The appropriate setting of the transition time from vegetative growth to reproductive development is essential for successful achievement of plant life cycle and has also commercial significance for crop plants. The transition from vegetative to floral development in higher plants is programmed by the simultaneous occurrence of several environmental stimuli, notably photoperiod and temperature, and endogenous developmental signals like hormones and carbohydrate assimilates.

B-box proteins (BBX) are zinc finger transcription regulators forming complex families in plants with 32 members in Arabidopsis and 30 in cultivated potato. Plant BBX proteins are characterized by the presence in the N-terminus of one single B-box domain or two arranged in tandem. In cultivated potato, BBX proteins are classified into five groups based on the presence and number of B-box and CCT domains. Plant BBX proteins widely differ in structure and fulfill distinct functions in the regulation of plant growth and development including seedling photomorphogenesis, photoperiodic regulation of flowering, shade avoidance. While in Arabidopsis the mechanisms controlling flowering have been well-known and the proteins belonging to the BBX family involved in the regulation of flowering have been well characterized in terms of their function, in crops the function of BBX proteins in vegetative and generative development is still poorly understood and only for a few BBX proteins was determined. Most of the data regarding the function of BBX proteins in the growth and development in crops refers to Arabidopsis CO (BBX1) homologs.

**In this project we want to explain a role of the StBBX20 protein in the regulation of flowering time and tubers characteristics in cultivated potato *Solanum tuberosum* L., cv. Desiree**.

To find out whether StBBX20 protein controls the expression of flowering-related genes and the genes that regulate the onset of tuber formation in cv. Desiree, the potato transgenic plants with suppressed expression of *StBBX20* gene and overexpressing *StBBX20* will be prepared. To find out the genes involved in the timing of flowering induction and flower development in cultivated potato, we intend to dissect transcriptome analysis of control plants and transgenic lines with overexpression and knockout of *StBBX20* gene at different stages of plant development and two different time points in the light phase. To find out which genes are involved in tuber formation, we intend to dissect transcriptome analysis of control plants and transgenic lines with overexpression and knockout of *StBBX20* at different stages of plant development. For final verification of the genes associated with flowering and tuberization which expression is controlled by StBBX20, we will use chromatin immunoprecipitation assay followed by high-throughput sequencing (ChiP-seq).

To identify a target protein interacting with StBBX20 in the chromatin complex in cultivated potato the ChAP (Chromatin Affinity Purification) technique will be applied.

**Understanding the function of the StBBX20 protein in the regulation of flowering time and tuberization allows for a better understanding of the mechanisms by which these processes are controlled. In addition, discovery of a protein interacting with StBBX20 in the chromatin complex exerts its effects on growth and yield and expand the knowledge of plants physiology**. **We believe that the integration of data from different experimental approaches will allow to indicate that StBBX20 is involved in the timing of flowering induction and tuber formation in cultivated potato. We also expect that the received data will allow us to find out whether there are common signaling steps in the flowering and tuberization regulatory pathways, and whether there is the cross-talk between them**.