Bundesministerium
für Ernährung
und Landwirtschaft

BMEL PhD-Program with the Islamic Republic of Iran

opTOMize – Modulation of trehalose biosynthetic gene expression to improve stress tolerance of tomato

country/countries	Islamic Republic of Iran
funding agency	Federal Ministry of Food and Agriculture – BMEL
project management	Federal Office for Agriculture and Food – BLE
project coordinator	Prof. Dr. Frederik Börnke
project partner(s)	Leibniz-Institute for Vegetable and Ornamental Crops
project budget	**122.863 €**
project duration	1.10.2017 – 30.06.2021

key words	Agricultural Biology, Plant Stress Physiology, Plant Molecular Biology, Biotechnology, Tomato, Trehalose
background	Due to global climate change, agricultural and horticultural production is increasingly threatened by environmental constraints imposed through abiotic stressors such heat, drought and salinity. To mitigate the vulnerability of horticulture to climate variation and associated environmental constraints we will need crop varieties, species or rootstocks with improved tolerance to stress conditions. In order to accelerate plant breeding, and the rational engineering of more resilient crop varieties, it is necessary to understand the molecular pathways underlying plant stress adaptation. The project aims to provide novel insights into plant stress signalling and adaptation of the important horticultural crop tomato with the aim to exploit this knowledge to increase stress tolerance in plants.
objective	An important metabolic pathway that has been linked to abiotic stress tolerance in plants is the trehalose biosynthetic pathway. Recent findings show that the metabolism of this nonreducing diglucoside is essential for normal plant growth and development. The role of any of the trehalose metabolic genes, particularly those displaying no apparent enzymatic activity but whose expression strongly responds to stress conditions, has not been studied in detail in any plant. Therefore, the objective of the project is to uncover how trehalose metabolism is involved in tomato response to abiotic stresses. This will identify and functionally characterize novel components of stress signal transduction and acclimation in this important horticultural species. A long term goal of the project is to utilize this knowledge to improve tomato stress tolerance by manipulating trehalose metabolism or the expression of its associated genes.
Results	- 10 TPS and 8 TPP encoding genes were identified in the tomato genome and the majority could be cloned - Enzymatic activity could be confirmed for two out of 10 tested TPS and for all four tested TPP isoforms

	- Tissue- and stress-specific expression patterns of TPS/TPP genes were determined by qPCR - Expression of a number of TPS/TPP genes is controlled by temperature - A workflow for the generation of stably transformed tomato plants was established - CRISPR-Cas9 mediated genome editing of selected TPS/TPP-genes in tomato so far was not successful. The number of primary transformants must be increased to enhance the successrate.
Recommendations	- The role of trehalose metabolism in stress resistance of tomato and other horticultural crops should be further investigated - Genome-editing technologies should be adapted and optimized for horticultural crops
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