

Description for the general public

The appearance of newly synthesized transcript does not guarantee a creation of functional RNA or protein in a cell. Already at the stage of synthesis RNA combines with proteins and other RNA particles, thanks to which it undergoes maturation, transporting to cytoplasm, translation, and finally degradation. During those processes a stoppage of maturation, a change in sequence, or directing RNA to another metabolic path can occur. Those mechanisms commonly appear in eukaryote cells and are called post-transcriptional regulation of gene expression (PTGR). Numerous publications appearing during the last decade point to a significant role played by PTGR in basic cell metabolism, development, and plants' response to stress. PTGR involves alternative splicing, edition, interference, but also less thoroughly studied processes such as localization, stabilization or RNA storing.

Our previous research have demonstrated that new nuclear structures associated with PTGR in plants are Cajal bodies (CB). Inside them, the presence of poly(A) RNA, including a number of mRNAs has been discovered. On the other hand, CBs lack II RNA polymerase, newly synthesized RNA and SR proteins essential for splicing. Research was also conducted on plants undergoing oxygen deficiency stress (hypoxia), which was most frequently the result of flooding. It allowed to determine that during hypoxia there is a large increase in the amount of poly(A) RNA in Cajal bodies. Further research have revealed that *ncb-1 Arabidopsis thaliana* mutants which do not have Cajal bodies are less tolerant to oxygen deficiency than wild plants (WT type). It is accompanied by a fourfold drop in the amount of poly(A) RNA in *ncb-1* cell nucleus in comparison to WT. However, the mechanism and the biological function of poly(A) RNA accumulation in CBs remains unknown.

On the basis of the abovementioned data, we have formulated a research hypothesis that Cajal bodies are associated with post-transcriptional regulation of gene expression in plant cells in physiological conditions and in the conditions of abiotic stress.

To test this hypothesis, we will perform the following:

- a) conduct a sequencing and comparison of transcriptomes of Cajal bodies, cell nuclei and whole plant cells; it will allow to determine the function of CBs in post-transcriptional gene regulation. On the other hand, the comparison of RNA in WT plants with *ncb-1* will allow to find out what influence Cajal bodies have on the content and functioning of transcriptome in plant cells,
- b) compare the transcriptome of plants' Cajal bodies in physiological conditions and in the conditions of hypoxic stress in order to explain the CB's function in stress conditions,
- c) study the localization, speed of movement and the duration of transcripts' stay in CBs and in the nucleus in physiological conditions and during hypoxic stress in root cells; it will allow to learn the nature and mechanism of RNA accumulation in Cajal bodies.