Elucidation of the role of ARGONAUTE proteins in post-transcriptional regulation of gene expression in germinating seeds of *Arabidopsis thaliana*

The seed habit is the most complex and successful method of sexual reproduction in vascular plants, allowing these settled organisms to reproduce independently of water. These organs play an essential role in the plant life cycle, as they store genetic information necessary for the next generation of plants to disperse, reproduce and maintain in various ecosystems. Seeds exhibit species-specific differences in their structure and the composition of their storage compounds. The embryo of mature seeds of most species of higher plants including *Arabidopsis thaliana* (one of the most commonly used model species in biological sciences) is encased by two covering layers: the living endosperm and the dead testa (seed coat). The seed coat - a protective layer, together with the endosperm – directly covering embryo and often playing a role as a storage tissue important for sustain growth, give seeds their superior evolutionary advantage. When the dry seeds come into contact with water under favourable conditions, the germination process begins. Nonetheless, the seed live is accompanied also with the existence of dormancy, defined as the failure of viable mature seeds to germinate even under favourable conditions. This phenomenon is assumed to be an important adaptive trait in nature, improving survival of the next generation by optimization of the distribution of germination over the time.

A major goal for modern seed biology is to unravel the complex series of biochemical and cellular processes resulting in the biosynthesis and/or degradation of defined cellular components, essential for regulation of seed dormancy and germination. Up to date, many studies have shown that besides the environmental stimuli's such as light, also the internal factors - plant hormones (i.e. gibberellins - GA and abscisic acid – ABA) play a crucial role in modulation processes occurring in seeds. Interestingly, several lines of evidences studies of plant signaling indicated that reactive oxygen species (ROS) previously regarded mainly as a co-product of oxygen metabolism, showing an extremely harmful effect on living organisms, have also significant, positive role for the proper functioning of plant cells. The ground-breaking research conducted by Dr. Krystyna Oracz, has proven that dormancy alleviation is correlated with an increase in ROS level and oxidation of specific proteins. However, to avoid oxidative cellular damages, ROS level must to be constantly controlled by actively functioning antioxidant system consisting of molecule antioxidants (i.e. carotenoids, vitamin C and E, etc.), as well as scavenging enzymes such as: catalase (CAT), superoxide dismutase (SOD), etc.

Seeds possess numerous specialized receptors and regulatory proteins enabling to perceive various changes in the surrounding environment. Both, environmental and endogenous factors produced within a seed, induce cascade of protein-protein interactions, involving many enzymes, regulators and transcription factors resulting in changes in expression profiles of defined genes. It is well known also that both transcription and translation are required for the completion of seed germination and seedling establishment; nonetheless the abundance of a gene transcript is not necessarily correlated with presumed translation and protein synthesis. The common mechanisms operating in all eukaryotic organisms, including post-transcriptional regulation of gene expression, are essential for selection of transcripts further used for translation of proteins throughout development including seed related events, or in response to environmental stimuli (i.e. light, temperature). Although, regulatory proteins (i.e. ARGONAUTE, AGO) are expected to participate in key cellular and organismal processes by modulation of specific transcript levels, the knowledge about their function in seed physiology is lacking. Therefore, a major challenge of this particular project and perhaps one of the most exciting aspects of the future research performed in the research team - SeedExplorerGroup (www.seedexplorer.eu) headed by Dr. Krystyna Oracz, would be to elucidate the role of AGO proteins in regulation of Arabidopsis thaliana seed dormancy and germination. Looking for the answer for the question about the biological function of AGO in post-transcriptional regulation of gene expression in light stimulated germination of dormant A. thaliana seeds, several experiments using a variety of research methods, such as: germination tests, quantitative Real-Time PCR analysis of gene expression, measurements of the activities of antioxidant enzymes, microscopic observations, flow cytometry and microarrays analyses, and many other will be used. Obtained data will allow proposing novel molecular actors in seed-related events, revealing new regulatory levels for the control of seed germination by dormancy. The detailed characteristic of such regulatory mechanisms will have a strong impact on the development of research in the field of cellular signaling and biology of plant development. When successful, these data can be also used for the improvement of seeds having increased tolerance to changing environment conditions and helpful in searching methods for improving seeds germinability.