

Catecholamines are biogenic aromatic monoamines widespread in animals, where they are neuromodulators and stress hormones. These compounds have been also identified in plants, though their function in these organisms was not fully recognized. It is known, that after binding with other phenolics they can reinforce cell wall either by constituting a physical barrier for pathogens or increasing its antioxidative potential. Catecholamines are strong antioxidants and can neutralize free radicals (including those resulting from pathogen infection). In plants catecholamines are also precursors for biosynthesis of alkaloids (e.g. morphine, mescaline) or pigments (betalains, melanins). However, there is data that beside structural function, catecholamines may play a more complicated role of regulatory molecules in plants. In animals, one of the most identified hormonal functions of catecholamines is their influence on sugar metabolism (glycogen breakdown). In plants, starch fulfills analogous function to glycogen – storage form of sugar and energy reservoir. Studies on catecholamines in potato suggest that in plants catecholamines show some resemblance in function – influence starch breakdown and lead to increased contents of soluble sugars. In other studies (i.a. in tobacco) catecholamine influence on plant growth was demonstrated, probably resulting from interaction with phytohormones. However, there are no data that would confirm the regulatory activity of catecholamines in plants, thus our aim is to identify the role of catecholamines in regulation of plant physiological processes. Our preliminary research indicate that catecholamines influence expression of some genes and lead to changes in metabolite and also, in protein phosphorylation level in plants. Phosphorylation of proteins (especially enzymes, transcription factors or receptors) is connected with their activity modulation.

We plan to achieve our goal in multi-stage approach. First of all we will establish the conditions of plant treatment with catecholamines, which will be verified by analysis of expression levels of genes connected with phenylpropanoid pathway, which, based on our previous studies, may be regulated by catecholamines and by measurements of corresponding metabolite contents. Next we will investigate whether catecholamines influence genetic expression by analyzing the whole transcriptome of plants exposed to catecholamines. We will pay special attention to the genes connected with secondary metabolism and stress response of plant, and we will verify their expression changes by means of quantitative Real Time PCR (qRT-PCR). As correlation between gene methylation of expression change (especially under stress conditions) is observed, our next step will be examining the methylation status of genes selected based on the transcriptome analysis and the whole genome methylation pattern after catecholamine treatment. In the next stage, because of our preliminary observation that catecholamines may lead to changes in phosphorylation status of proteins, we will investigate phosphoproteome of plants exposed to catecholamines. In this way we will identify proteins that undergo this posttranslational modification due to catecholamine activity. Considering potential signaling role of catecholamines, we will simultaneously measure levels of cAMP – the secondary messenger in cell. As catecholamines were shown to be involved in stress response of plants, potato plants will be submitted to various stressogenic conditions and catecholamine level in correlation to secondary metabolite changes and genes connected with their synthesis will be assayed. Selection of potato as the subject of study results from our earlier studies of catecholamines in this plants. Large experience in working with this plant, knowledge of its metabolic pathways and well established methodology, will all help to successfully complete this project. Moreover, potato is an important crop, hence the results of our study can be further developed in more applied projects, especially important for food industry.