



Additional file 2: Figure S1. Bayesian consensus phylogram of Dipsacoideae focussing on *Knautia* based on plastid *petN(ycf6)*-*psbM* sequences. Values above and below branches are parsimony bootstrap values > 50 and posterior probabilities derived from Bayesian analysis > 0.80, respectively. Population IDs, provenance countries and ploidy are printed after the species names. The print colour follows the haplotype groups in Fig. 2A. Terminal branches are coloured according to ploidy level: black, diploid; red, tetraploid; green, hexaploid.