

Abstract

A common alga of oligotrophic slightly acidic fresh water habitats, *Synura sphagnicola*, has never been suspected for a presence of cryptic diversity. The publicly available SSU rDNA sequences showed very slight genetic differences between the *S. sphagnicola* isolates. However, I suspected that if any cryptic lineages exist, the sequencing of ITS region will show the differences between them.

A total of 37 *S. sphagnicola* sequences (36 from Europe and 1 from Korea) were analyzed in this thesis. The ITS rDNA sequencing clearly recognized the presence of two distinct cryptic species, referred here as lineage SP1 and SP2. The morphological analysis of 14 cultivated strains (6 belonging to the lineage SP1 and 8 to the lineage SP2) validated the genetic distinction. The statistical analyses showed that 4 morphological aspects (length of a scale, width of a scale, length of a spine, length of a rim) were found to have significant differences in length of measured factors between species. The most visible difference is in the length of a spine that is connected to the scale. The analysis of published *S. sphagnicola* scales showed that the two lineages can be morphologically distinguished also in natural conditions. According to the morphological analyses, the lineage SP2 (species with a longer spine) corresponds with the description of *S. sphagnicola*. The SP1 lineage probably represents yet unsubscribed species.

Despite the species can co-occur in nature, analysis of ecological data showed that their optima of some environmental conditions slightly differ. Whereas the species SP2 prefers low conductivity, the species SP1 occurs in a wider range of conductivity. The conductivity is probably connected with the amount of precipitation, since the species SP2 occurs in more rainy regions.