

Figure 1. Schematic presentation of secondary metabolites detected in species of *Parmelinopsis* treated in this study, as detected using modified Solvent C (200:30 toluene:glacial acetic acid) following Lendemer (2011). Lane 1 consists of standards from *Lepraria finkii*, at = atranorin, z = zeorin, nt = norstictic acid, st = stictic acid. Lanes 2-11 are the species treated here: 2 = *H. afrorevoluta*, 3 = *H. appalachensis*, 4 = *H. cryptochlora*, 5 = *H. horrescens*, 6 = *H. kauffmaniana*, 7 = *H. mcmulliniana*, 8 = *H. minarum*, 9 = *H. revoluta*, 10 = *H. showmanii*, 11 = *H. spumosa*. Abbreviated names (right) correspond to the following substances in descending order: 4,5-di-O-methylhiascic acid, 3-methoxy-2,4-di-O-methylgyrophoric acid, methyl hiascate, 2,4,5-tri-O-methylhiascic acid, 2,4-di-O-methylgyrophoric acid, 5-O-methylhiascic acid, gyrophoric acid, spumosa unknown.



Figure 2. Phylogeny of *Hypotrachyna* inferred from mtSSU sequence data with *Myelochroa* selected as the outgroup based on Crespo et al. (2010) and presented as the most likely tree. Subgenera are labeled following Divakar et al. (2013), except that the two lineages of *Parmelinopsis* are indicated with roman numerals. The complete phylogeny of *Hypotrachyna* is inset (right) with individual sequences collapsed to illustrate the overall relationship and support for subgenera. The detailed sampling for subgenus *Parmelinopsis* is presented on the left, and includes subgenus *Hypotrachyna*. Maximum likelihood bootstrap support values  $\geq 50$  are labeled, support of 100 is indicated with an asterisk (\*), and branches with  $\geq 70$  support are thickened. Note that sequence labels for previously published data from NCBI should be cross-referenced with Table 1.

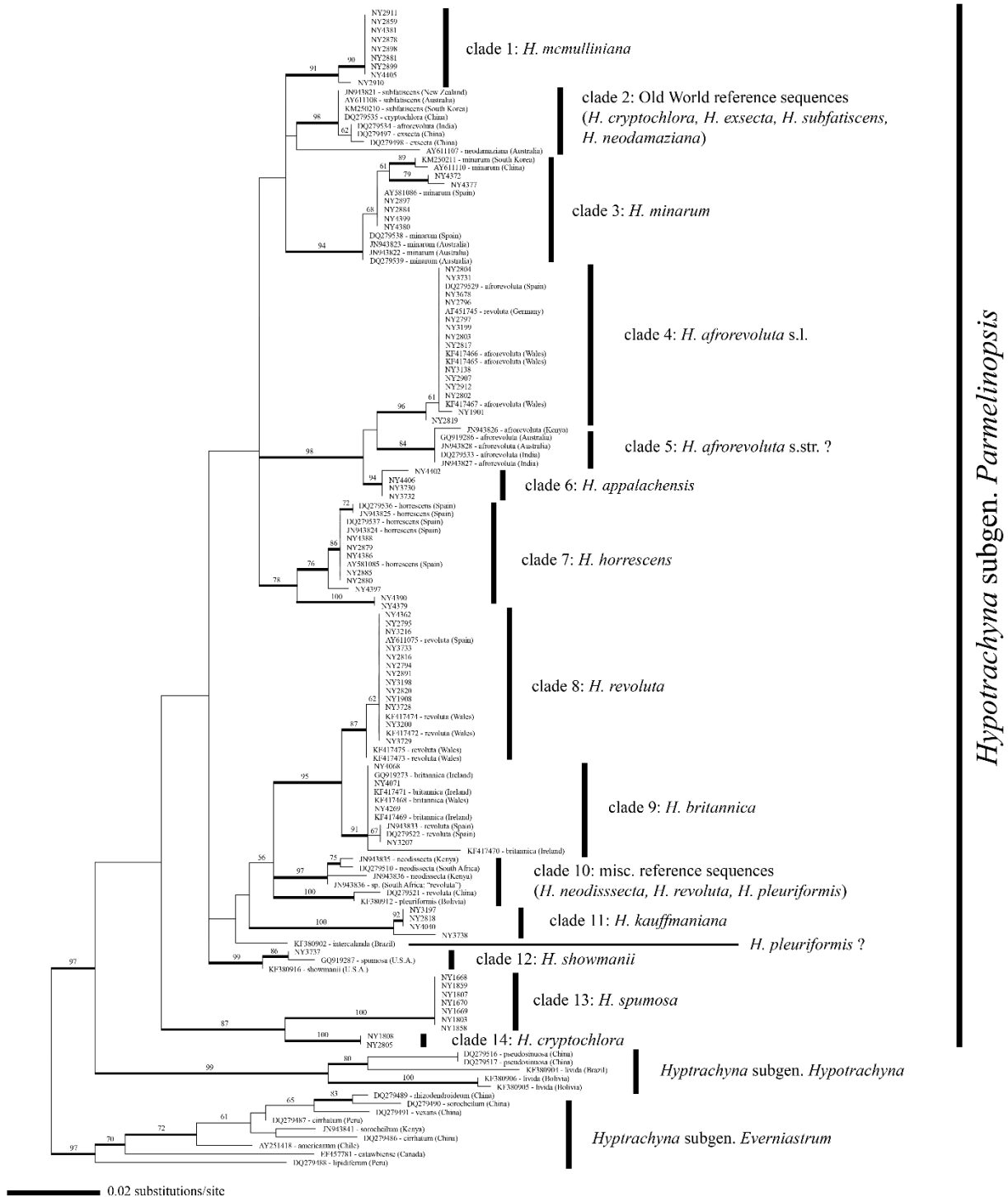


Figure 3. Phylogeny of subgenus *Parmelinopsis* inferred from ITS sequence data with subgenus *Everniastrum* selected as the outgroup based on Divakar et al. (2013) and presented as the most likely tree. Maximum likelihood bootstrap support values  $\geq 50$  are labeled, support of 100 is indicated with an asterisk (\*), and branches with  $\geq 70$  support are thickened. Species names applied to each clade are given following the clade number, and clade numbers are cross-referenced with the discussion in the main text of this contribution. Note that sequence labels for previously published data from NCBI should be cross-referenced with Table 1.