**Supplementary Material**

Supplementary Fig. S1. Morphology of example specimens. a. *Parmelia serrana*, with very light brown and rounded lobe tips; b. *P. ernstiae* with very light brown and squared lobe tips; c. *P. ernstiae* with light brown and rounded lobe tips; d. *P. serrana* with light brown and squared lobe tips; e. *P. saxatilis* with brown and rounded lobe tips; f. *P. saxatilis* with brown and squared lobe tips.

Supplementary Fig. S2. Maximum likelihood phylogeny of unique sequences types, as determined using CD-HIT Suite, of nr ITS sequences of *Parmelia saxatilis* aggregate samples from Scotland along with reference samples. Thickened branches have bootstrap support over 70%. A sequence of *Parmelia adaugescens* (AY036992) was used as the outgroup.

Supplementary Fig. S3. Classification tree using morphological and presence/absence data only for chemical characters for 161 specimens of the *P. saxatilis* aggregate sampled across Scotland, excluding cases with missing data. The overall error rate was 16·7%. The terms *ern*, *sax* and *ser* correspond to specimens of *Parmelia ernstiae, P. saxatilis* s. str. and *P. serrana* respectively. The extent of pruinose layer is indicated as follows: + = few tips with pruina; ++ = many tips with pruina; +++ = pruina throughout.