Information about development and biological functions of organisms is encoded in genes – fragments of deoxyribonucleic acid (DNA) which is maintained in almost each cell. The complete DNA sequence of the given organism is named genome. Genetic information is revealed during gene expression – the process starting from transcription of genes to ribonucleic acid (RNA). Transcripts (RNA fragments generated by gene transcription) are templates for synthesis of proteins.

DNA is wrapped around histones forming so called chromatin. Interaction between DNA and histones has to be temporarily released before transcription starts. Enzymes called histone acetyltransferases attach chemical acetyl residues to histones and make genes accessible for RNA polymerase, the enzyme that transcribes DNA to RNA. There are also enzymes that attach or remove directly to/from DNA another chemical component named methyl group. Methylation of DNA may either make transcription easier or vice versa, depending on the DNA region where it appears.

1. The main goal of the project and the research hypothesis

Elongator is an enzyme which associates with RNA polymerase and facilitates transcription. Elongator has two activities – acetylates histones and modifies methylation of DNA. It has the same complex structure of six subunits in yeast, plants and humans. In plants, Elongator is necessary for growth, development, response to stress and defense against pathogens.

The main goal of this project is to explain the role played by Elongator when very young plant seedlings develop in light, this process is named photomorphogenesis. We will investigate the role of Elongator in the model plant *Arabidopsis thaliana*.

Following germination, plant seedlings elongate very fast while cotyledons (the first leaves) are folded. When seedlings reach the soil surface and are exposed to light, the photomorphogenesis starts and elongation of seedlings is inhibited, while cotyledons expand. Plants having defective Elongator (*elo* mutants) are hyposensitive to light (are longer than normal plants and their cotyledons are less expanded). We found that in the *elo* mutant the genes encoding positive regulators of photomorphogenesis are less active while the gene encoding protein that stimulate elongation in darkness is more active.

Our working hypothesis is that during photomorphogenesis Elongator regulates important genes via histone acetylation or/and modification of DNA methylation.

2. Experiments

We will compare gene activity during photomorphogenesis in the *elo* mutants and in the wild type plants to identify genes which are more or less active in the mutant. In parallel we will identify genes bound by Elongator in the Arabidopsis genome. Genes revealed by both approaches will be most likely regulated by Elongator during photomorphogenesis. Subsequently, we will check how much the histones of the selected genes are acetylated or how much the DNA is methylated to verify which of the Elongator's activities, histone transacetylase or cytosine methylase respectively, is responsible for regulation of these genes. We will also cross *elo* mutant with plants which have super-active the same genes which are less active in the mutant. We hope that super-active genes will compensate for decreased activity in mutant proving that the defects observed in the *elo* mutant occurred indeed due to inefficient gene transcription.

3. Reasons to perform the project

In this project we would like to continue our recently published research concerning the earlier unknown role of Elongator in photomorphogenesis. Explanation of the function of Elongator in photomorphogenesis will allow to better understand epigenetic control of physiological processes in plants, in particular in light regulated plant development.