Transposable elements (TEs) are DNA segments capable to change localization in the host genome in the process called transposition. TEs constitute a large genomic fraction of eukaryotic organisms, among them miniature inverted repeat transposable elements (MITEs), that do not possess any enzymatic machinery necessary for transposition. These non-autonomous elements are likely mobilized by a transposase supplied by related autonomous transposons. State of the arts relatively little is known about mobilization of MITEs in dicotyledonous and open-pollinated plants such as carrot *(Daucus carota* subsp. *sativus*). A growing body of evidence suggests that TEs, including MITEs, are important players in crop evolution, domestication and improvement, providing *de novo* variability subjected to natural selection and genetic novelty utilized by early farmers and recent breeders. The carrot genome sequencing project provided the reference genome assembly and high-throughput genomic data to explore, which were used to study TEs and led to the identification of a group of *Daucus carota Stowaway*-like (*DcSto*) MITEs. Related putatively autonomous *Mariner*-like elements *DcMar*s, possibly providing the transposition machinery to *DcSto*s were also identified. Based on our preliminary research, we hypothesize that the ***DcMar* transposases are responsible for the mobilization of *DcSto* MITEs**. Thus, we intend to analyze functional interactions between *DcMar*s transposases and *DcSto* MITEs.

The aim of the project is to answer the question whether transposases originating from autonomous DNA transposons (*DcMar*s) are capable of mobilizing *DcSto* miniature inverted repeats transposable elements present in the carrot genome.

To achieve the goal, we intend to use of a protocol allowing tracking *DcMar* transposase-driven transposition of carrot *DcSto* elements in *Saccharomyces cerevisiae* yeast. The yeast transposition assay enables unambiguous observation whether transposition has occurred. To verify the hypothesis we would like to construct vectors for yeast transformation comprising functional *DcMar* transposases and several *DcSto* MITEs and subsequently carry yeast transposition assay. It will be achieved first through the yeast transformation and next tracking transposition events. Verification of transposition including identification and analyses of excision and insertion sites of an activated MITE will be conducted.

The proposed research is innovative, no interactions between transposases of putatively active autonomous DNA transposons and related MITEs present in carrot genome have been examined. The implementation of research tasks included in the project will allow for significant broadening of the knowledge about TE activity in the carrot genome and the relation between autonomous and non-autonomous elements. Thorough investigation of mechanisms of MITE mobilization is crucial in the perspective of understanding the role of mobile elements in shaping genomes of carrot and other plants. The results obtained using co-transformation of yeast in the project will be an interesting starting point for further exploration of *DcMar/DcSto* genomic ecology and to study mechanistic issues of *DcSto* transposition. At the same time, the developed molecular tools for the yeast transposition assay can be further used to study other carrot genome-derived transposase/MITE interactions.