

## CANDIDATE GENES CONTROLLING FRUIT QUALITY IN A TOMATO INTROGRESSION LINE TOLERANT TO WATER DEFICIT

VASCO M.\*, DE STEFANO R.\*, DI MATTEO A.\*, PUNZO B.\*, MOLISSO M.\*, LOTTI C.\*\*,  
RICCIARDI L.\*\*\*, BARONE A.\*

\*) Department of Soil, Plant, Environmental and Animal Production Sciences, University of Naples “Federico II”, Via Università 100, 80055 Portici (Italy)

\*\*) Department of Agro-Environmental, Chemistry and Crop Protection, University of Foggia, Via Napoli 25, 71100 Foggia (Italy)

\*\*\*) Department of Biology and Chemistry Agro-Forestal and Environmental, Genetics and Plant Breeding Unit, University of Bari, Via Amendola 165/A, 70125 Bari (Italy)

*Solanum pennellii* introgression lines (ILs), fruit quality, antioxidants, water deficit tolerance

Fruit quality is an important criterion for marketing of tomatoes and of paramount importance to guarantee consumer satisfaction. It involves a combination of many traits mostly expressing a quantitative variation and controlled by complex gene networks. In addition, fruit quality can be dramatically reduced by environmental constraints such as drought. Thus identifying genetic reservoirs of drought tolerance and elucidating genetic mechanisms controlling the interaction between drought stress and fruit quality traits may be beneficial for breeders to develop new tomato genotypes combining increased drought tolerance to high fruit quality. The aim of this research was to identify major genes and molecular networks controlling fruit quality under drought conditions in tomato.

Introgression lines (ILs), in which individual homozygous segments of wild chromosome are carried in the genomic context of the cultivated species, are useful for resolving complex traits in QTLs and identifying candidate genes. Screening ILs from *S. pennellii* allowed to identify IL 9-2-5 as a more drought tolerant genotype than the control M82. When grown at a lower water regime, IL9-2-5 also revealed to perform higher concentration of fruit reduced ascorbate (AsA). A comparative transcriptomic analysis allowed to select 62 transcripts differentially expressed in red ripe fruit of IL9-2-5 with respect to M82. Candidate genes for controlling fruit quality in tomato were identified among antioxidant pathways, signal transduction pathway, hormonal metabolism, transcription regulation process. In particular, the concentration of fruit AsA well correlated with the transcript abundance of cell wall-associated genes such as a polygalacturonase and a polygalacturonate-4-alpha-galacturonosyltransferase and with three monodehydroascorbate reductase genes.

Functional characterization of candidate genes will prove their involvement in fruit quality control and provide additional genetic means to breeders for tomato quality enhancement in sustainable cropping systems.