

The inner organisation of organisms originates from the information contained within its DNA. In addition, the size of the genome itself may influence the function of the organism. Unlike many other groups of organisms, genome size is only known for a very limited number of lichen mycobionts.

So far it has been only speculated whether there is a connection between genome size, the ecology and the traits of lichens. The goal of my thesis is to measure genome size of a sufficient amount of lichen mycobionts to be able to determine possible connection between genome size and ecology or functional traits of these lichen species.

I successfully measured the genome size of 50 lichen species using flow cytometry (FCM). I did molecular phylogenetic analysis of 141 taxa with known genome size in order to recognize the influence of phylogeny on genome size of these species.

Two genes – ITS and mtSSU – were used for the phylogenetic analysis. Statistical analysis was performed using measured genome sizes, ecologically relevant traits of lichen species and my phylogenetic tree.

I found that genome size might be connected to substrate preference, vegetative reproduction or the type of the lichens' photobiont. A correlation of genome size and life strategy – larger genome sizes connected to K-strategy, whereas smaller genomes connected to r-strategy – can be found in certain groups of lichens.

I have newly determined genome sizes of many species of lichens. I used a method new to lichenology (FCM) to do it. My thesis presents one of the first investigations into effects of genome sizes in lichens.