMUNITY BEEH – Frugivory**

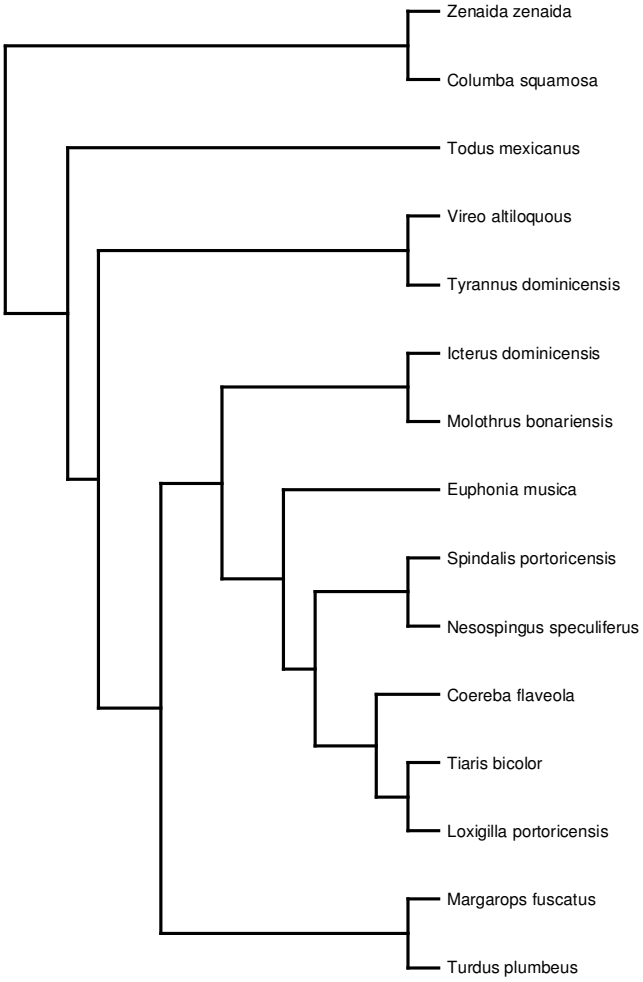



**AN_BEEH**
(not included in analysis)

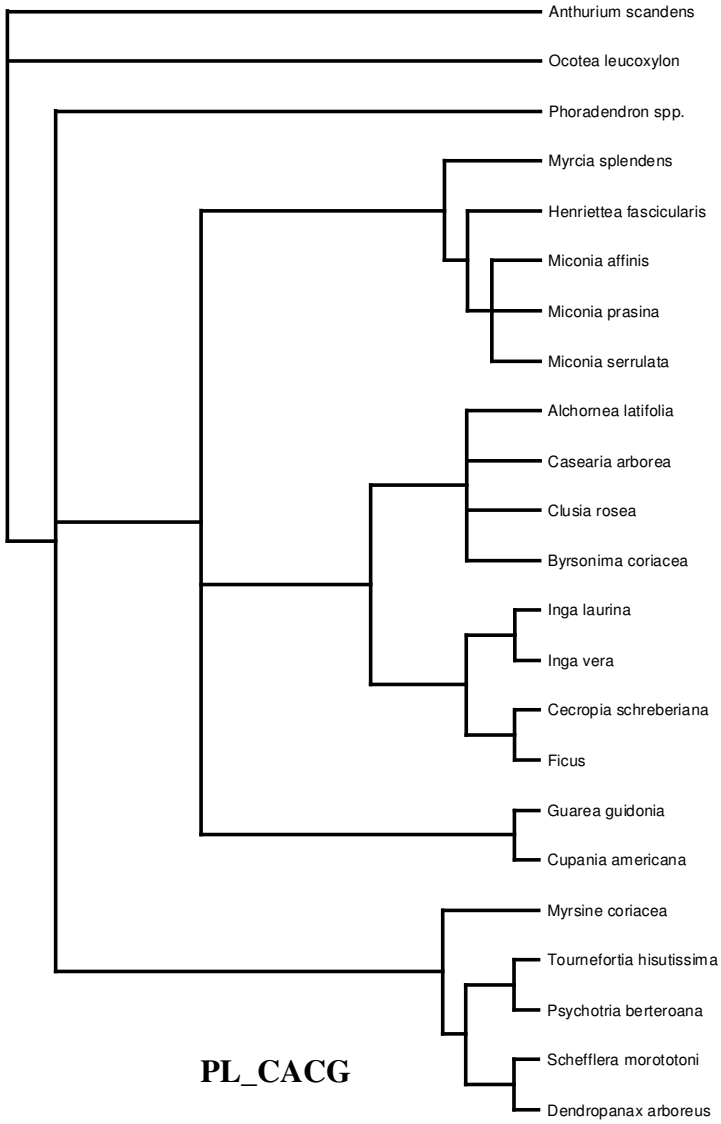



**PL_BEEH**

## COMMUNITY CACG – Frugivory

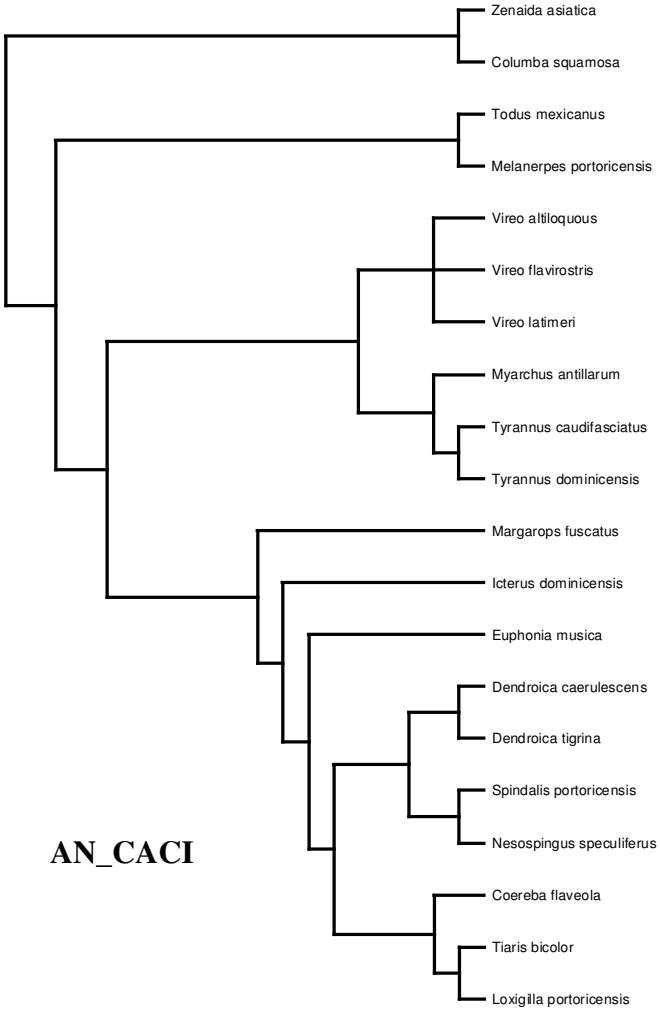



**AN_CACG**

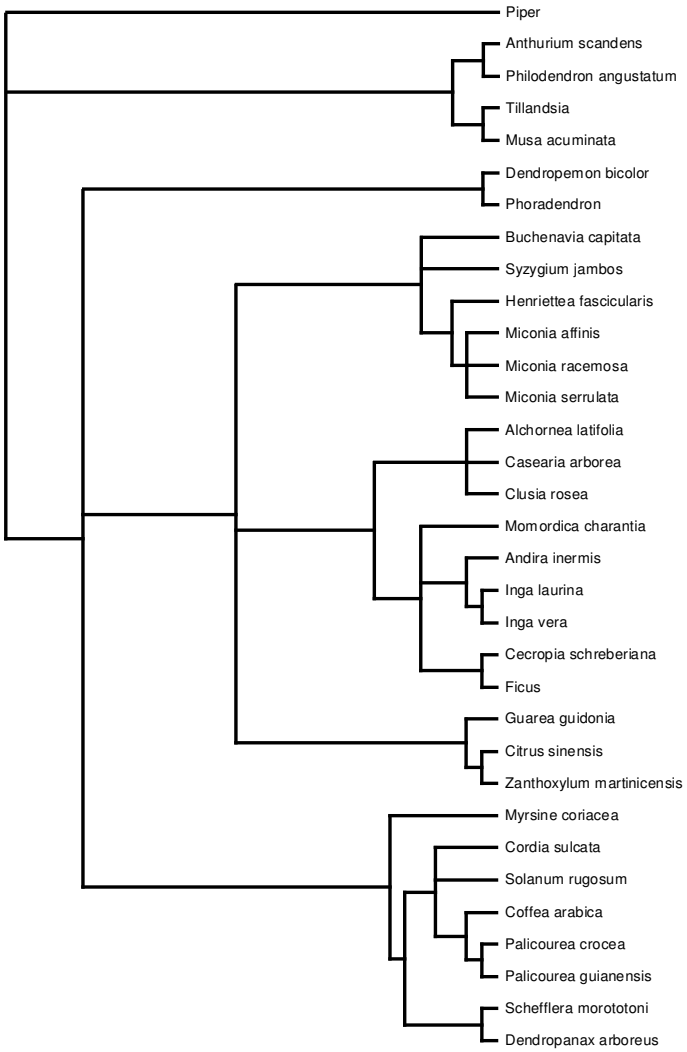



**PL_CACG**

## COMMUNITY CACI – Frugivory

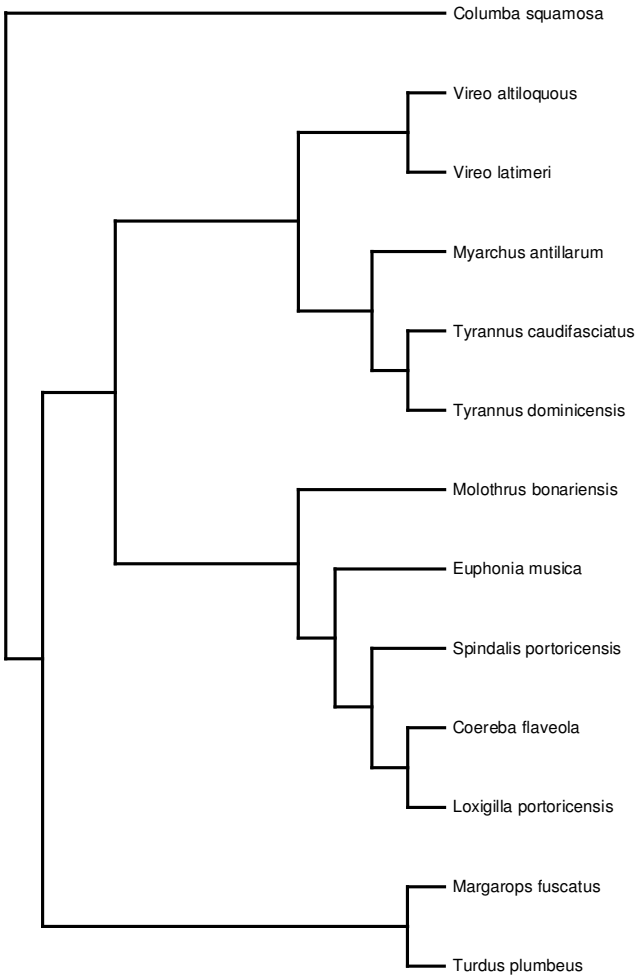



**AN_CACI**

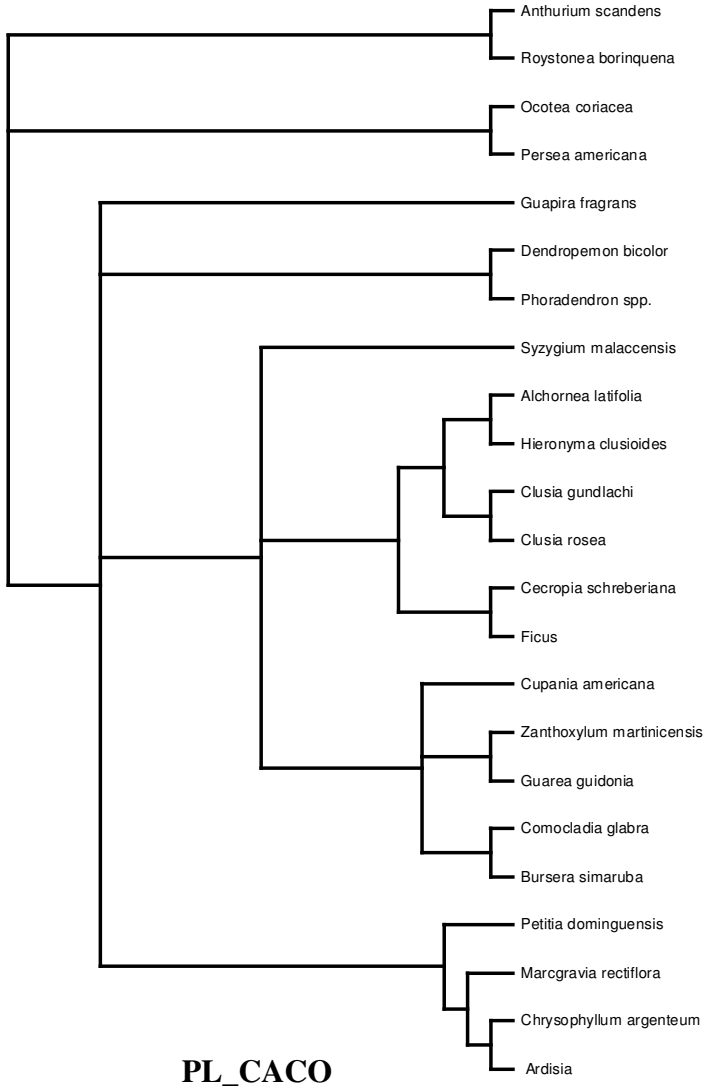



**PL_CACI**

## COMMUNITY CACO – Frugivory

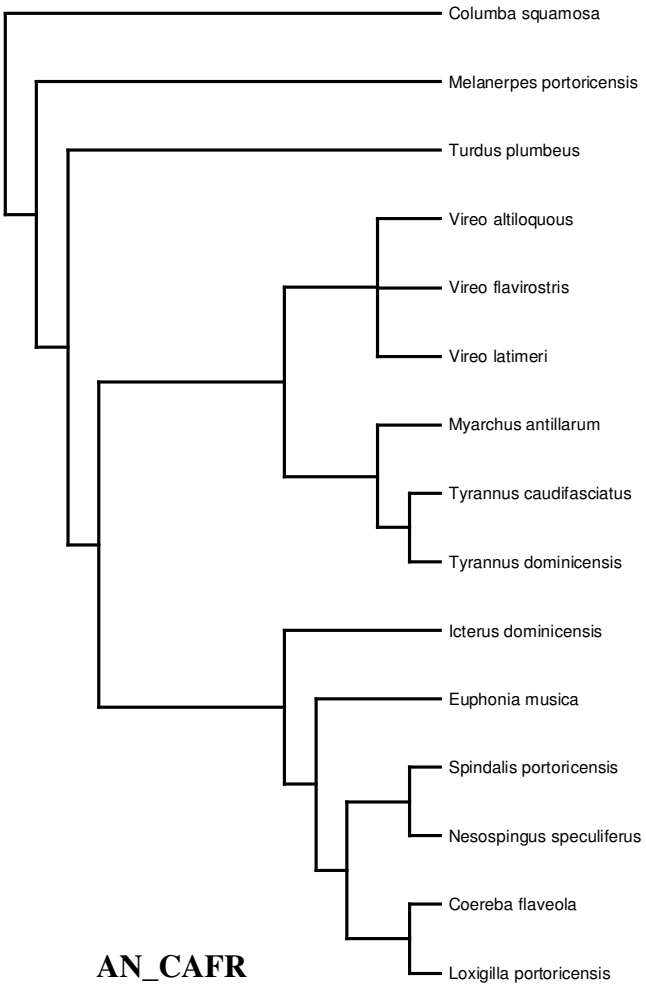



**AN_CACO**

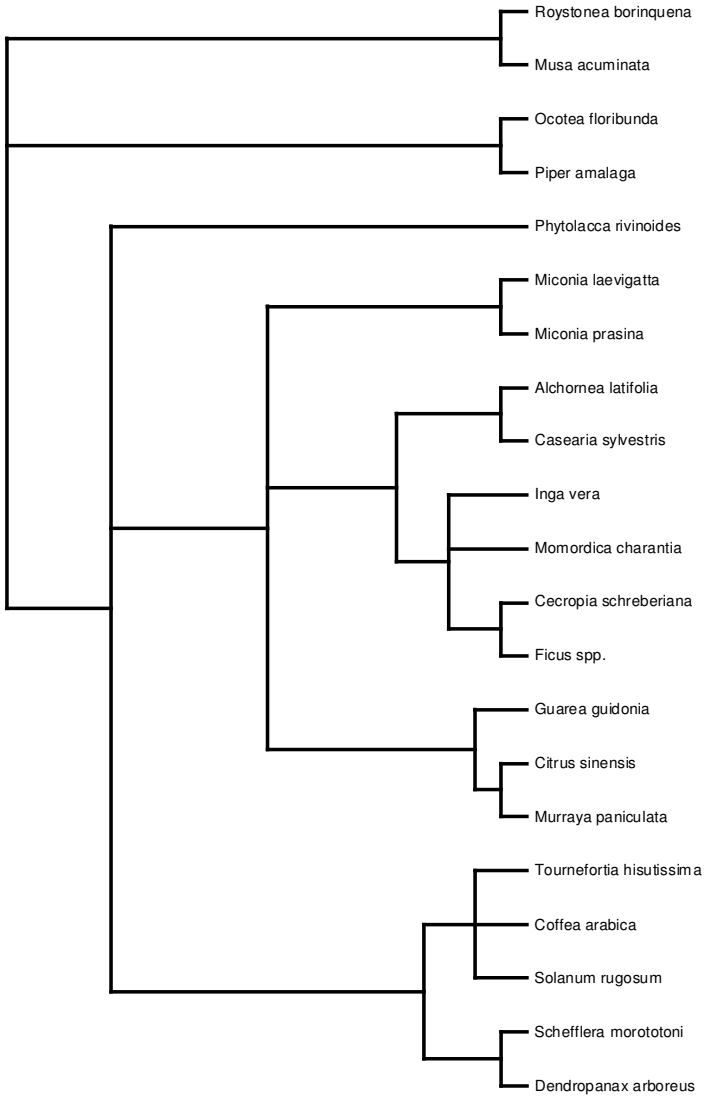



**PL_CACO**

## COMMUNITY CAFR – Frugivory

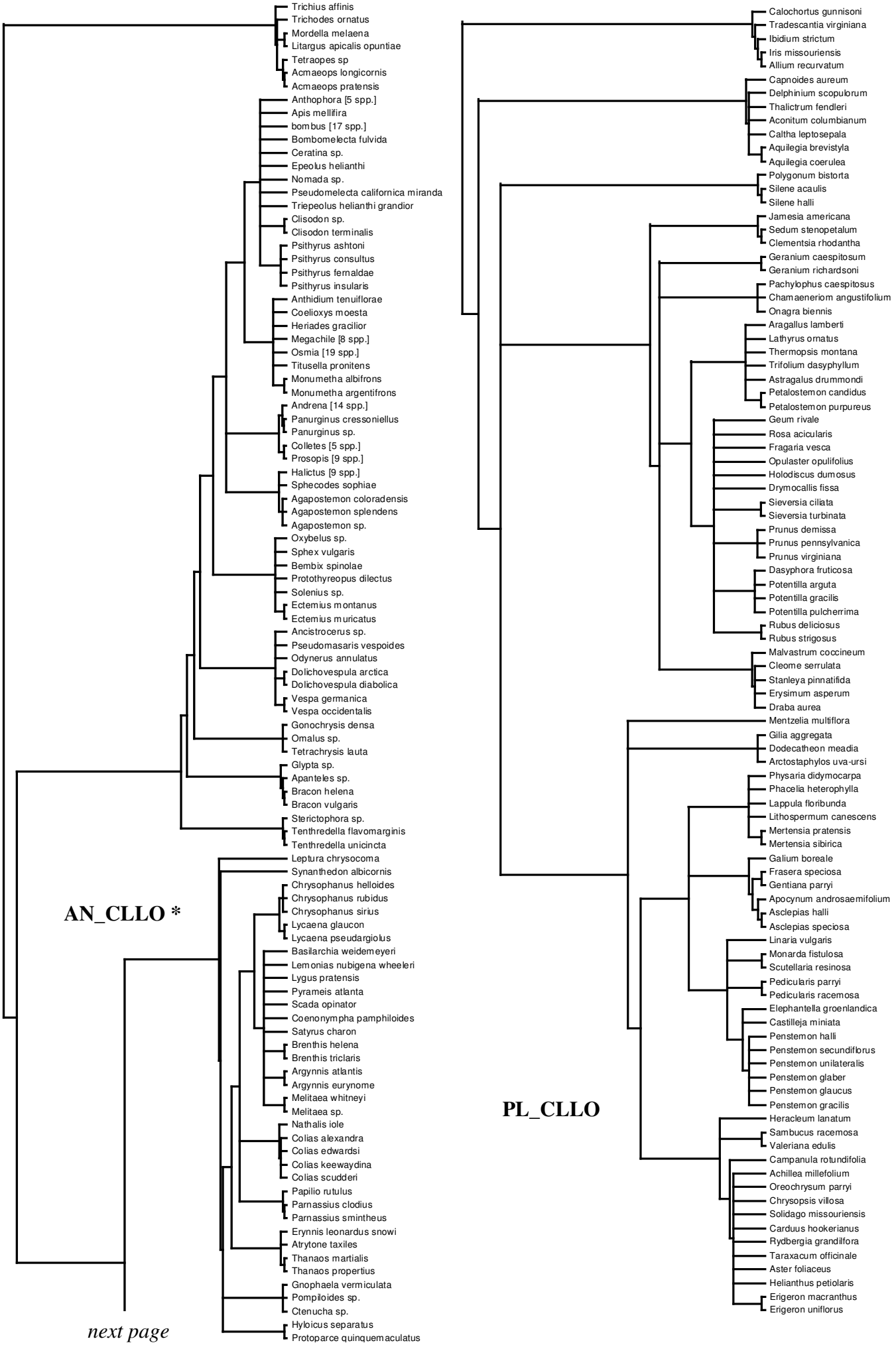



**AN_CAFR**

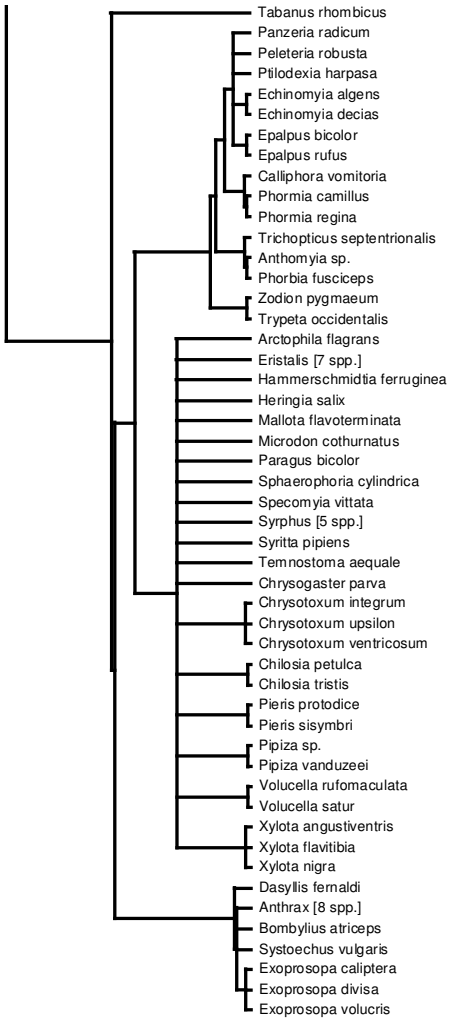



**PL_CAFR**

## COMMUNITY CLLO– Pollination



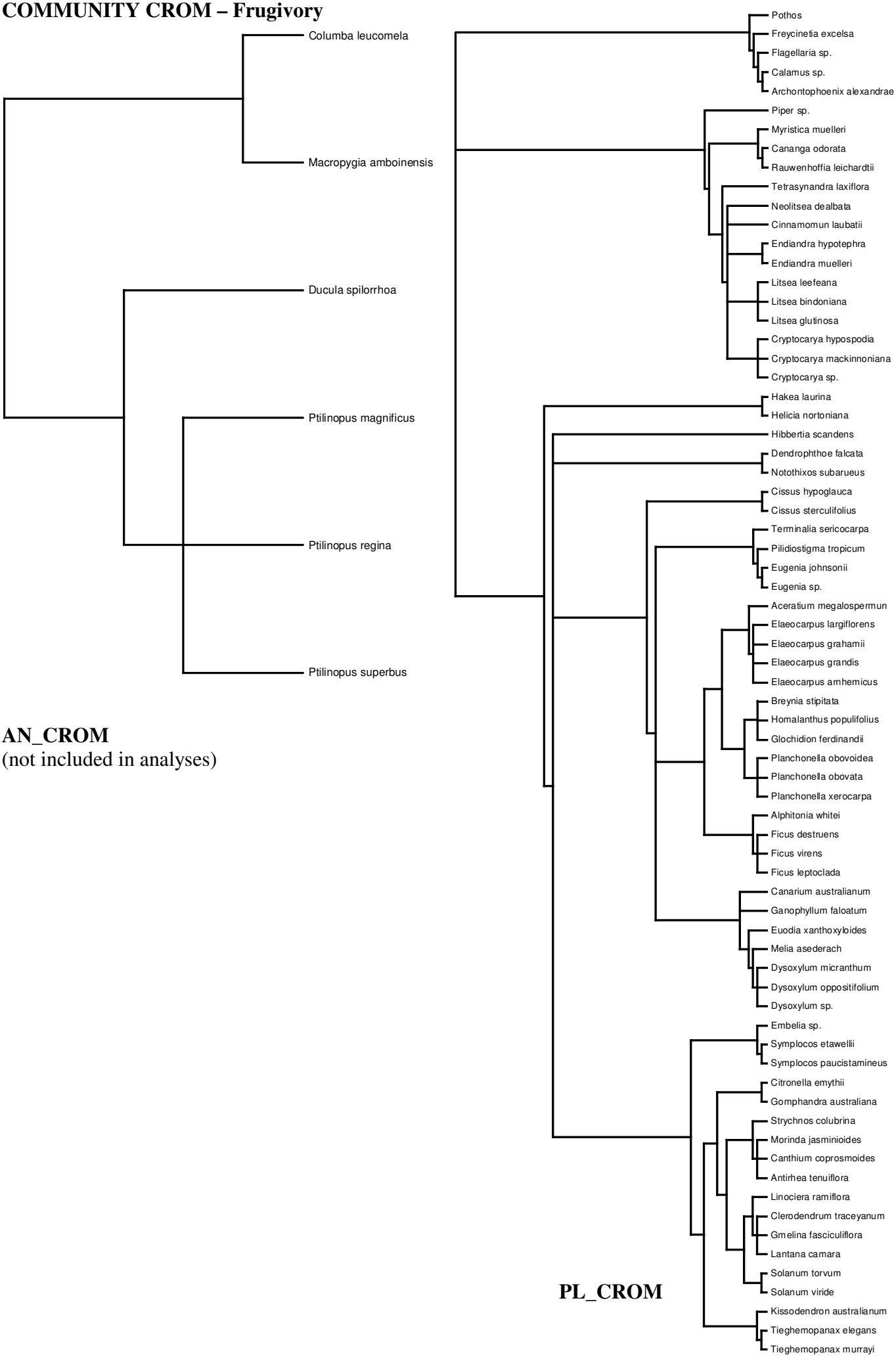
Community CLLO *(continued)*




**AN_CLLO ***

***** 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.

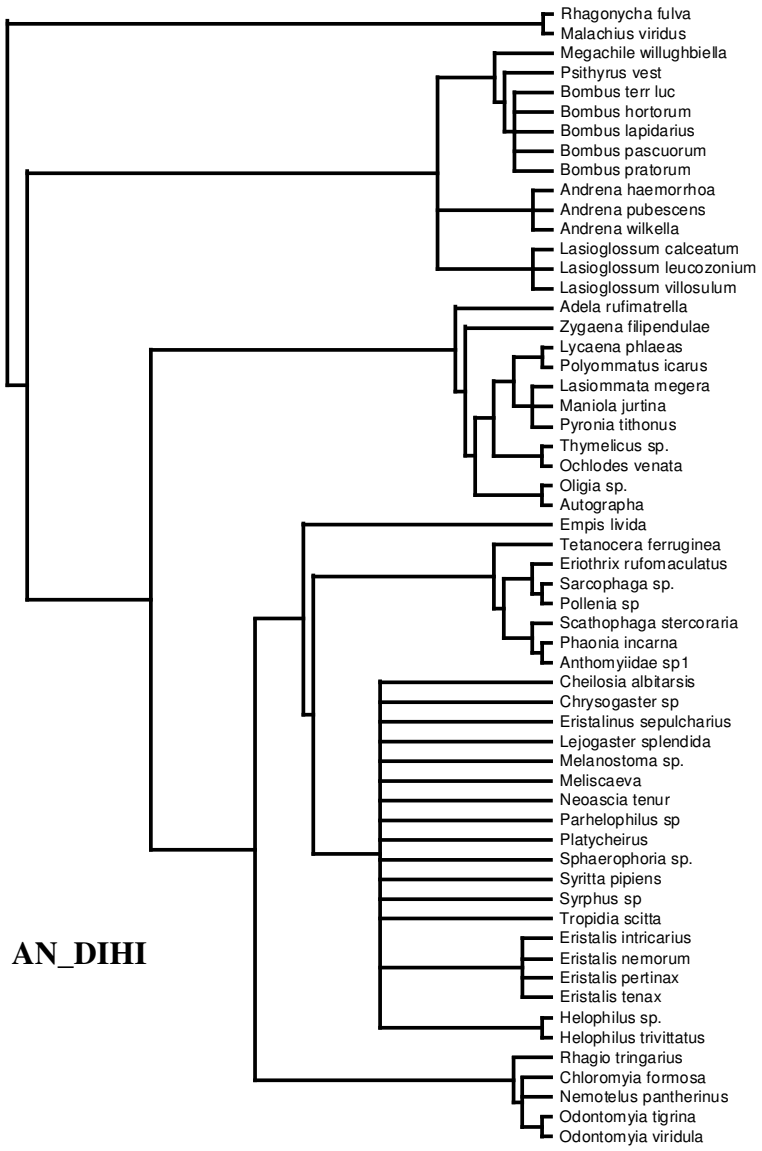
**COMMUNITY CROM – Frugivory**

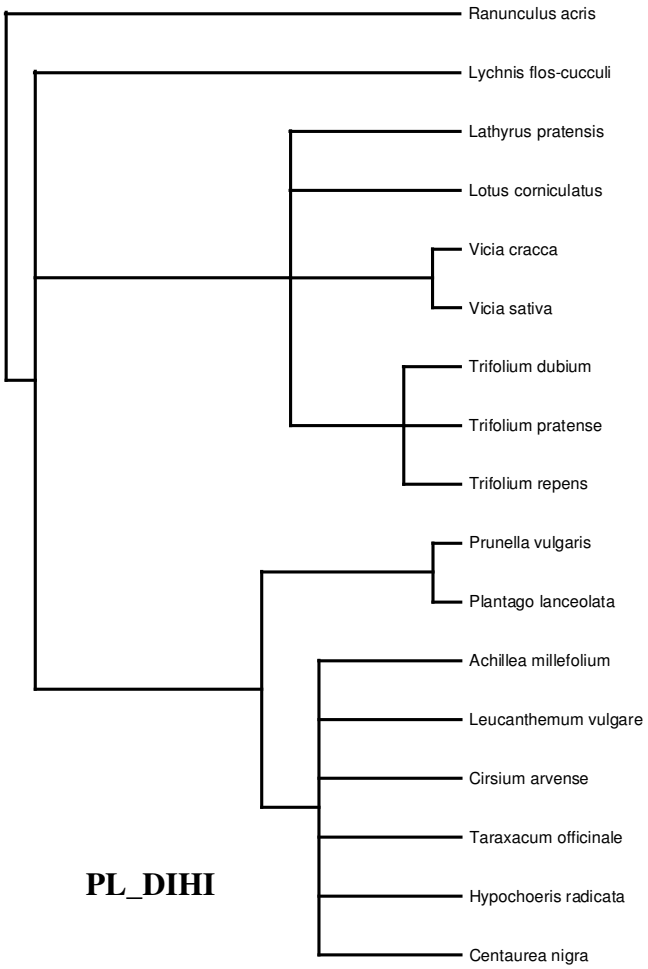



**AN_CROM**
(not included in analyses)

**PL_CROM**

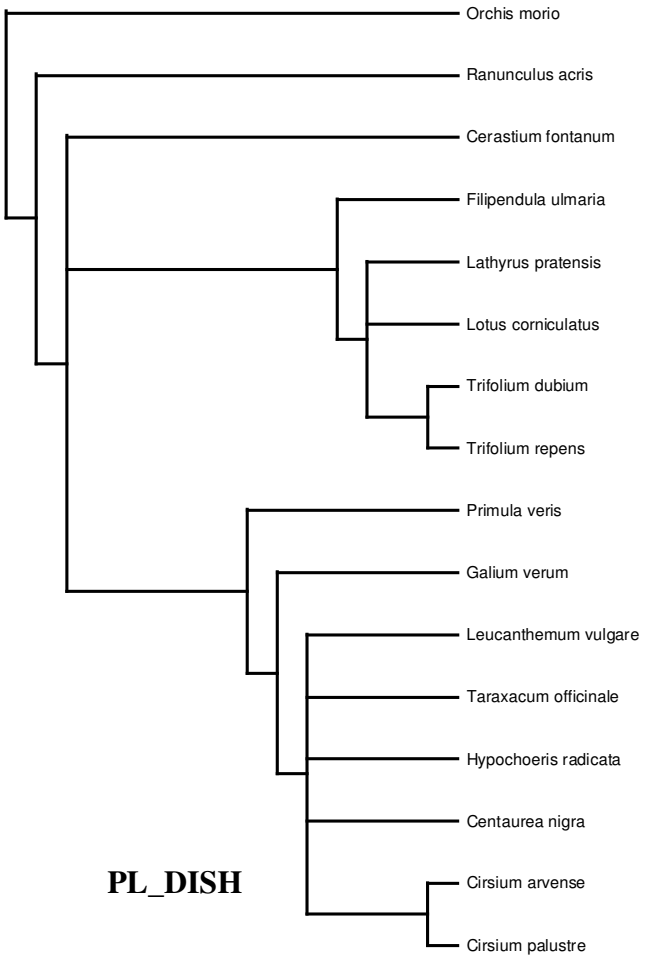
## COMMUNITY DIHI – Pollination



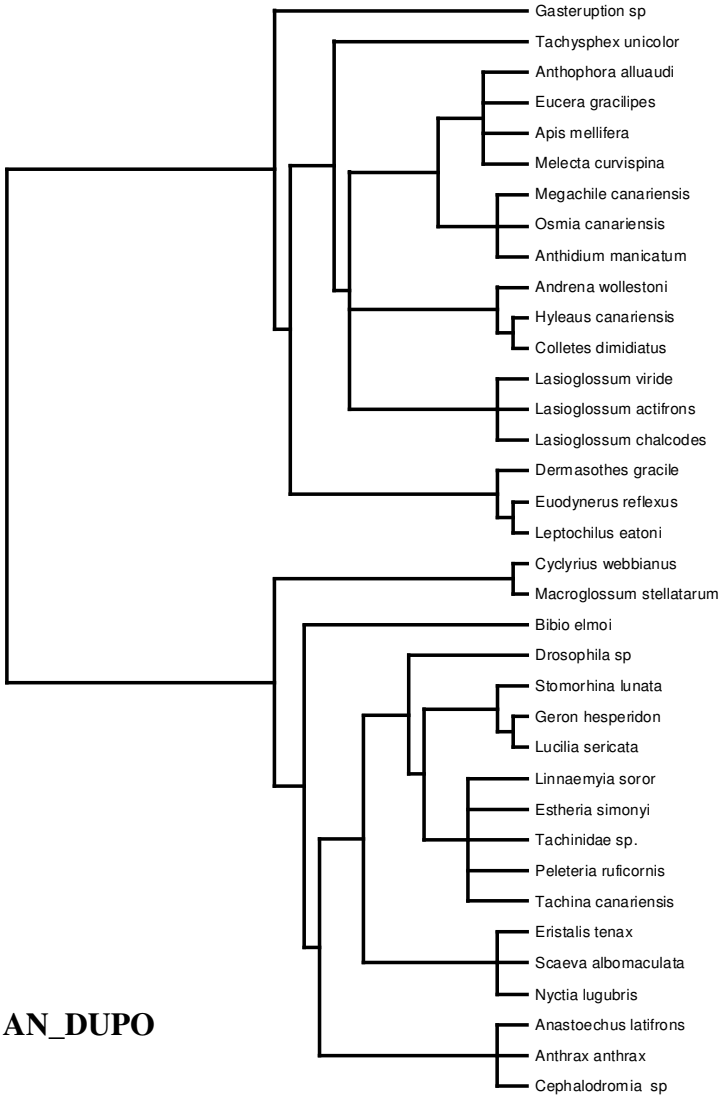
## COMMUNITY DISH – Pollination

**AN_DISH**

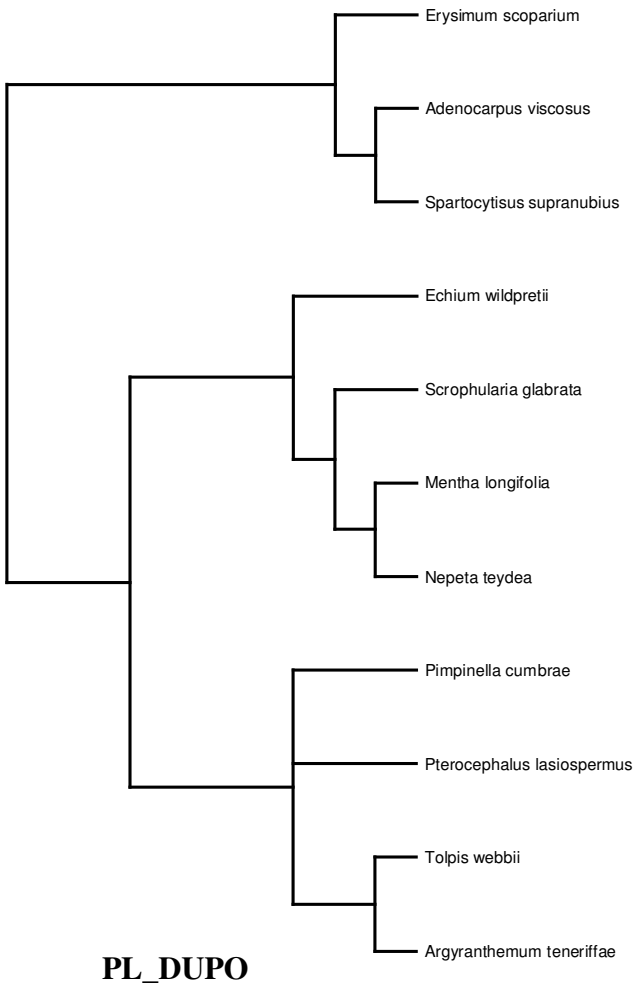



**PL_DISH**

## COMMUNITY DUPO – Pollination



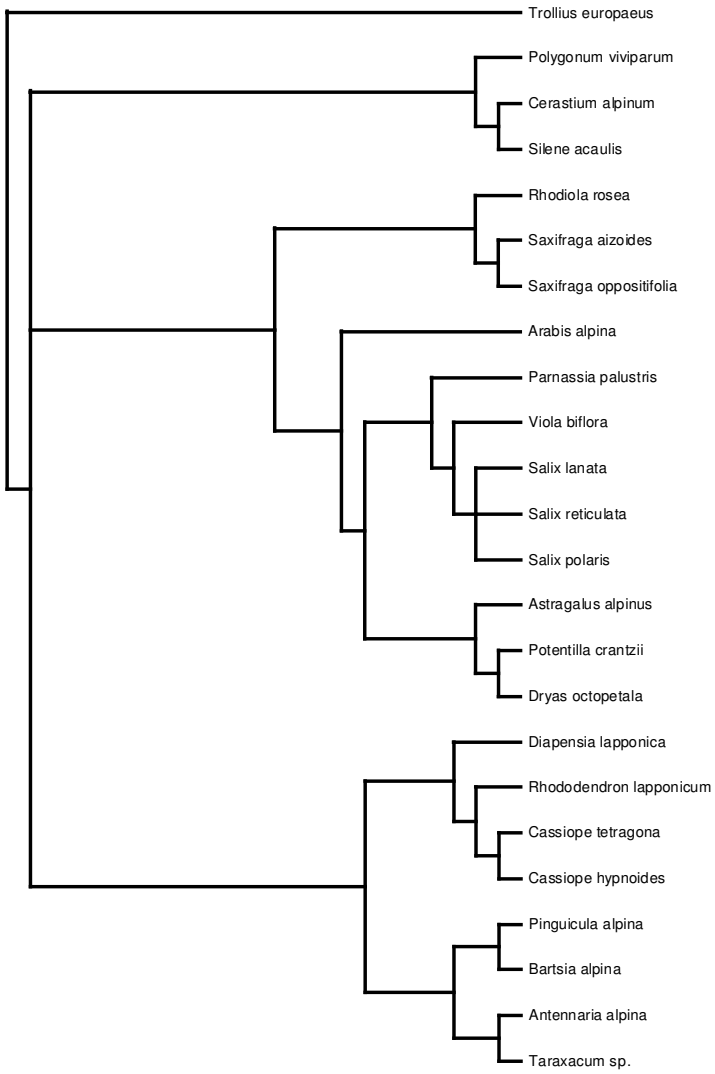

**AN_DUPO**




**PL_DUPO**

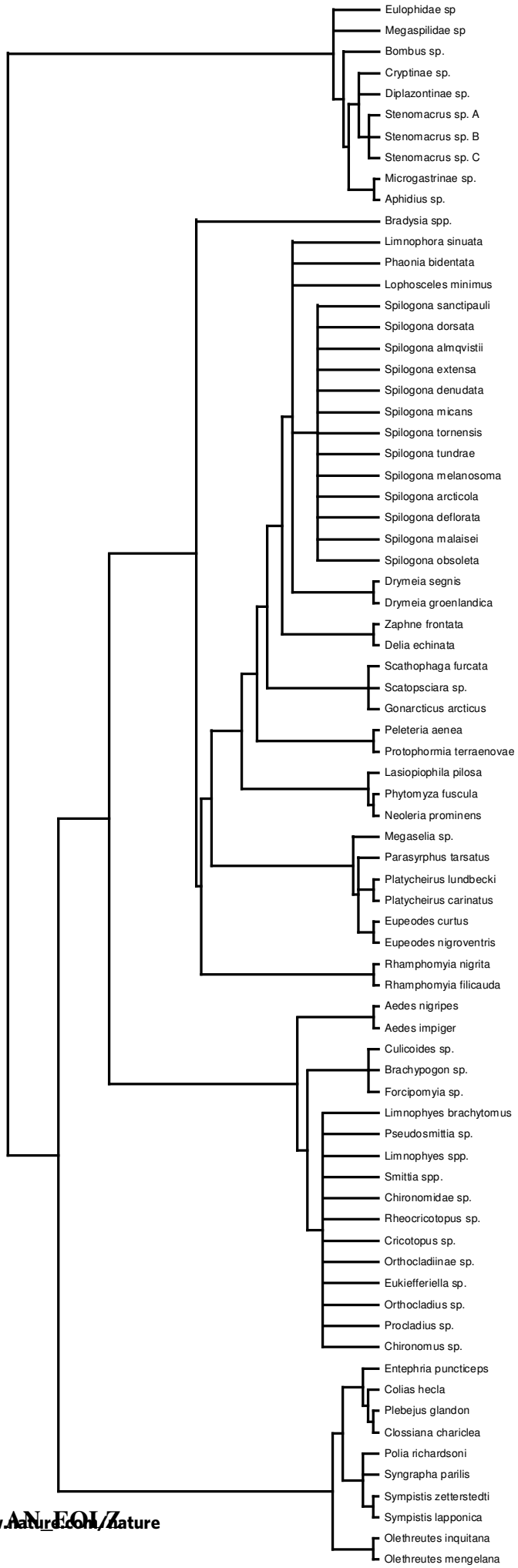
## COMMUNITY EOL – Pollination

**AN_EOL**

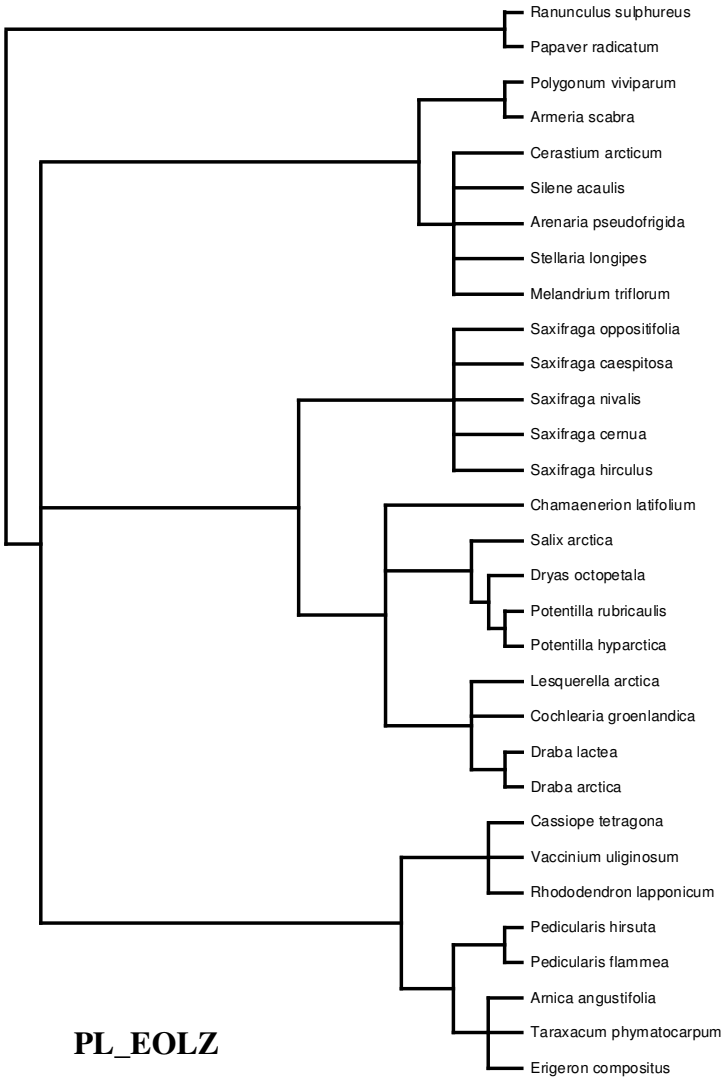



**PL_EOL**

**COMMUNITY EOLZ – Pollination**

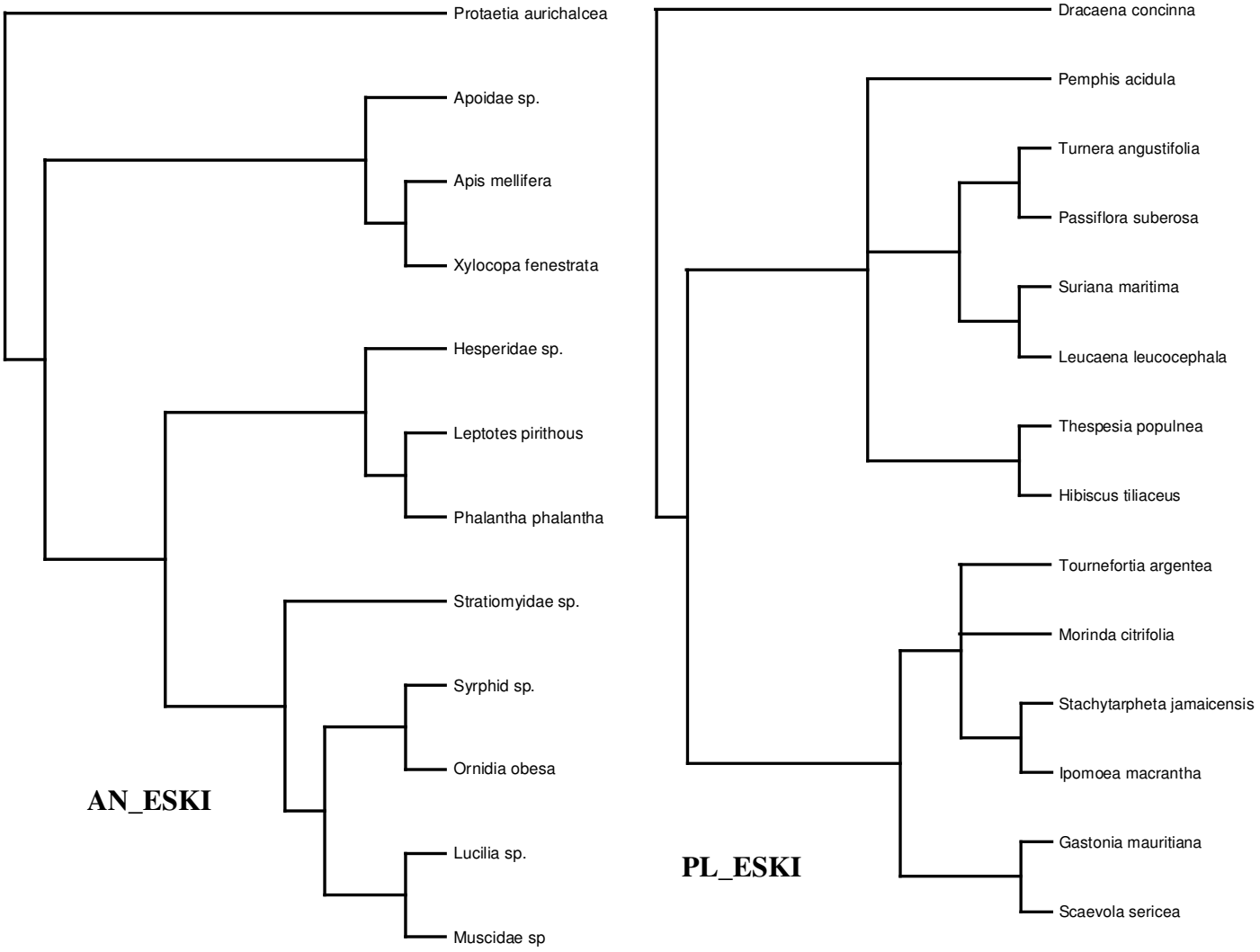



**AN_EOLZ**

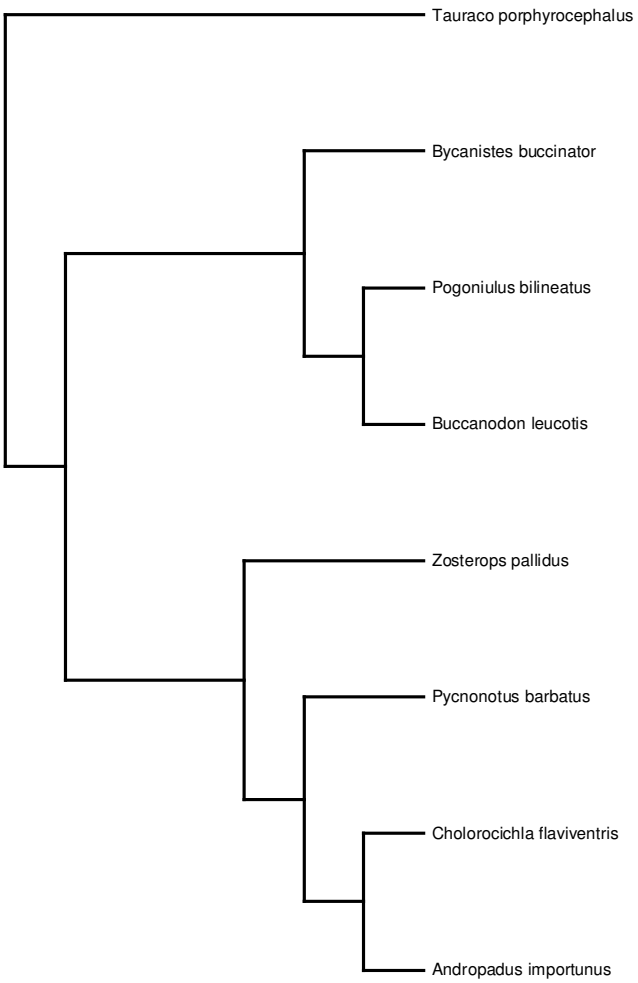



**PL_EOLZ**

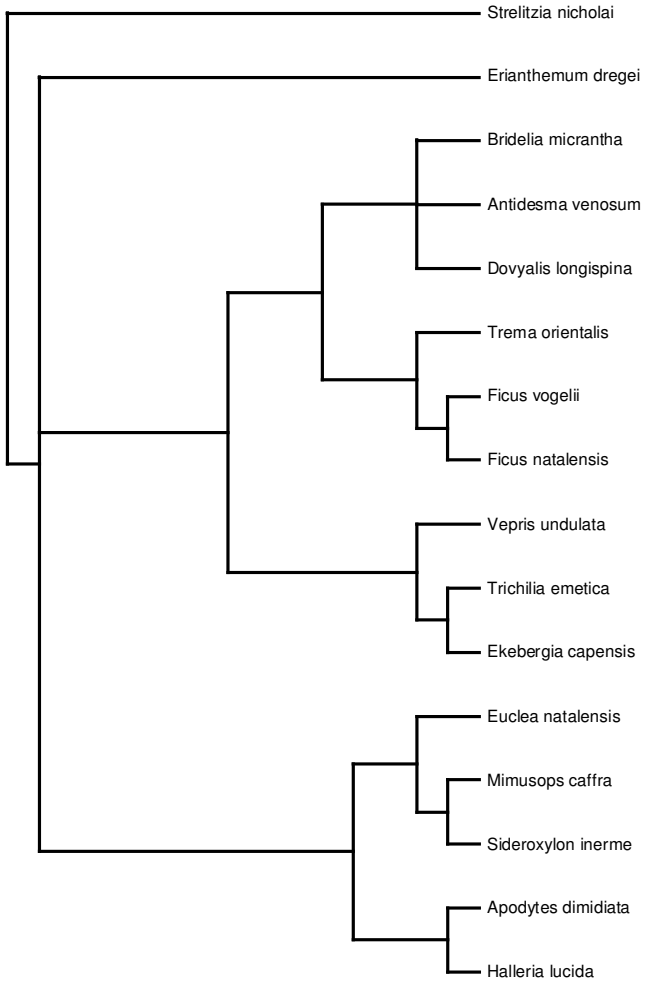
## COMMUNITY ESKI – Pollination



**COMMUNITY FROS – Frugivory**

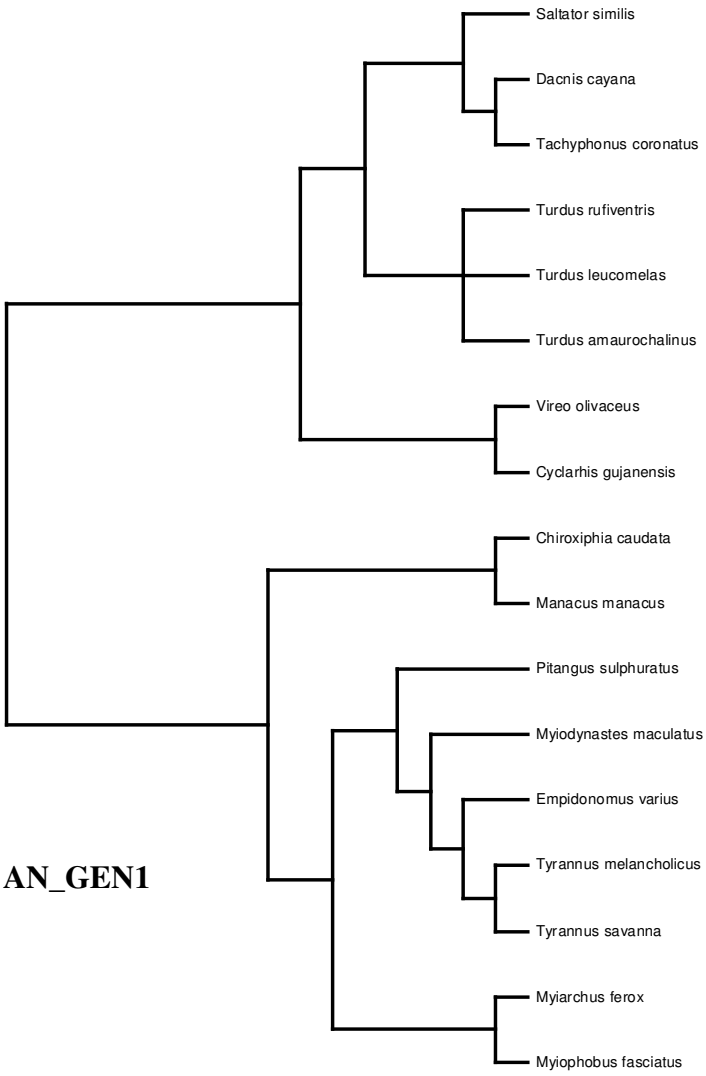



**AN_FROS**
(not included in analyses)

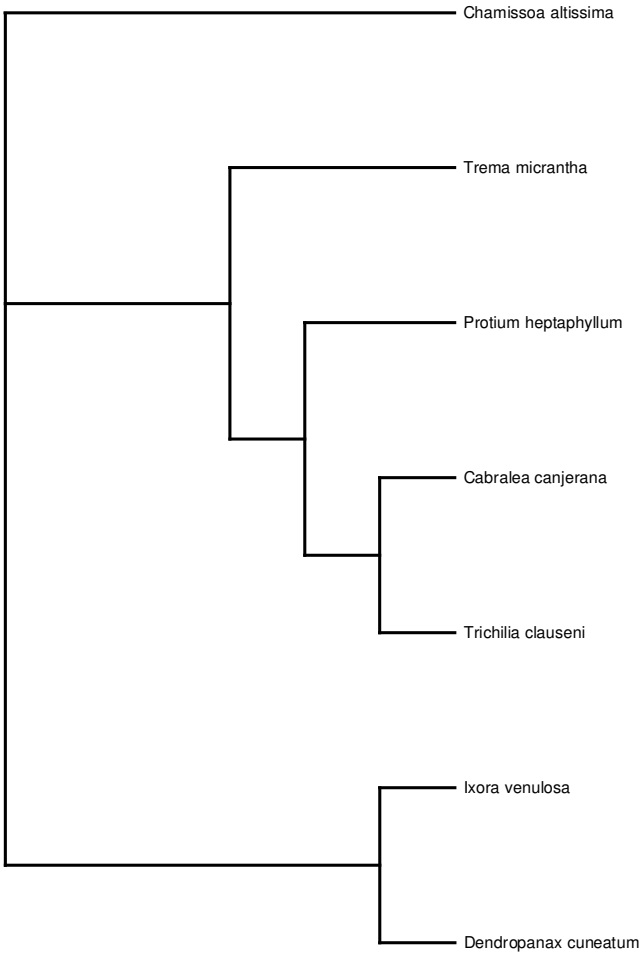



**PL_FROS**

## COMMUNITY GEN1 – Frugivory

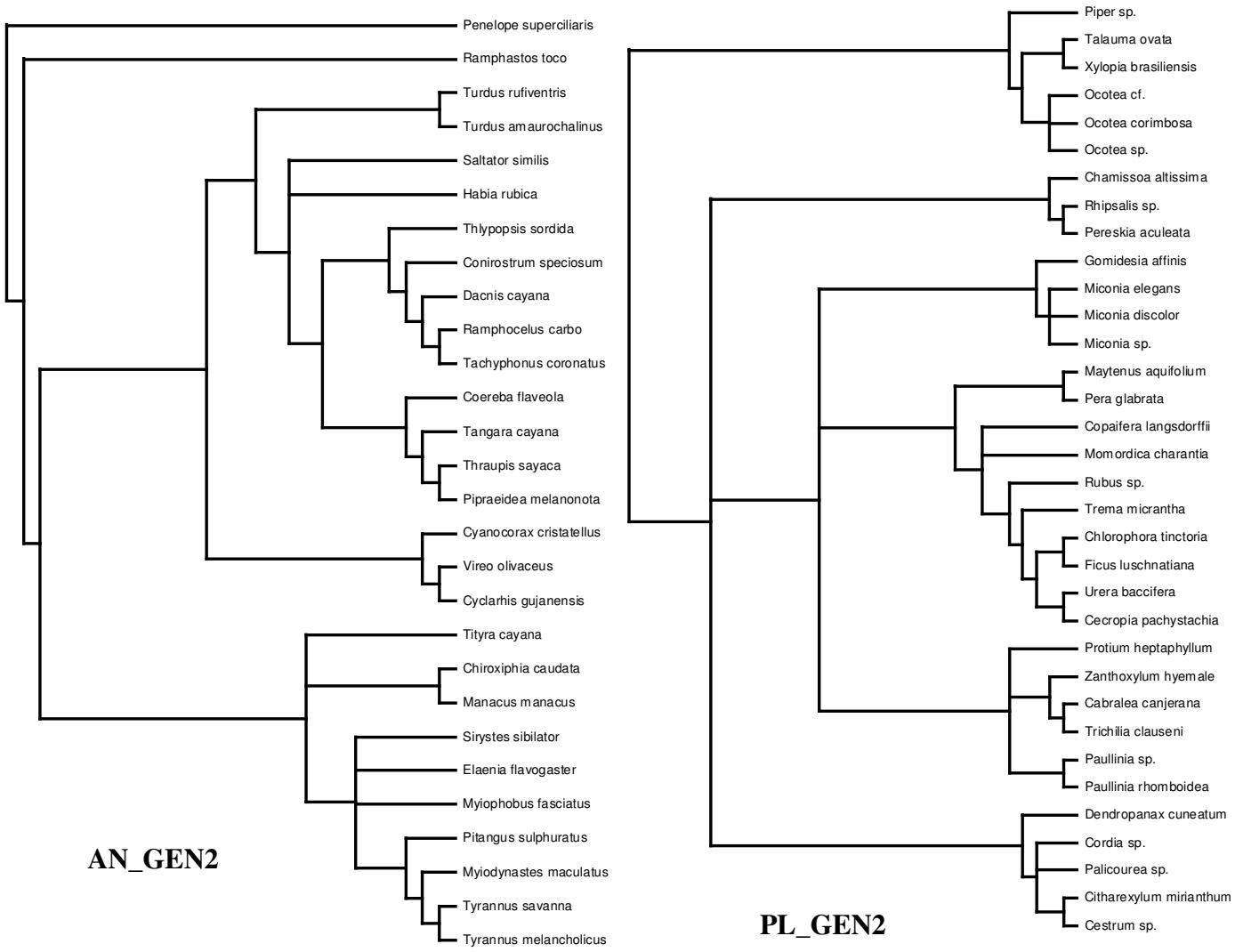



**AN_GEN1**

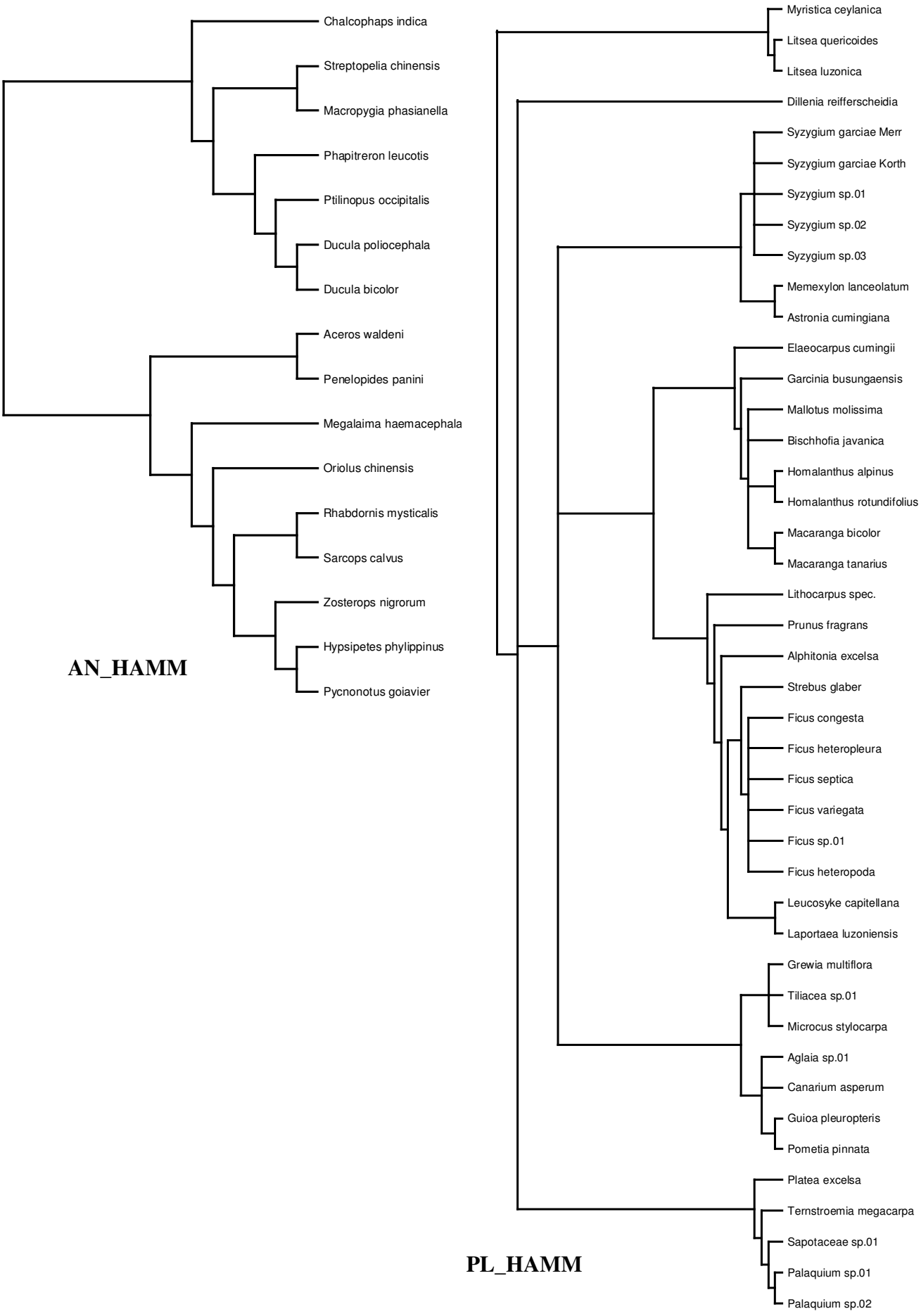


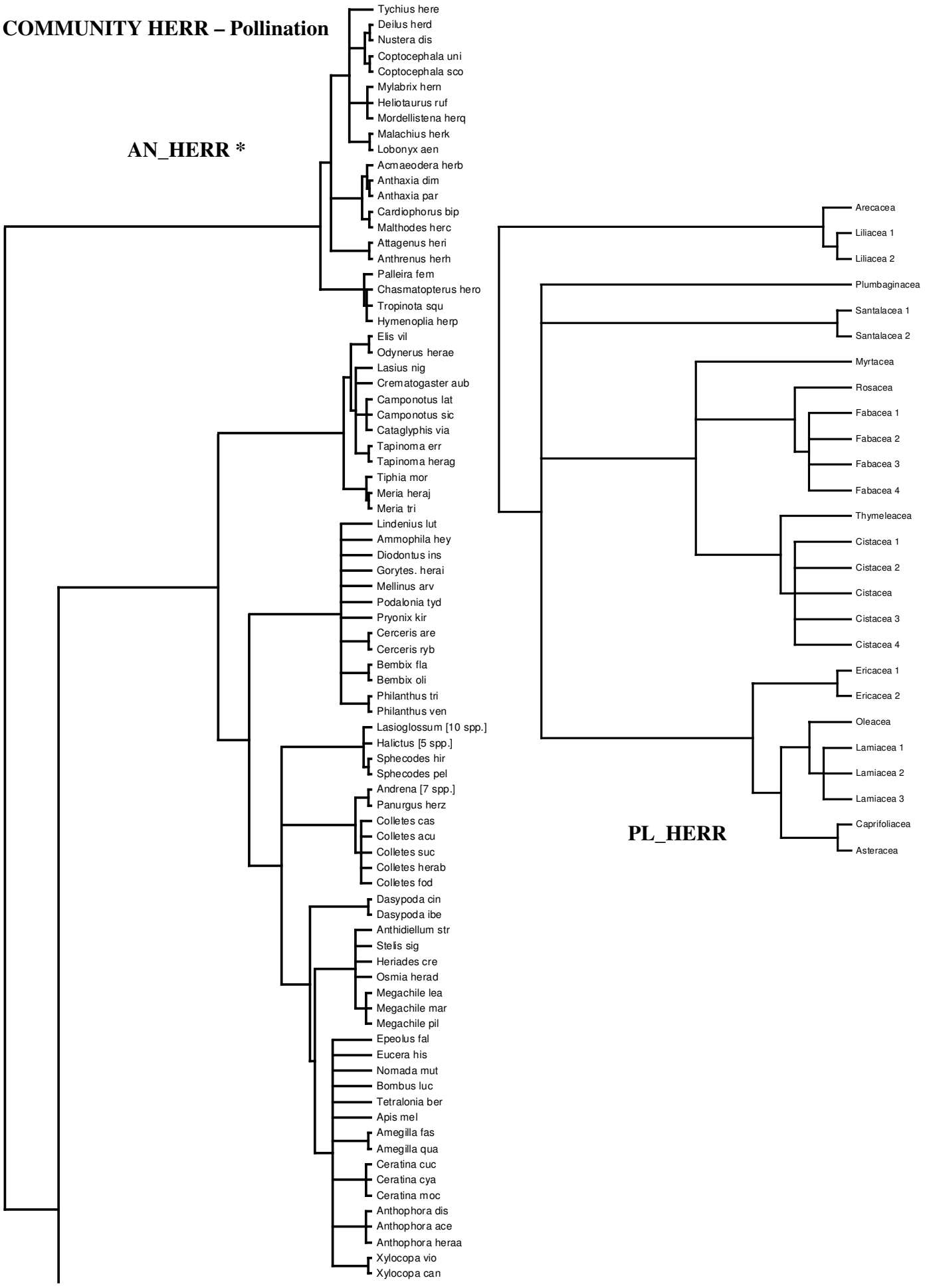

**PL_GEN1**
(not included in analyses)

## COMMUNITY GEN2 – Frugivory



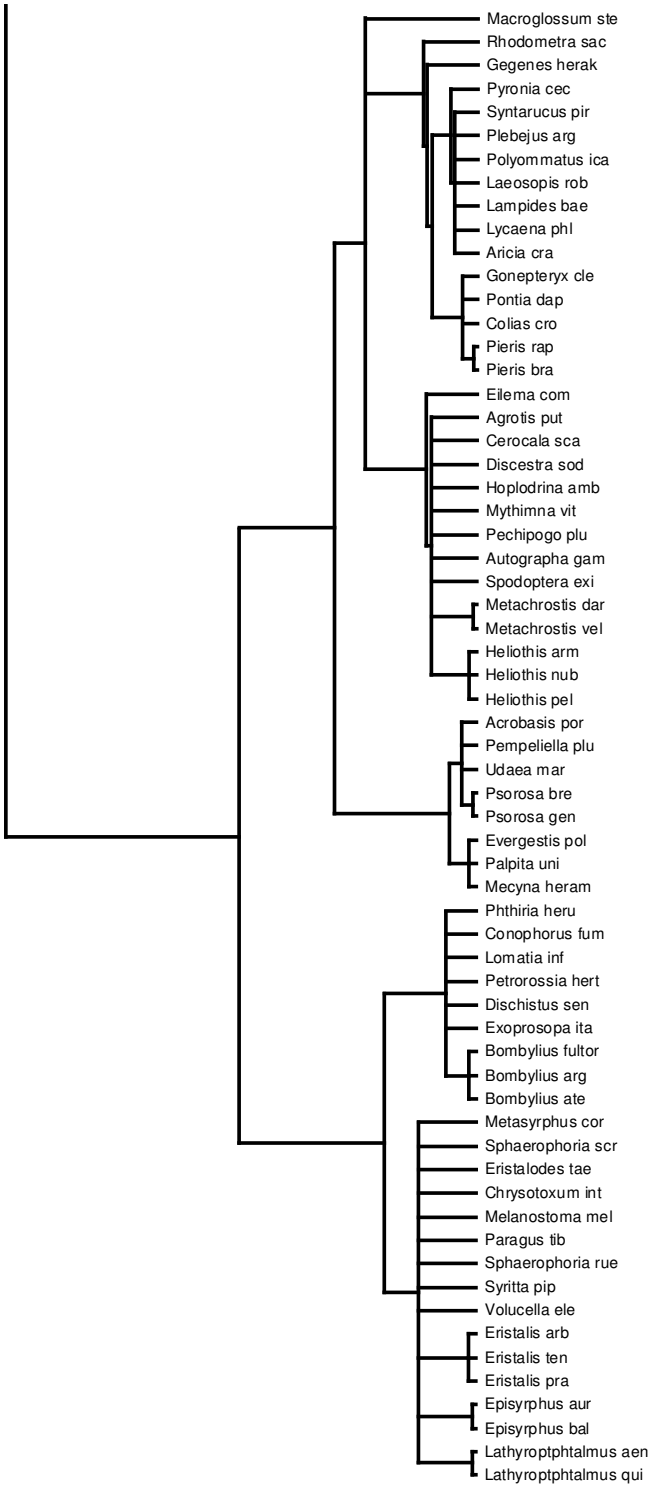
## COMMUNITY HAMM – Frugivory




COMMUNITY HERR – Pollination
AN_HERR *
Tychius here
Deilus herd
Nustera dis
Coptocephala uni
Coptocephala sco
Mylabrix hern
Heliotaurus ruf
Mordellistena herq
Malachius herk
Lobonyx aen
Acmaeodera herb
Anthaxia dim
Anthaxia par
Cardiophorus bip
Malthodes herc
Attagenus heri
Anthrenus herh
Palleira fem
Chasmatopterus hero
Tropinota squ
Hymenoplia herp
Elis vil
Odynerus herae
Lasius nig
Crematogaster aub
Camponotus lat
Camponotus sic
Cataglyphis via
Tapinoma err
Tapinoma herag
Tiphia mor
Meria heraj
Meria tri
Lindenius lut
Ammophila hey
Diodontus ins
Gorytes. herai
Mellinus arv
Podalonia tyd
Pryonix kir
Cerceris are
Cerceris ryb
Bembix fla
Bembix oli
Philanthus tri
Philanthus ven
Lasioglossum [10 spp.]
Halictus [5 spp.]
Sphecodes hir
Sphecodes pel
Andrena [7 spp.]
Panurgus herz
Colletes cas
Colletes acu
Colletes suc
Colletes herab
Colletes fod
Dasypoda cin
Dasypoda ibe
Anthidiellum str
Stelis sig
Heriades cre
Osmia herad
Megachile lea
Megachile mar
Megachile pil
Epeolus fal
Eucera his
Nomada mut
Bombus luc
Tetralonia ber
Apis mel
Amegilla fas
Amegilla qua
Ceratina cuc
Ceratina cya
Ceratina moc
Anthophora dis
Anthophora ace
Anthophora heraa
Xylocopa vio
Xylocopa can
Arecacea
Liliacea 1
Liliacea 2
Plumbaginacea
Santalacea 1
Santalacea 2
Myrtacea
Rosacea
Fabacea 1
Fabacea 2
Fabacea 3
Fabacea 4
Thymeleacea
Cistacea 1
Cistacea 2
Cistacea
Cistacea 3
Cistacea 4
Ericacea 1
Ericacea 2
Oleacea
Lamiacea 1
Lamiacea 2
Lamiacea 3
Caprifoliacea
Asteracea
PL_HERR

*next page*

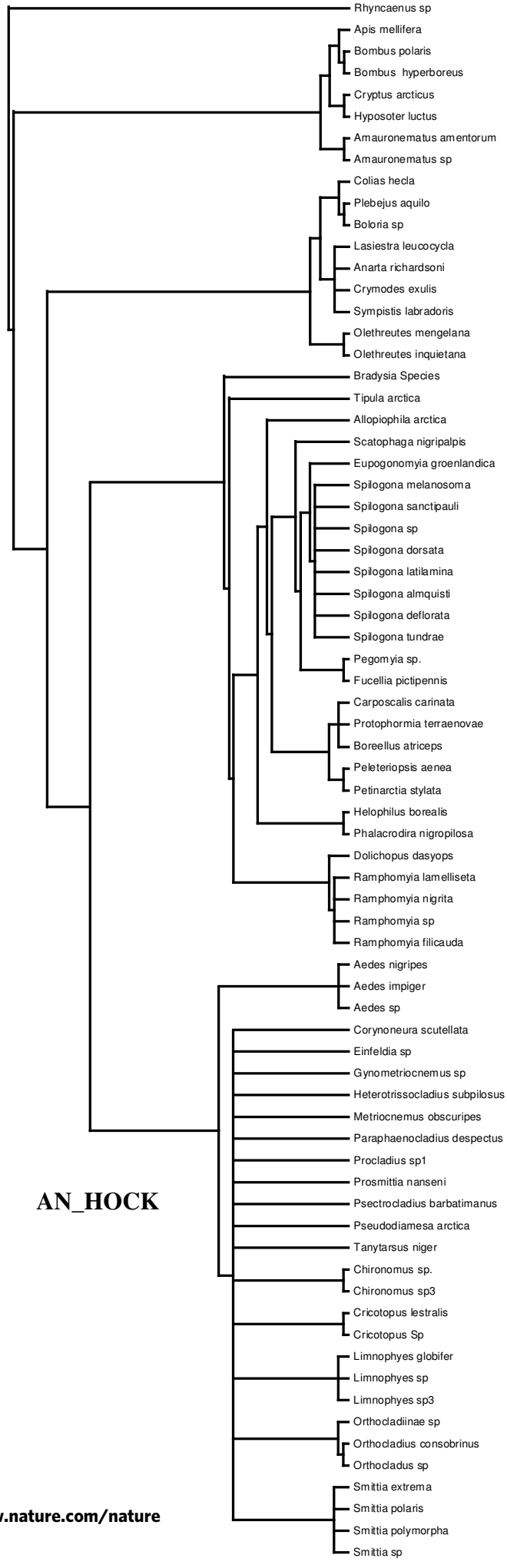
Community HERR *(continued)*



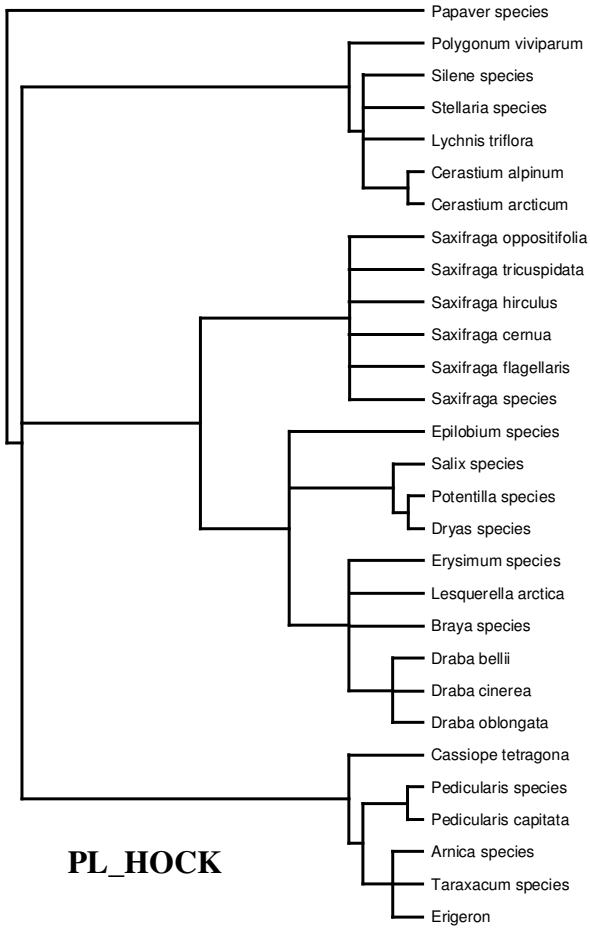

**AN_HERR ***

***** 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

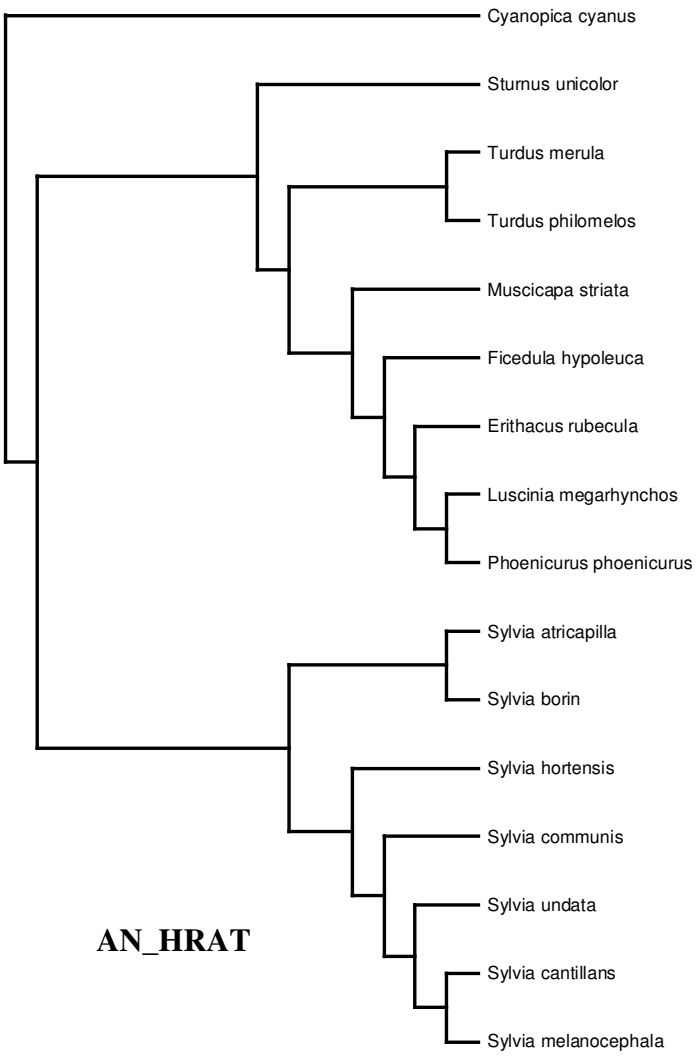


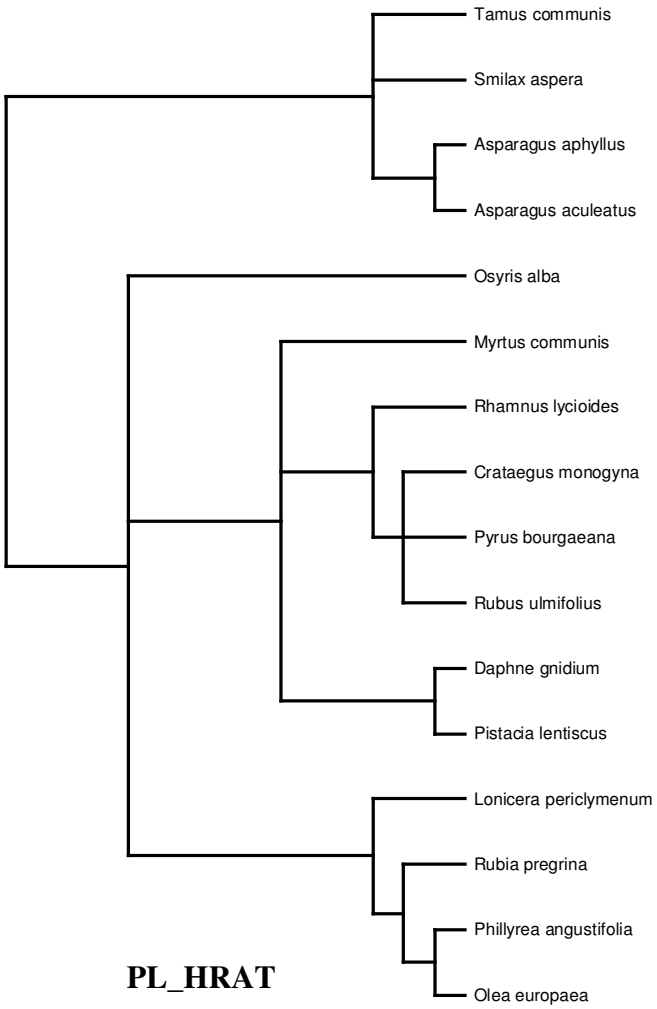

**AN_HOCK**



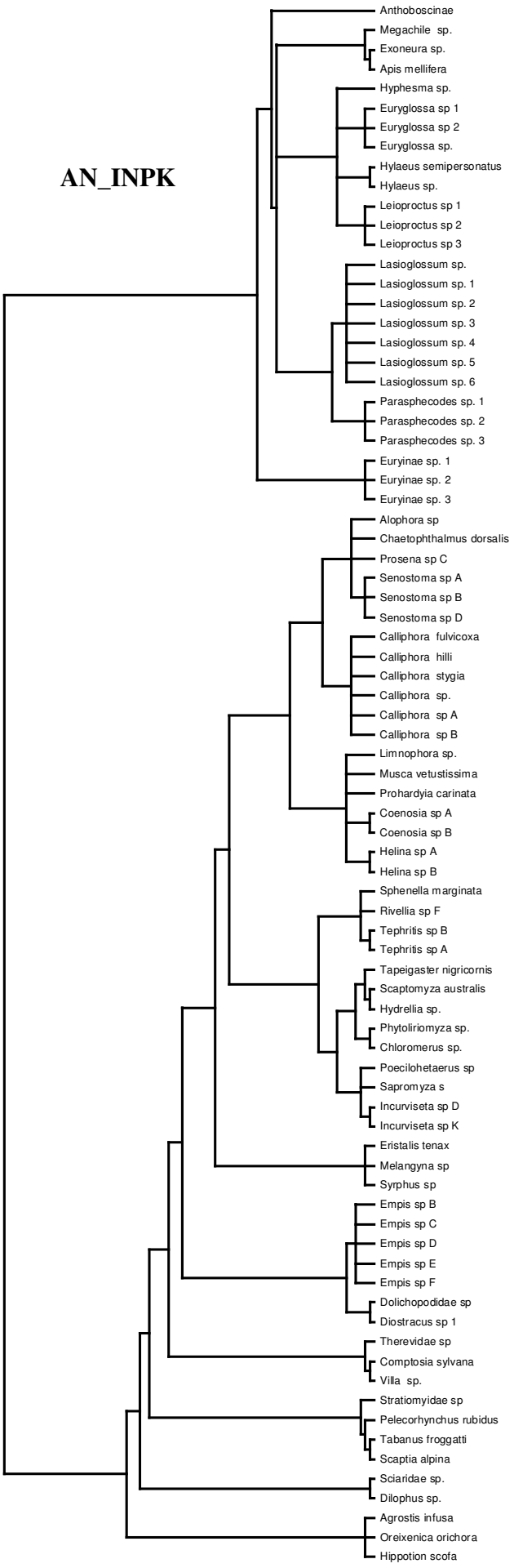

**PL_HOCK**

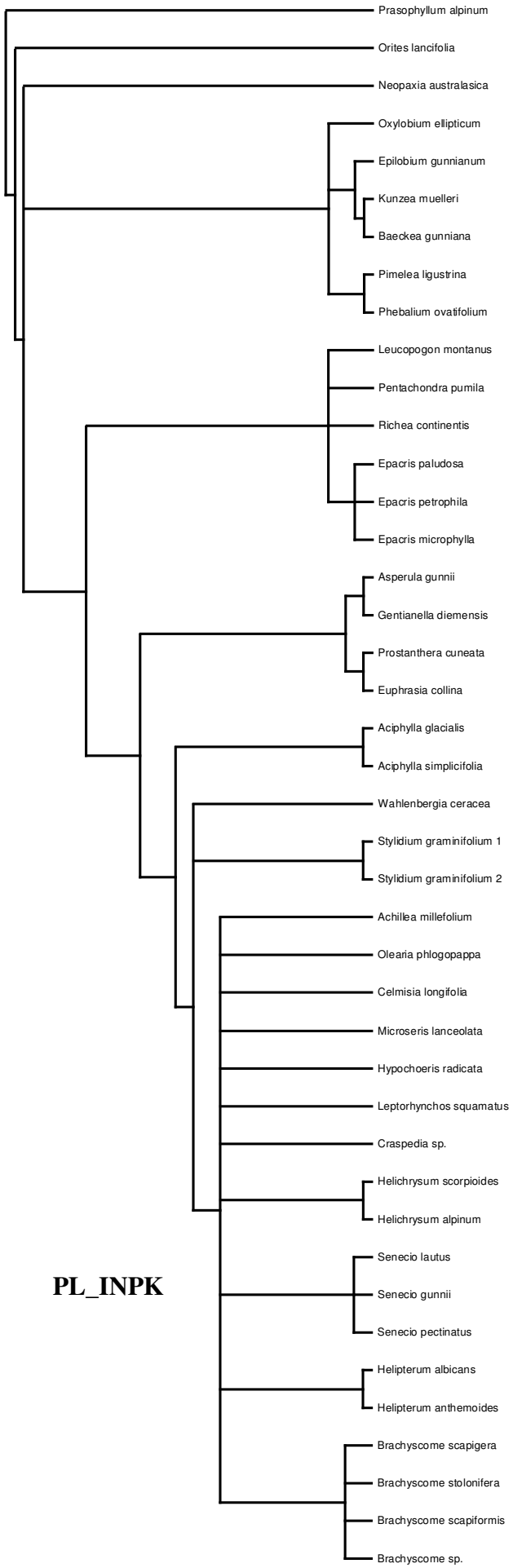
## COMMUNITY HRAT – Frugivory



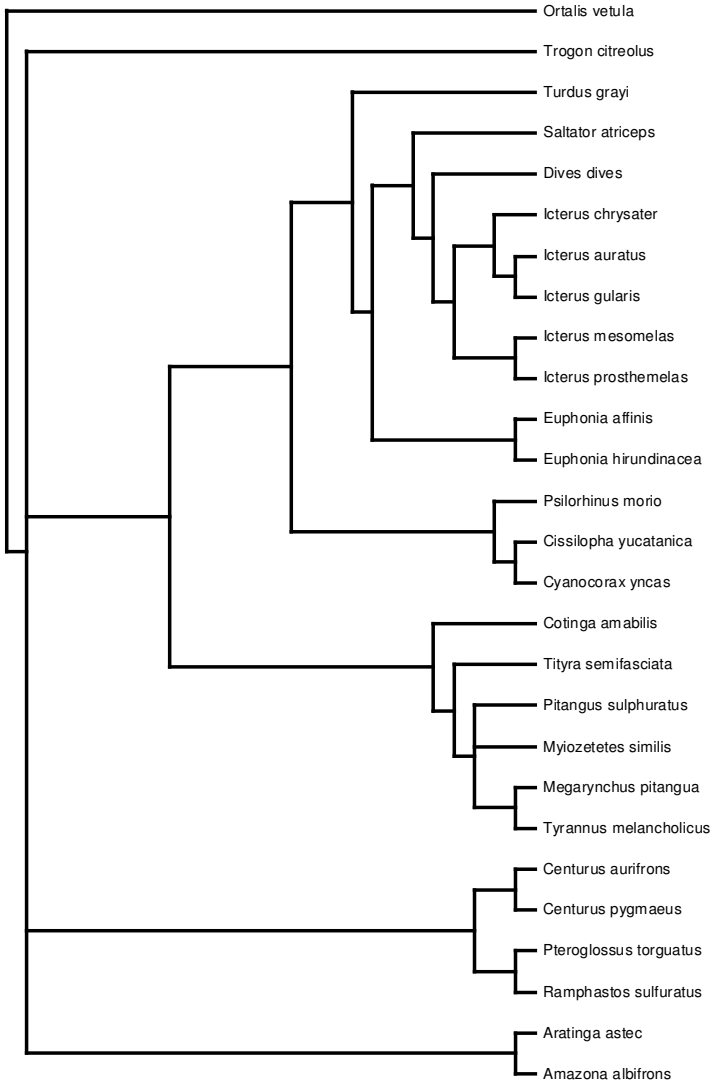



## COMMUNITY INPK – Pollination

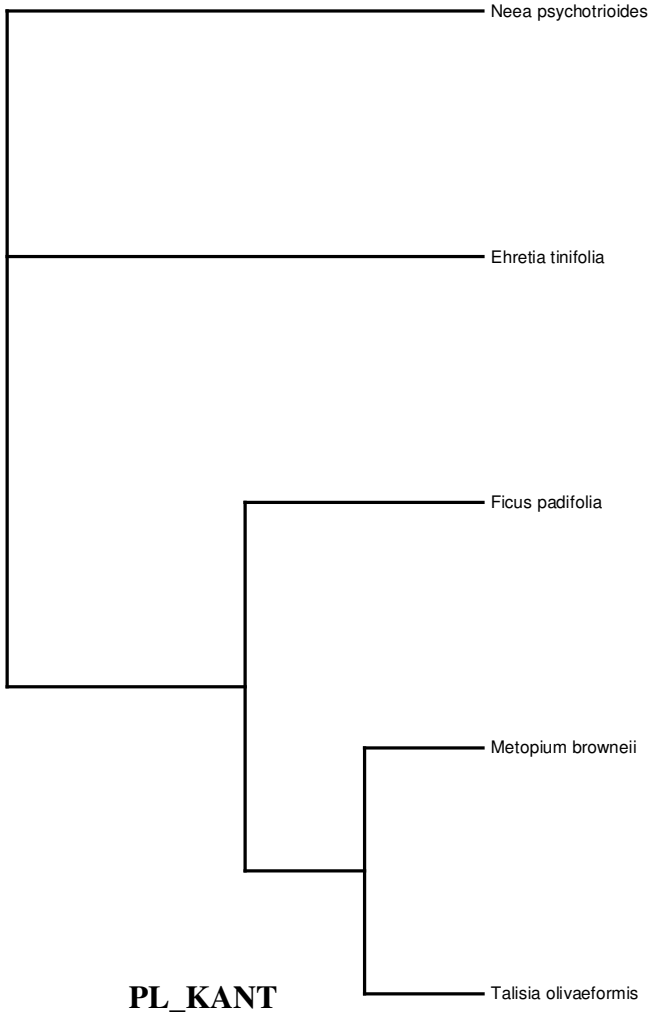


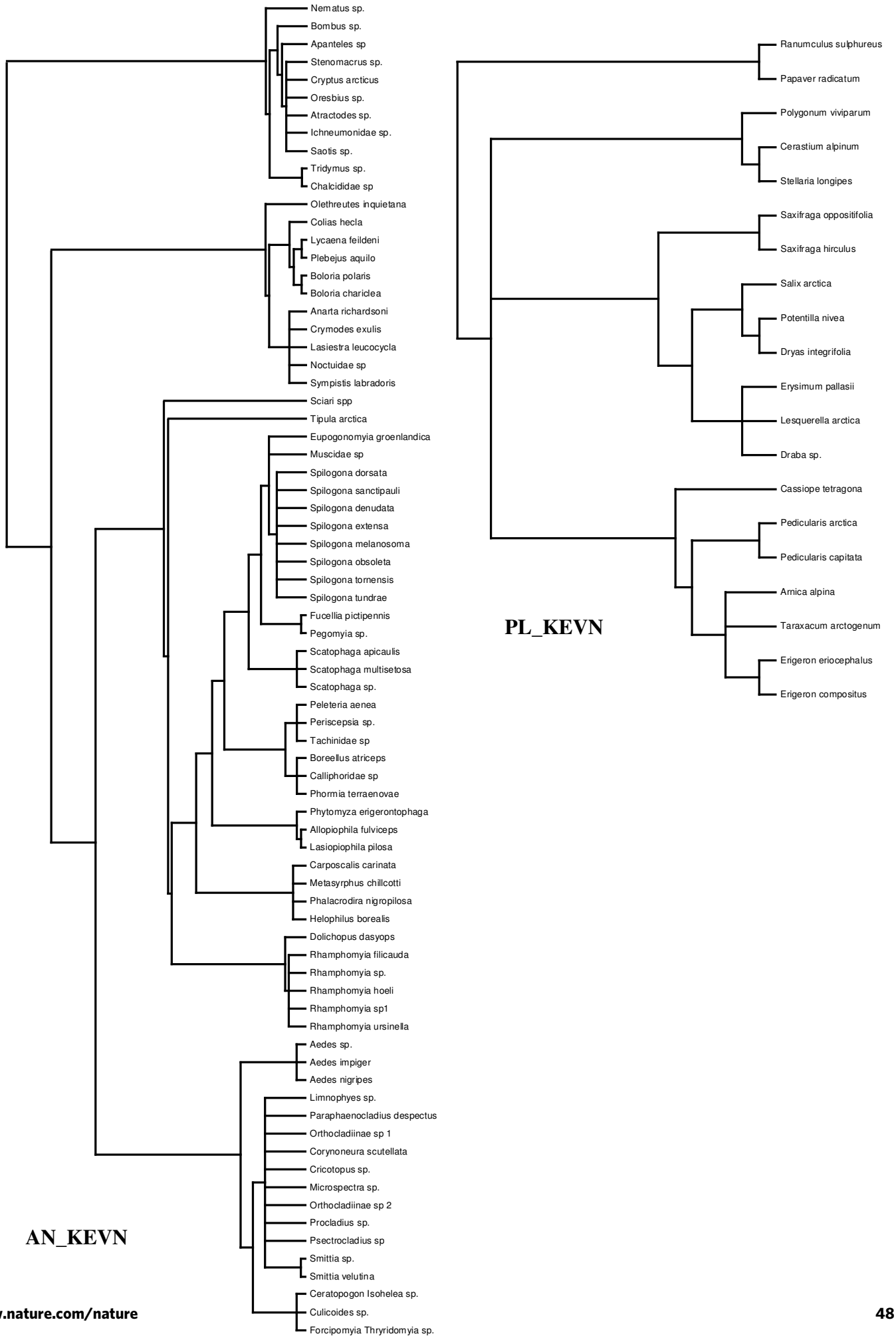
**COMMUNITY KANT – Frugivory**



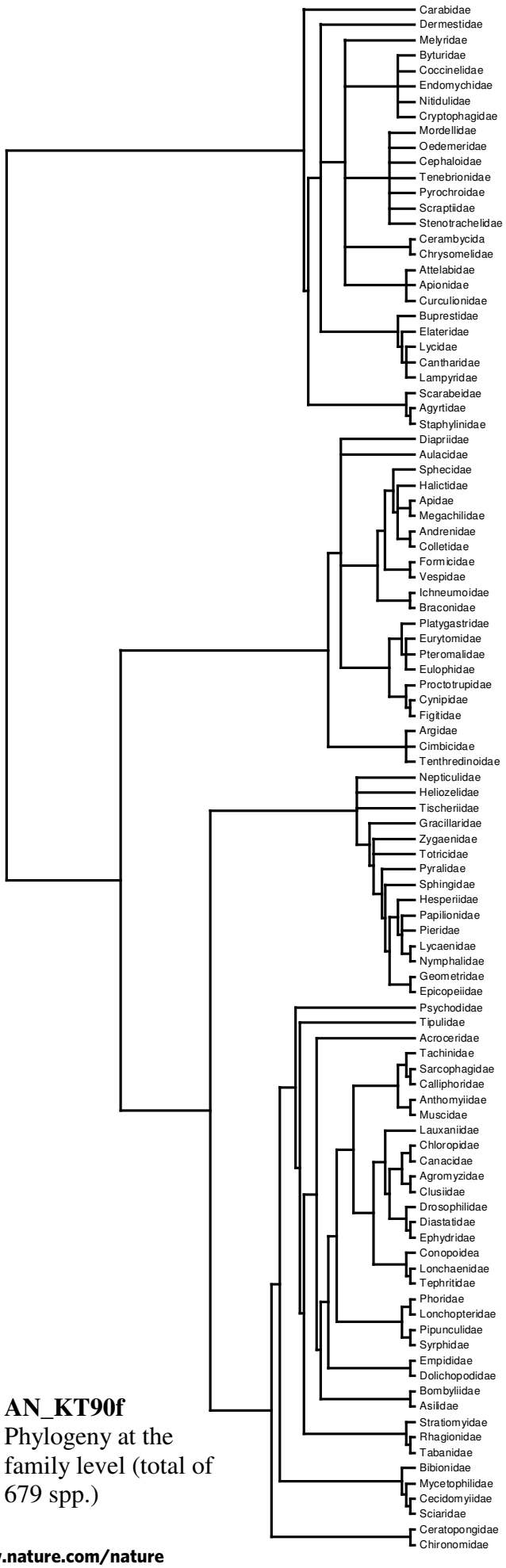

**AN_KANT**



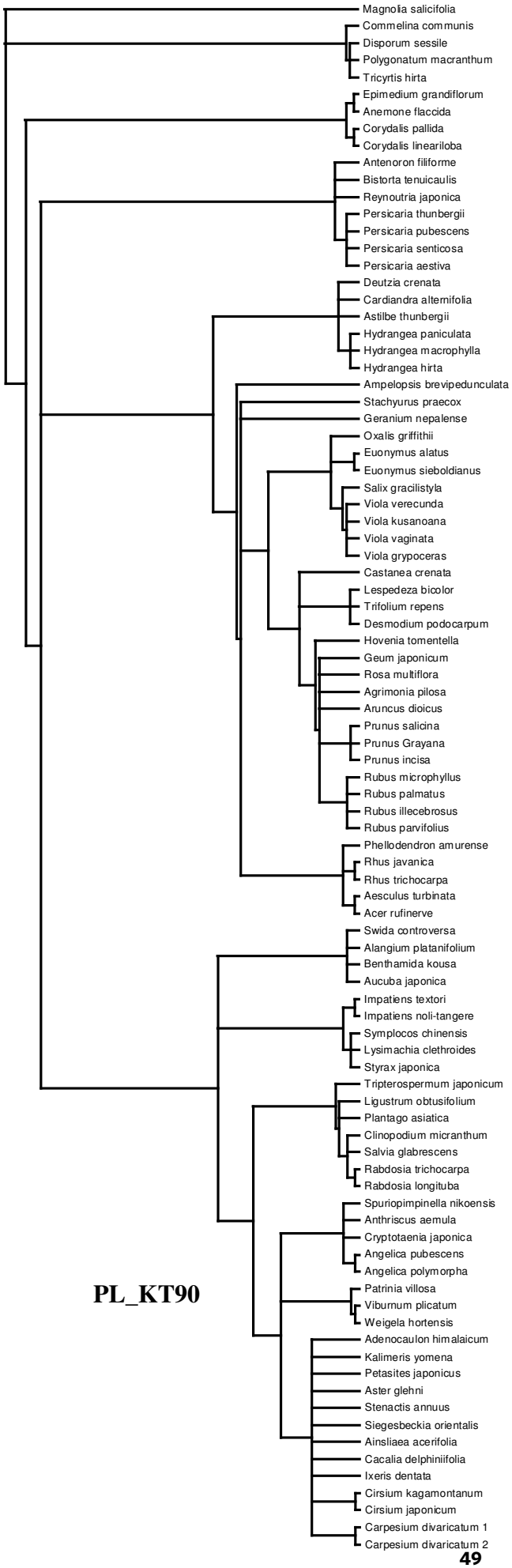

**PL_KANT**
(not included in analyses)


COMMUNITY KEVN – Pollination
Nematus sp.
Bombus sp.
Apanteles sp
Stenomacrus sp.
Cryptus arcticus
Oresbius sp.
Atractodes sp.
Ichneumonidae sp.
Saotis sp.
Tridymus sp.
Chalcididae sp
Olethreutes inquietana
Colias hecla
Lycaena feildeni
Plebejus aquilo
Boloria polaris
Boloria chariclea
Anarta richardsoni
Crymodes exulis
Lasiestra leucocycla
Noctuidae sp
Sympistis labradoris
Sciari spp
Tipula arctica
Eupogonomyia groenlandica
Muscidae sp
Spilogona dorsata
Spilogona sanctipauli
Spilogona denudata
Spilogona extensa
Spilogona melanosoma
Spilogona obsoleta
Spilogona tornensis
Spilogona tundrae
Fucellia pictipennis
Pegomyia sp.
Scatophaga apicaulis
Scatophaga multisetosa
Scatophaga sp.
Peleteria aenea
Periscepsia sp.
Tachinidae sp
Boreellus atriceps
Calliphoridae sp
Phormia terraenovae
Phytomyza erigerontophaga
Allopiophila fulviceps
Lasiopiophila pilosa
Carposcalis carinata
Metasyrphus chillcotti
Phalacrodira nigropilosa
Helophilus borealis
Dolichopus dasyops
Rhamphomyia filicauda
Rhamphomyia sp.
Rhamphomyia hoeli
Rhamphomyia sp1
Rhamphomyia ursinella
Aedes sp.
Aedes impiger
Aedes nigripes
Limnophyes sp.
Paraphaenocladius despectus
Orthocladiinae sp 1
Corynoneura scutellata
Cricotopus sp.
Microspectra sp.
Orthocladiinae sp 2
Procladius sp.
Psectrocladius sp
Smittia sp.
Smittia velutina
Ceratopogon Isohelea sp.
Culicoides sp.
Forcipomyia Thryridomyia sp.
AN_KEVN
Ranumculus sulphureus
Papaver radicatum
Polygonum viviparum
Cerastium alpinum
Stellaria longipes
Saxifraga oppositifolia
Saxifraga hirculus
Salix arctica
Potentilla nivea
Dryas integrifolia
Erysimum pallasii
Lesquerella arctica
Draba sp.
Cassiope tetragona
Pedicularis arctica
Pedicularis capitata
Arnica alpina
Taraxacum arctogenum
Erigeron eriocephalus
Erigeron compositus
PL_KEVN

## COMMUNITY KT90 – Pollination

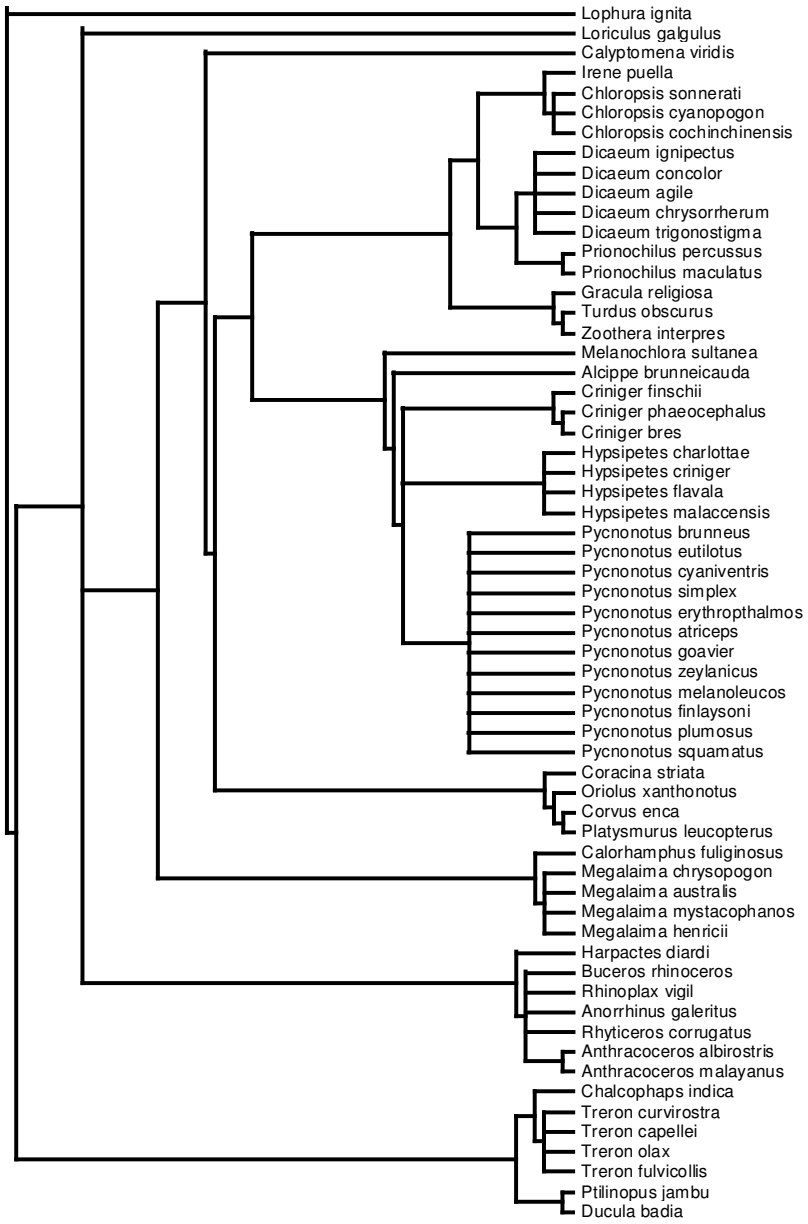



**AN_KT90f**
Phylogeny at the family level (total of 679 spp.)




**PL_KT90**

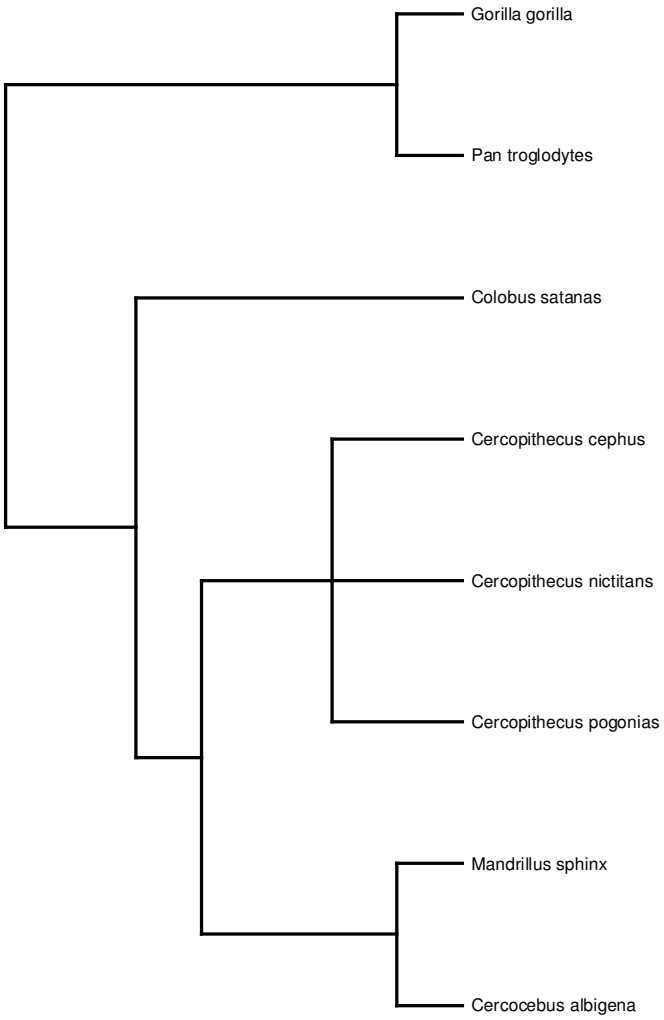
**COMMUNITY LAMB – Frugivory**



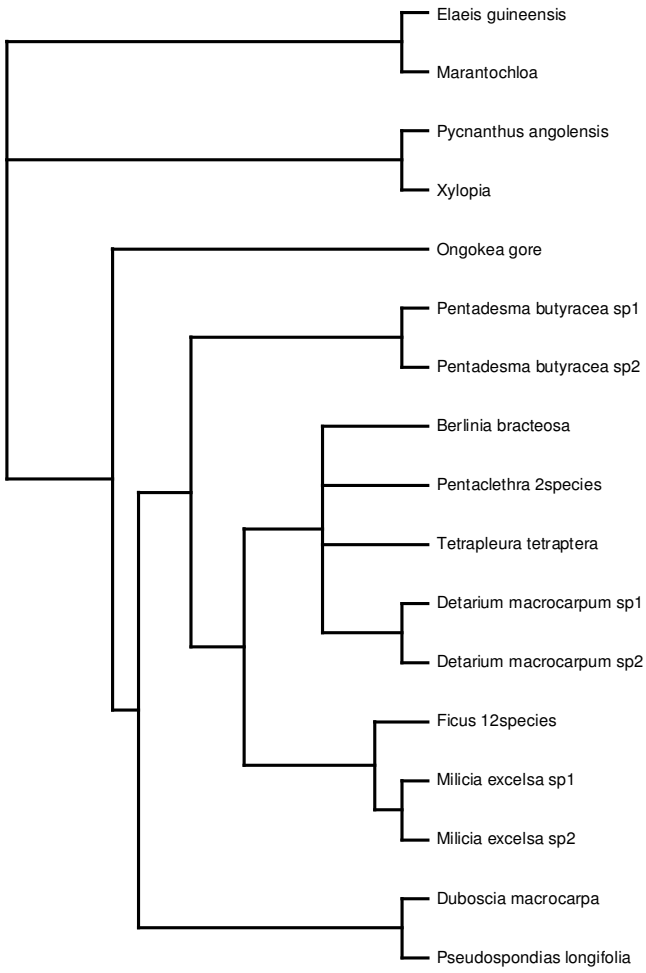

**AN_LAMB**

**PL_LAMB not available**
(not included in analyses)

**COMMUNITY LOPE – Frugivory**

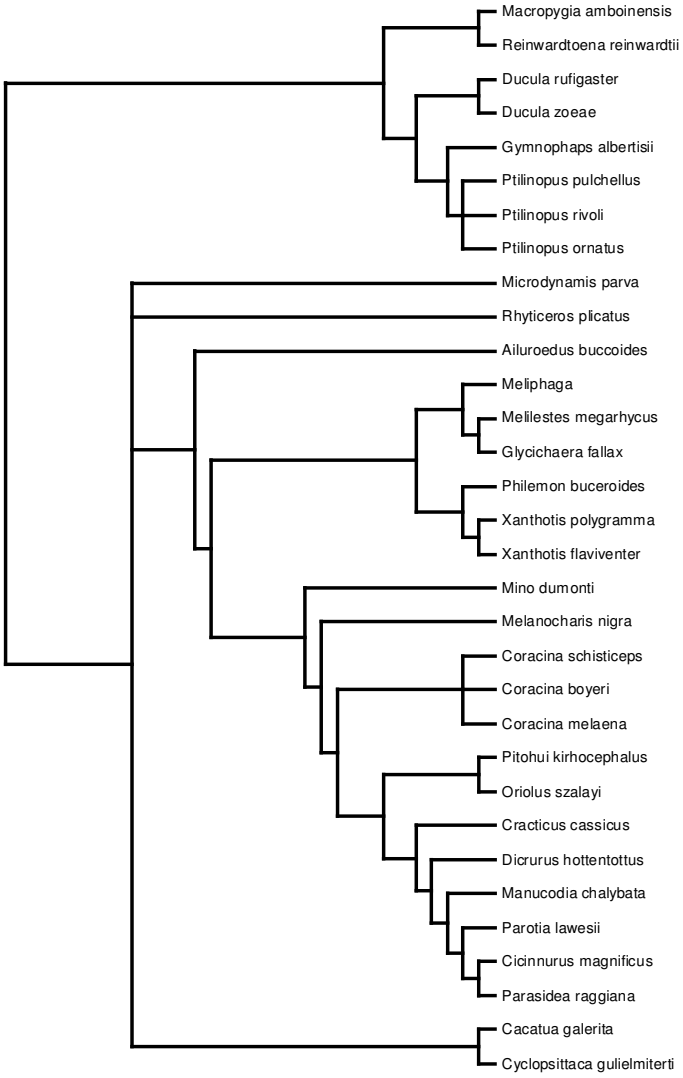



**AN_LOPE**
(Primate phylogeny, not included in analyses)

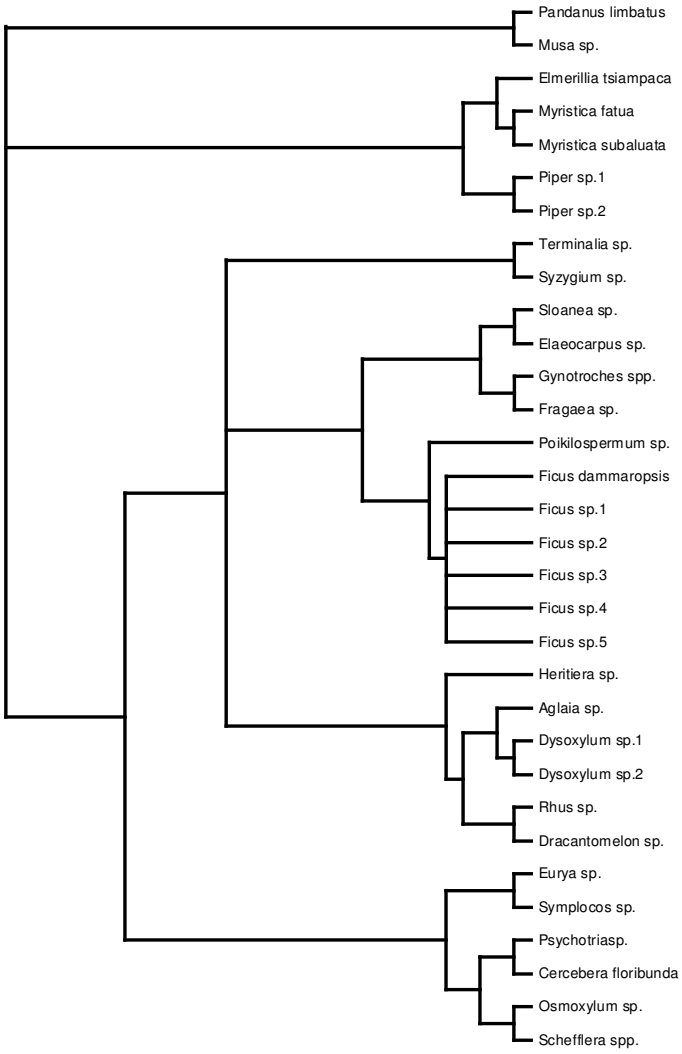



**PL_LOPE**

## COMMUNITY MACK – Frugivory

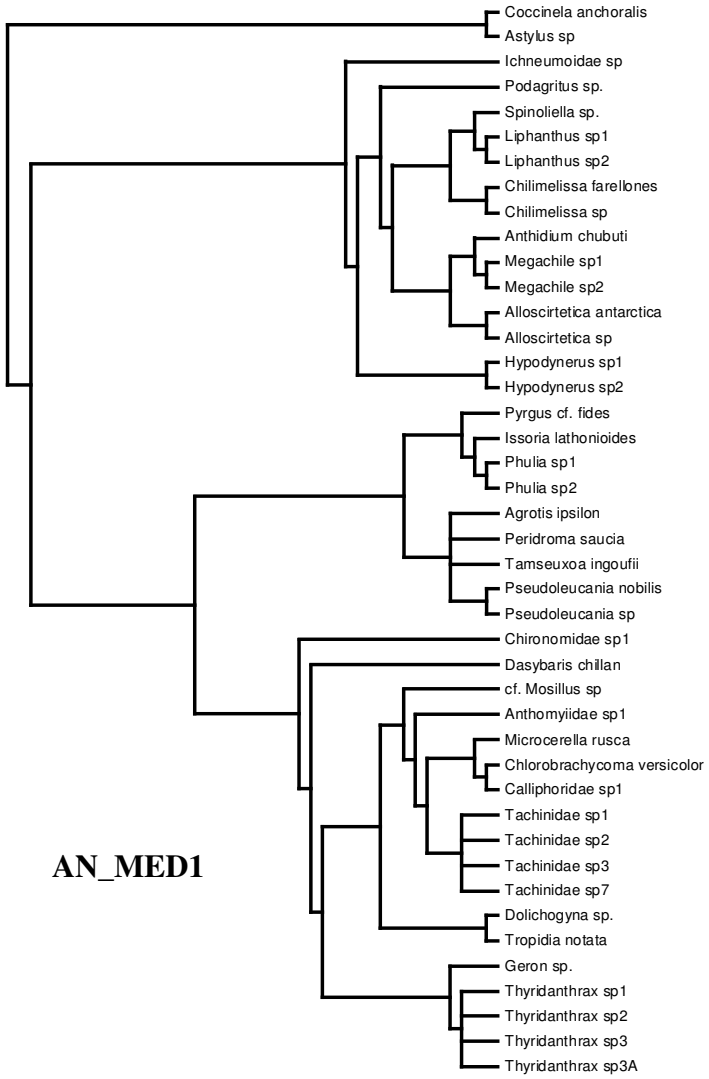


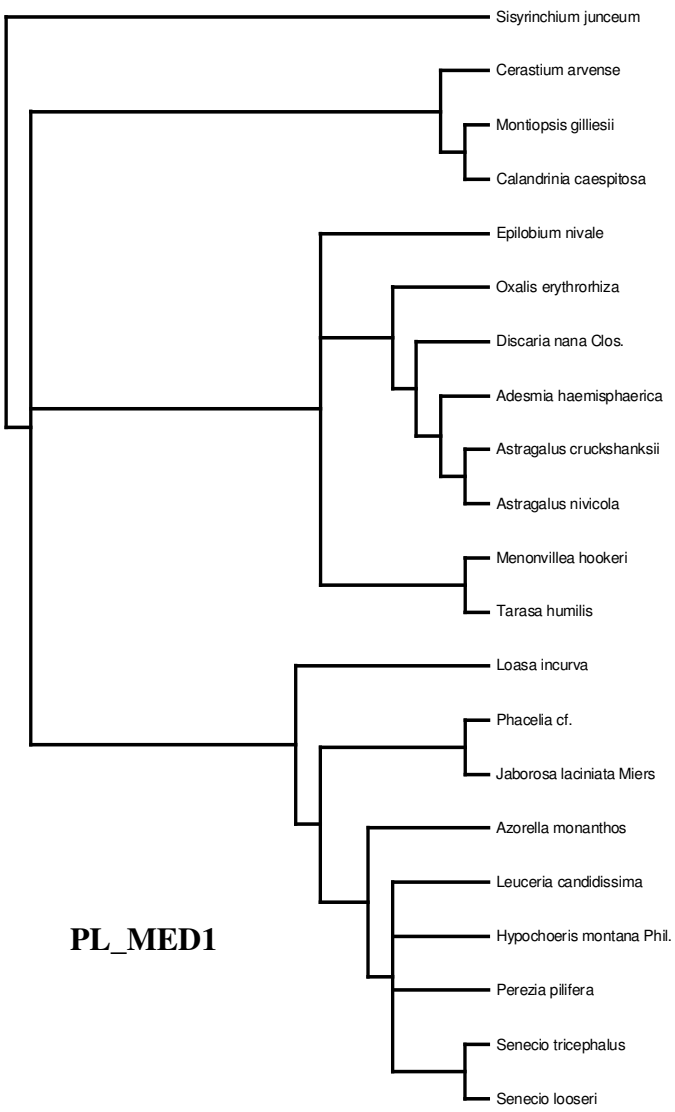

AN_MACK



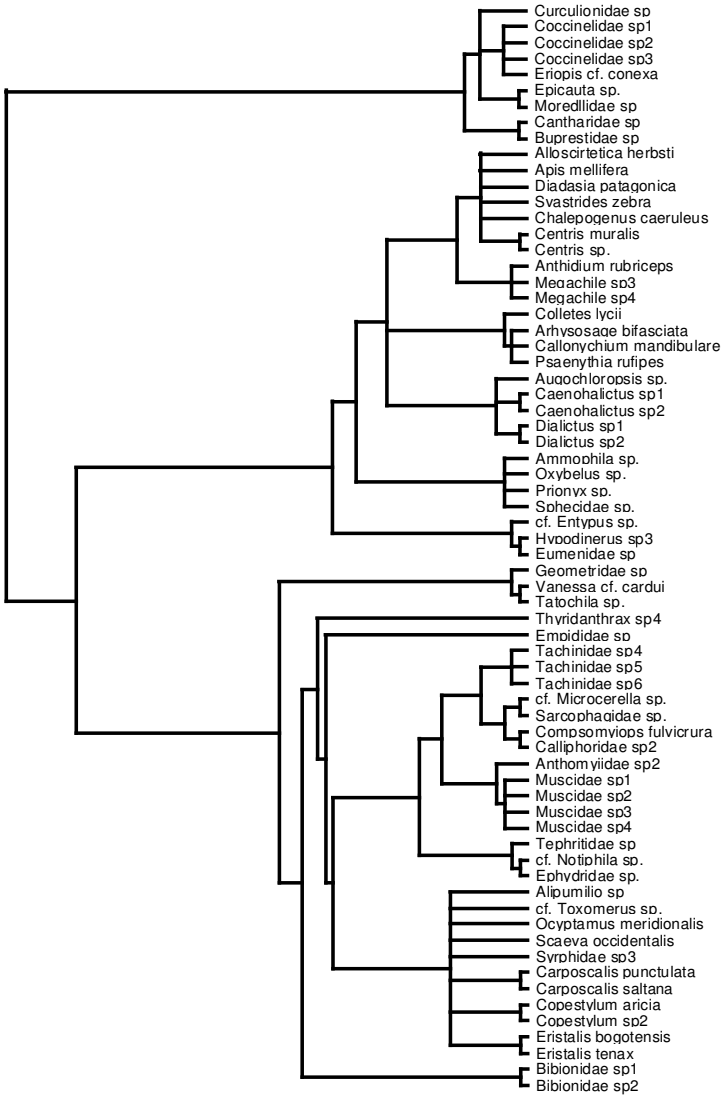

PL_MACK

## COMMUNITY MED1 – Pollination

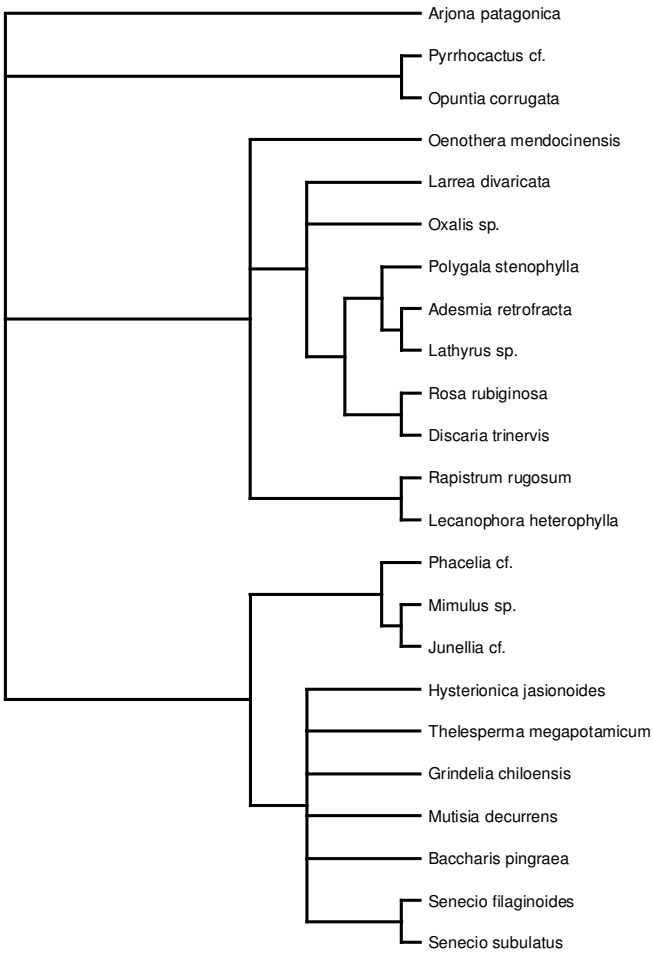


## COMMUNITY MED2 – Pollination

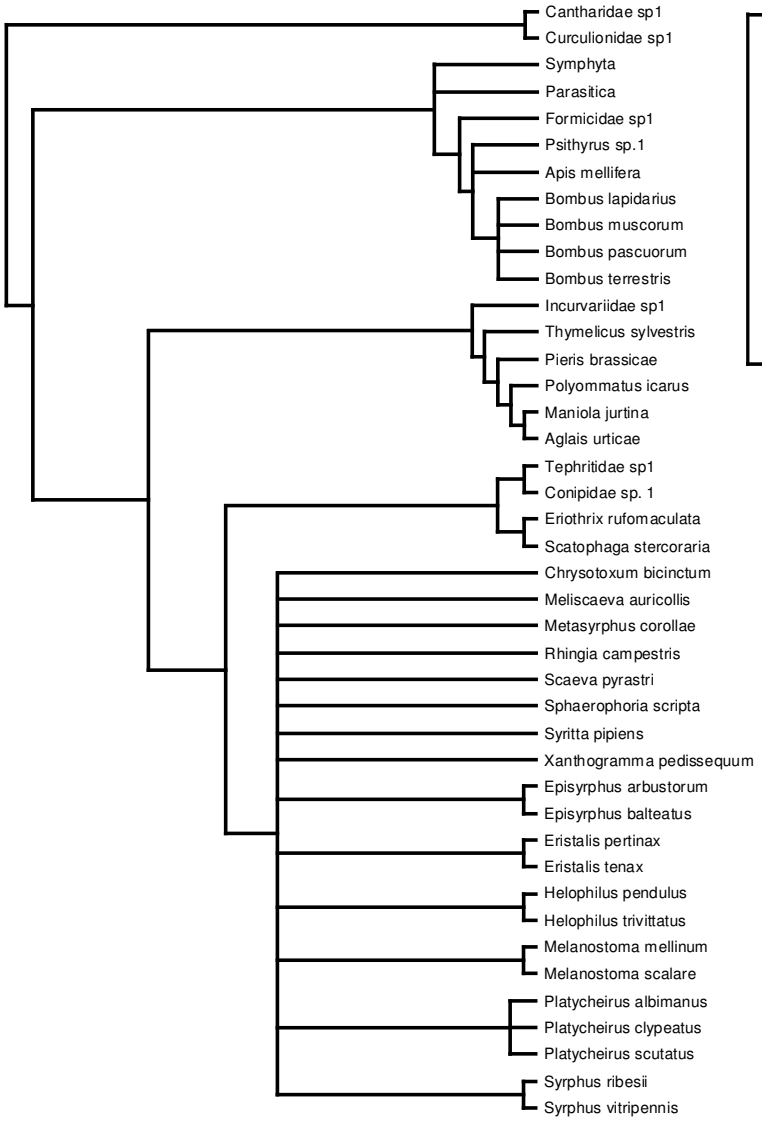



AN_MED2

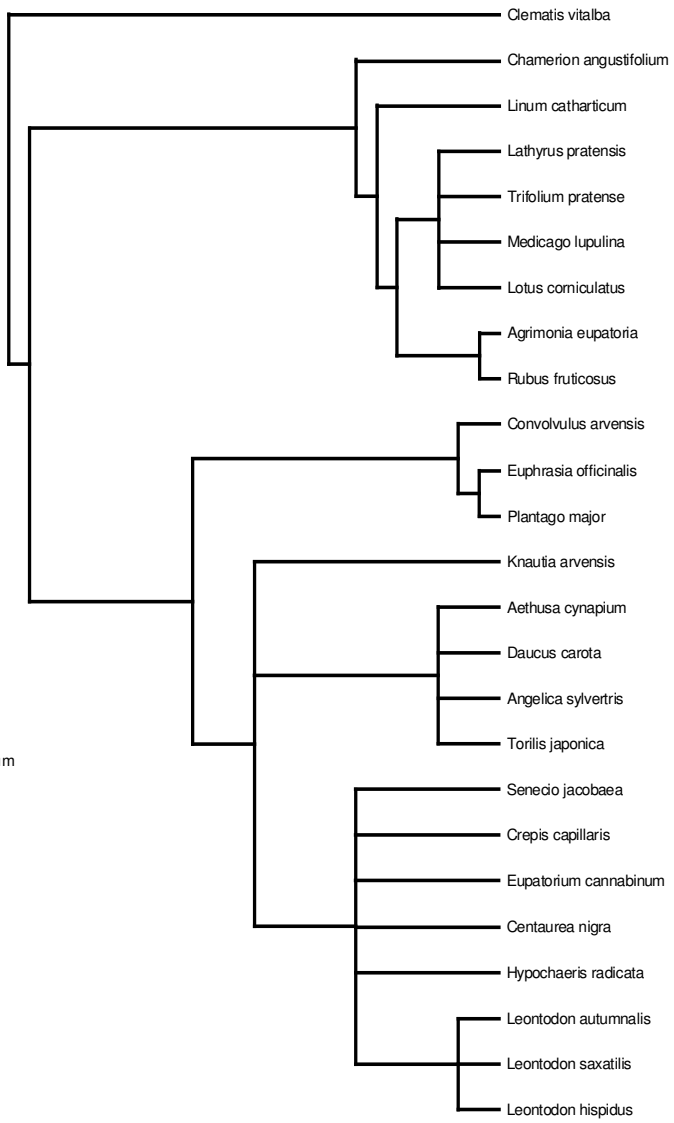



PL_MED2

## COMMUNITY MEMM – Pollination

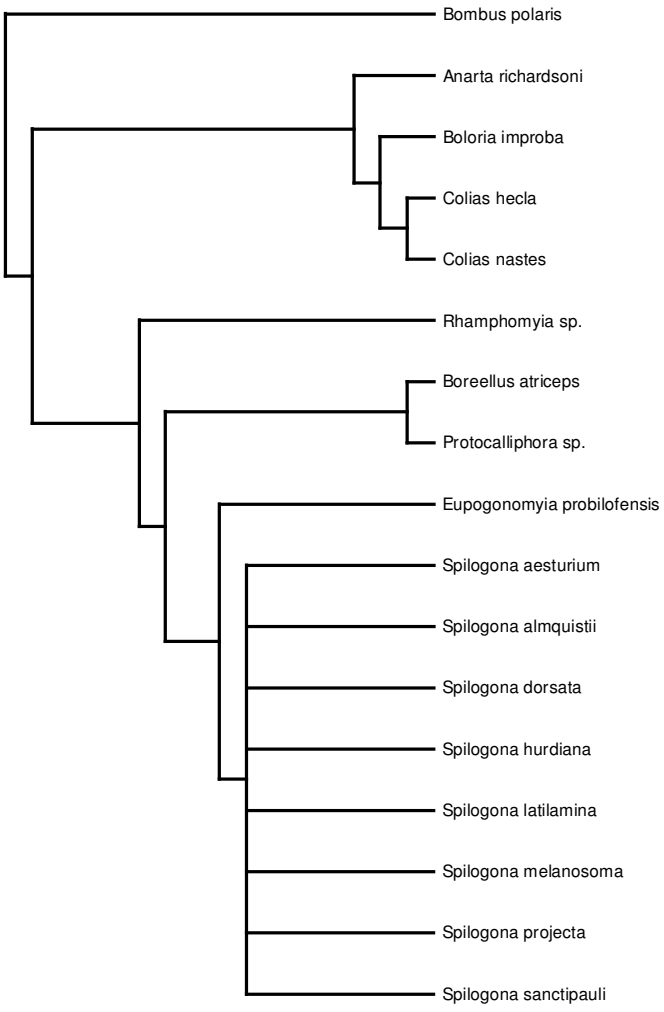



AN_MEMM

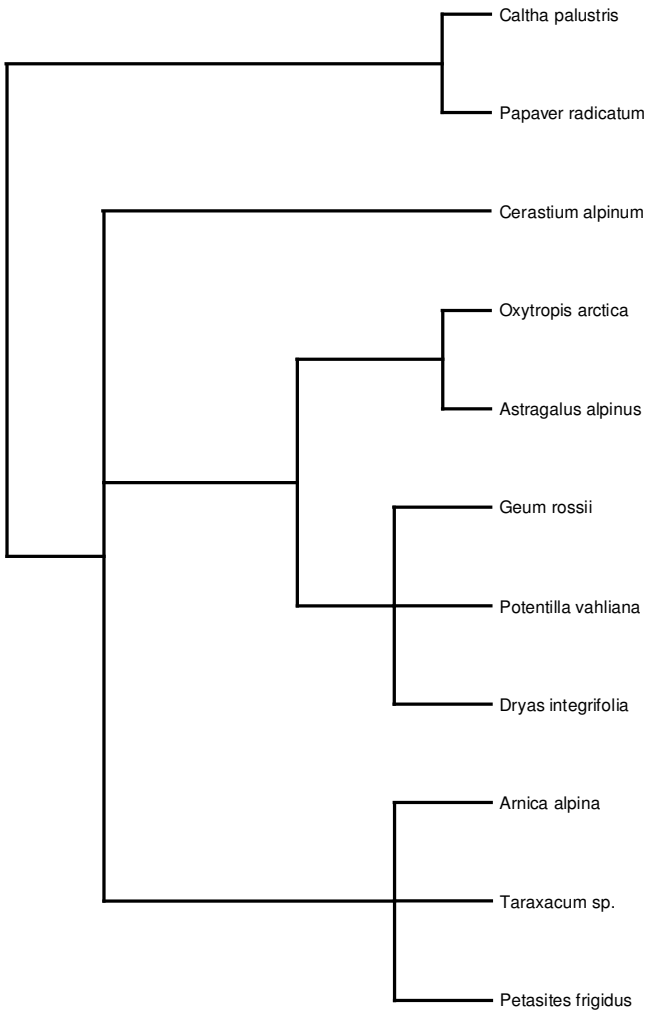



PL_MEMM

## COMMUNITY MOMA – Pollination

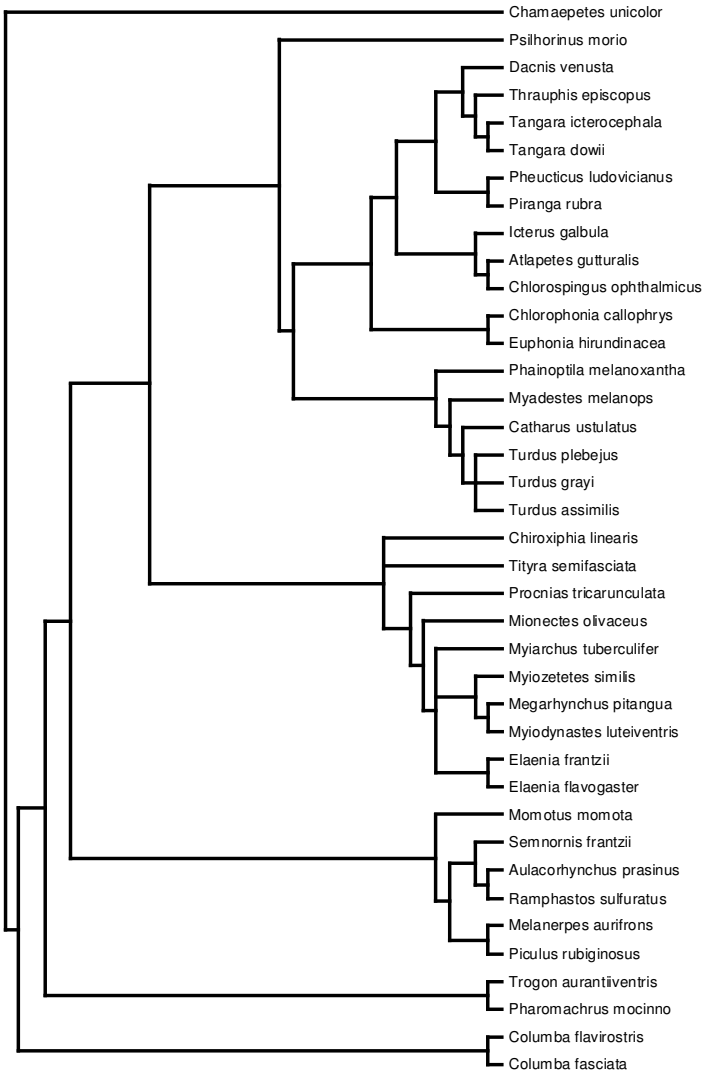



**AN_MOMA**

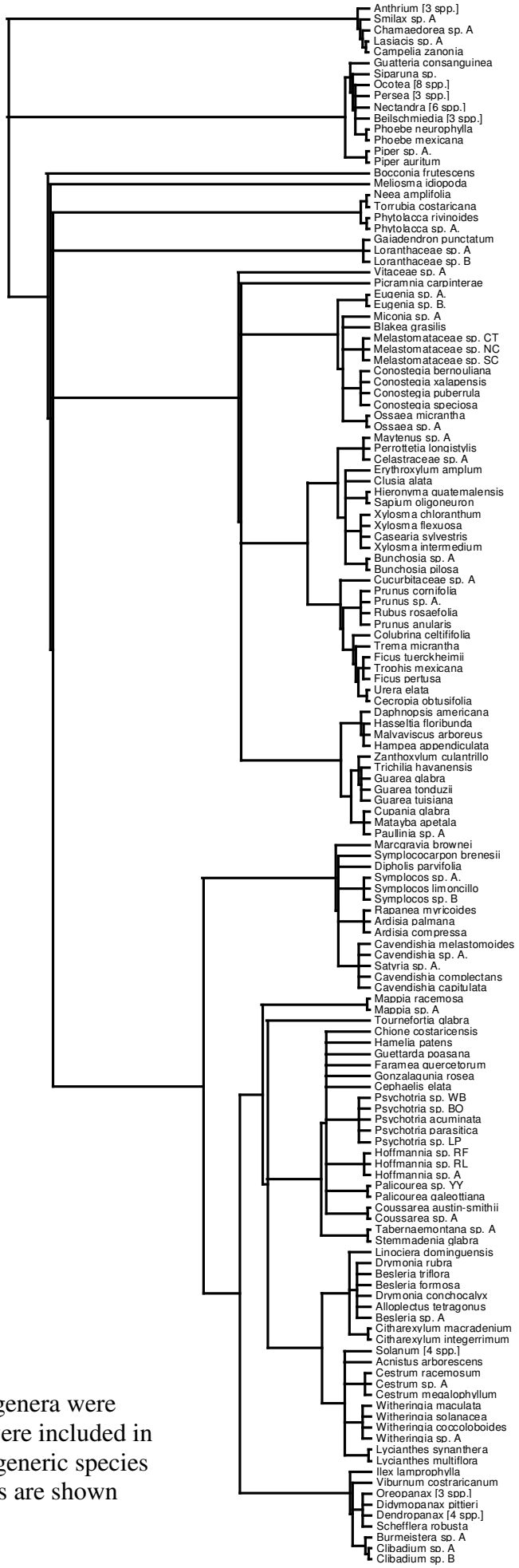



**PL_MOMA**

## COMMUNITY MONT – Frugivory



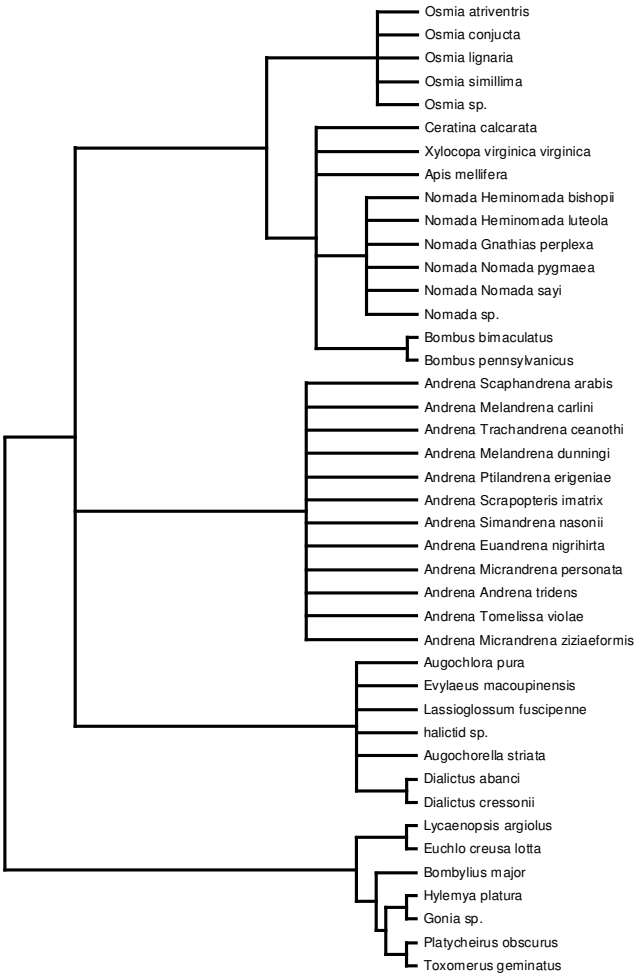

**AN_MONT**



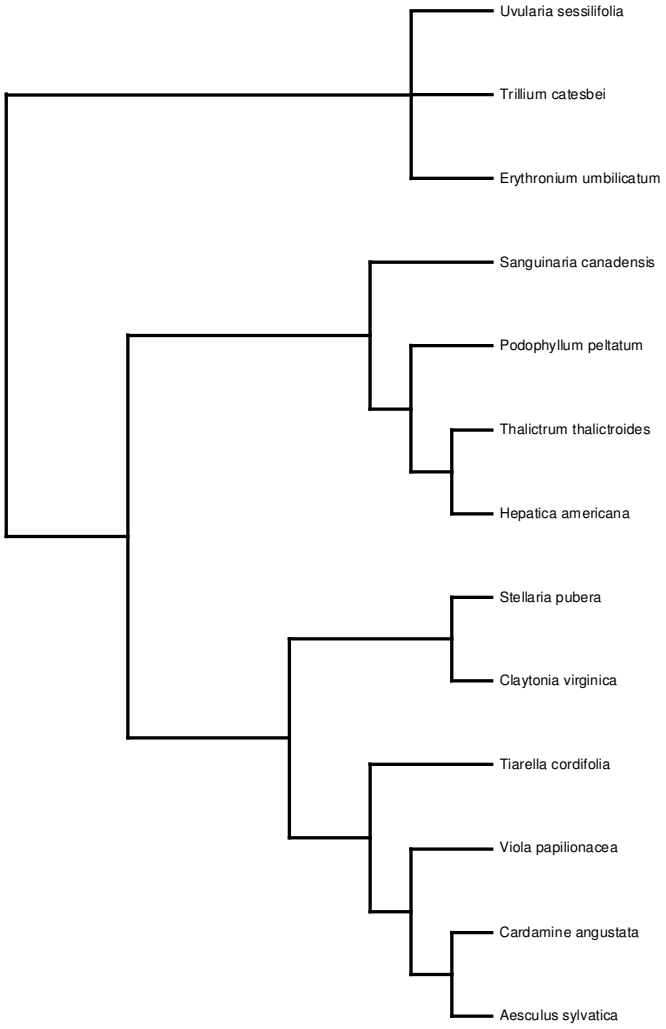

**PL_MONT ***

* 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

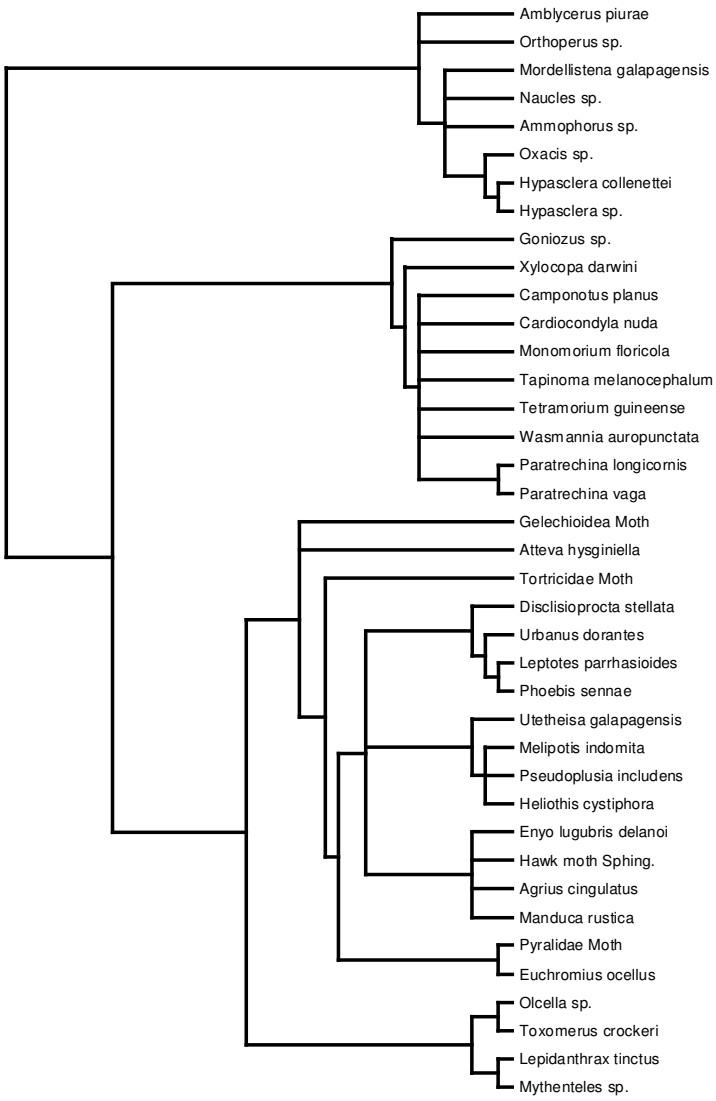



AN_MOTT

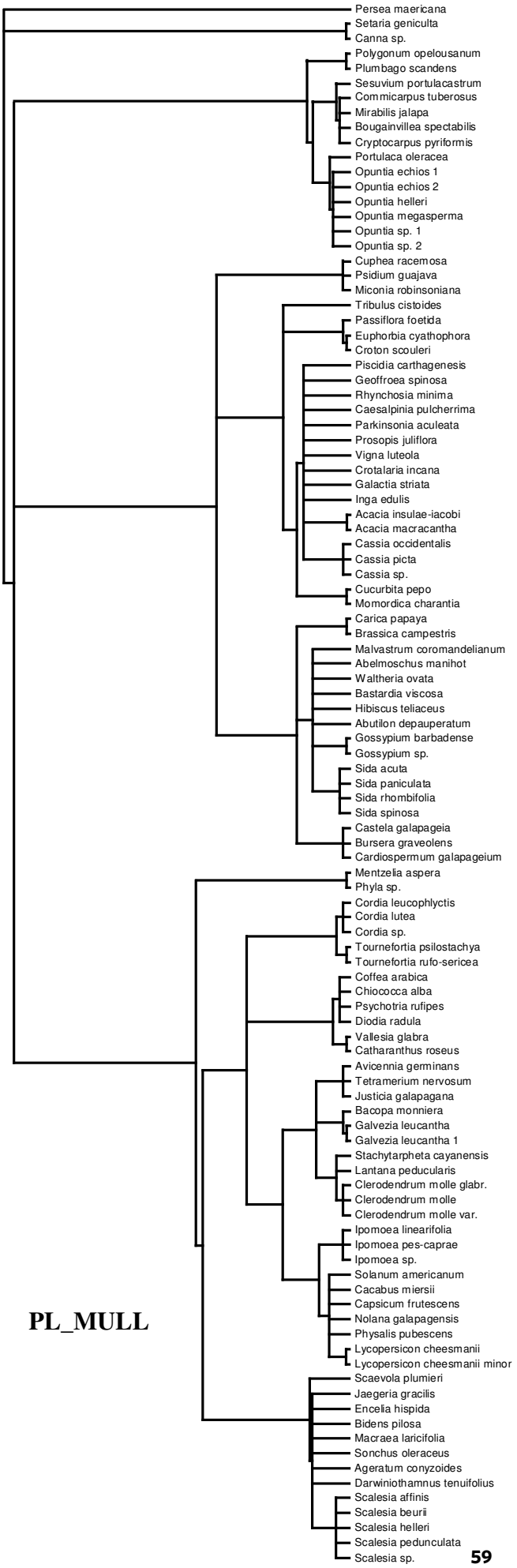



PL_MOTT

## COMMUNITY MULL – Pollination

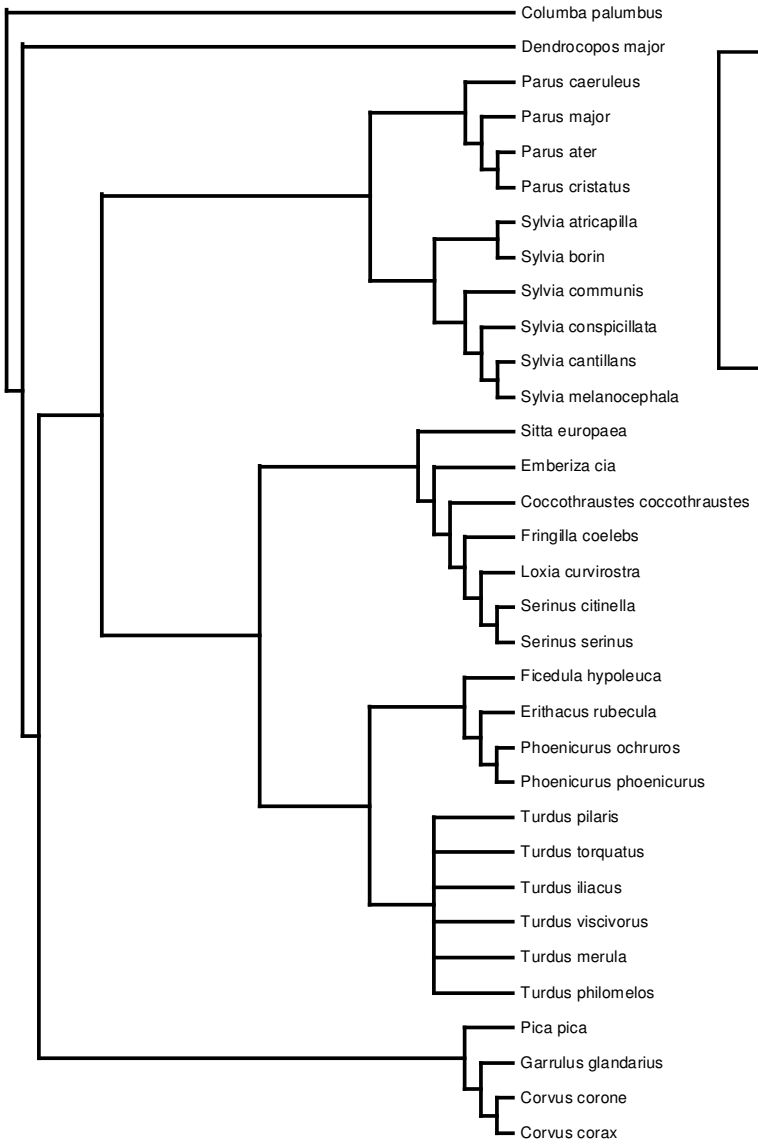



**AN_MULL**

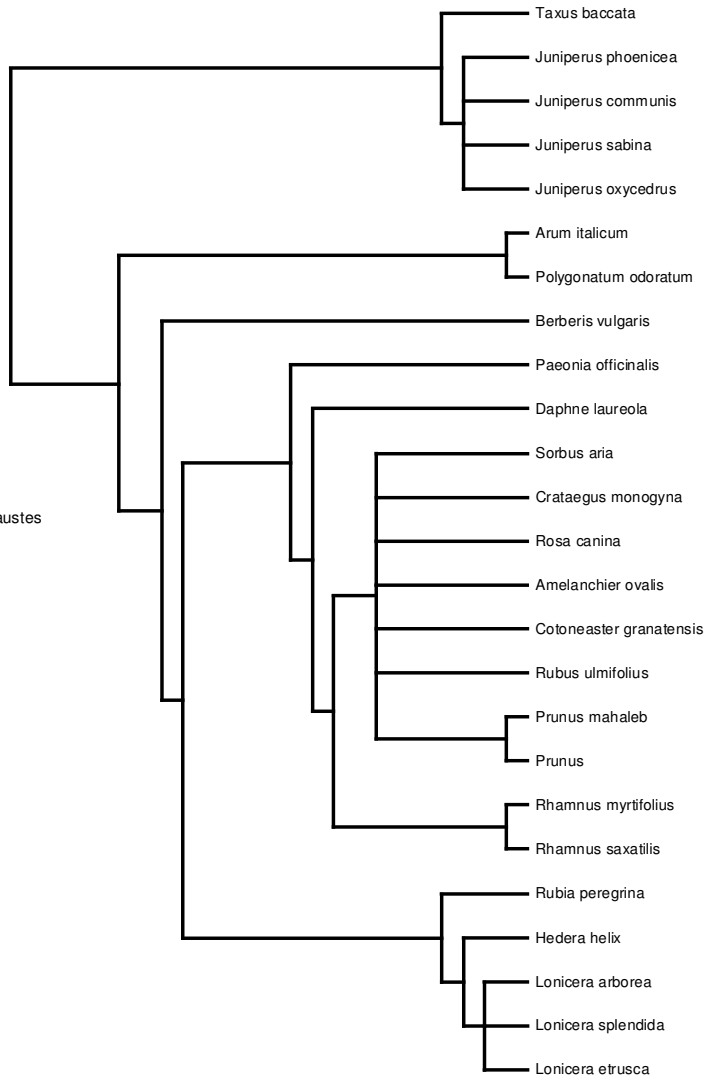



**PL_MULL**

## COMMUNITY NCOR – Frugivory

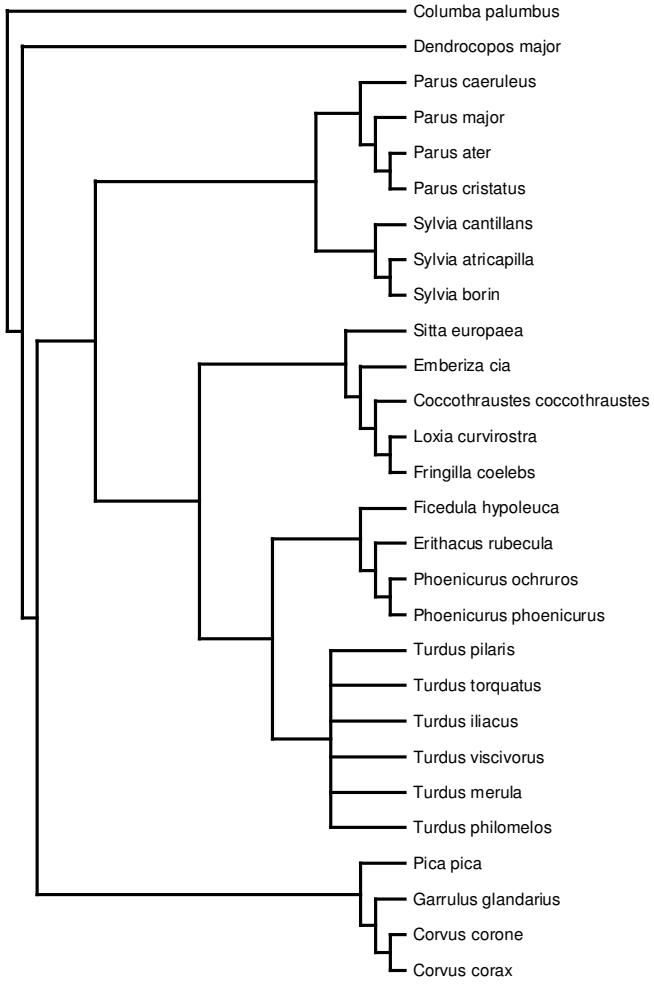



**AN_NCOR**

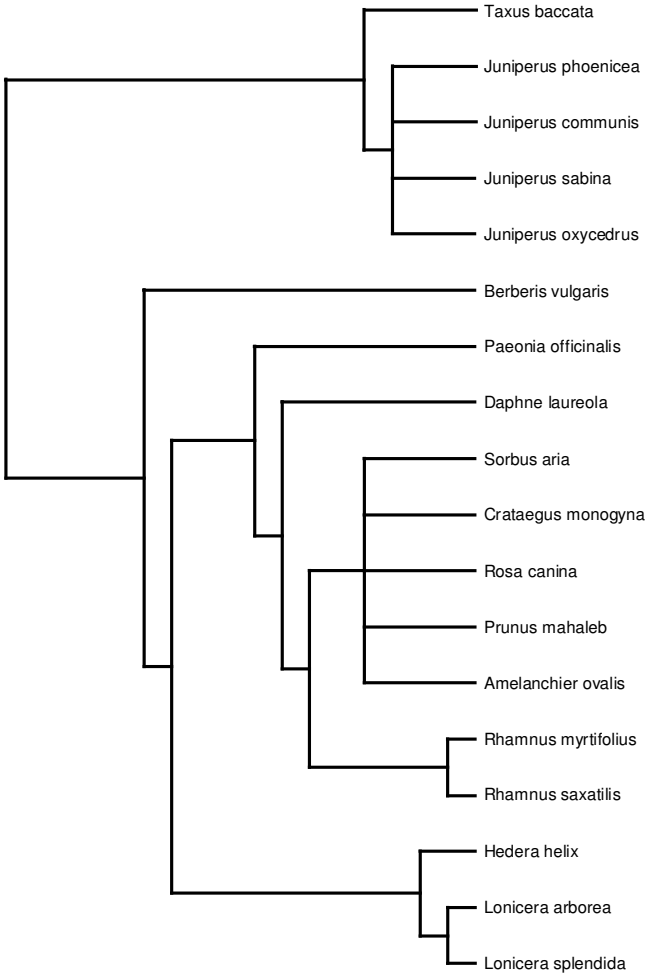



**PL_NCOR**

## COMMUNITY NNOG – Frugivory



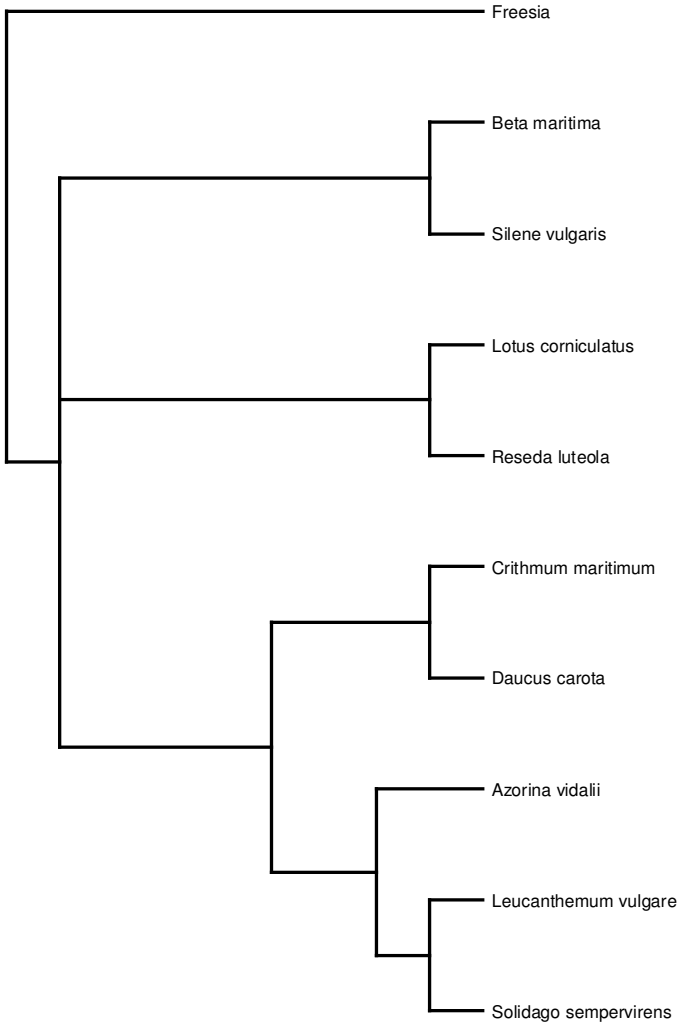

AN_NNOG




PL_NNOG

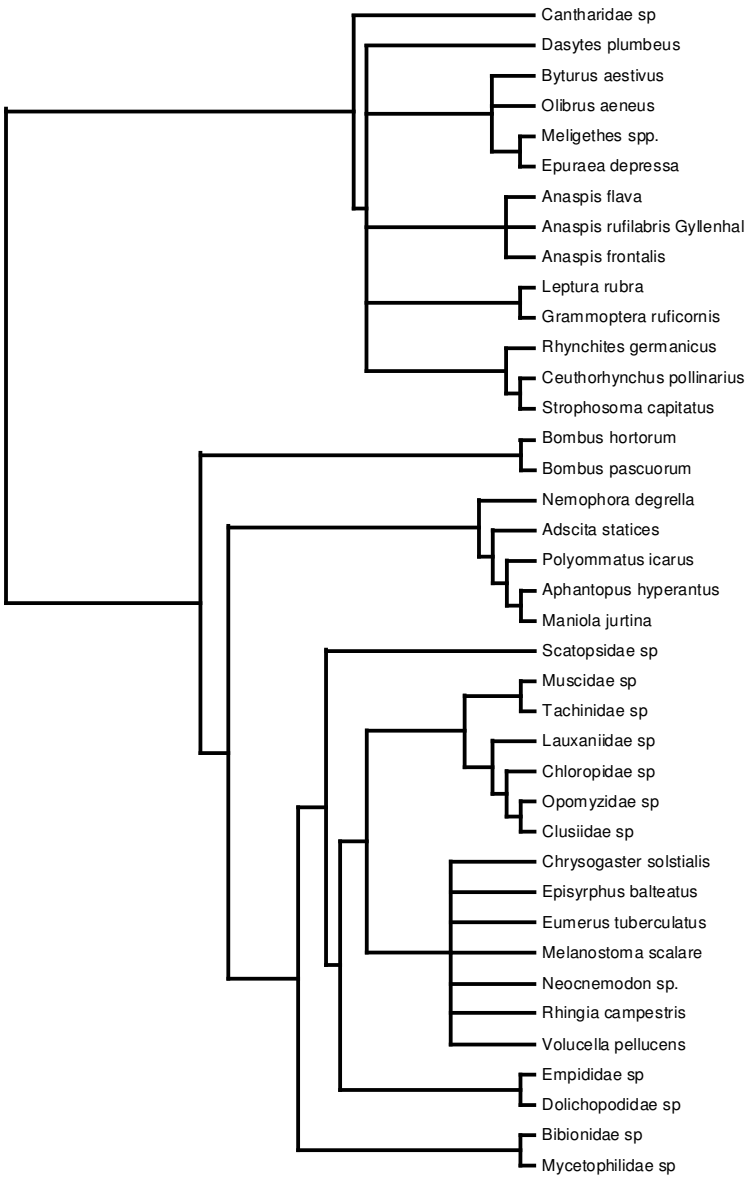
**COMMUNITY OFLO – Pollination**

**AN_OFLO not available**
(not included in analyses)




**PL_OFLO**

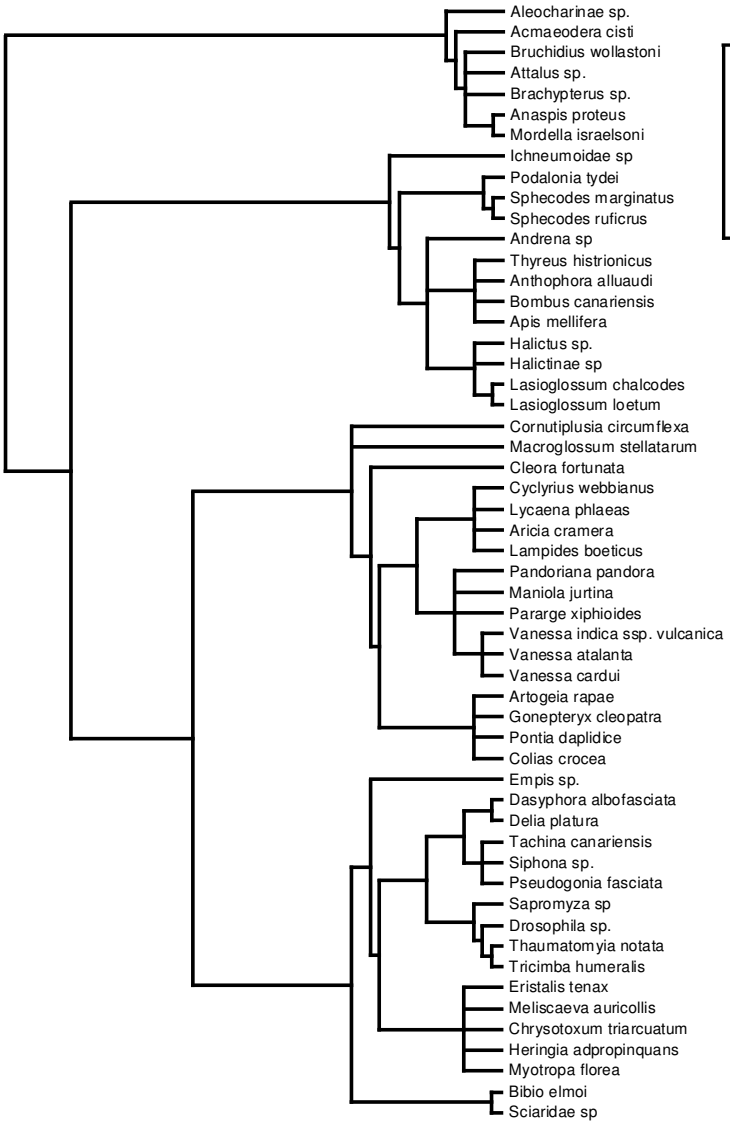
**COMMUNITY OFST – Pollination**



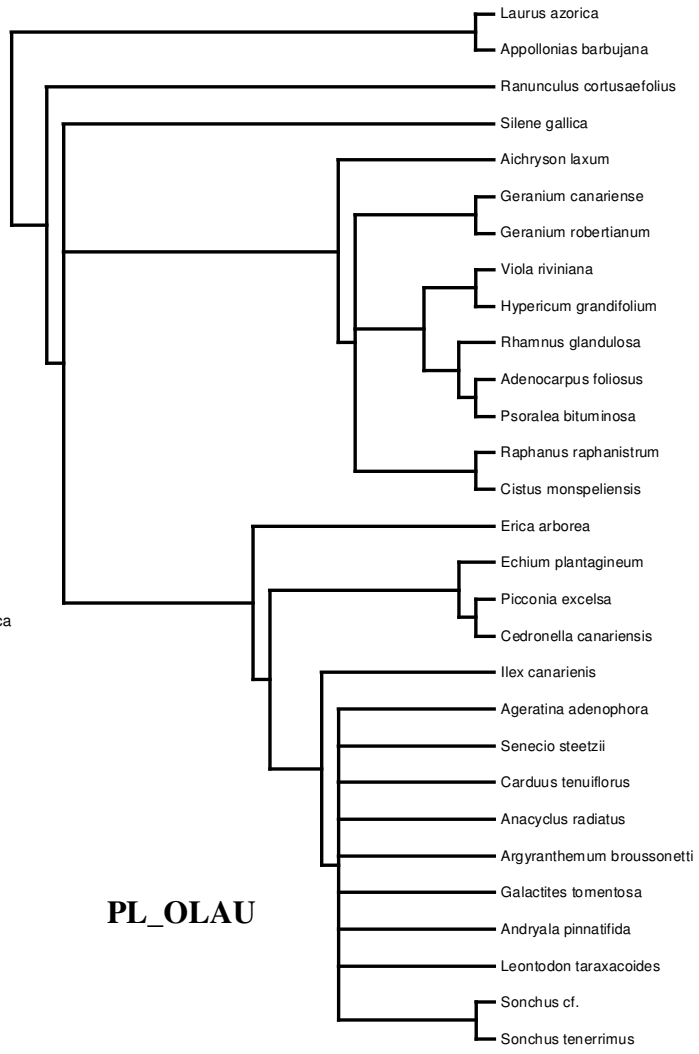

**PL_OFST not available**
(not included in analyses)

**AN_OFST**

## COMMUNITY OLAU – Pollination

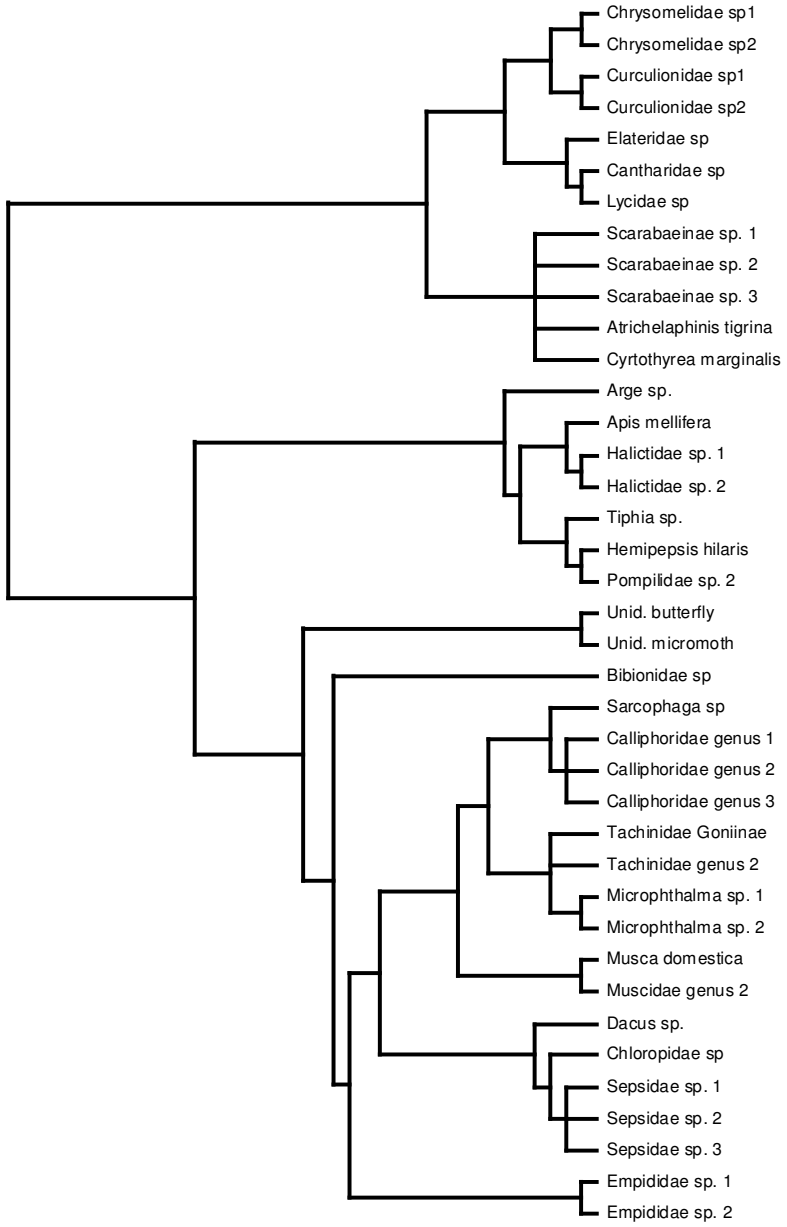



**AN_OLAU**




**PL_OLAU**

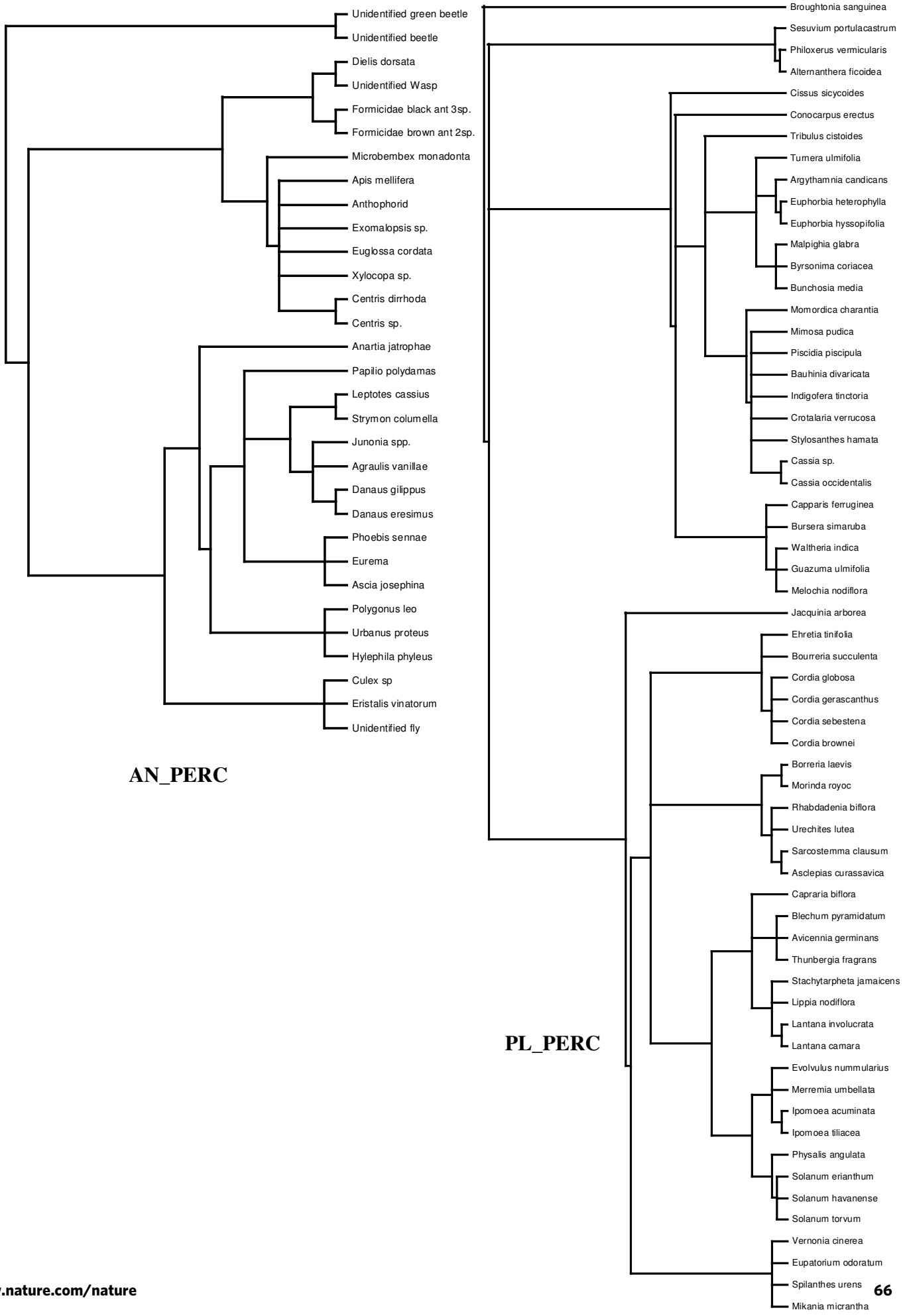
**COMMUNITY OLLE – Pollination**



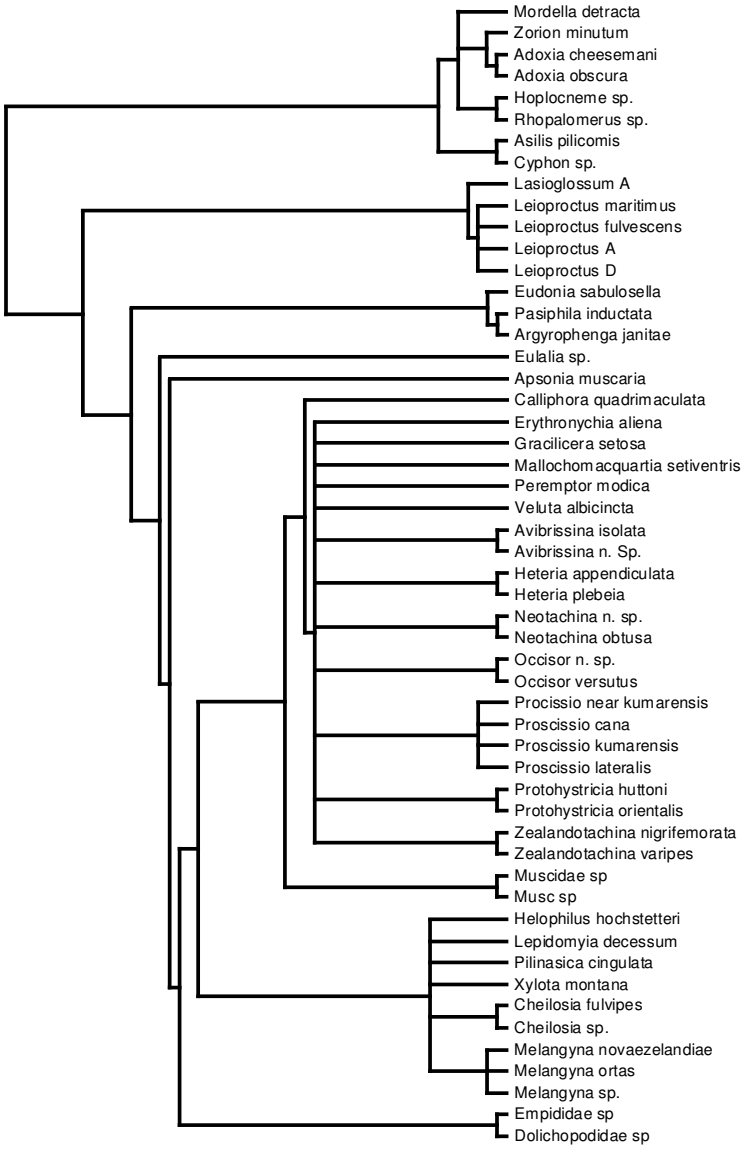

**AN_OLLE**

**PL_OLLE not available**
(not included in analyses)

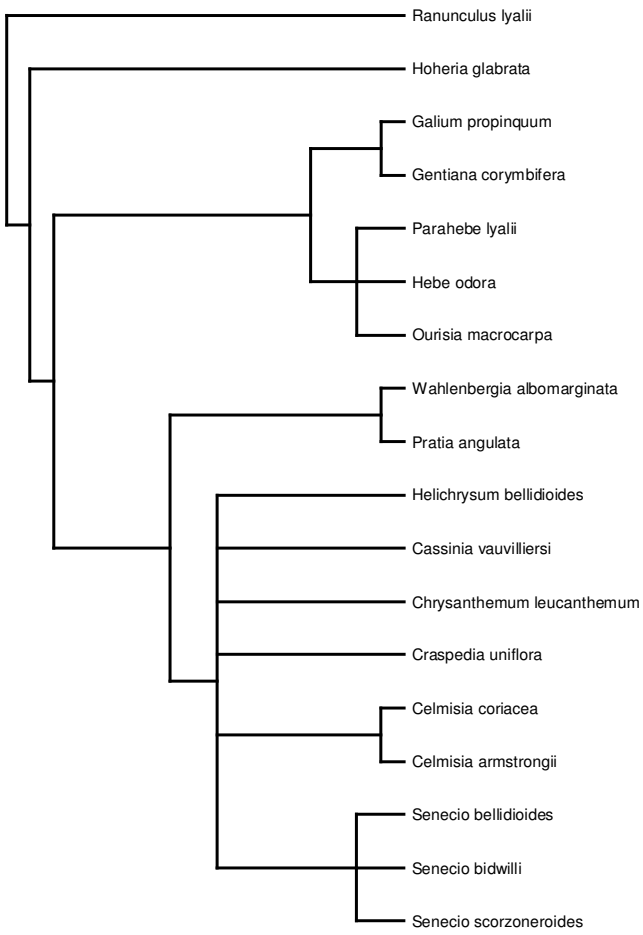
## COMMUNITY PERC – Pollination



## COMMUNITY PRAP – Pollination

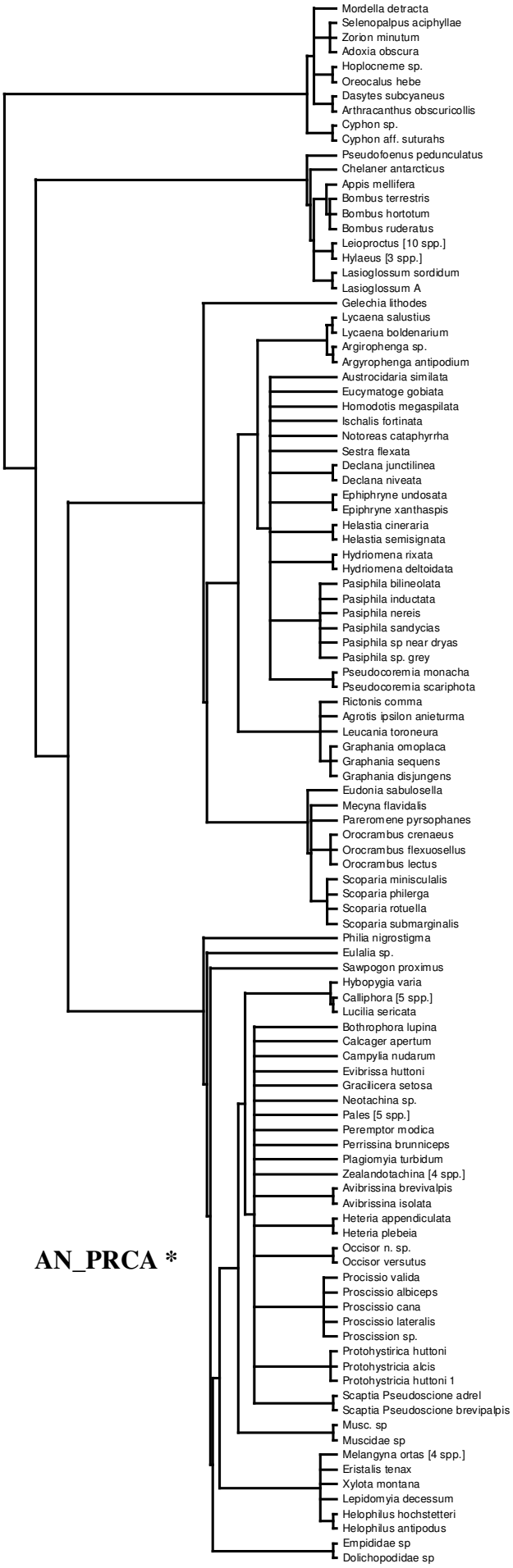



**AN_PRAP**

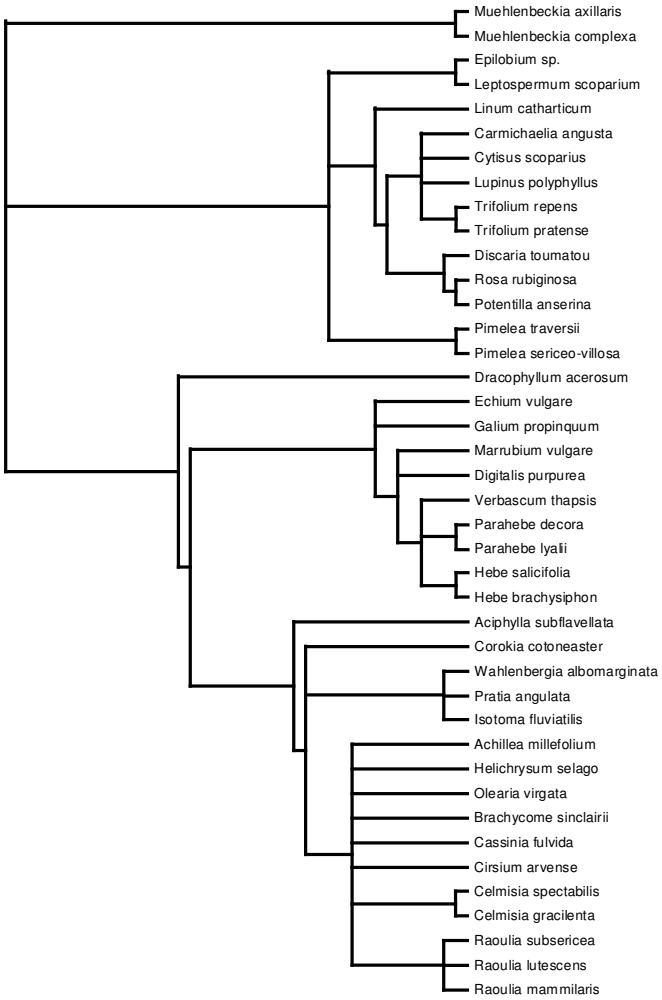



**PL_PRAP**

## COMMUNITY PRCA – Pollination



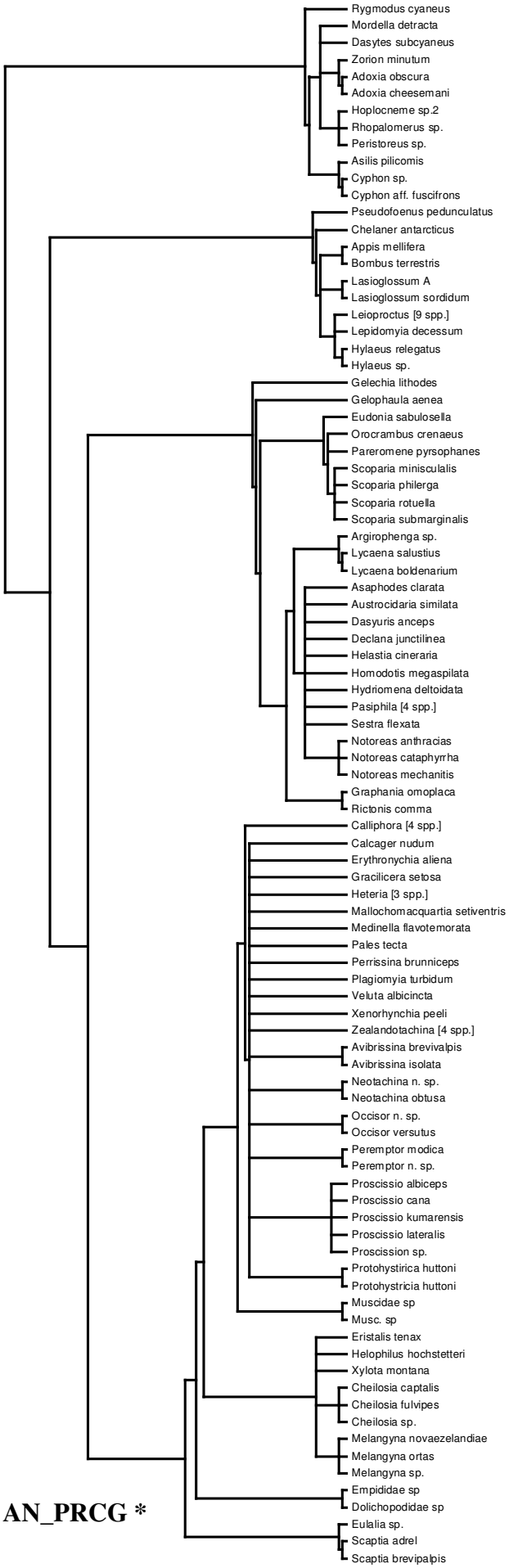

**AN_PRCA ***



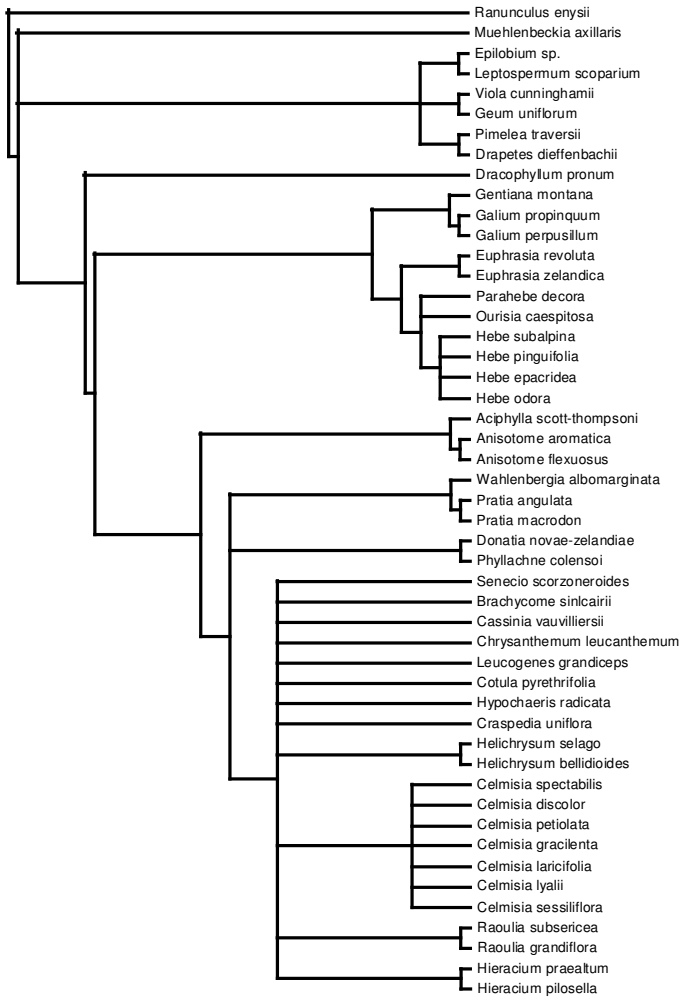

**PL_PRCA**

* 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



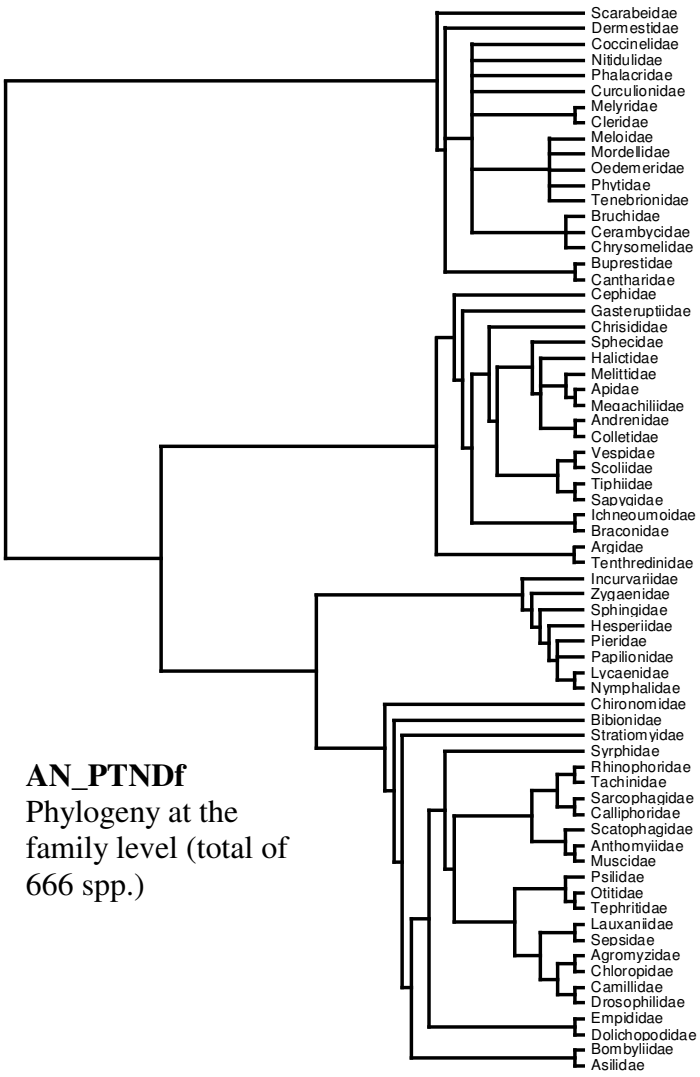

**AN_PRCG ***



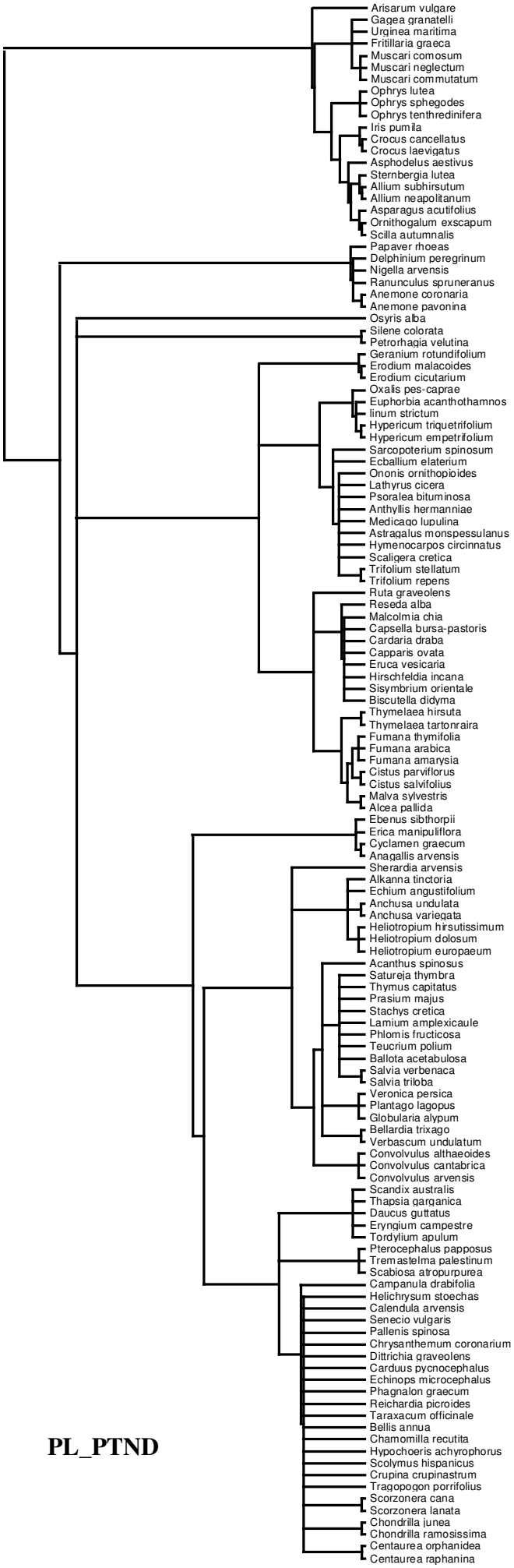

**PL_PRCG**

* 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 PTND – Pollination

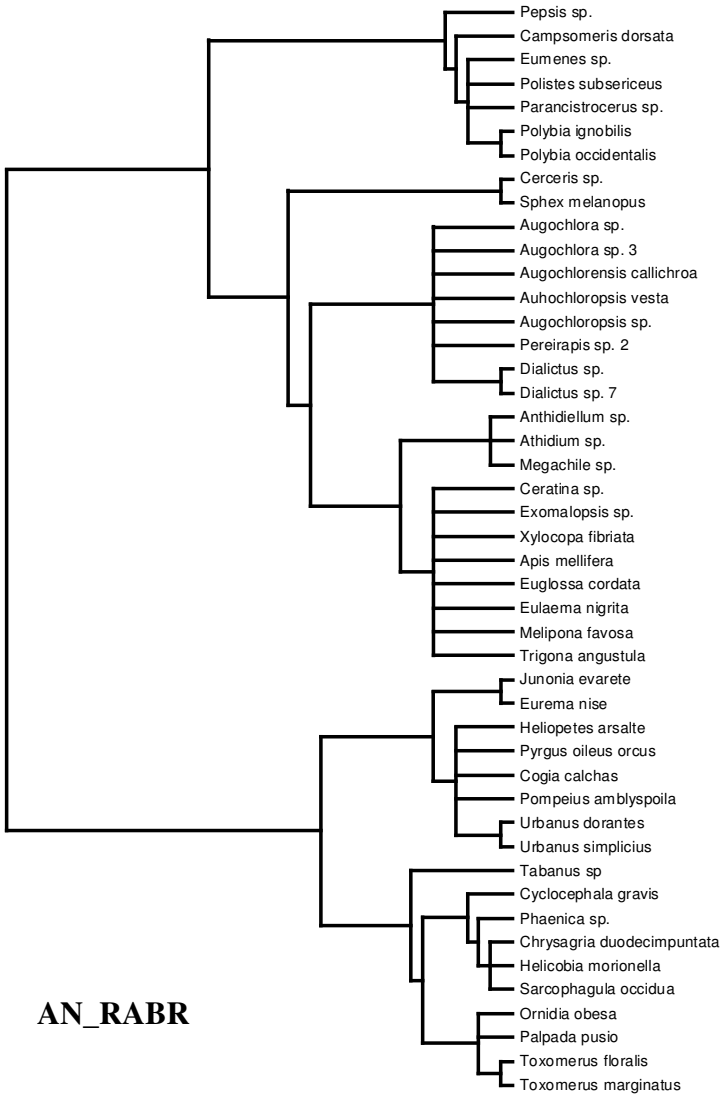



**AN_PTNDf**
Phylogeny at the family level (total of 666 spp.)

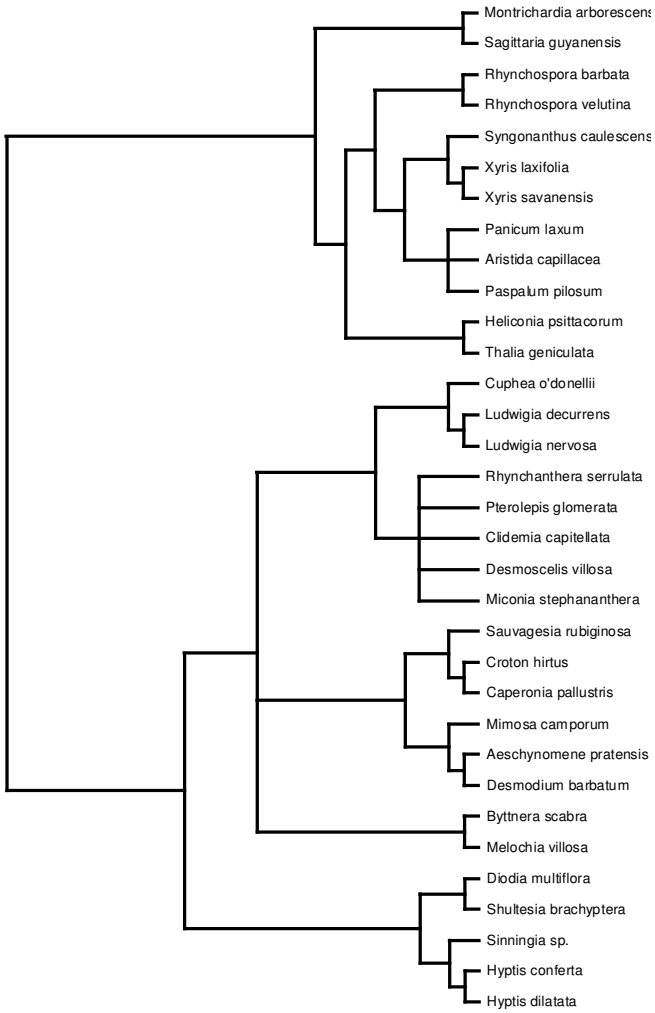



**PL_PTND**

## COMMUNITY RABR – Pollination

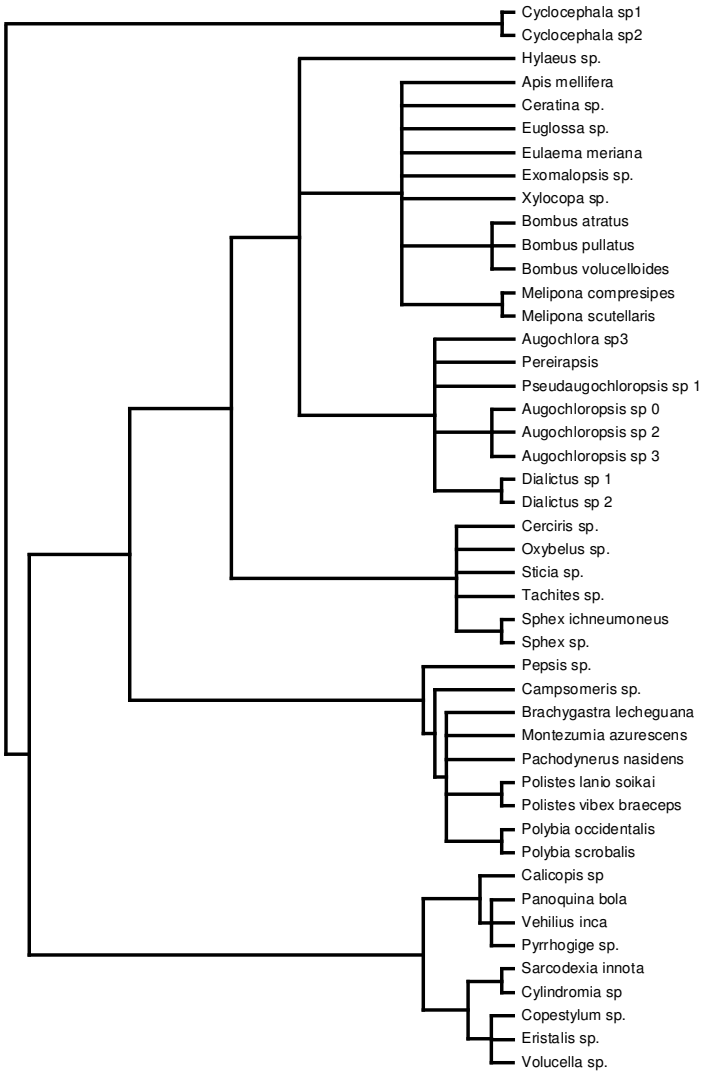



**AN_RABR**

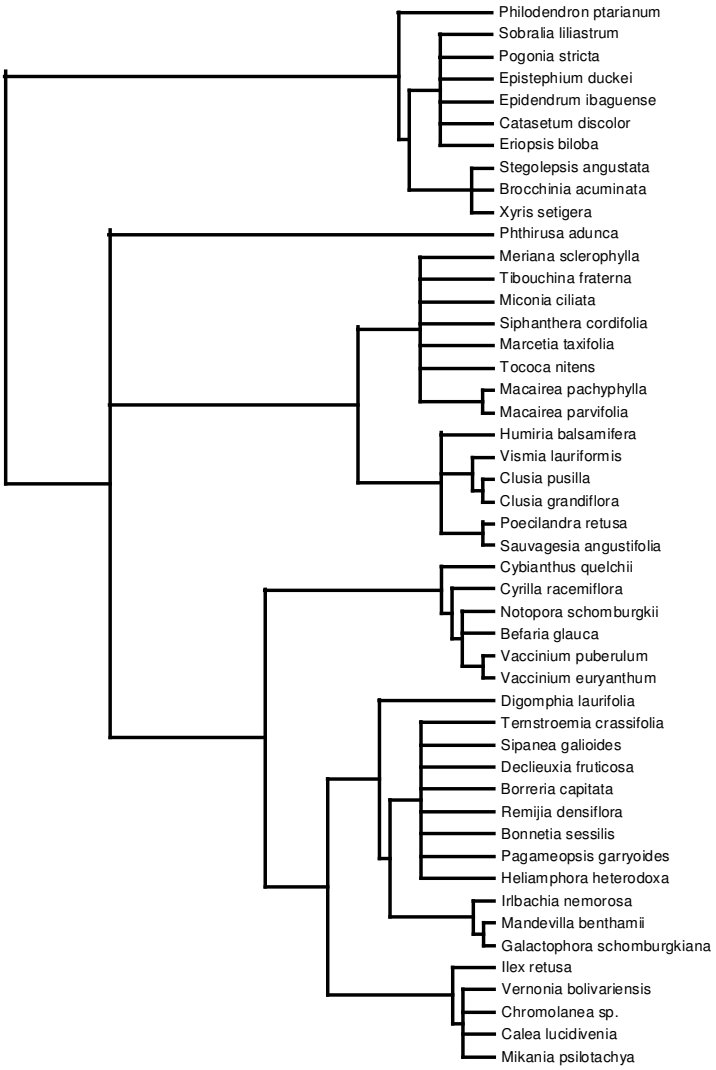



**PL_RABR**

## COMMUNITY RMRZ – Pollination

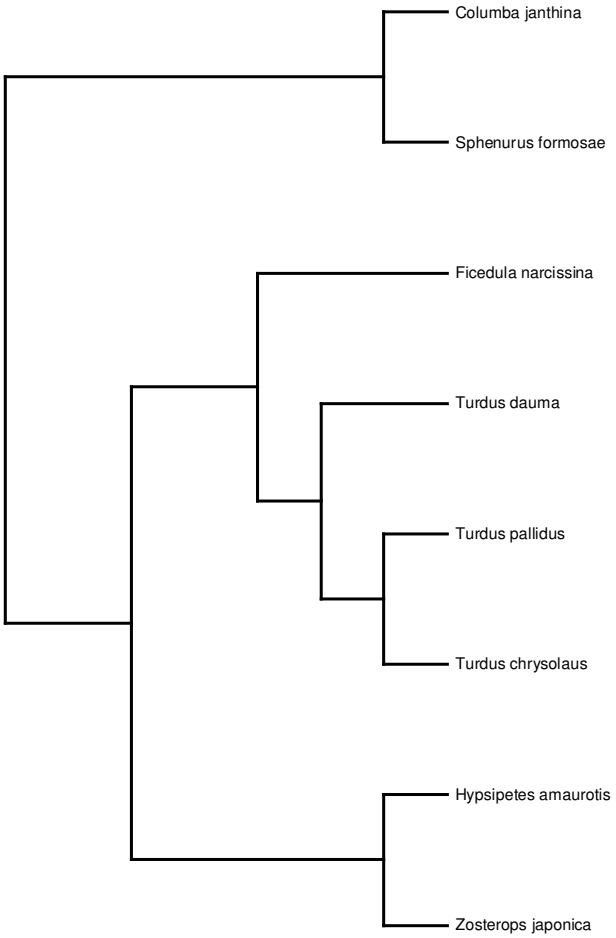



**AN_RMRZ**

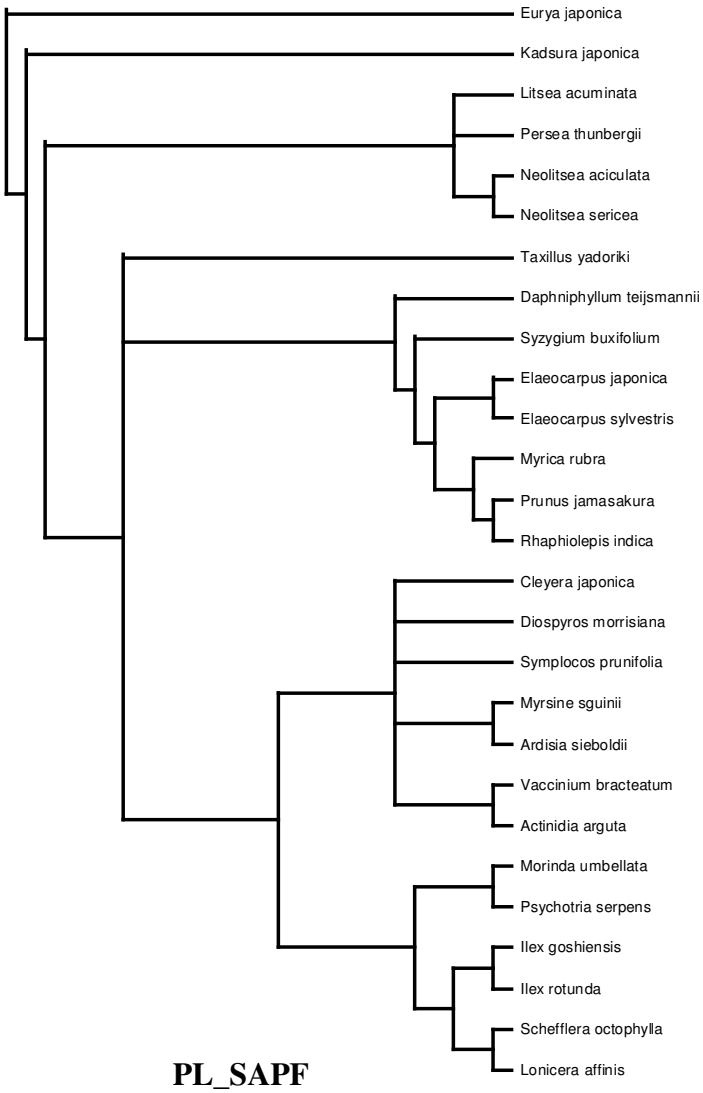



**PL_RMRZ**

## COMMUNITY SAPF – Frugivory

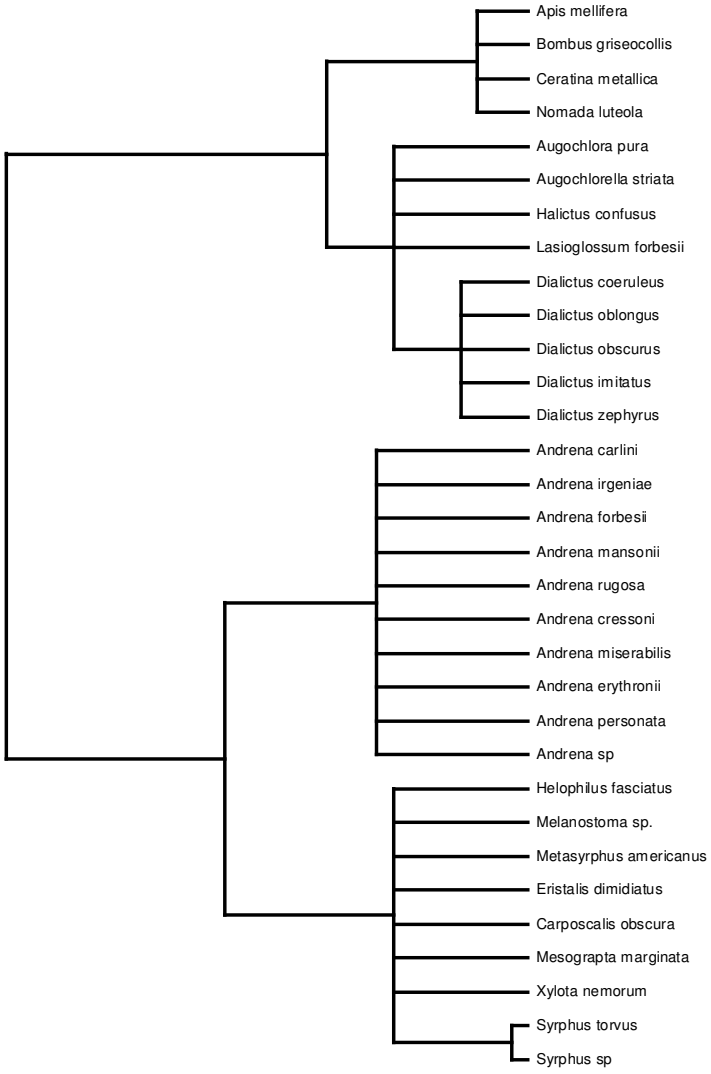



**AN_SAPF**
(not included in analyses)

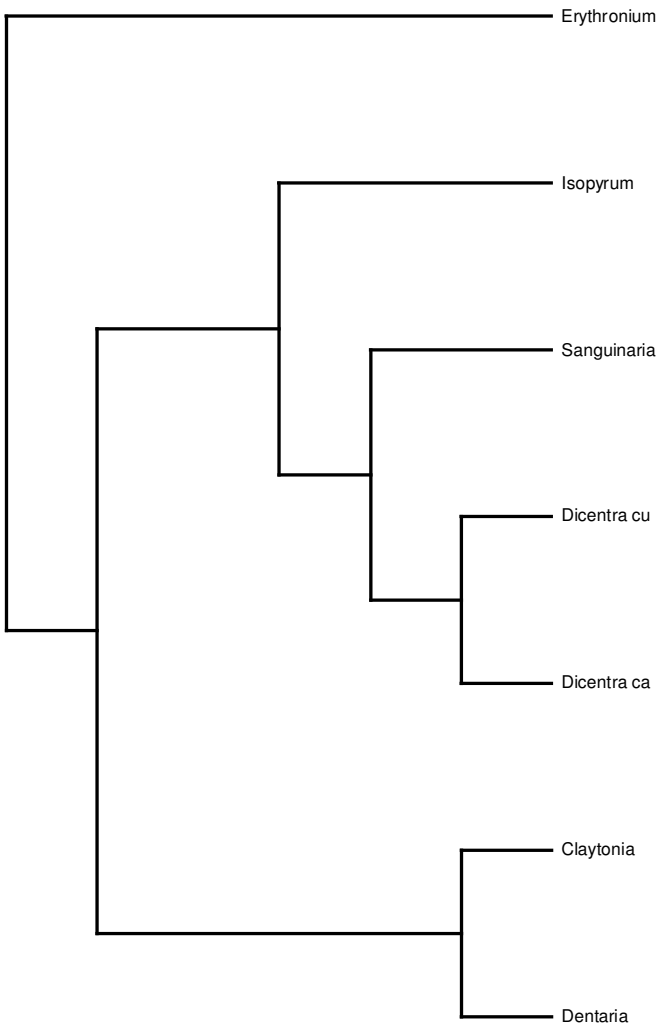



**PL_SAPF**

**COMMUNITY SCHM – Pollination**

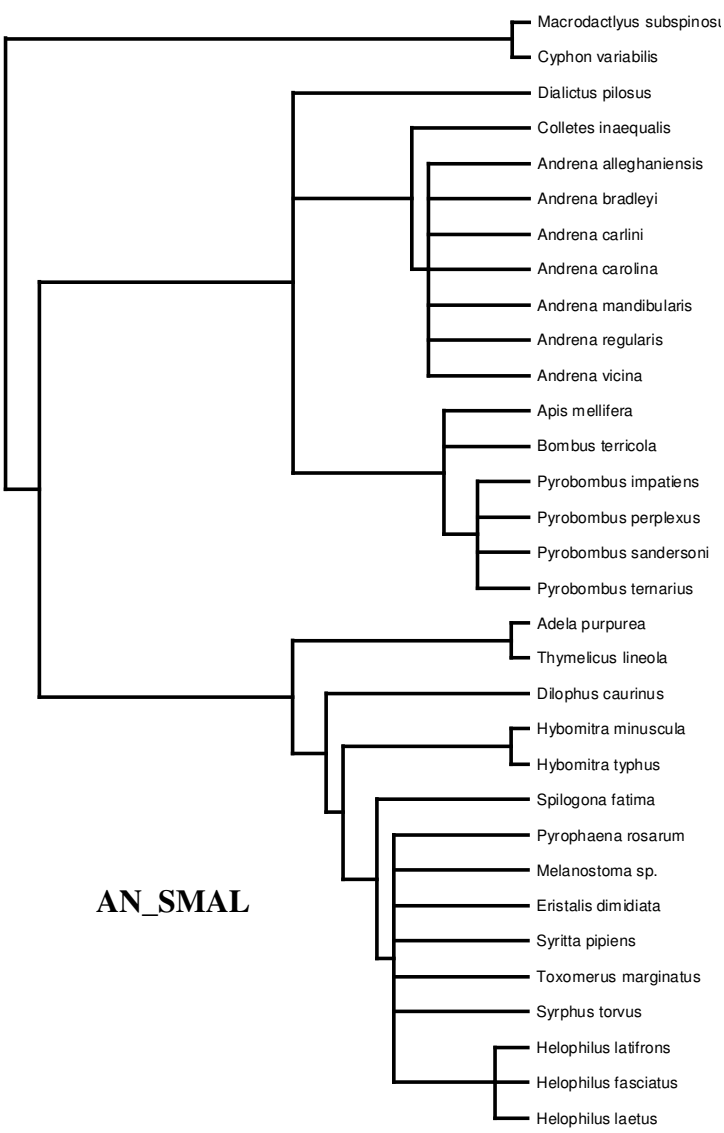



**AN_SCHM**

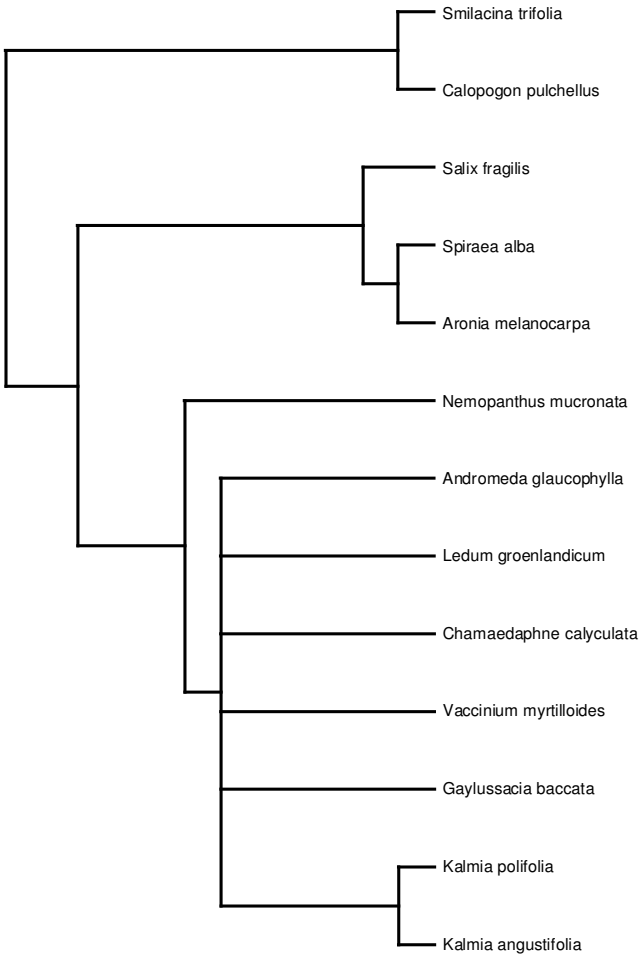



**PL_SCHM**
(not included in analyses)

## COMMUNITY SMAL – Pollination

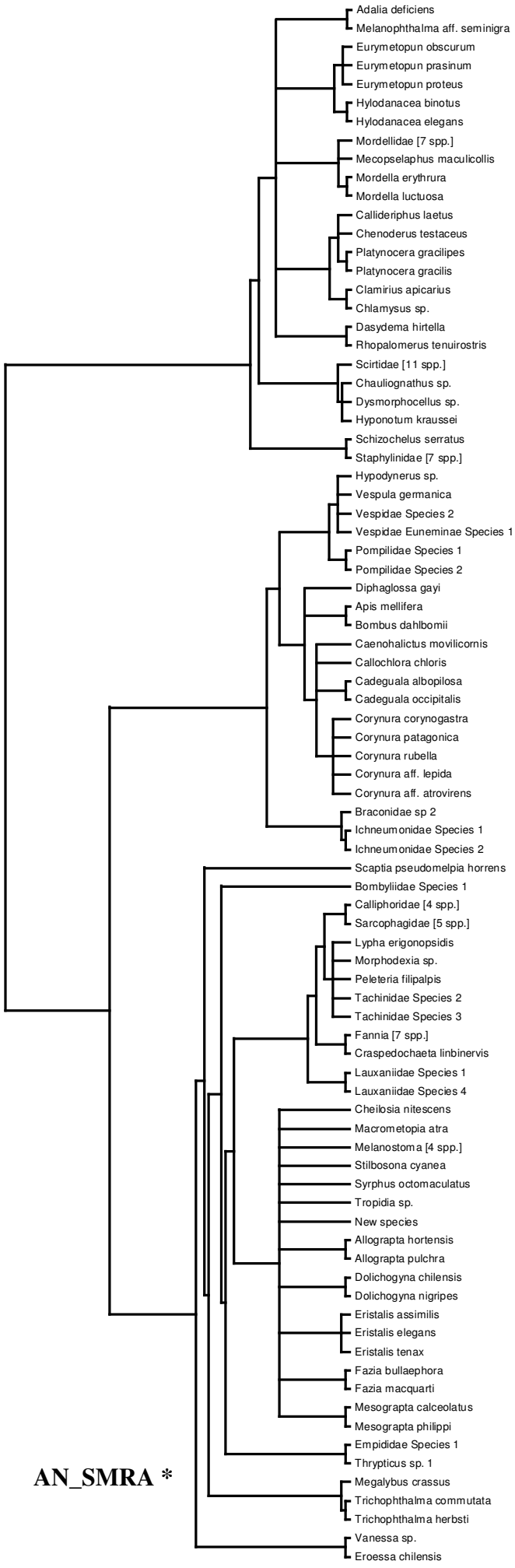



**AN_SMAL**

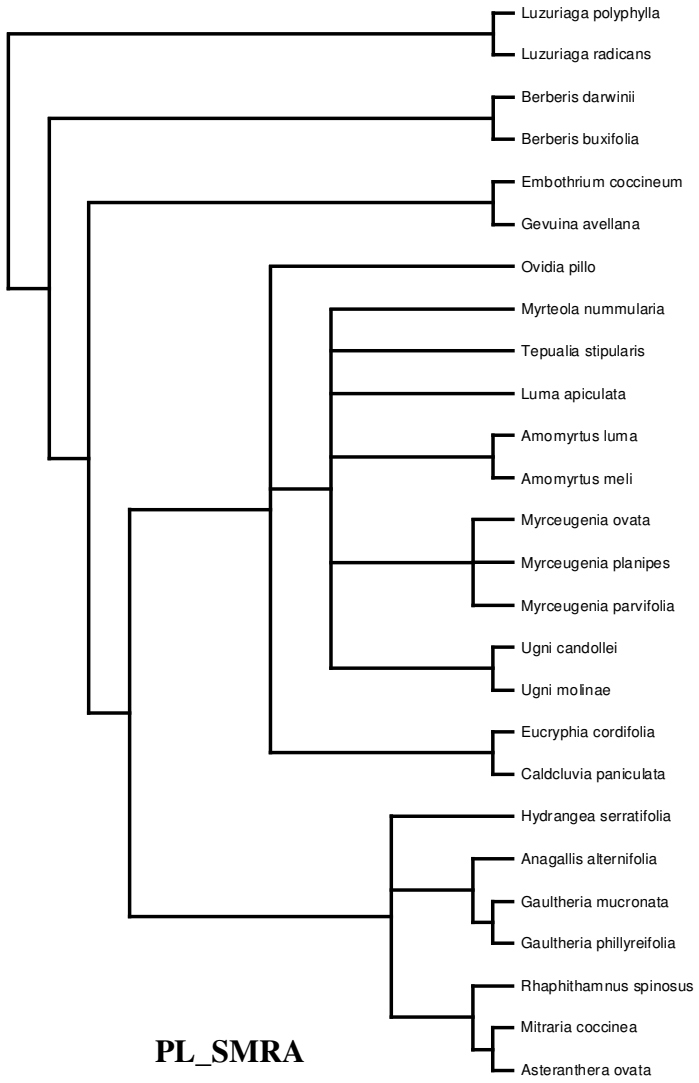



**PL_SMAL**

**COMMUNITY SMRA – Pollination**



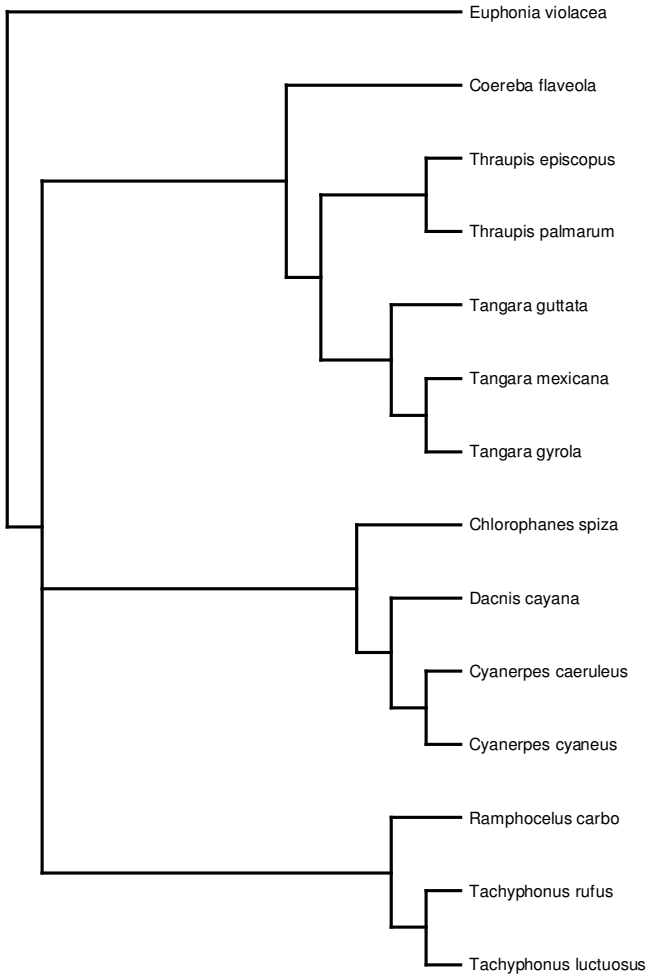

**AN_SMRA ***



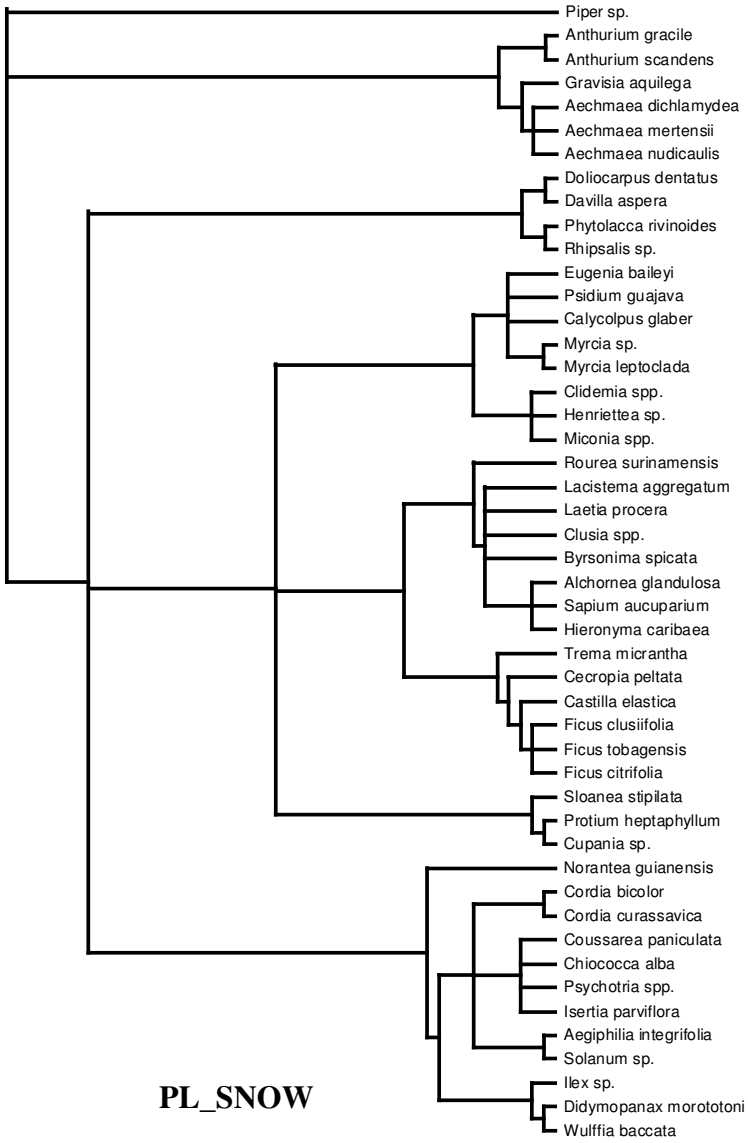

**PL_SMRA**

* 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.

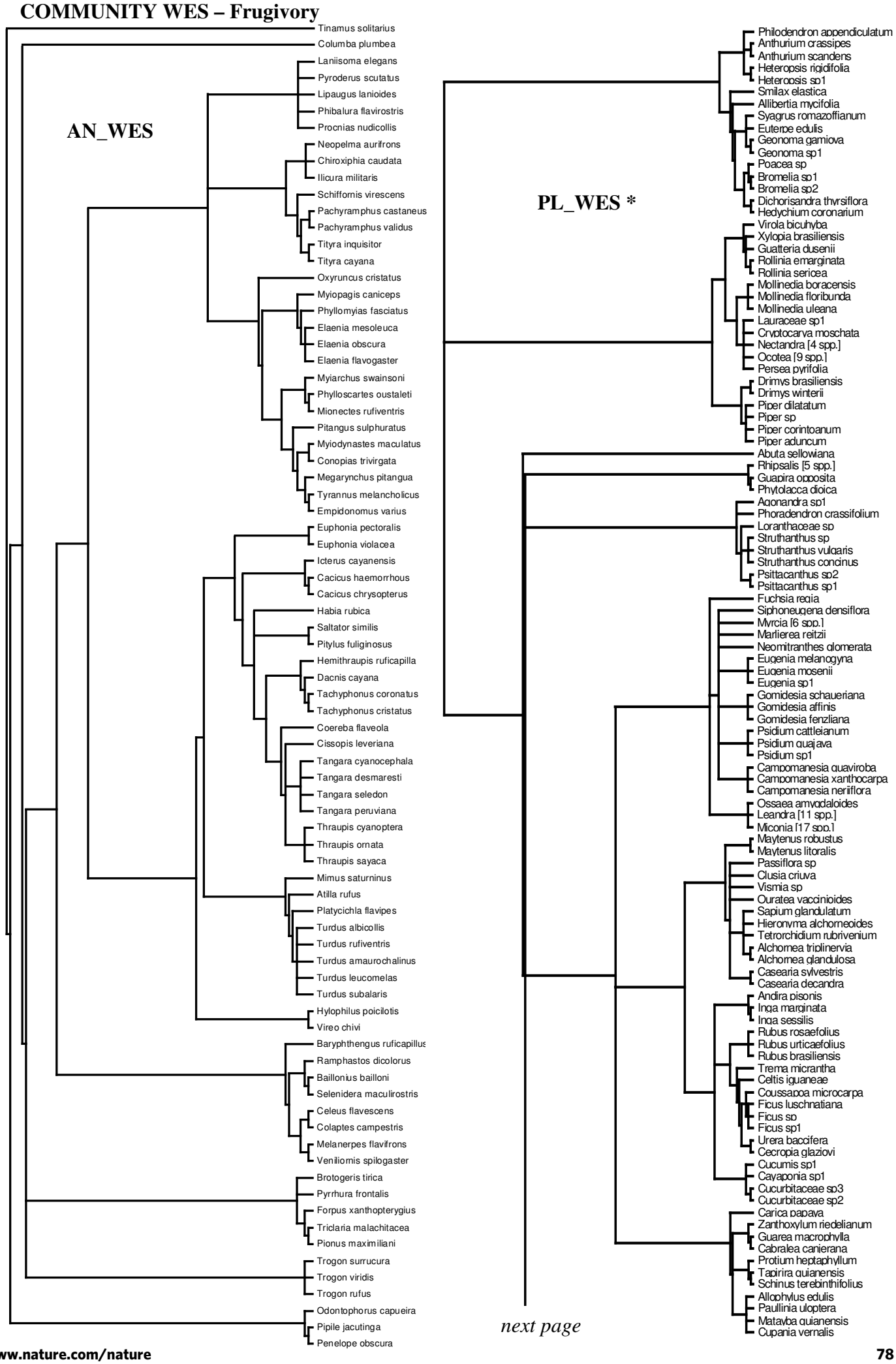
## COMMUNITY SNOW – Frugivory




**AN_SNOW**

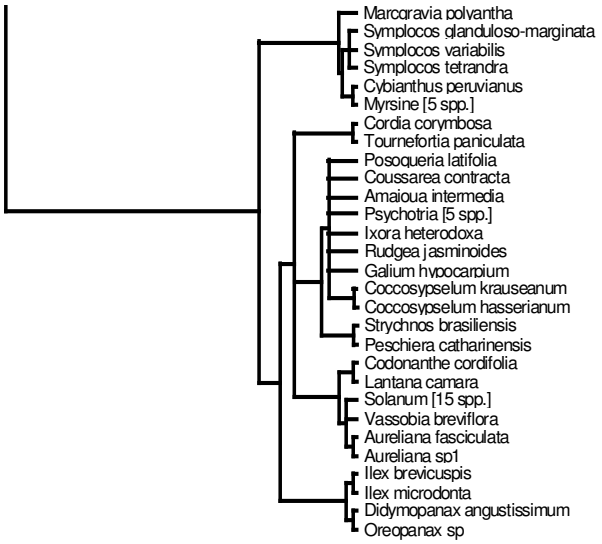



**PL_SNOW**

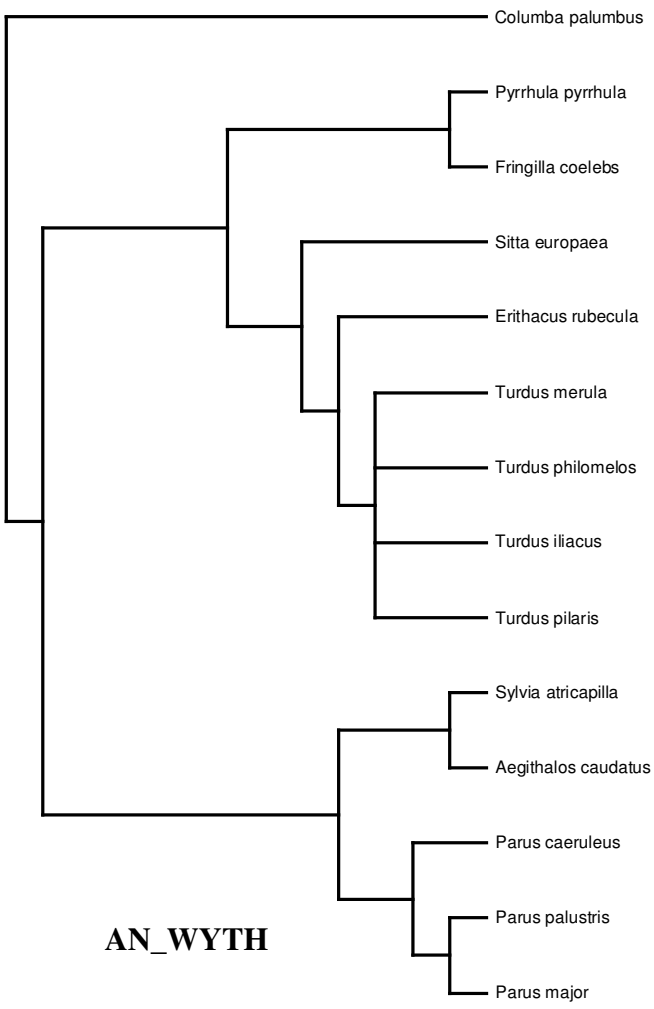
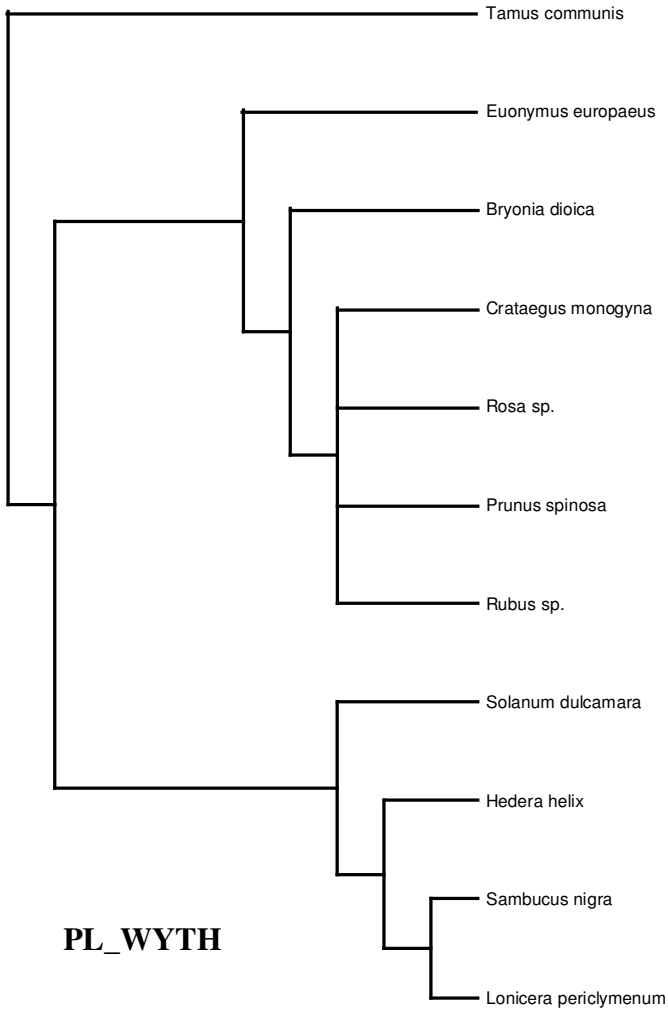

COMMUNITY WES – Frugivory
AN_WES
Tinamus solitarius
Columba plumbea
Laniisoma elegans
Pyroderus scutatus
Lipaugus lanioides
Phibalura flavirostris
Procnias nudicollis
Neopelma aurifrons
Chiroxiphia caudata
Ilicura militaris
Schiffornis virescens
Pachyramphus castaneus
Pachyramphus validus
Tityra inquisitor
Tityra cayana
Oxyruncus cristatus
Myiopagis caniceps
Phyllomyias fasciatus
Elaenia mesoleuca
Elaenia obscura
Elaenia flavogaster
Myiarchus swainsoni
Phylloscartes oustaleti
Mionectes rufiventris
Pitangus sulphuratus
Myiodynastes maculatus
Conopias trivirgata
Megarynchus pitangua
Tyrannus melancholicus
Empidonomus varius
Euphonia pectoralis
Euphonia violacea
Icterus cayanensis
Cacicus haemorrhous
Cacicus chrysopterus
Habia rubica
Saltator similis
Pitylus fuliginosus
Hemithraupis ruficapilla
Dacnis cayana
Tachyphonus coronatus
Tachyphonus cristatus
Coereba flaveola
Cissopis leveriana
Tangara cyanocephala
Tangara desmaresti
Tangara seledon
Tangara peruviana
Thraupis cyanoptera
Thraupis ornata
Thraupis sayaca
Mimus saturninus
Atilla rufus
Platycichla flavipes
Turdus albicollis
Turdus rufiventris
Turdus amaurochalinus
Turdus leucomelas
Turdus subalaris
Hylophilus poicilotis
Vireo chivi
Baryphthengus ruficapillus
Ramphastos dicolorus
Baillonius bailloni
Selenidera maculirostris
Celeus flavescens
Colaptes campestris
Melanerpes flavifrons
Veniliornis spilogaster
Brotogeris tirica
Pyrrhura frontalis
Forpus xanthopterygius
Triclaria malachitacea
Pionus maximiliani
Trogon surrucura
Trogon viridis
Trogon rufus
Odontophorus capueira
Pipile jacutinga
Penelope obscura
PL_WES *
Philodendron appendiculatum
Anthurium crassipes
Anthurium scandens
Heteropsis rigidifolia
Heteropsis sp1
Smilax elastica
Allibertia mycifolia
Syagrus romazoffianum
Euterpe edulis
Geonoma gamiova
Geonoma sp1
Poacea sp
Bromelia sp1
Bromelia sp2
Dichorisandra thyrsiflora
Hedychium coronarium
Virola bicuhyba
Xylopia brasiliensis
Guatteria dusenii
Rollinia emarginata
Rollinia sericea
Mollinedia boracensis
Mollinedia floribunda
Mollinedia uleana
Lauraceae sp1
Cryptocarya moschata
Nectandra [4 spp.]
Ocotea [9 spp.]
Persea pyrifolia
Drimys brasiliensis
Drimys winterii
Piper dilatatum
Piper sp
Piper corintoanum
Piper aduncum
Abuta sellowiana
Rhipsalis [5 spp.]
Guapira opposita
Phytolacca dioica
Agonandra sp1
Phoradendron crassifolium
Loranthaceae sp
Struthanthus sp
Struthanthus vulgaris
Struthanthus concinus
Psittacanthus sp2
Psittacanthus sp1
Fuchsia regia
Siphoneugena densiflora
Myrcia [6 spp.]
Marlierea reitzii
Neomitranthes glomerata
Eugenia melanogyna
Eugenia mosenii
Eugenia sp1
Gomidesia schaueriana
Gomidesia affinis
Gomidesia fenzliana
Psidium cattleianum
Psidium guajava
Psidium sp1
Campomanesia guaviroba
Campomanesia xanthocarpa
Campomanesia neriiflora
Ossaea amygdaloides
Leandra [11 spp.]
Miconia [17 spp.]
Maytenus robustus
Maytenus litoralis
Passiflora sp
Clusia criuva
Vismia sp
Ouratea vaccinioides
Sapium glandulatum
Hieronyma alchorneoides
Tetrorchidium rubrivenium
Alchornea triplinervia
Alchornea glandulosa
Casearia sylvestris
Casearia decandra
Andira fraxinifolia
Inga marginata
Inga sessilis
Rubus rosaefolius
Rubus urticaefolius
Rubus brasiliensis
Trema micrantha
Celtis iguanaea
Coussapoa microcarpa
Ficus luschnatiana
Ficus sp
Ficus sp1
Urera baccifera
Cecropia glaziovi
Cucumis sp1
Cayaponia sp1
Cucurbitaceae sp3
Cucurbitaceae sp2
Carica papaya
Zanthoxylum riedelianum
Guarea macrophylla
Cabralea canjerana
Protium heptaphyllum
Tapirira guianensis
Schinus terebinthifolius
Allophylus edulis
Paullinia uloptera
Matayba guianensis
Cupania vernalis

*next page*

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