SERRATE (SE) is an essential protein for development and proper functioning of plants. It is involved in many processing steps of various classes of RNAs. It plays a significant role in the production of small regulatory RNAs (microRNAs), the excision of introns and the transcription of certain groups of genes. Our last studies on proteins associated with SE revealed many RNA binding proteins (RBPs) as well as a large group of helicases. RBPs bind specific RNA sequence motif, while helicases are capable of RNA refolding. Most RBPs recognise RNAs containing specific sequence motifs that are usually located within their single-stranded fragments. On the other hand, DEAD-box helicases do not show sequence-specificity.

In our preliminary study we showed that SE interacts directly with three helicases: DRH1, RH46 and RH40, which belong to the DDX5/Dbp2 subfamily. Moreover, we identified proteins associated with DRH1 and we found that DRH1 is in complexes with at least 12 RNA binding proteins which were also detected among proteins associated with SE by us previously. Based on our preliminary results we hypothesize that the helicases that interacts with SE enable RBPs to recognize and bind to specific sites of RNA molecules.

RBPs that associated with both SE and DRH1 (as identified by us previously) can be divided into a few groups involved in different RNA metabolism processes. In this proposal we will focus only on those RBPs that are involved in RNA degradation or mRNA export. We decided to start with RNA degradation because our knowledge about the involvement of SE in degradation of RNA is most extensive and in our preliminary results we showed that RBM7 a subunit on NEXT complex (which is involved in RNA degradation) interacts directly with both: SE and DRH1.We also chose to study RNA export, because: (i) it has been shown that DRH1 interacts with nuclear pore complex; (ii) in a mutant that does not express DRH1 protein, there is an accumulation of polyadenylated mRNA in the nucleus, and (iii) human homolog of SE – ARS2 is involved in mRNA export to cytoplasm.

These data suggest that SERRATE is a protein that interacts with DEAD-box helicase(s) that unwinds secondary structure of RNA as well as with RBP(s) which can bind the specific RNA sequence motif within an unwound fragment. The research planned in this project will focus on the mechanism of such SE-mediated coordination in RNA degradation and export of RNA from the nucleus to the cytoplasm. In this project, we plan to confirm interaction between RNA binding proteins involved in mRNA export with the helicases as well as SE. In the next stage of this project, we will perform an analysis of the changes in the transcriptome and secondary structure of RNA in triple helicase mutant (*drh1 rh40 rh46*).We also plan to identify RNA motifs recognized by selected RBPs in plants with and without helicases activity. The observations from *in vivo* experiments will also be confirmed using *in vitro* techniques. The results of the presented project will be an extension of our knowledge about RNA processing and thus, increase of understanding of fundamental processes occurring in eukaryotic cells. Moreover, the planned experiments will allow us to discover the role of poorly described plant helicases and RNA binding proteins. We will also be able to characterize the role of trimeric complex that is capable of RNA remodelling and binding.