

Liverworts of the genus *Riccia* represent a valuable research model due to several advantages. They are characterized by a simple life cycle with haploid dominance, ease of cultivation and cloning, and the ability to live both in water and on land. These features make them excellent subjects for studies in plant physiology, molecular biology, development, and evolution.

The main goal of this research is to verify the hypothesis that UV-B radiation induces diverse transcriptomic and epitranscriptomic changes in *Riccia fluitans* and *Riccia sorocarpa*, revealing specific adaptive mechanisms for amphibious and typically terrestrial plants. In the project, we will analyze gene expression profiles, RNA methylation modifications, poly(A) tail lengths, and identify potential sites of RNA pseudouridylation. Additionally, we will conduct a series of molecular pathway analyses in response to UV-B radiation in the context of environmental plasticity. The research will be conducted using modern molecular biology methods, including long-read sequencing of native RNA molecules. This will allow us to obtain actual RNA molecules without RNA amplification methods and identify complete mRNA variants. However, the most intriguing aspect of this project will be the use of non-sequencing signals of chemical RNA modifications, such as m6A, m5C, and psU, to characterize the epitranscriptome of the studied plants. The long-read sequencing method from Oxford Nanopore, used in this experiment, was acclaimed as the method of the year in 2022. We will also utilize modern computer software and publicly available biological databases to thoroughly analyze the transcriptomic and epitranscriptomic data for the studied species.

This project will contribute to expanding knowledge about the adaptation of amphibious and typically terrestrial plants to cyclical climate changes, such as increasing UV-B radiation. It will broaden our understanding of the molecular processes accompanying epigenetic modifications. We assume that the results obtained in this project will serve as a starting point for similar research in other plants. Additionally, they will contribute to a better understanding of plant physiology.