**FIGURE 9.** Preliminary maximum parsimony (MP) phylogram randomly chosen with 447 terminals modified from Barfuss (2012) based on the nDNA *PHYC* (*Phytochrome C*) and *PRK* (*Phosphoribulokinase*) (complete for all taxa) and ptDNA *trnK*-*matK*-*trnK*, *atpB*-*rbcL*, *rbcL*, *trnL* intron and *trnL*-*trnF*, and *rps16* intron sequence data (only for 97 taxa from Barfuss *et al.* 2005a). Numbers above branches are bootstrap support values of MP bootstrapping and Bayesian Inference (BI) posterior probabilities (PBS/BPP), missing values (-/-) indicate values less than 50% PBS or 0.50 BPP, respectively; numbers below branches are branch lengths of variable DNA characters. Technical details can be found in Barfuss (2012). Taxa are labelled with their newly proposed names according to the revised classification. An asterisk before species names indicate terminals, for which also ptDNA sequence data was available. For other accessions only *PHYC* and *PRK* was available, with missing data coded as ‘?’ for the ptDNA loci. Two asterisk before species names indicate terminals where ptDNA and nDNA sequence data came from different accessions of the same species.

***Note:*** Species relationships should be taken with caution as only one of the many possible phylogenetic hypothesis is shown. Branches are often unsupported due to missing ptDNA sequence data and high levels of homoplasy in nDNA sequence data. Several species are unplaced (*incertae* *sedis*). However, circumscriptions of higher taxonomic groups are mostly identical to the 210 taxa set, but the taxon sampling is more inclusive. This expanded sequence data set will be published in a separate publication with GenBank accession numbers and voucher details.