

Mark, K. et al 2016. Evaluation of traditionally circumscribed species in the lichen-forming genus *Usnea*, section *Usnea* (Parmeliaceae, Ascomycota) using a six-locus dataset. *Organisms Diversity and Evolution* 16: 497-524.

Looked at species from all over Europe and N America, sorediate and sexually reproducing, long and shrubby species.

-Molecular info: ITS (internal transcribed spacer region), IGS (intergenetic spacer region), Bt (beta-tubulin), MCM7 (Minichromosome Maintenance Complex Component 7, used for protein coding) and RPB1 and RPB2 (RNA polymerases).

-Morphological characters: looked at many including thallus form (long or shrubby), branching, papillae, reproduction, CMA, medulla density etc.

Using all of this information they found that many "species" described from morphological characters grouped in clusters of two or more. Many currently accepted diagnostic morphological characters do not prove useful for delimiting these clusters. CMA was informative.

Three from our area appeared monophyletic:

U. cavernosa

U. silesiaca

U. wasmuthii

Usnea lapponica and *U. substerilis* appear to be conspecific, Mark et al. synonymize under *U. lapponica*.

Very high chemotypic variation within morphology-based entities may indicate the need for phylogenetic reevaluation of some chemotypes in species boundaries.

Spribille et al. 2016:

The assumption that these substances are exclusively synthesized by the lecanoromycete must now be considered untested.

Daphne's thoughts: I propose that using spot-test reactions may not always help in delimiting species, and that there may be different yeasts in the cortex of *Usnea* spp. producing different chemistry confounding identification.

Also, sort of circular reasoning where they identified the specimens then said that those species were grouped with others. Perhaps the original ID's were faulty. One example *U. barbata* from OR, which McCune & Geiser do not recognize as from here?