Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 8.32

RESOLVING GENE NETWORK THAT CONTROLS PHENOLICS ACCUMULATION IN TOMATO FRUIT

DI MATTEO A.*, RUGGIERI V.*, SACCO A.*, CARRIERO F.**, RIGANO M.M.*, LOMBARDI N.*, BARONE A.*

*) Department of Soil, Plant, Environmental and Animal Production Sciences, School of Biotechnology, University of Naples "Federico II", Via Università 100, 80055 Portici (Italy)
**) Metapontum Agrobios, S.S. Jonica 106, km 448.2, 75010 Metaponto (Italy)

Phenolics, antioxidants, tomato fruit quality, Solanum pennellii introgression lines, transcriptomics

Phenolic compounds are plant secondary metabolites that are important determinants in both sensory and nutritional quality of fruits and vegetables. In addition, in the last few years many studies studies support the increasing evidence of the possible role of phenolic compounds in prevention of chronic diseases such as cardiovascular disease and cancer [Nakajima et al., 2007, Life Sciences 80: 370–377]. Tomatoes are one of the valuable sources of antioxidants such as phenolic compounds (flavonoids and hydroxycinnamic acid derivatives). Therefore, increasing phenolics in tomato fruit is a major claim of breeding in order to meet consumer requirements and create new market opportunities. So far, many key genes have been reported that control the accumulation *in planta* of phenolic compounds. However, additional insights are required in order to highlight genetic and physiological mechanisms controlling phenols accumulation in tomato fruit and to support breeding programs for increased fruit quality. The aim of the work was the identification of major genes and gene networks that regulate the level of phenols in tomato fruit.

The screening of *Solanum pennellii x S. lycopersicum* introgression lines (ILs) [Eshed and Zamir, 1995, Genetics 141:1147-1162] over three year trials in greenhouse and open field environments allowed the identification of a stable QTL for increased fruit content of total phenolics in the IL7-3. In particular, chlorogenic acid mainly accounted for the higher performance of this line. Therefore, to investigate candidate genes controlling phenols synthesis and accumulation in IL7-3 fruit, we performed a comparative transcriptomic analysis in tomato pericarp between this line and the control *cv*. M82 over two consecutive years. The transcriptomic approach allowed to identify 149 up-rgulated and 142 down-regulated probes. Based on functional annotation, clustering and networking outputs, subsets of differentially expressed transcripts were used to develop model networks that describe mechanisms controlling accumulation of phenylpropanoids in tomato fruit. The network explains the variation in phenols levels in terms of interactions between ethylene signalling, plant responses to stress and biosynthesis of phenolics. Upon validation of key transcripts of our model by RT-qPCR we undertook a functional characterization of candidate genes by the TILLING (Targeting Induced Local Lesion IN Genomes) approach [Minoia et al., 2010, BMC Research Notes 3:69]. In particular, tomato plants homozygous for mutations in the coding sequence of two transcription factors involved in ethylene response (e.g. ERF1 and EIN3) revealed to drive ripening-associated phenol accumulation in fruit. These results suggested us to design new strategies of precision breeding for increased fruit nutritional quality in tomato.