Water deficiency is a major abiotic factor that influences carbon uptake by photosynthesis and limits the growth and development of plants. At present, water deficiency seems to be a widespread and worsening problem because of global climate change and human activities. In the light of this, it is important to make the effort to understand plants' responses to abiotic stresses, specifically to drought stress.

Bryophytes are interesting objects to study, particularly the changes they exhibit during drought stress. These organisms were the first plants to leave an aquatic environment and adapt to life on land. For this purpose, some of the bryophyte species developed a remarkable ability to tolerate long periods of nearly complete desiccation.

Peat mosses (*Sphagnum*) comprise a group of bryophytes of high ecological and economic importance. These organisms are the main components of peatlands, which significantly contribute to global climate formation by capturing greenhouse gases such as carbon dioxide, methane, or nitrogen oxides. The extremely high water-holding capacity of peat mosses shapes local water relations. Thus, large peatlands play an important role in controlling floods and droughts. However, many of these areas undergo significant levels of erosion that are the result of water shortages and intensive peat digging. Because of the importance of peatlands, it is critical to take actions to protect and restore these valuable areas. However, current understanding of water deficiency on different metabolic processes in desiccation-sensitive mosses is based on sparse and scattered data.

The object of the studies, *Sphagnum denticulatum*, can occupy contrasting habitats. This plant was found growing on both land and underwater. Sphagnum representing terrestrial populations are periodically endangered by drought, whereas those growing at the bottom of the lake are completely immersed during their lifetimes and probably never experience water deficiency. The working hypothesis of the project is that the drought tolerance and response of plants from these two environments will be diverse.

Within the project, genotypes of *S. denticulatum* sampled from the aquatic and terrestrial habitats will be examined. To eliminate the effect of the environment, experimental plants will be cultivated in strictly controlled homogenous conditions for an extended duration. The plants representing each genotype will be treated with drought and/or subsequent rehydration and compared to a control not treated with water stress. Plants from two experimental groups will be studied in terms of their cell ultrastructure, gene expression, and physiological parameters.

The aims of this study are to (1) evaluate gene expression level, and to detect (2) physiological, and (3) ultrastructural changes in ecotypes/genotypes of *S. denticulatum* under drought stress and rehydration.

The quantitative technique of a real-time polymerase chain reaction (qPCR) will be applied to identify and evaluate expression levels of candidate genes involved in *S. denticulatum*'s response to water stress. The plant response to drought at the physiological level will be examined by measuring the chlorophyll fluorescence parameters (Fv/Fm, θPSII, NPQ, 1-qP), and pigment contents (chlorophyll a, chlorophyll b, and carotenoids). Cell ultrastructural changes triggered by desiccation and rehydration will be evaluated by electron microscopy studies. In particular, the appearance of the organelles, and the integrity of cell membranes will be examined.

A complete image of complex stress reactions in these plants will be obtained by considering drought stress at different levels. A more exhaustive knowledge and a better understanding of the molecular base of drought stress tolerance may help to protect these endangered taxa. The studies will shed light on genetic variation within the *S. denticulatum* genome. The results of the project may provide insight into the origin of abiotic stress adaptation/acclimation in plants. From a further perspective, a number of stress-inducible genes will be detected within the genome, which may be used to improve the stress tolerance of plants by gene transfer.