

## **DESCRIPTION FOR THE GENERAL PUBLIC**

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It is estimated that up to 20% of cultivated area is affected by uncontrolled concentration of salt in the soil. Soil salinization is a growing problem for agriculture worldwide and poses a serious threat to crop yield and future food production. The situation is likely to worsen owing to the anticipated effect of the global climate warming. Carrot is one of the most important root vegetable crops grown worldwide on more than one million hectares. Carrot is considered as a salinity-sensitive species, however, there are several regions in Asia, where landraces adapted to high soil salinity are being cultivated and can be useful sources of germplasm for breeding cultivars with increased tolerance to salt. Identification of genetic factors determining tolerance is a prerequisite for their successful utilization in crop improvement.

The objective of the present project is to pinpoint genes decreasing plant sensitivity to salt in the soil, by application of modern analytical tools. We will investigate the whole genome, i.e. the total genetic information written in carrot DNA, comprising over 400 million nucleotides and containing more than 32 thousand genes. We will mine for differences in gene expression between salt-tolerant plants originating from Asia and salt-sensitive plants of European cultivar, ultimately resulting in changes in their phenotypes, i.e. visible trait variants. We will also indicate regulatory factors, microRNAs, associated with response to salt stress and controlling gene expression. In parallel we will study the changes in the chemical composition and the ability to photosynthesis in these plants. We will identify potential physiological mechanisms enabling the growth of plants tolerant to increased salt content in the soil.

Comprehensive genetic analysis combined with biochemical and physiological analyses will allow identification of genes potentially responsible for the tolerance of the used carrot plants to salinity. The role of these genes will be verified by making their precise genetic modification involving the removal of a gene fragment, which will result in its functional knockout. Alternatively, we will induce an enhanced expression of these genes. Plants with such modified genes will be subjected to salt stress in the laboratory and observed for changes in their sensitivity or tolerance to salinity. As we will use high-throughput technologies generating large datasets, beside the experimental part, we will be using computer-aided data analysis (bioinformatics) uploaded to a high-performance computer cluster.