



Fig. 8.2.1.1 (Larger version of Fig 2.4) Bayesian phylogenies constructed with (a) plastid marker *trnL-F* and (b) nuclear marker *ITS (1+2)* for *Polytrichastrum alpinum*, *Polytrichum piliferum*, *P. strictum* and *P. juniperinum*. Posterior probabilities and bootstrap support are shown next to branches (* = conflict between topologies of Bayesian and ML tree; see Figs. 8.2.1.2 and 8.2.1.3 in the Appendix for ML phylogenies). Colours refer to different geographical regions (see map); outgroups are indicated in black. The scale bar represents the mean number of nucleotide substitutions per site. ABGD species delimitation clusters with different P_{max} -values are shown in grey next to (b).