

Supplementary material

**Genetic variation and phylogeography of the Australian and New Zealand fern
Asplenium flabellifolium (Aspleniaceae)**

*Daniel J. Ohlsen^{A,D}, Lara D. Shepherd^B, Leon R. Perrie^B, Patrick J. Brownsey^B
and Michael J. Bayly^C*

^ARoyal Botanic Gardens, Private Bag 2000, Birdwood Avenue,
South Yarra, Vic. 3141, Australia.

^BMuseum of New Zealand Te Papa Tongarewa, PO Box 467, 55 Cable Street,
Wellington, 6140, New Zealand.

^CSchool of BioSciences, The University of Melbourne, Royal Parade,
Parkville, Vic. 3010, Australia.

^DCorresponding author. Email: ohlsend@gmail.com

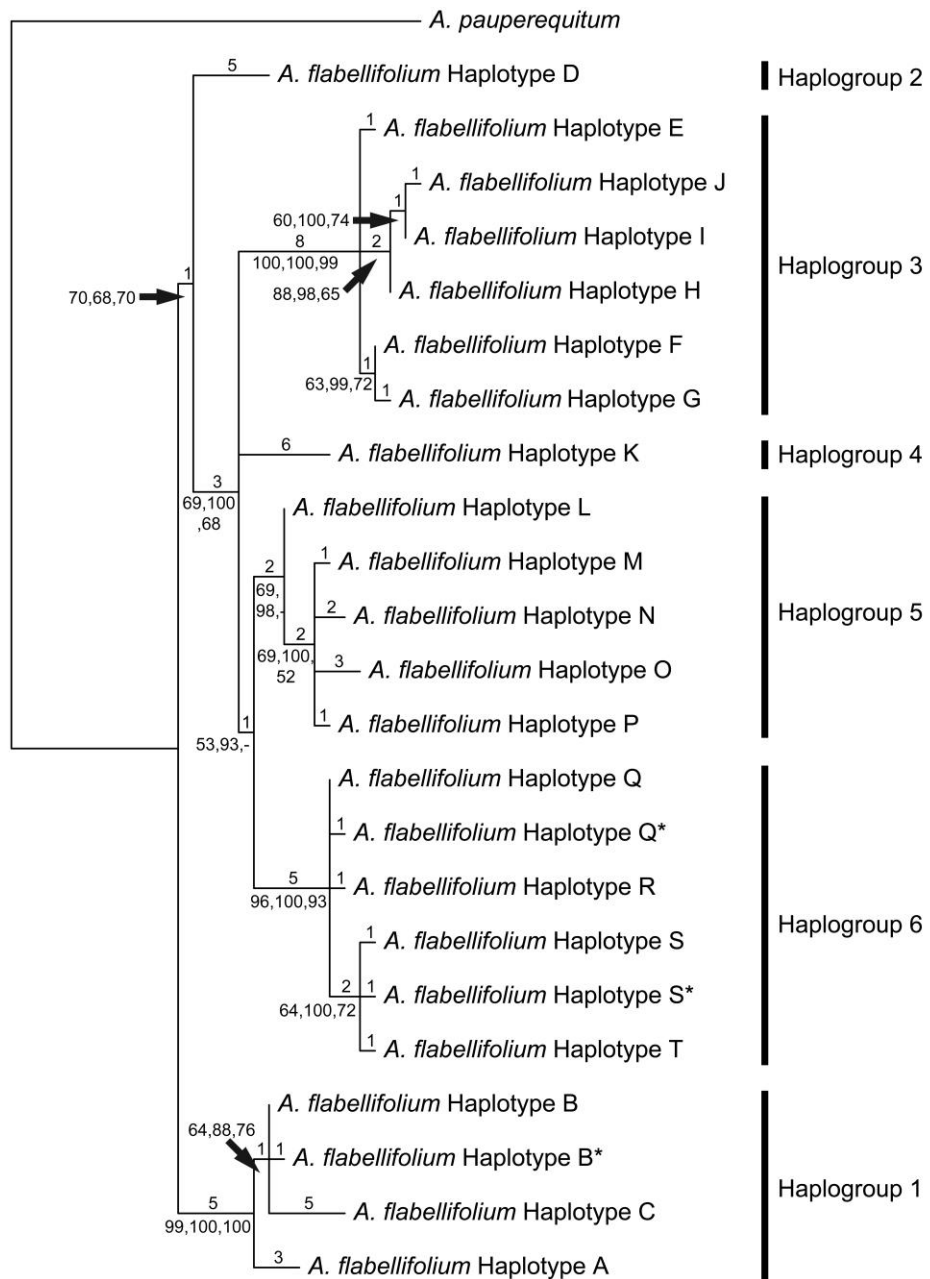


Fig. S1. One of fourteen most parsimonious trees (length = 107, consistency index = 0.925, retention index = 0.943) from the alignment of *trnL-trnF* and *rps4-trnS* of all *Asplenium flabellifolium* haplotypes, with *A. pauperequitum* as an outgroup. Branch lengths are given above branches and maximum-parsimony bootstrap support values, followed by Bayesian posterior probabilities and maximum-likelihood bootstrap support values are given below.