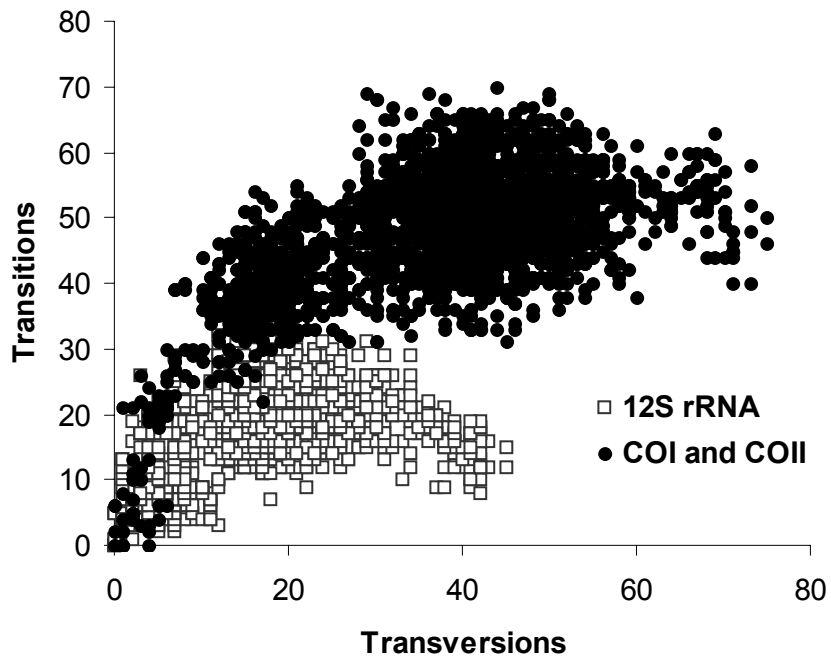


FIGURE 2. Substitution rates shown as transitions/transversions for the 12S and CO regions.



Opposite page:

FIGURE 3.

Phylograms of the three data sets in this study. A – 12S, one of the 750 MP trees based on 12S rRNA sequences (length 807, CI 0.32 excluding uninformative characters, RI 0.614); B – CO, one of the six MP trees based on COI-tRNA leucine-COII sequences (length 2280, CI 0.248 excluding uninformative characters, RI 0.613); C – morphology, one of the 18 MP trees based on 67 morphological characters (length 554, CI 0.484 excluding a single uninformative character, RI 0.612). Thick branches indicate nodes with bootstrap values > 75%, and dotted branches indicate nodes that collapse in the Strict consensus. Labelled nodes: A = *Arytainilla*, AR = *Arytaina*, L = ‘core *Livilla*’, M = ‘Macaronesian clade’. Where samples occur on different host plants, these are indicated (abbreviated from Table 2). Abbreviated codes for sample origin and labelled nodes (Figs 3-5): Scotland – SC, Portugal – PO, Spain – SP, Morocco – MO, Madeira – MA, Canary Islands – CI: Gran Canaria – C, Tenerife – T, La Gomera – G, La Palma – P, El Hierro – H.

Opposite page:

FIGURE 4.

One of the eight MP trees based on the combined 12S rRNA and COI-tRNA leucine-COII sequences (length 3112, CI 0.265 excluding uninformative characters, RI 0.609). Thick branches indicate nodes with bootstrap values > 75%, and dotted branches indicate nodes that collapse in the Strict consensus. Labelled nodes: A = *Arytainilla*, AR = *Arytaina*, L = 'core *Livilla*', M = 'Macaronesian clade'. MED – Mediterranean, see Figure 3 for other distribution codes. Note: as this analysis includes all individuals sampled for 12S and CO, branch lengths will be proportionally shorter for those taxa/individuals only represented in one data set (sampling is given in Table 2).

Opposite page:

FIGURE 6.

Phylogram of one of the eight MP trees from the total evidence analysis – combined molecular and morphological data, reduced to include all the Macaronesian taxa (plus intraspecific sampling) and selected continental sister taxa. Unequivocal colonizations of the Canary Islands, and equivocal colonizations of Madeira and the continent are mapped onto the tree, as are colonizations of host genera (using ACCTRAN optimization for the continental and Madeiran species). Distributions for all the Canary Island species are illustrated.

Opposite page:

FIGURE 7.

Cladogram of the combined molecular analysis, including those species for which the host associations have been established. Host groups are mapped as an unordered character using ACCTRAN optimization. Major geographic colonization events in the psyllid group (i.e. between: Canary Islands/continent/Madeira; indicated by *) were apparently accompanied by selection of a host related to the original host (i.e. in the same major plant groups) suggesting an important role for preadaptation to particular hosts in colonizing psyllids. White branch tips indicate possible ambiguity in host group assignment for *Laburnum*: *Cytisus* group; and *Spartium* and *Chamaespartium tridentatum*: *Genista* group.