# Revealing the component of epigenetic aging in monocarpic plant leaves

Biological aging is associated with variability in life across different ecological scales and reflects an age-related decline in organismal functions. Aging is accompanied by highly dynamic changes in DNA methylation, which have already been modelled into epigenetic clocks and used to predict the chronological age of vertebrates, including humans. Although evidence suggests that DNA methylation patterns may also describe plant aging, the development of plant epigenetic clocks remains in its pioneering stages. Previous observations, however, indicate that, like animals, plants likely possess their own epigenetic clocks.

The project aims to investigate changes in DNA methylation in barley and tomato during the aging process of these plants. The collected data could contribute to the construction of epigenetic clock, which have not yet been developed for monocarpic plants. In this project, I will use transgenic tomato plants characterized by accelerated or delayed aging. I intend to determine whether these altered aging phenotypes result from delayed or accelerated epigenetic aging.

Epigenetic clocks have numerous potential applications in plant biology research. Precise measurements of biological age could be useful for testing theories of plant biological aging, optimizing agronomic modelling to enhance productivity, diagnosing age-related responses to stress or climate change, and selecting varieties resistant to (a)biotic environmental factors, among many other possibilities