Starch is the most abundant reserve carbohydrate in plants, which is accumulated as granules in the chloroplasts (transitory starch) and in the amyloplasts of tubers, roots and seeds (storage starch). Cultivated potato (*Solanum tuberosum* L.) is the fourth most important crop in the world. There is a large variation in starch content present in tubers of cultivated potato, between 11-30% starch of tuber fresh weight. Starch is not only the source of energy for human diet or for production of valuable products used in many industries. Two components of starch, amylose and amylopectin, are polymers of glucose. For non-food applications, the polymer amylopectin is of interest. Amylopectin is the major, highly branched, polysaccharide and constitutes about 70-90% of starch. Amylose is regarded as an impurity. In 2006, using biotechnological tools amylase-free potato plants were generated. However, because of a strong opposition against genetic modification of plants in Europe, the cultivar Amflora has not been introduced into industry.

Therefore, a challenge for fundamental potato science is the identification of natural variation in genes involved in tuber starch metabolism. Understanding of the molecular aspects of starch biosynthesis and degradation will be the impulse for generation novel starches with altered properties, useful for industry. On the other hand, knowledge about relationship between genetic variation in gene sequences and the phenotypic variation is important for basic research of source-sink interactions in net carbon accumulation in plants.

Starch biosynthesis is the dominant pathway of carbohydrate metabolism in potato tubers. This is the typical quantitative trait being under control of many genetic and environmental factors. In potato tubers, starch synthesis and breakdown serve as the suitable model pathways for genetic analysis of quantitative traits. Quantitative trait loci (QTL) analysis requires phenotypic evaluation, molecular profiling, and statistical analysis of a segregating population. QTL mapping provides valuable information in terms of the minimal number and approximate genomic position of the factors controlling a complex trait, but does not identify their molecular basis. Recent molecular technologies have fundamentally changed the way genetic research in plant science. Large scale transcription profiling technologies, such as DNA microarrays and RNAseq technology, have allowed the analysis of gene expression patterns at the genome level. These approaches provide a valuable tools for determination of the gene expression profiles in different tissues, stages of growth and in response to different growing conditions and to abiotic and biotic stresses.

In potato, genomic studies have significantly grown when the first physical map of potato genome has been described by the international Potato Genome Sequencing Consortium in 2011. Since the publication of the potato genome sequence (genomics) the progress is observed in detection of up and down-regulated genes (transcriptomics), proteins produced (proteomics) and the metabolic processes influenced by these proteins (metabolomics). However, to date, knowledge concerning genome-wide expression profiling related to starch content in potato tubers remains poor. In the present project comparative transcriptome analysis in diploid potato tubers will be performed. Our aim is finding transcription factors overlapping with QTL for starch content using the next generation sequencing (NGS) technology. NGS data will be applied for discovery of genes overlapping with the QTL. Transcription factors co-localizing with QTL will be selected and the specific DNA markers will be developed. Their significance for tuber starch content will be evaluated. The knowledge about genes underlying the tuber starch content in diploid potato will be the impulse for study of tetraploid germplasm to improve the cultivated potato. This study will also be the basis for further experiments in potato and heterotrophic organs in other plant species at the physiological, biochemical and molecular levels.