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One of the specialized RNA quality control mechanisms, protecting from formation of potentially harmful proteins is NMD (Nonsense-Mediated Decay). This mechanisms recognizing and removing mRNAs containing premature termination codons (PTC) and simultaneously affects the level of the normal transcripts. It is estimated that in *Arabidopsis thaliana*, similar to mammals and yeast, NMD regulates expression about 10% of all genes. Abnormal functioning of NMD can leads to many human diseases, including a number of cancers (BRCA1, p53, WT1) also Duchenne muscular dystrophy, β -thalassemia, cystic fibrosis, Hurler syndrome and mental retardation. Moreover, the core components of NMD are essential for the survival of the organisms, such as flies, zebrafish, mice and also plants including Arabidopsis.

Knowledge about the NMD mechanisms is relatively wide in different groups of eukaryotes, while plant NMD is still poorly understood. So far, there have been identified only essential proteins of plant NMD active components: AtUPF1, AtUPF2, AtUPF3, AtSMG7 and proteins comprising the complex EJC (Exon junction Complex). Therefore, explanation of the regulation and mechanism activity factors responsible in NMD is crucial for required understanding molecular basic processes, including hormonal homeostasis and regulation of gene expression related with pathogen response.

Scientific goal of this project is to confirm participation and preliminary analysis of function newly identified factors which can be involved in NMD using *Arabidopsis thaliana* as a model organism and plant *Nicotiana benthamiana*. Subsequently, we plan to investigate at what stage of NMD, this potential new interactors of active complex are involved in this mechanisms and whether are they crucial for NMD.

In this project will be realized aspects of molecular biology, research involves basic and advanced molecular biology techniques such as northern blots, RT-PCR, qRT-PCR, immunoprecipitation, western blots, protoplasts isolation and VIGS-NMD technique.