

Progressive environmental degradation resulting from climate warming and habitat destruction is leading to an irreversible loss of biodiversity. The increasing dynamics of this phenomenon forces scientists to develop new strategies and new tools to protect both wild species and populations and cultivars of crop species. Cryobiotechnology meets these needs. Thanks to the research conducted on cold and freeze tolerance basis, innovative concepts, technologies, and protocols for the preservation of cells, tissues and organisms in cryogenic conditions and their subsequent restoration of life functions are being developed.

The goal of this project is to understand and characterize the gene regulatory network responsible for deep freeze tolerance. The research will be conducted on winter vegetative buds of apples. This material can be considered as a model for this type of analysis. We now have extensive theoretical and practical knowledge of how to freeze apple buds so that a fruiting tree can be regenerated after thawing. In addition, the apple genome is small, and its sequence is already known. High-throughput Next Generation Sequencing (NGS) will be used in this study. This will provide insight into the expression of genes key to cold, freeze and cryopreservation tolerance and the way they are regulated.

The results of the project will significantly improve the state of knowledge on molecular aspects of cryopreservation. As a result, it will be possible to develop new or improve existing protocols for preserving germplasm at ultra-low temperatures, thus increasing the chances of preserving plant species that are not tolerant to drying and/or freezing.