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Maize, apart from being one of the most important crop plants, is recently becoming accepted as an attractive model plant. From both, the basic and applied points of view, the adaptation mechanisms driven by artificial selection seem to be among the most important and intriguing problems to be studied in maize. Thanks to its large, highly redundant genome and phenotypic diversity, maize has been adapted to diverse conditions in regions far away from its place of origin, Mexico. Artificial selection drove maize domestication by Native Americans several thousand years ago and allowed its further widespread distribution. Artificial selection is still used by modern breeders to improve different crop traits. Nowadays, transformation of maize and other crop plants is an auxiliary method to obtain new valuable traits, but artificial selection is still the main tool for breeders in the production of new inbred lines and hybrids.

This project is designed to discover the mechanisms that could allow the further adaptation of maize to the temperate climate of Eastern and Central Europe with cold periods in spring. In that context, very early growth stage seems to be of particular importance. At this stage seedlings grow from a seed (in maize it is called kernel) and become autotrophic, i.e. their further growth depends fully on photosynthesis. Subjecting maize at this stage to ca. 13°C can have dramatic consequences, since, *in extremis*, seedlings of some inbred lines have been observed to die having fully exhausted the seed reserves before development of photosynthetic apparatus. Better tolerance of maize to low temperature stress at this stage would allow for early sowing, prolongation of the vegetation season and finally higher yield.

On the basis of our recent results we hypothesise that several distinct and possibly independent mechanisms exist that would ensure increase of the maize adaptability to cold springs in temperate climate. It seems that at least five main types of response to cold at early growth stage among several dozen tested inbred lines exist. Some genotypes are not able to germinate at cold, for others leaves appear, but under prolonged chilling seedlings die. However, many inbred lines could function well under cold conditions. First phenotype combines fast growth and production of effective photosynthetic apparatus. Second phenotype is distinguished by fast growth of seedlings and forming of the green leaves at low temperatures despite low photosynthetic efficiency. The third phenotype rely on remarkable ability to regrowth at elevated temperatures. We aim to reveal and describe mechanisms responsible for described phenotypes at molecular levels. To this end we will use two high-throughput techniques: automated plant phenotyping and transcriptomics.

In the physiological part of the project, we shall follow the growth of seedlings of selected inbred lines under cold conditions by using fully automated multispectral 3D scanner that provide a dozen morphological and spectral data on plant performance. Automated plant phenotyping using non-invasive and digital technologies is a modern technique that is recently increasingly used in plant physiology. It captures plants non-destructively and delivers precise and objective plant parameters in real time. Thus, we expect to choose inbred lines being better adapted to cold periods. In the molecular part of the project, we will follow the gene expression global profile in seedlings at the shift from low to optimal growth temperature. We will use inbred lines selected as those representing the mechanisms that warrant adaptation of maize to cold springs. Finally, we are going to design several models of maize early development at low temperatures and we will perform bioinformatic analyses to present overall conclusions on their molecular basis for mechanisms.

Fulfilment of the project's targets may lead to significant increase of our knowledge on high plasticity of maize response to low temperatures in highly changeable environment of temperate climate. Also the project would provide valuable information to breeders seeking for new approaches that would allow them selecting maize genotypes better adapted to cold springs.