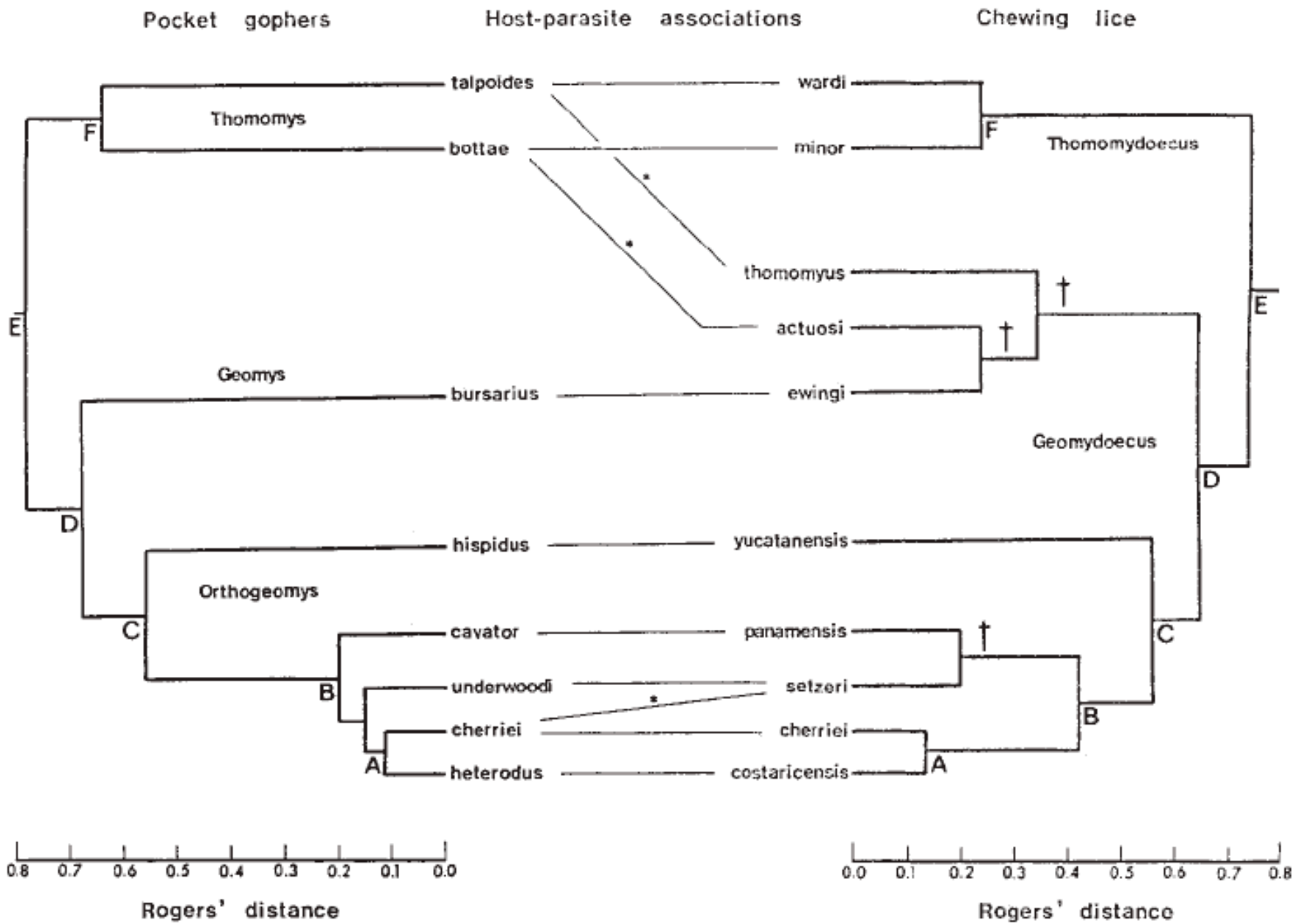


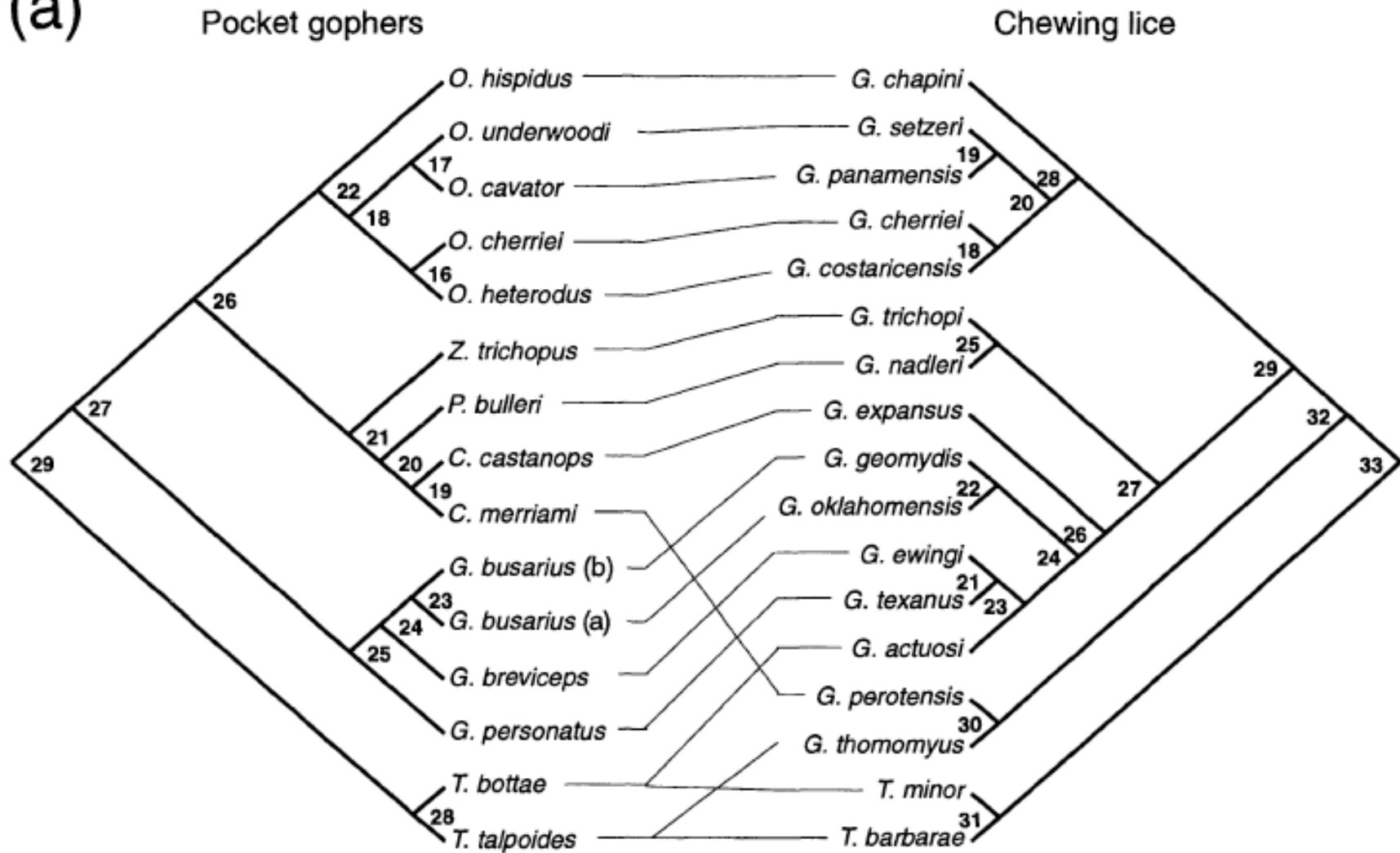
FIGURE 2. A host and parasite phylogeny showing a cospeciation event (●), a duplication (■), a host switch (▶), and a sorting event (○).

3 kinds of speciation events for parasite

sorting: extinction; failure to speciate; 'miss the boat'; missed collection



(a)



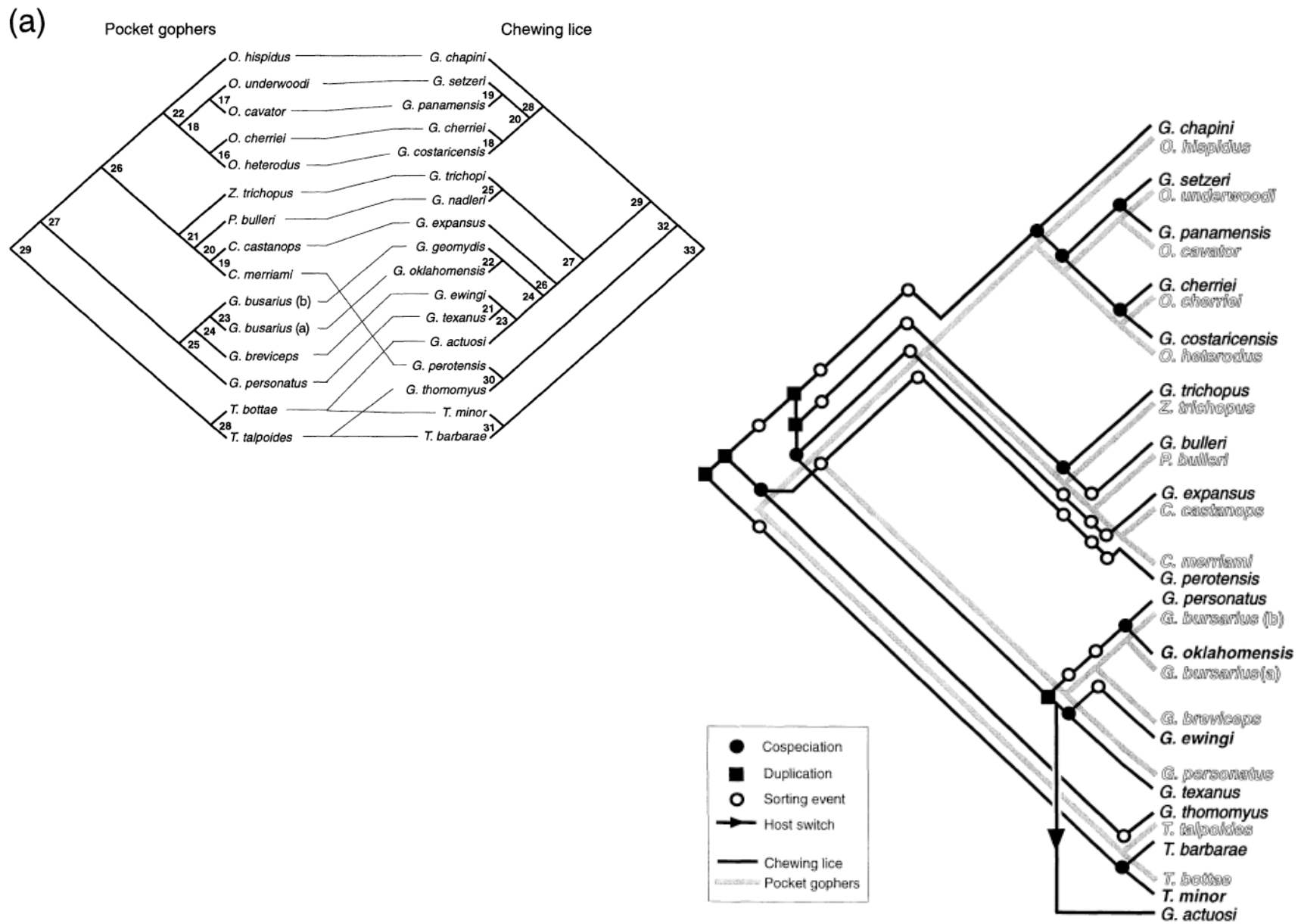


FIGURE 3. A possible reconstruction of the history of the gopher–lice association that postulates 10 cospeciation events, five duplications (in situ speciation of the lice on the same host), 20 sorting events (instances where lice lineages have been lost or remain undetected), and a single host switch (by *Geomydoecus actuosus*)

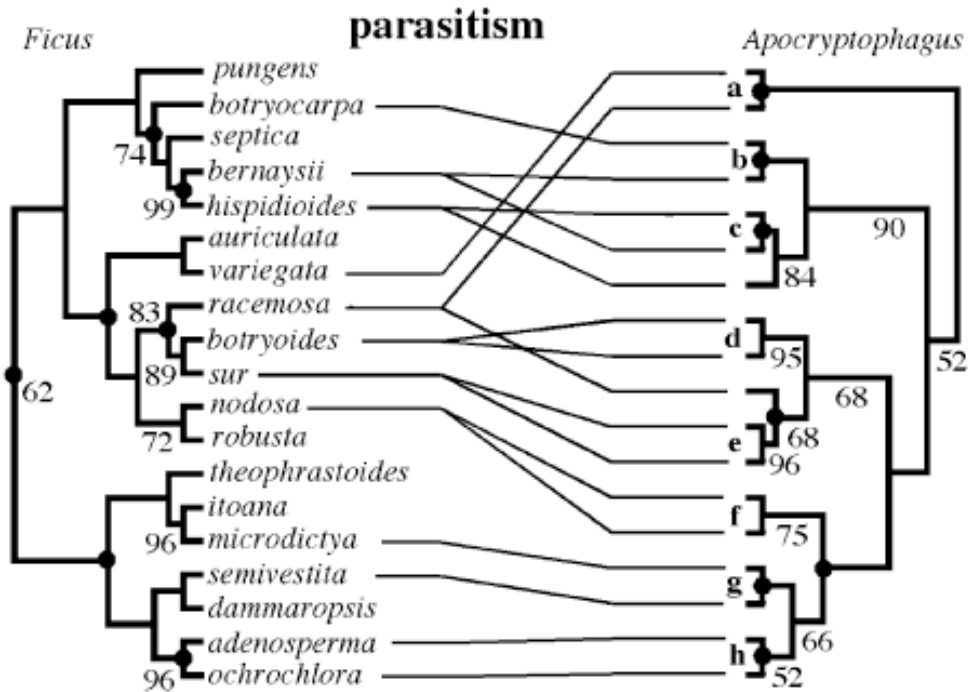
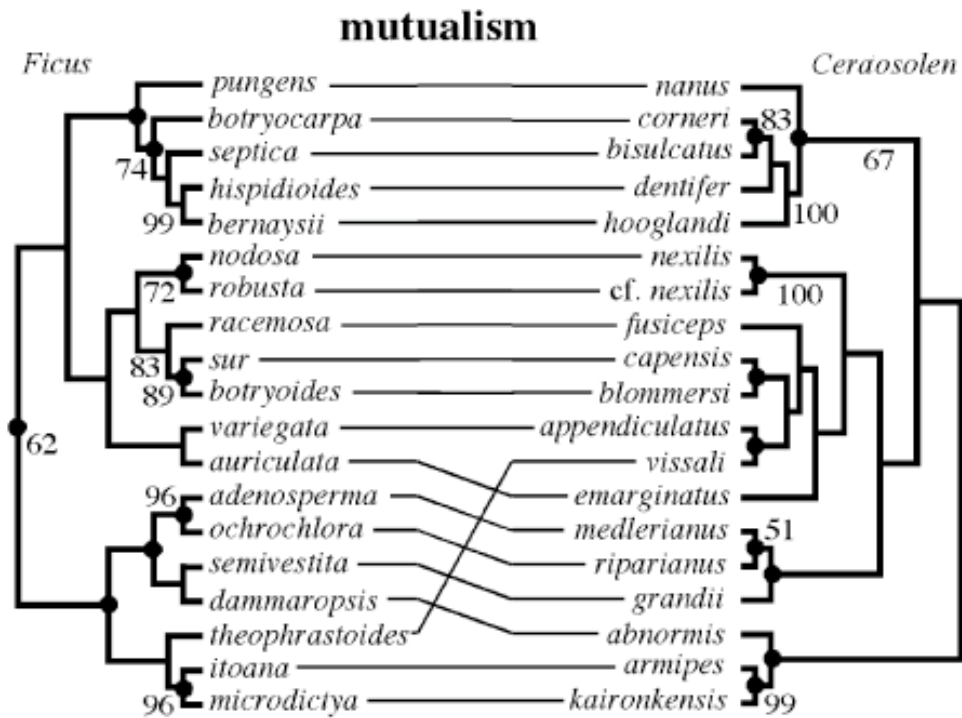


Fig. 2 Evolutionary patterns of host association in pollinating mutualists and nonpollinating parasites of *Ficus* subgenus *Sycomorus sensu lato*. Species associations between pollinating *Ceratosolen* and *Sycomorus* are pairwise, in contrast to *Apocryptophagus*, where multiple unnamed parasite species may attack a single host species and some host species are not attacked at all. Cospeciating nodes inferred from reconciled trees are marked by dots. Bootstrap percentages > 50% based on 1000 replicates are listed below the nodes. Phylogenies are based on parsimony analyses of nuclear ribosomal ITS sequences for *Ficus* and mitochondrial COI sequences for fig wasps. (a–h) refer to species pairs in Fig. 3.

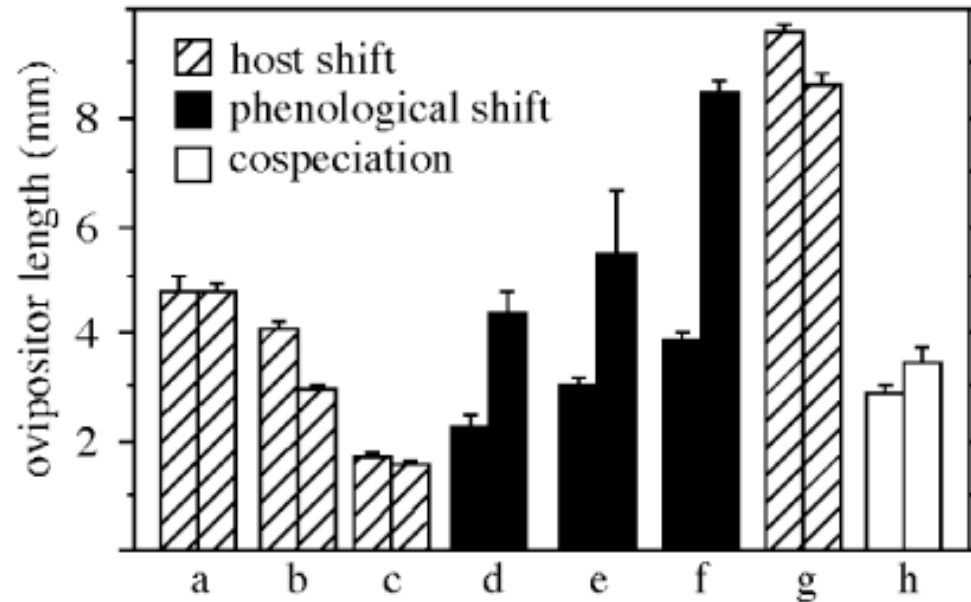


Fig. 3 Sister group comparisons of ovipositor length in the fig parasite, *Apocryptophagus*, under three alternative modes of speciation. (a–h) refer to sister groups in Fig. 2. Sister species (h) attacking sister hosts, *F. adenosperma* and *F. ochrochlora*, represent cospeciation. In contrast (a–c, g) are sister species on nonsister hosts, indicating potential instances of host switching. Closest relatives attacking the same host are represented by (d–f). We predict less divergence in ovipositor length between sister species in cases of cospeciation and host switching than in the case of a phenological shift, where divergence results from a shift in the relative timing of oviposition. Greater ovipositor length divergence between sister species (d–f) indicates a relatively large shift in the timing of oviposition, as the thickness of the fig wall increases during development (Kerdelhue & Rasplus 1996).

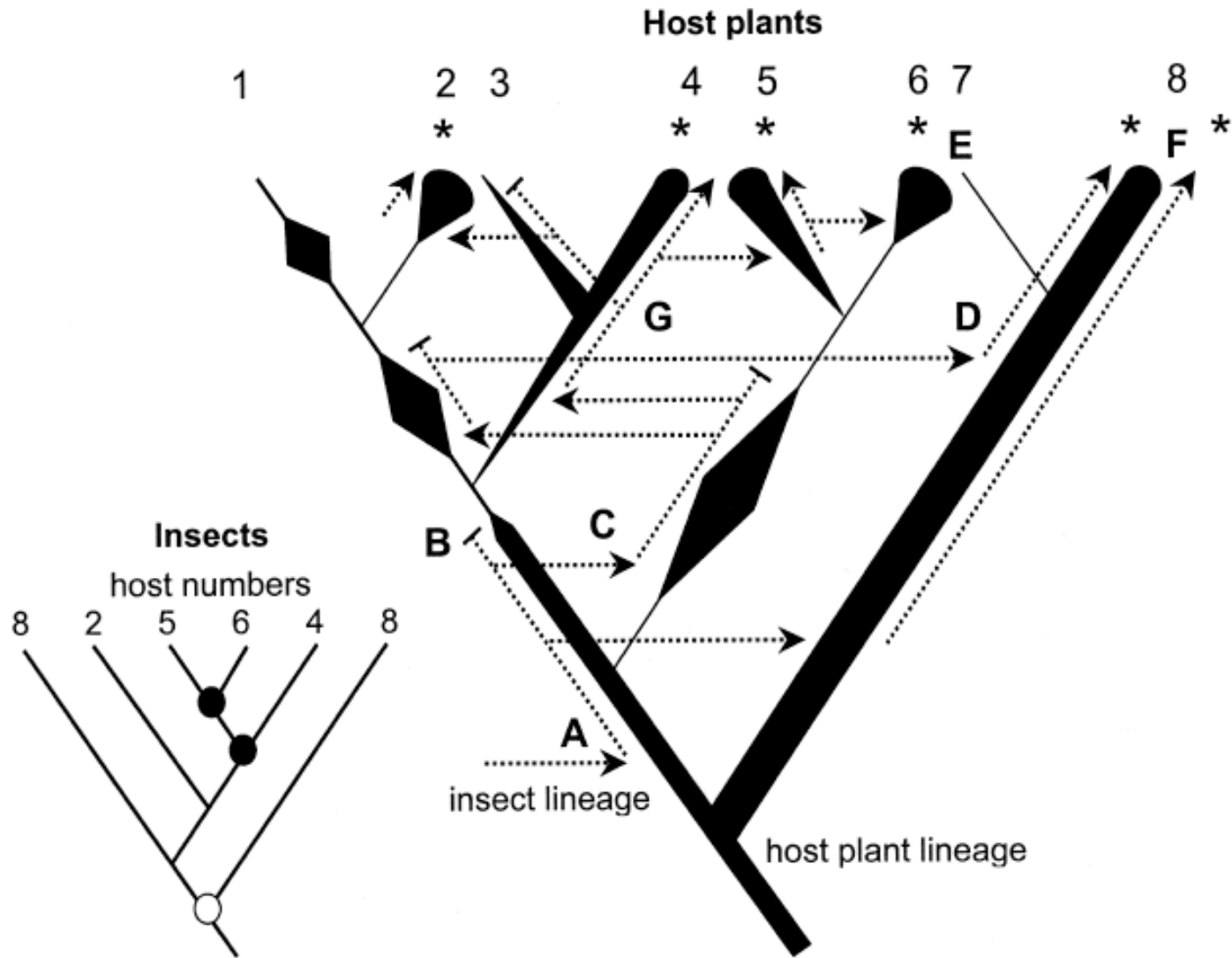


FIGURE 1. A hypothetical fluctuating host plant lineage (right), illustrating the factors that may influence how an insect lineage interacts with a fluctuating plant lineage and an interpretation of the resultant phylogenetic patterns (left). This model takes into account the susceptibility factors for host switching suggested by examination of the ecology of Canary Island psyllids and their legume hosts. Host abundance is indicated by line width. Examples of different events are labeled: A = colonization of preexisting host lineage by insect lineage; B = loss of insect due to extinction; C = increase in host abundance after bottleneck leads to vacant host, usually filled by near host switching from related plants; D = abundant host and geographical proximity may lead to wide host switching; E = rare plants are unlikely to be colonized; F = temporally stable host lineages may sustain multiple insect lineages; G = occasional cospeciation events. The asterisks indicate extant insect taxa, whose phylogeny is shown (left). Given the two phylogenies, certain events would be misinterpreted in a TreeMap analysis: the solid circles are cospeciation events, and the open circle is a duplication event (speciation of parasites in situ on the host).

colonization of the
Genisteae by psyllids:

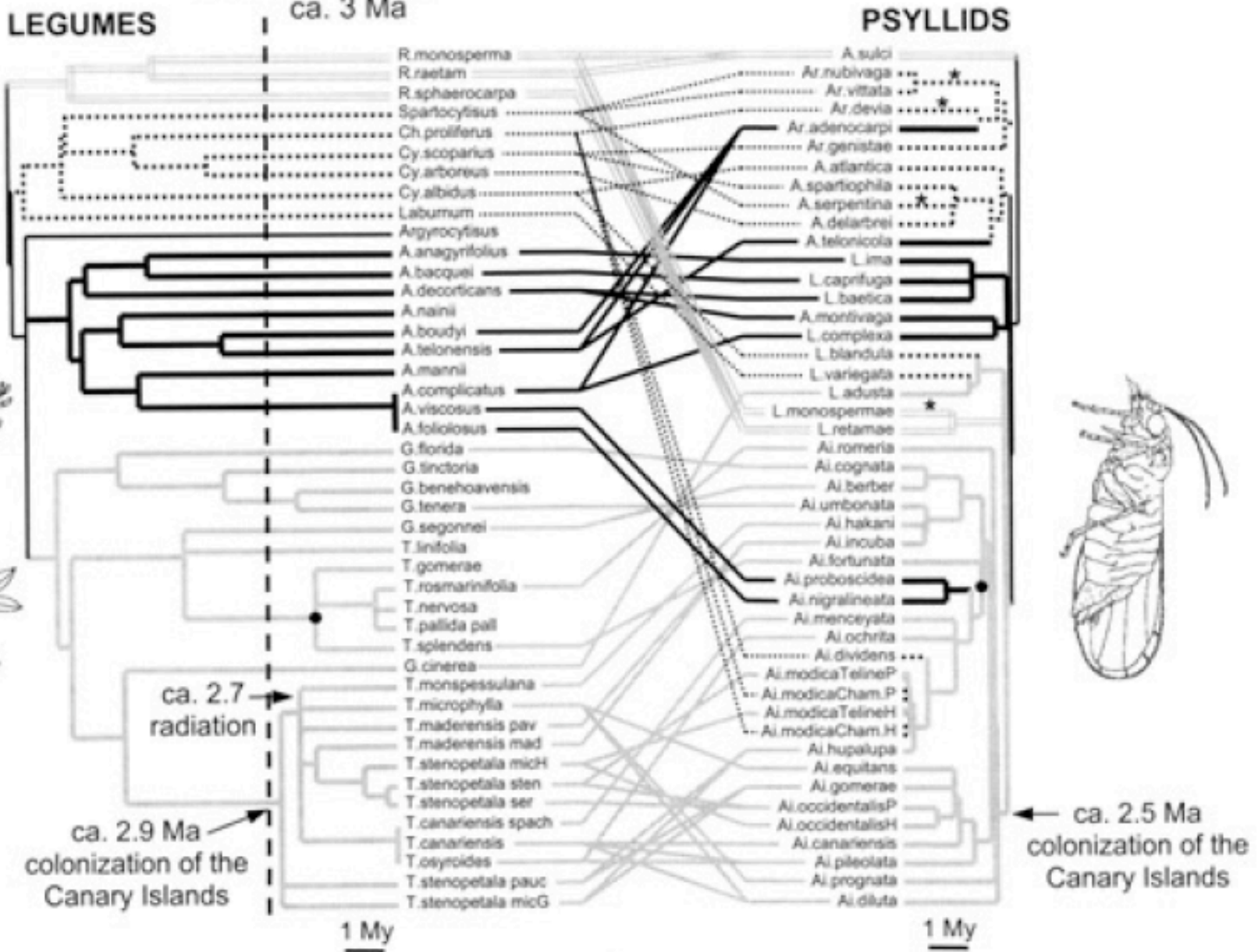


FIGURE 2. A tanglegram of the insect–host–plant relationships of a group of legume-feeding psyllids (right) and their Genisteeae (broom) hosts (left). Four main legume lineages are distinguished: *Retama* (double gray line), *Cytisus* (dotted black line), *Adenocarpus* (thick black line), and *Genista* (thick gray line). The psyllids on these hosts are indicated by the same type of branches. Most of the psyllids on each host group are from a single psyllid group, but some psyllid–legume associations have involved a wide host switch between legume groups. The dates on the psyllid tree are much younger than the dates on the legume tree, indicating a colonizing, not a cospeciating, psyllid, lineage. Calibration points are indicated by solid circles. Of several independent colonizations of the Canary Islands by legumes and psyllids, only one could have been contemporaneous (around 2.5 and 2.9 MY ago), with a single potential cospeciation event during the radiation of legumes and psyllids in the Canary Islands (Fig. 3). The evolution of other island psyllid lineages (indicated by asterisks) substantially postdate the evolution of their island legume hosts. Psyllid genera: *Arytaina* (Ar.), *Arytainilla* (A.), *Arytinnis* (Ai.), *Livilla* (L.); legume genera: *Chamaecytisus* (Ch.), *Cytisus* (Cy.), *Genista* (G.), *Teline* (T.).

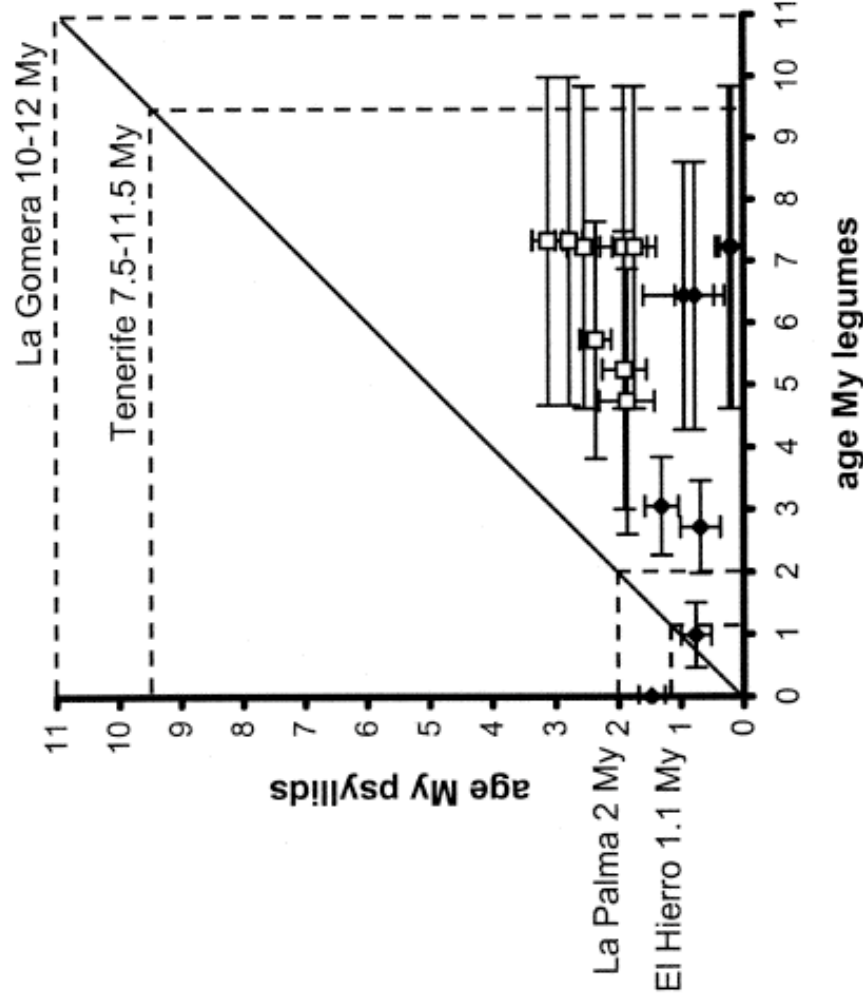
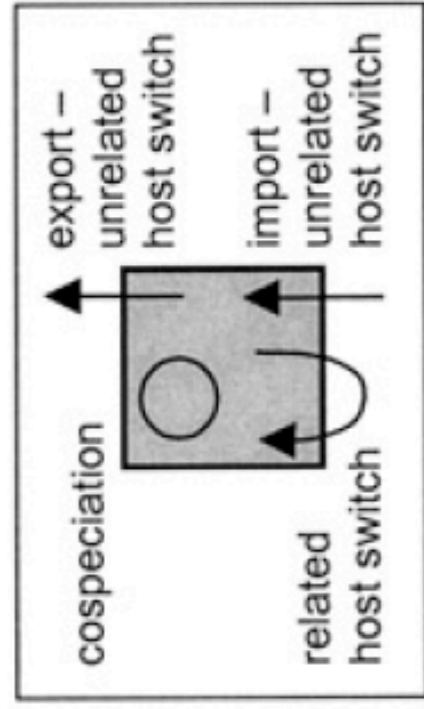
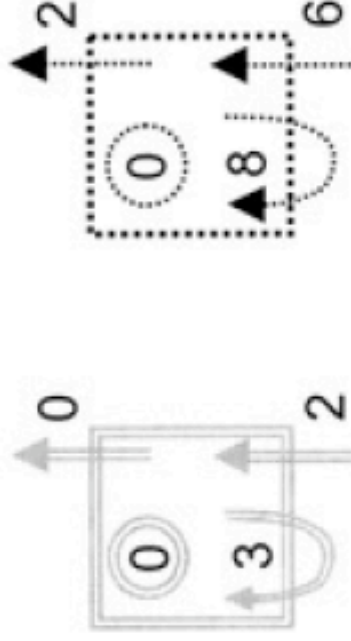


FIGURE 3. Comparative ages of 16 putative cospeciation events suggested by TreeMap (□ = continental; ◆ = island). Reconciled psyllid and legume phylogenies, without considering dates of divergence, produce associated legume nodes that are much older than the putatively synchronous psyllid nodes. This plot shows the cospeciation events determined by TreeMap, which optimizes a psyllid node onto the most recent common ancestor of all its host plants (i.e., no assumption of host switching). All but one of the results are temporally implausible. The dates plotted represent the means and SDs of 100 bootstrap replicates.



Retama *Cytisus* group



Adenocarpus *Genista* group

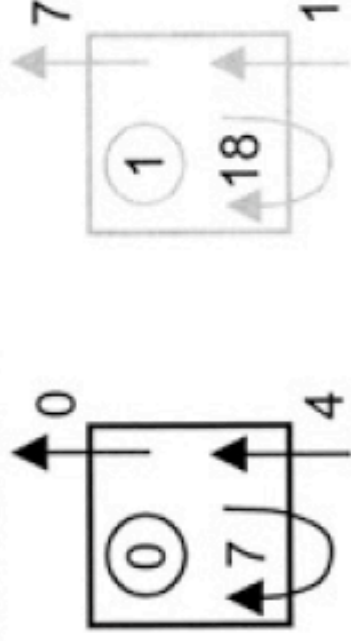


FIGURE 4. The levels of different types of host switching and cospeciation implied for the four major legume lineages, on the assumption that the presence of asynchronous nodes rules out cospeciation over most of the association. The legume lineages are coded as in Figure 2: *Retama* (double gray line), *Cytisus* (dotted black line), *Adenocarpus* (thick black line), and *Genista* (thick gray line). The only possible cospeciation events are found in the *Genista* group, abundant in the Canary Islands and Madeira, where there has been a recent radiation of both legumes and psyllids. The majority of the host switching (61%) apparently occurred between related hosts (within major legume lineages) and produced some shared phylogenetic patterns that can be misinterpreted as cospeciation.