

TABLE 1. Genbank accession numbers for 11 additional sequences used in this study.

species	Genbank accession number	reference
<i>Calicotome villosa</i>	Z72252 + Z72253 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Chamaecytisus proliferus</i>	Z72234 + Z72235 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Chamaespartium tridentatum</i>	Z72280 + Z72281 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Cytisus albidus</i> (= <i>Chamaecytisus mollis</i>)	AF007472 (ITS1-5.8S-ITS2)	Aïnouche & Bayer, 1999
<i>Cytisus arboreus</i>	Z72240 + Z72241 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Cytisus scoparius</i>	Z72246 + Z72247 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Laburnum anagyroides</i>	Z72226 + Z72227 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Retama monosperma</i>	Z72302 + Z72303 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Retama raetam</i>	Z72304 + Z72305 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Retama sphaerocarpa</i>	Z72306 + Z72307 (ITS1 + ITS2)	Käss & Wink, 1997
<i>Spartocytisus supranubius</i>	Z72250 + Z72251 (ITS1 + ITS2)	Käss & Wink, 1997

Opposite page:

FIGURE 1.

Tanglegram showing a complex pattern of host associations between psyllids and their legume hosts.

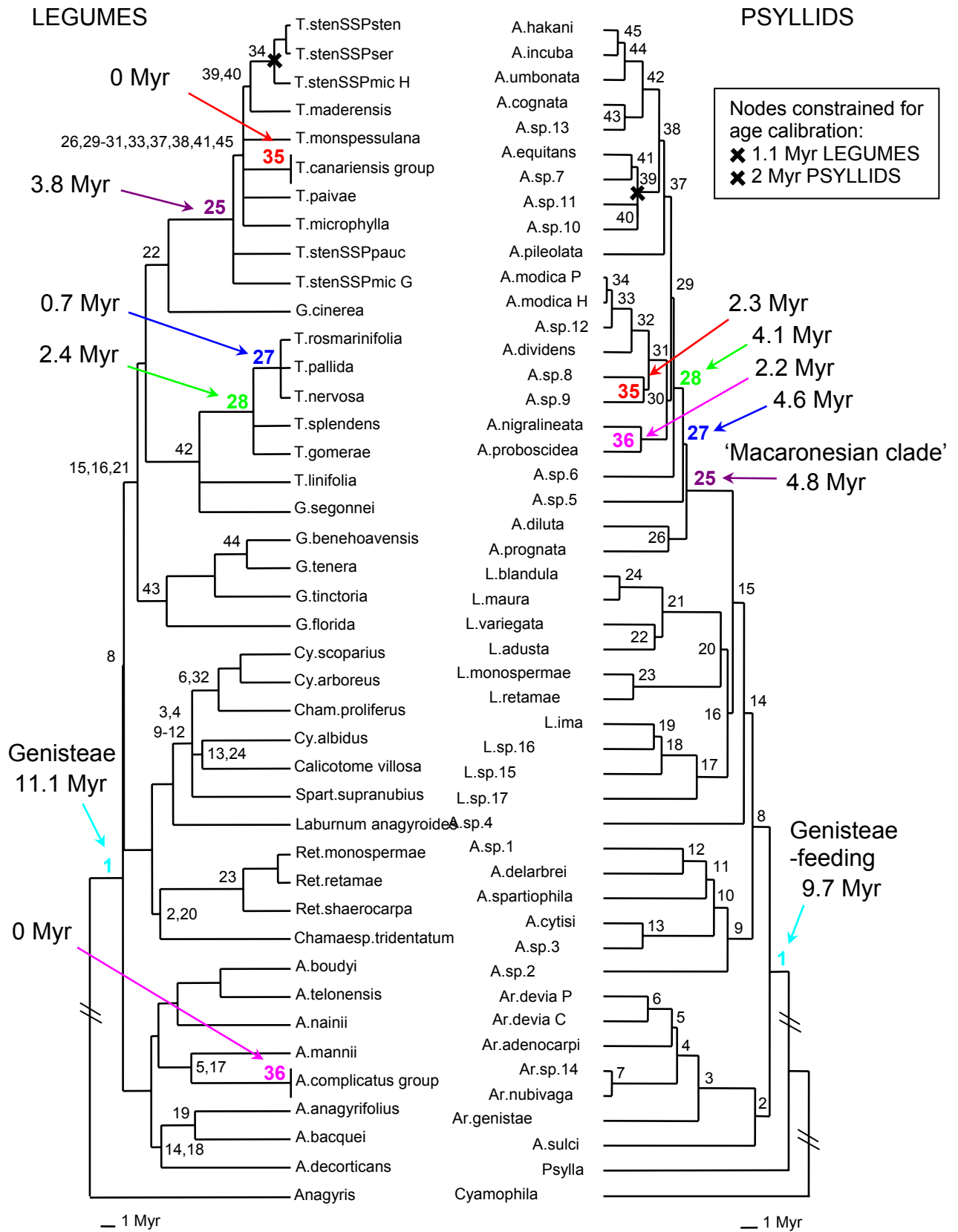


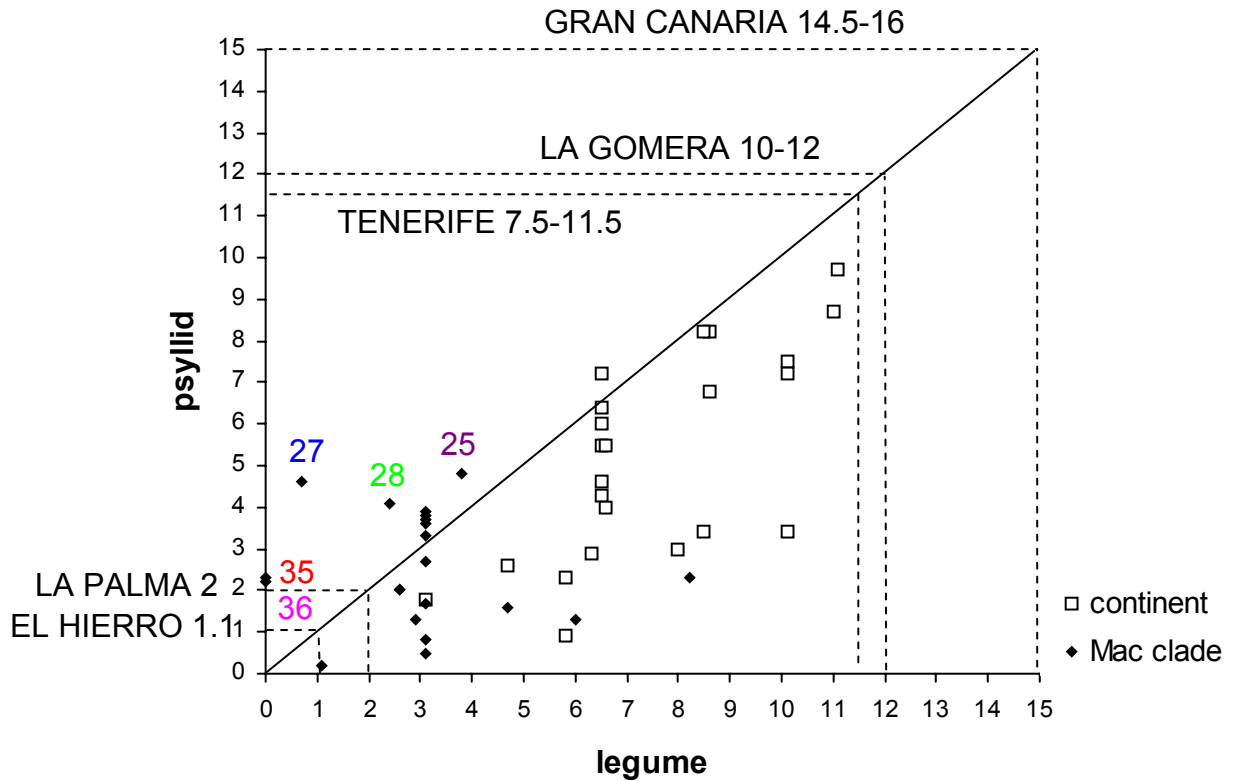
FIGURE 2. NPRS (nonparametric rate-smoothed) trees for the legume hosts and psyllids. Numbered nodes correspond to those in Table 2, and represent the psyllid nodes and the comparative host taxon/group node. The majority of the node ages on the psyllid tree are younger than the age of the corresponding node on the legume tree (i.e. sequential, see Figure 3), including ‘node 1’ which represents the initial diversification of the Genistee and the Gensiteae-feeding psyllids. Several nodes (numbered) in the ‘Macaronesian clade’ of psyllids appear to predate the corresponding node in the legume tree and these are discussed in the text.

TABLE 2. Node number and corresponding ages of nodes in legume and psyllid phylogenies.

node no.	age (Myr) of legume node	age (Myr) of psyllid node
1	11.1	9.7
2	8.6	8.2
3	6.5	5.5
4	6.5	4.3
5	6.6	4
6	4.7	2.6
7	–	0.5
8	11	8.7
9	6.5	7.2
10	6.5	6.4
11	6.5	6
12	6.5	4.6
13	5.8	2.3
14	8.5	8.2
15	10.1	7.5
16	10.1	7.2
17	6.6	5.5
18	8.5	3.4
19	6.3	2.9
20	8.6	6.8
21	10.1	3.4
22	8	3
23	3.1	1.8
24	5.8	0.9
25	3.8	4.8
26	3.1	3.8
27	0.7	4.6
28	2.4	4.1
29	3.1	3.9
30	3.1	3.7
31	3.1	2.7
32	4.7	1.6
33	3.1	0.5
34	1.1	0.2
35	0	2.3
36	0	2.2
37	3.1	3.6
38	3.1	3.3
39	2.6	2
40	2.6	2
41	3.1	1.7
42	8.2	2.3
43	6	1.3
44	2.9	1.3
45	3.1	0.8

↓ 'Macaronesian clade'

Node age (Myr) for psyllid and legume phylogenies



Age (Myr) of 'cospeciation nodes' for psyllid and legume phylogenies

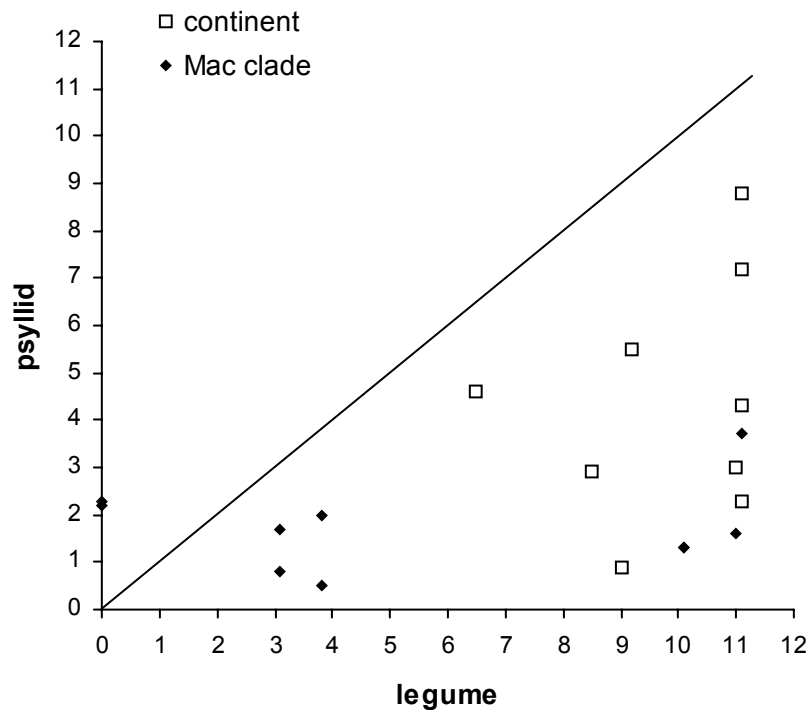


FIGURE 3. Comparative ages of psyllid and legume nodes are shown relative to island age. The majority of the node ages on the psyllid tree are younger than the age of the corresponding node on the legume tree (upper plot). Nodes which represent 'cospeciation events' when optimized in TreeMap are shown (lower plot). These would be expected to fall on, or near to the diagonal if they represented contemporaneous speciation events.

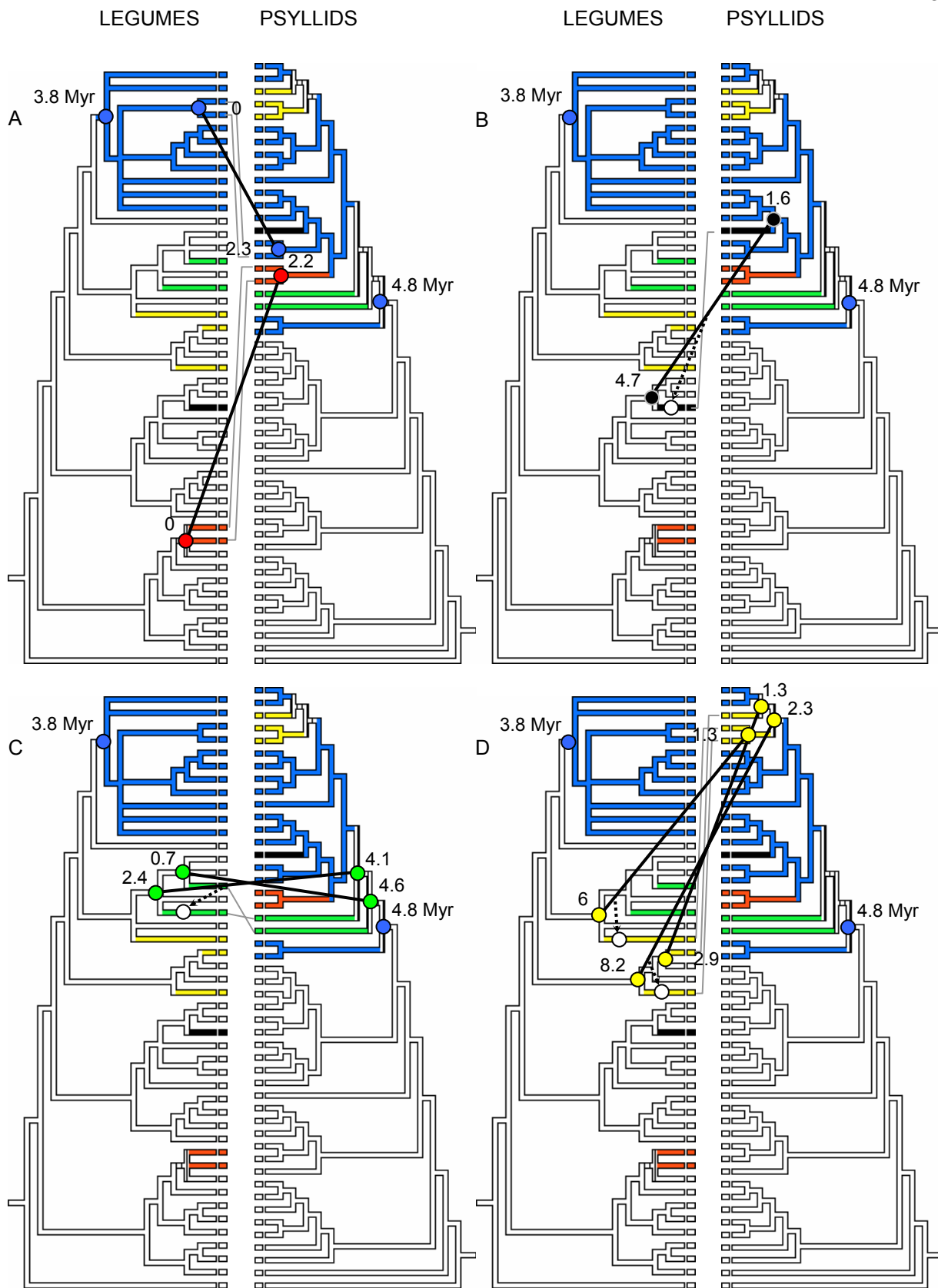


FIGURE 4. Illustration of methods used for associating psyllid nodes with host nodes. Numbers at nodes indicate age (Myr). See text for discussion of optimization methods and interpretation of nonlinear and noncontemporaneous node ages.

HOSTS

- *T. monspessula* group
- *T. linifolia* group
- *Genista*
- *Adenocarpus*
- *Chamaecytisus*

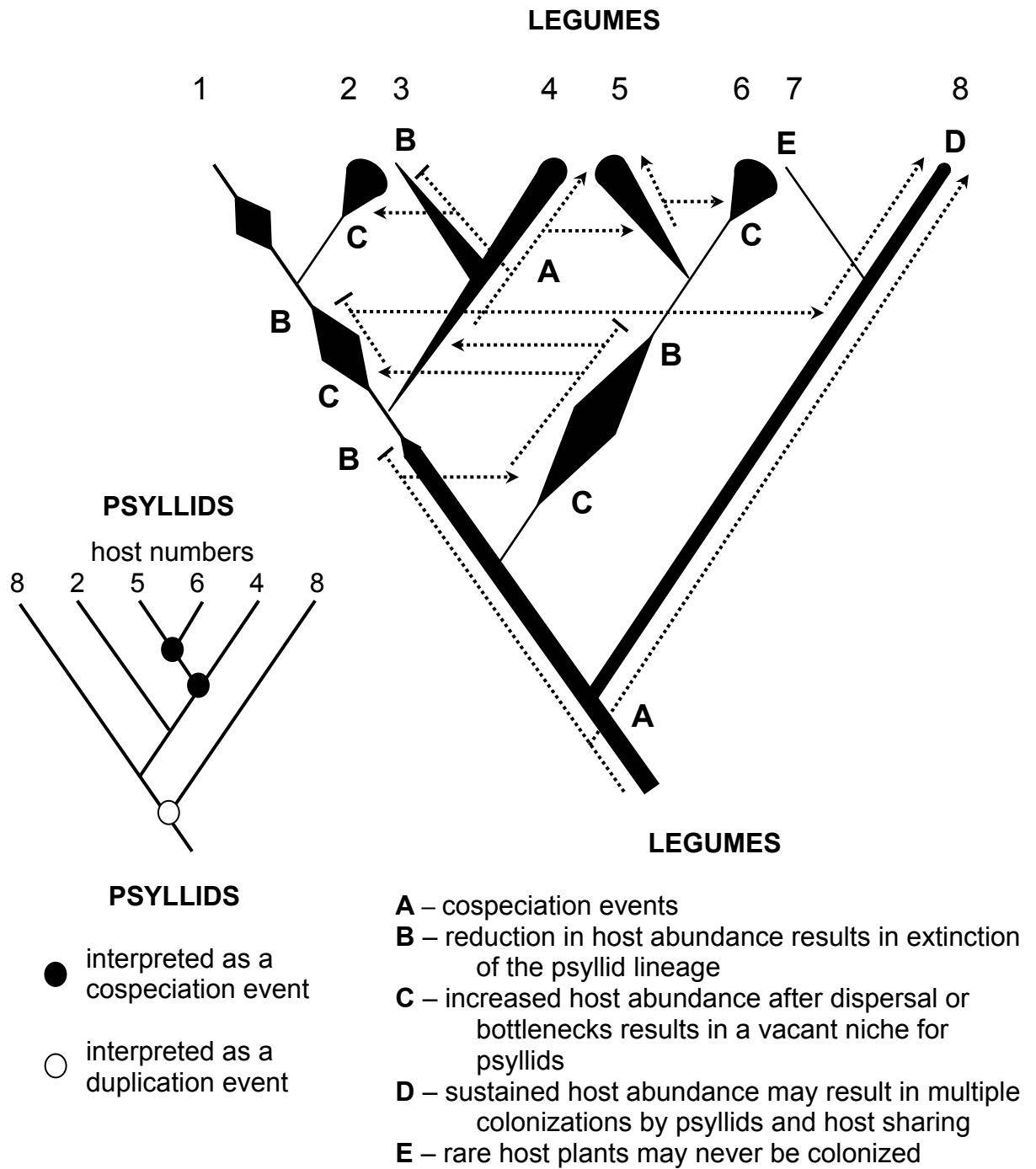


FIGURE 5. Hypothetical reconstruction of a fluctuating host lineage, and in response, opportunistic host switching by psyllids. There are some cospeciation events, but there is a greater degree of host switching, typically between closely related hosts. This history of host switching could not be reconstructed from the resultant psyllid phylogeny shown, and several misinterpretations of the historic associations may arise: such as the divergence of psyllids on hosts 4, 5 & 6, these could be interpreted as cospeciation events as they are sister taxa on sister hosts, but the reconstruction shows that the events are neither contemporaneous, nor is there sustained phylogenetic tracking (i.e. association by descent); another case for possible misinterpretation presents the cospeciation event at the base of the phylogeny as a duplication event which assumes sympatric speciation of psyllids on the same host (8) without host switching.