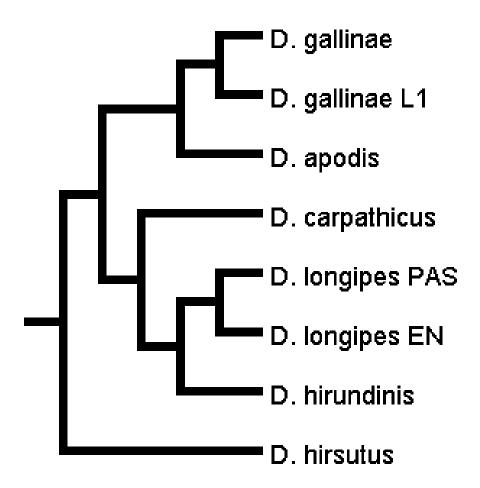
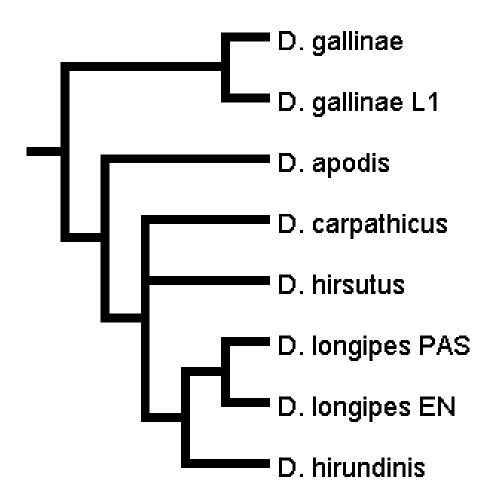
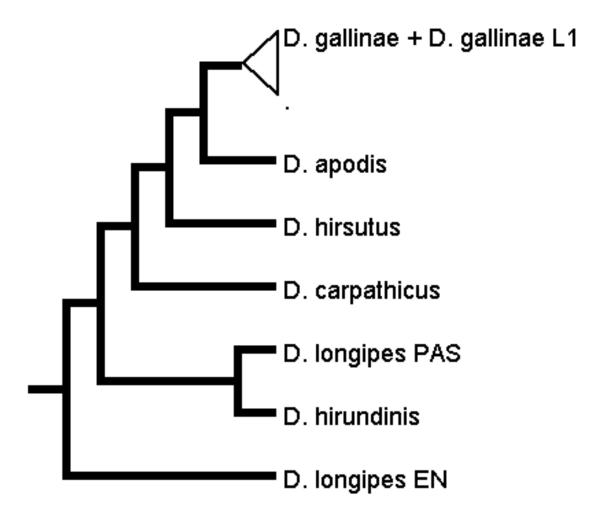
Appendix 5

The different topologies obtained at the specific level within *Dermanyssus* in multi-gene analyses and in multi-isolate analyses.

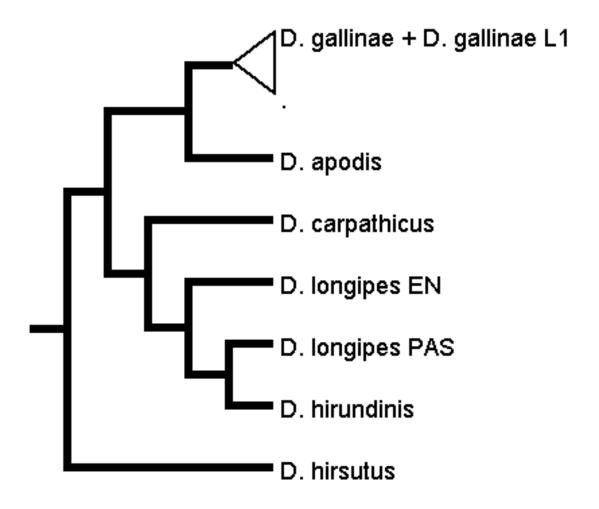
A triangle followed by D. gallinae + D. gallinae L1 represents a D. gallinae clade from within which the clade of L1 isolates is branching.



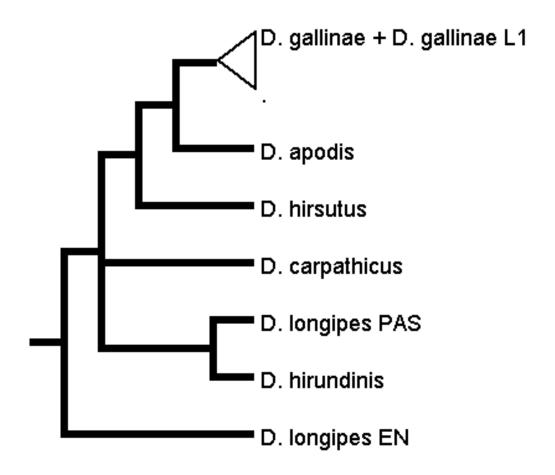


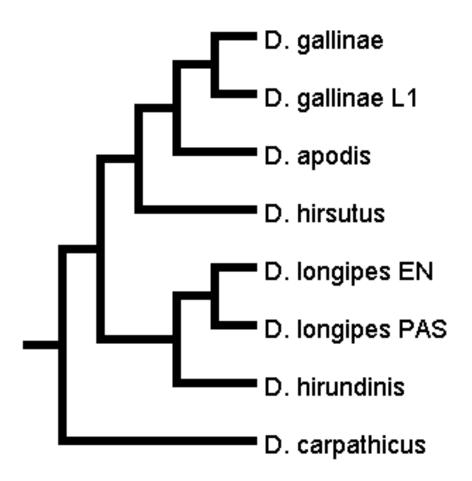


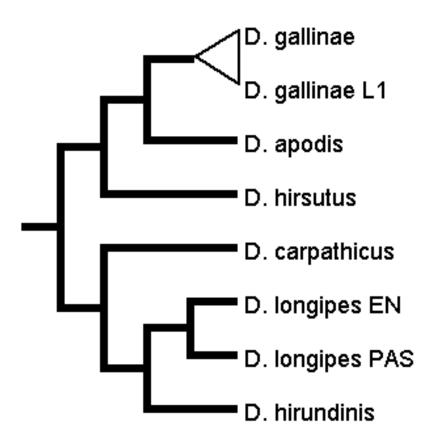
Top6

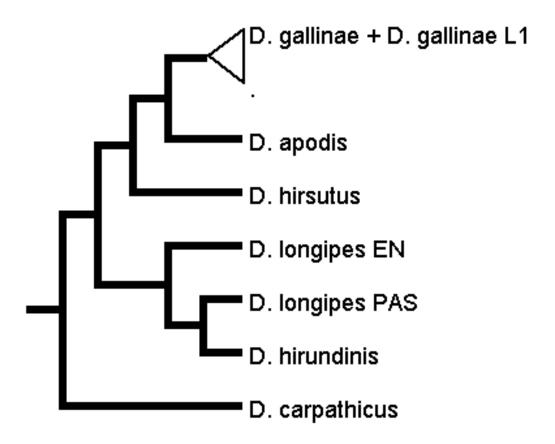


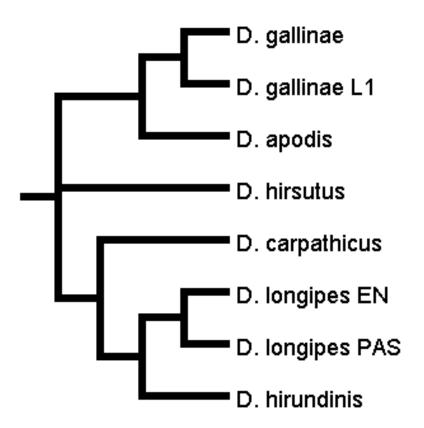
Top7

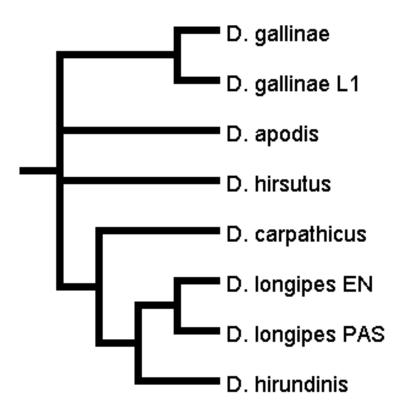


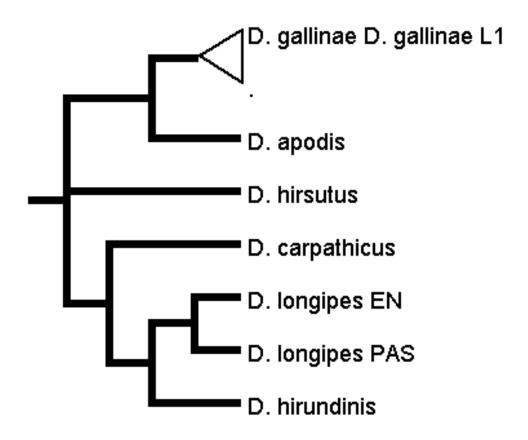


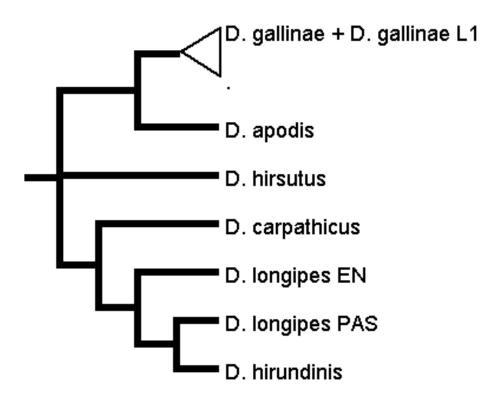


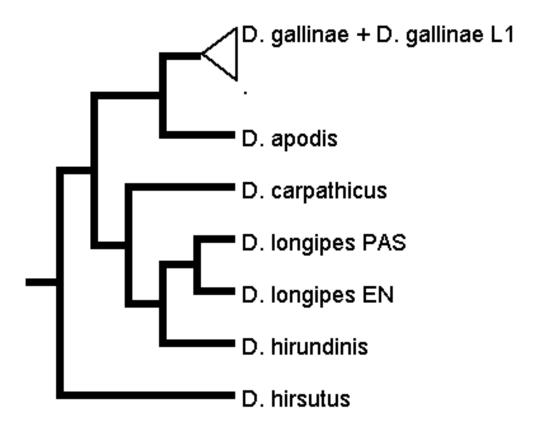


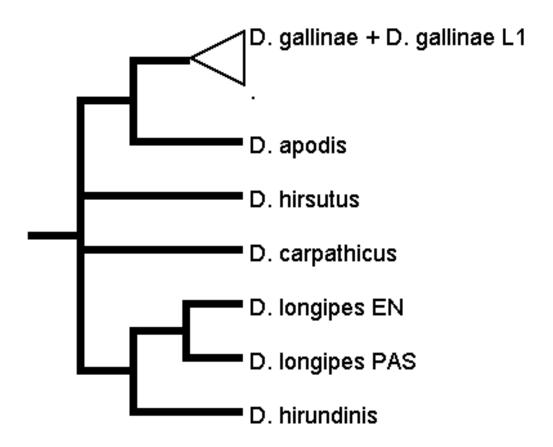


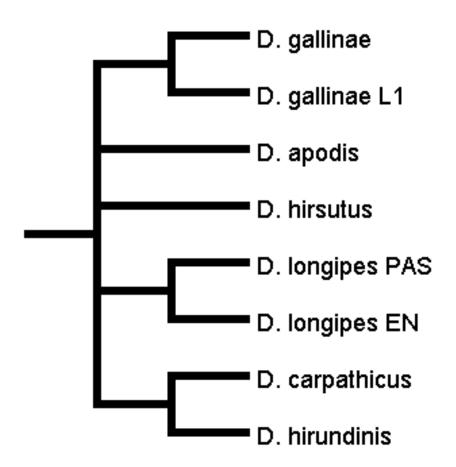


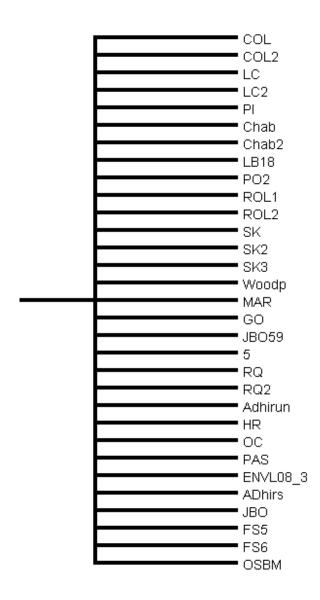




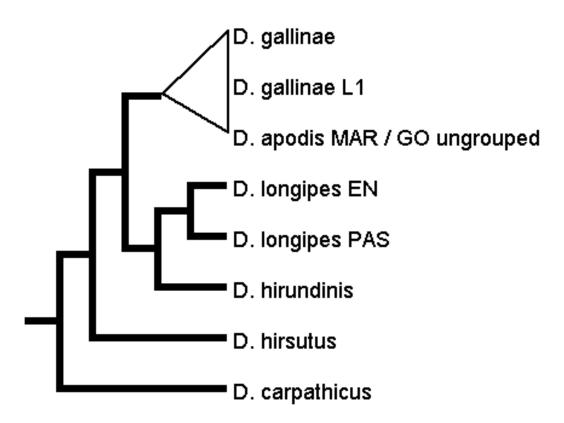


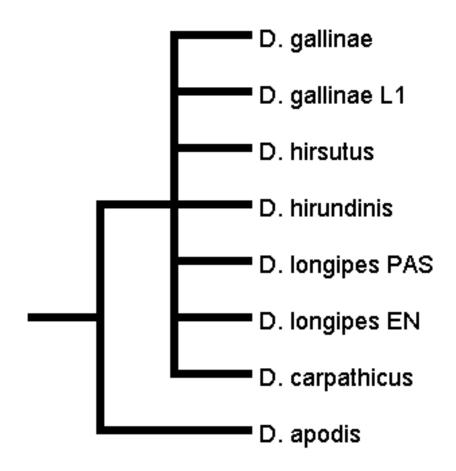


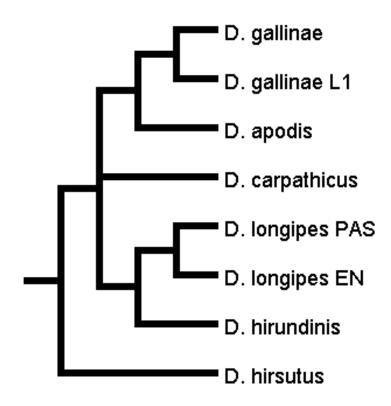


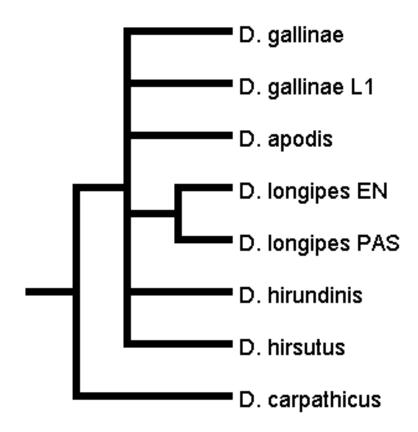


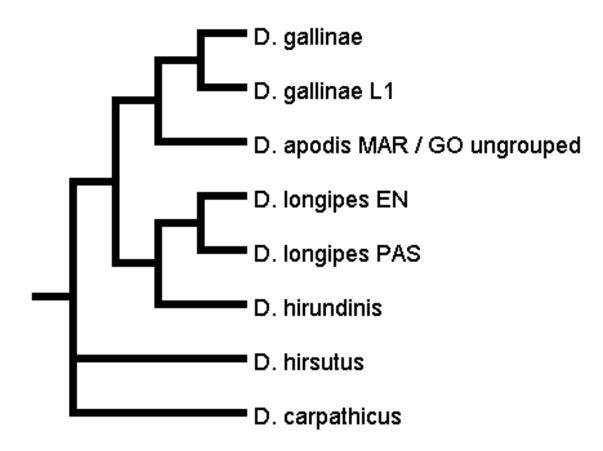
Top20

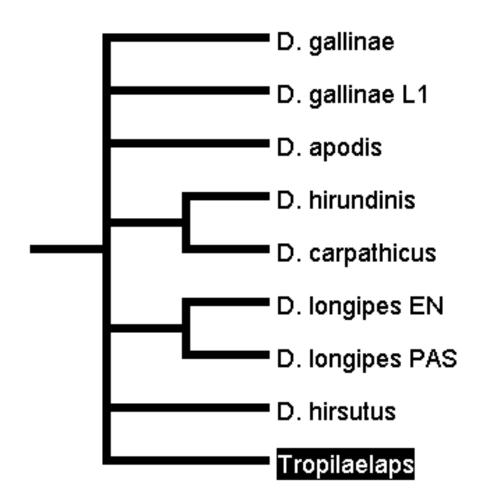


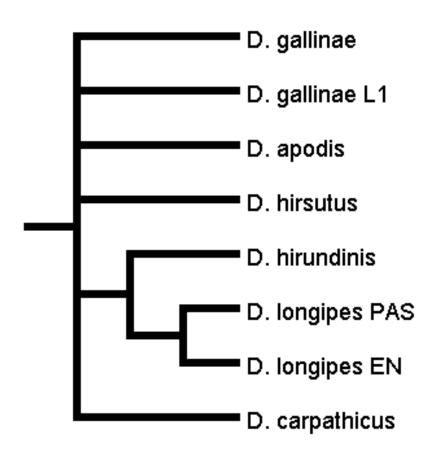


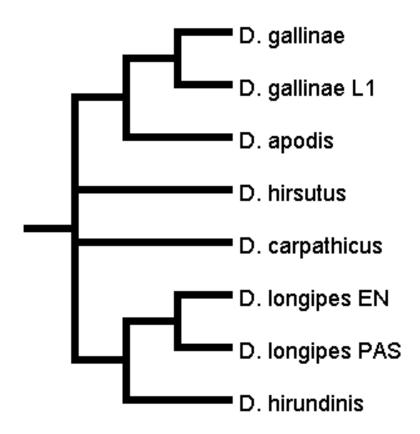


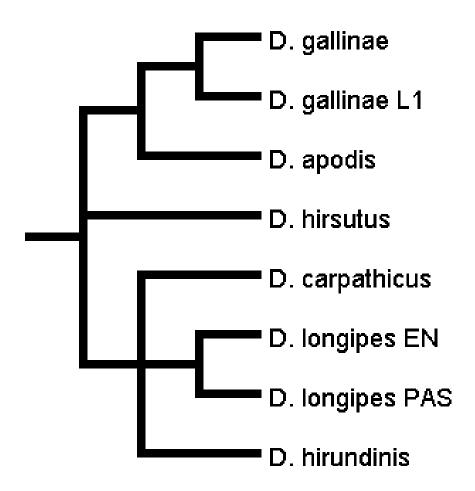


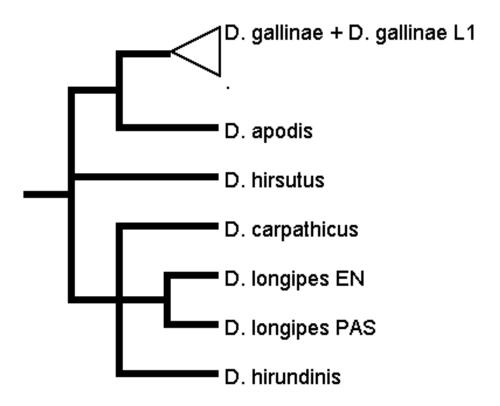


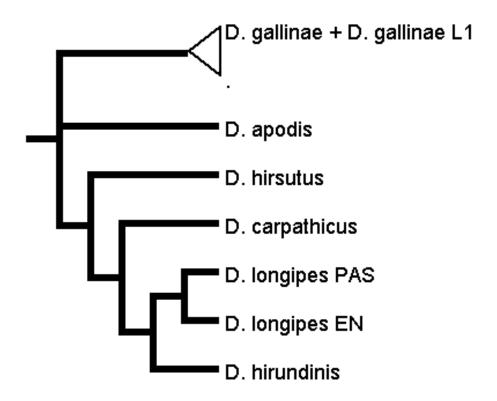


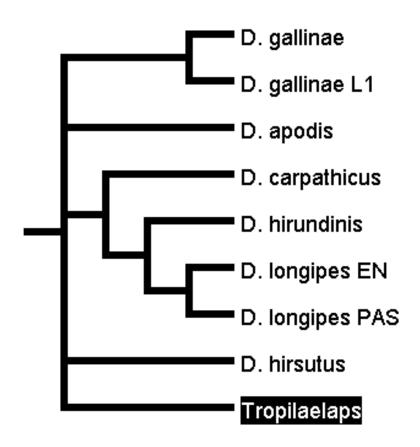


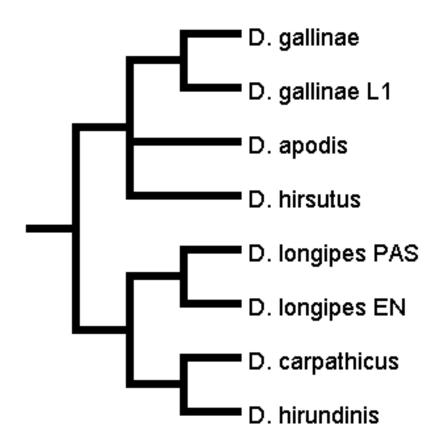


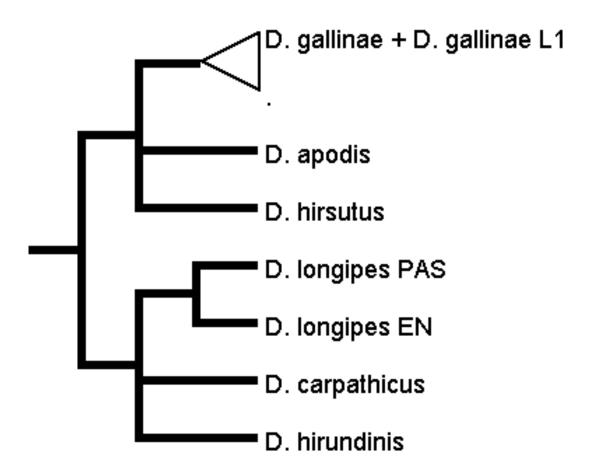


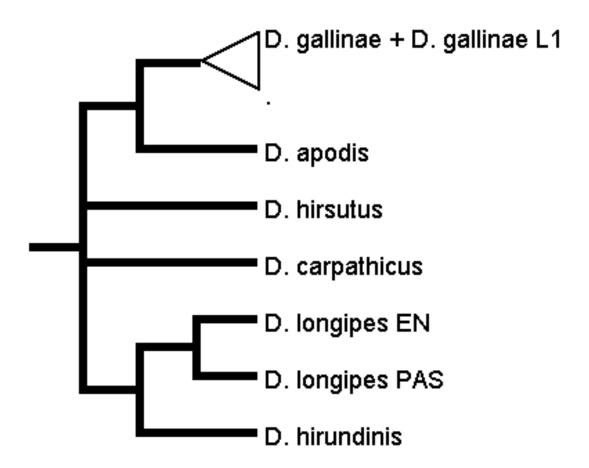


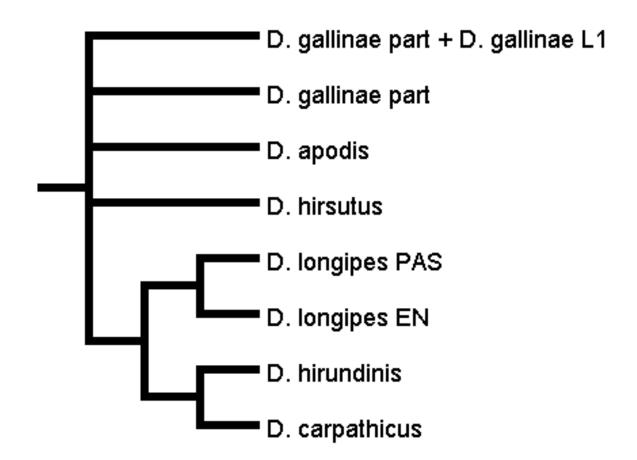


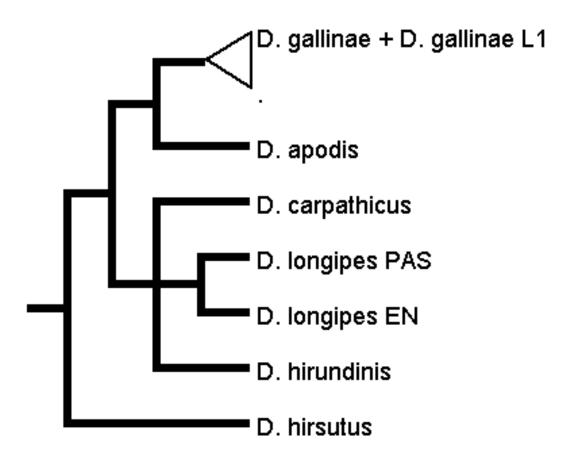


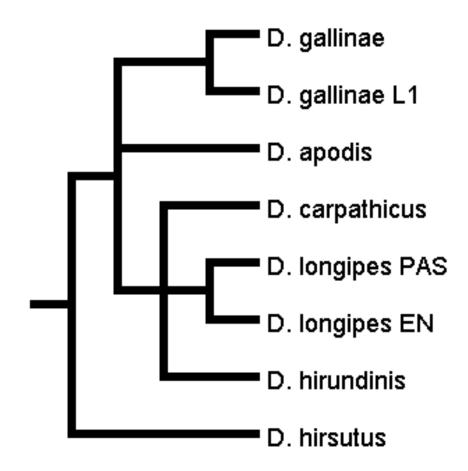


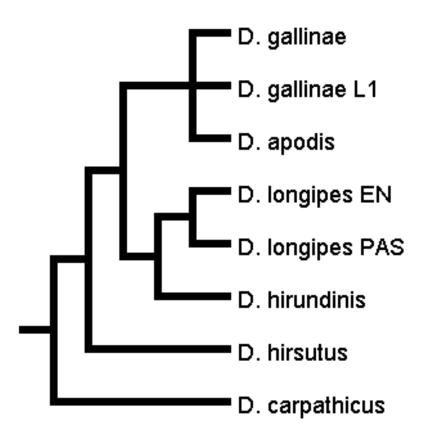


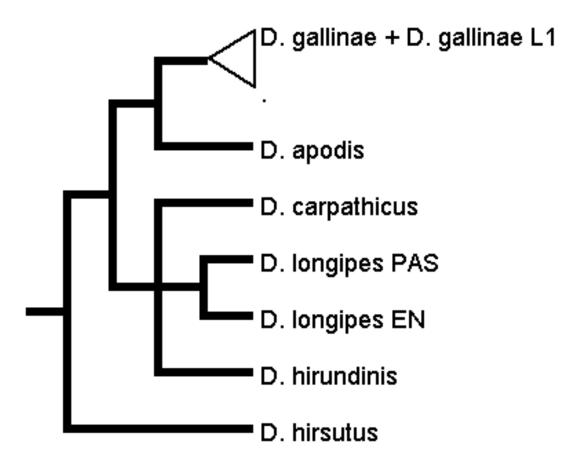


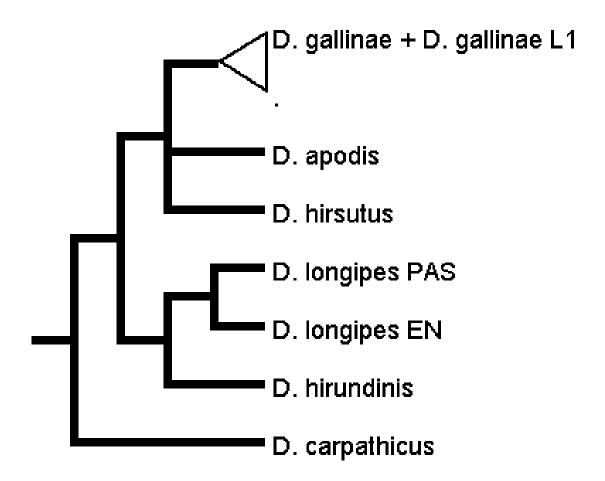


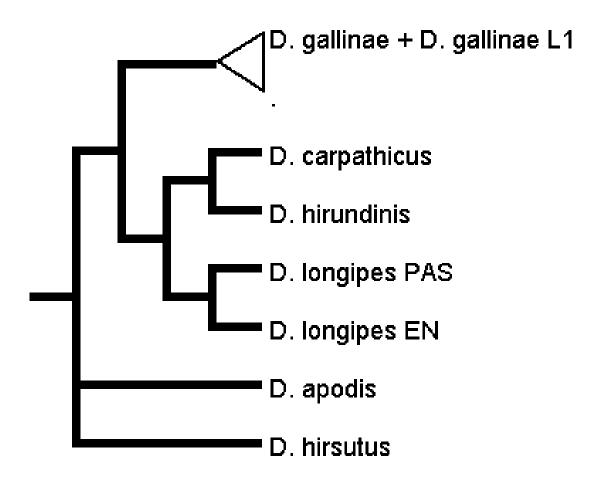


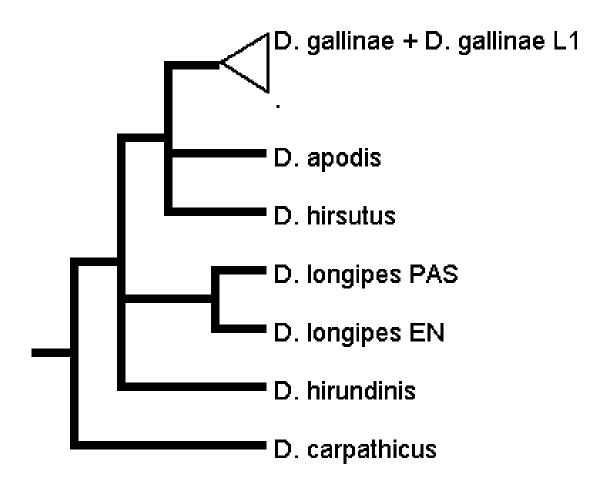


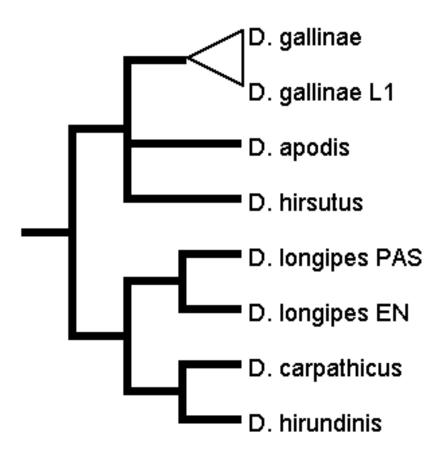












Frequency of occurrence of topologies obtained in the different combinations tested in multi-gene analyses ordered according to the level of resolution. Solid bars represent the percentage of occurrence of topologies in MP analyses treating with gaps as the fifth state, open bars with gaps as missing data. Level of tree resolution was assessed considering *Dermanyssus* exclusively as follows: 0 = a single node (monophyly of *Dermanyssus*), 1 = a specific entities delineated, 2 = 1 + a one internal node, 3 = 2 + a one internal nodes, and so on until 9 = a specific entities delineated + all interrelationships resolved.

