

Are Miniature Inverted-repeat Transposable Elements involved in fine-tuning of gene expression in carrot?

Transposable elements (TEs) are DNA segments that are able to change their chromosomal localization in a process called transposition. TEs are present in genomes of virtually all living organisms and, as a result of their replicative nature, may constitute a significant portion of the genome. TEs have been called 'jumping genes' and are commonly considered as 'selfish' or 'parasitic'. Miniature Inverted-repeat Transposable Elements (MITEs) are a group of short (> 600 bp) DNA transposons that do not have any coding capacity and are mobilized by related autonomous elements. Interestingly, MITEs are preferentially found in genic regions. Around 45% of the carrot genome is attributed to TEs. Carrot MITEs comprise more than 400 families varying in terms of their copy numbers, from few to thousands of copies. Our analysis of 14 *Stowaway*-like MITE families showed that their genomic distribution was very diverse, depending on the origin of carrot accessions, they were frequently inserted close to genes, and much more numerous in carrot, as compared to other plants. Overall, it suggests their putative impact on genes.

TEs, especially retrotransposons and MITEs, play an important role in modifying gene expression. It is possible, as they may provide additional regulatory sequences to adjacent genes. MITE-derived transcription factors binding sites (TFBS), i.e. motifs to which regulatory proteins bind, may affect transcript levels. MITEs are a source of small RNAs, that in turn are responsible for gene regulation through cytosine methylation, that usually results in gene silencing. They can also affect the structure, stability, and cellular positioning of transcripts. MITE-related post-transcriptional modifications of gene expression may be associated with the presence of alternative polyadenylation sites (APAs) provided by MITEs inserted in 3'untranscribed regions (3'UTRs). APAs may result in formation of truncated transcripts encoding non-functional proteins, may affect transcript stability or their tissue specific localization. Importantly, these mechanisms are often activated and/or modified under abiotic stress conditions. Thus, it is likely that TEs are also involved in the host response to stress, increasing genome plasticity and transcriptome flexibility which is crucial to survive in adverse environmental conditions. Anecdotic examples of the role of MITEs in the regulation of gene expression and reaction to stress have been reported for model plants (e.g. thale cress, *Arabidopsis thaliana*) and were limited to the action of one or few genes.

We hypothesize that carrot MITEs are involved in fine-tuning of the expression of adjacent genes. The regulatory role of MITE may include usage of MITE-derived transcription factor binding sites (TFBS), involvement of MITE-derived small RNAs (sRNAs) providing epigenetic response to abiotic stressors, and usage of MITE-derived polyadenylation signals (PAS).

Advances in bioinformatics and high-throughput DNA sequencing technologies gives us an opportunity to perform global analysis of gene expression, sRNA and methylation status of carrot seedlings grown under salt, cold and heat stress and associate them with MITE insertions. As a result, we will verify the hypothesis that MITEs important in fine-tuning of gene expression and some MITE families are involved in the plant host reaction to particular stressors.