The project concerns investigating how low frequency alternating electromagnetic field modulates gene expression in plants. Electromagnetic field (EMF) is a factor that is present in the environment and that influences growth and development of living organisms. Extremely low frequency alternating electromagnetic field (ELF-EMF) is particularly important object of investigation, because in daily life, ELF-EMF exists around electric appliances and electronic devices or power lines. With the rapid development of technology and the increase in the number of electrical devices, the exposure of all living organisms to EMF generated by human drastically increases. While many organisms can move, and thus are temporarily and locally exposed to EMF, plants do not have that option. Once located in the nearby of EMF source, plants are permanently exposed to EMF. In particular, it refers to the crop plants growing in the vicinity of electric power transmission networks or traction networks. As there are reports of negative effects of EMF on the growth and development of plants in the literature, research in this area seems justified. However, literature reports mostly describe the effects of EMF on plant physiology, while the very mechanism of the EMF action remains unclear.

Our preliminary experiments showed that flax plants treated with ELF-EMF showed huge changes in gene expression (increased expression of 4778 genes, while 10178 genes were silenced). Primarily, genes involved in plant metabolism were altered, followed by genes connected with DNA/RNA processing, which in concert with signal transduction genes suggests an active and specific response to ELF-EMF. It has been demonstrated that promoter sequence motif nCTCTn identified in human HSP70 gene is involved in the response to EMF. Such motifs are present also in plant gene promoters; however, their involvement in the response of plants to EMF has not yet been verified. Of course, there might be other motifs which are the electromagnetic field response elements (EMREs) that are present in the promoters of genes. Identification of such motifs in plants is the main objective of this proposal.

For this purpose, we will determine promoter sequences of all the genes, whose expression has changed upon ELF-EMF treatment in flax, followed by bioinformatics analysis to identify short sequences (motifs) in promoter region that might be specifically sensitive to EMF. On this basis, we will select group of not more than 30 genes, whose promoter we expect to be modulated by EMF and whose expression showed biggest changes upon EMF treatment. Then, we will verify expression of these genes upon treatment with different intensities of ELF-EMF and different time exposures. This will allow further narrowing the number of potential motives that response to EMF. EMF might also alter gene expression through epigenetic changes, so we will determine the methylation status of selected promoters. To verify the previously selected motives, we will generate transgenic plants, with artificial promoters containing these motives using reporter gene system. We also generate promoter with mutation in investigated regulatory sequence. Finally, we will subject obtained transgenic plants to various stress conditions (such as pathogen infection, drought, cold, salinity etc.) to check whether these motives response only to EMF or are they part of a general plant response to stress conditions. One of the plant responses to stress is generation of free radicals and in consequence oxidative burst that initiate a various processes in plant including changes in gene expression. Thus, we will also check whether selected motives are sensitive to free radicals.

The knowledge gained during the realization of this project will contribute to a better understanding of regulation of gene expression in plants and potential modulators of plants growth and development. This knowledge is particularly beneficial in the case of crop plants, because transmission or traction networks often run through or near crop plant cultivations.