

C.1. DESCRIPTION FOR THE GENERAL PUBLIC

Research on the plants embryological development evolve very rapidly. As a result of the development of molecular techniques, intensive studies are being conducted on plant generative cells. Studies using these techniques have demonstrated the important role of regulation of expression of mRNAs encoding proteins necessary during cell growth. mRNAs generated in the nucleus in the process of transcription consist of coding sequences (exons) and non-coding sequences (introns) between the 5` and 3` ends. Processes of mRNA maturation consist of three steps: (1) capping at the 5` end (2) excising of introns, called splicing, (3) polyadenylation at the 3` end. All of these processes normally take place during transcription. Fully mature mRNA is next transported to the cytoplasm where it serves as a template in the process of translation to form a protein. However, recent studies indicate that generative line cells have developed a mechanism that allows temporal retention of polyadenylated RNA (poly(A) RNA).

Studies performed in our research team showed that in the male generative cells- European larch (*Larix decidua* Mill.) microsporocytes alternating periods of increased transcriptional activity related to the synthesis of significant quantities of polyadenylated transcripts (poly(A) RNA) occurs. The newly synthesized poly(A) RNA is not directly transported to the cytoplasm, where it would be translated, but is retained within the nucleus. Accumulation of poly(A) RNA including mRNA is observed both in the nucleoplasm and within nuclear domains called Cajal bodies (CB). Cajal bodies are highly specialized structures, which number and size depends on changes in the metabolic activity of cells. Newly discovered role of Cajal body is accumulation of poly(A) RNA. High levels of mRNA in the nucleus remains even after the silencing of transcription, and its transport to the cytoplasm takes place in the later stages.

Research carried out in recent years show that eukaryotic cells have evolved several mechanisms to prevent the transport of not fully mature mRNA to the cytoplasm. Temporal retention within the nucleus could serve as a way of coordinating the expression of proteins in various cellular processes, and preventing the synthesis of defective proteins. One of mechanism that prevents transport into the cytoplasm, is the retention not fully mature transcripts until the splicing is fully completed. Another mechanism is the preferential association of certain protein export factors to mature mRNA. The mechanism responsible for the retention of the mRNA in the cell nucleus is still not fully understood.

In light of these studies we suppose that in our research model there is a similar process of regulation of gene expression by nuclear retention of mRNAs necessary during the various stages of microsporocytes development. In our research we would like to see what particular transcripts of poly(A) RNA are retained in the cell nucleus, whether they are housekeeping genes transcripts and / or transcripts of meiotic genes. Microsporocytes probably transcribe a large amount of RNA, which is next temporarily retained in the nucleus for the next stages of development, when it could be rapidly translated during periods of very dynamic development of the male gametophyte. We also want to verify if the nuclear retention of transcripts is indeed due to accumulation for further export to the cytoplasm (in the certain time point of development), or if it rather a mechanism of nuclear degradation of excessive/defected RNAs. We would also define the dynamic expression of retained transcripts in the nucleus to determine at what stage of development certain genes are transcribed.

Our results will explain the phenomenon of posttranscriptional regulation of gene expression by retention of polyadenylated transcripts including mRNA in the nucleus. We hypothesize that both RNAs of genes involved in meiotic division, as well as the housekeeping gene transcripts are subject to temporal nuclear retention. Understanding this phenomenon will significantly expand our better understanding of the processes and mechanisms involved in the maturation of generative plant cells, and the fundamental processes taking place within them. It will enrich the recent knowledge on cell biology as well as developmental biology.