DROUGHT RESPONSE IN TOMATO: MOLECULAR AND PHYSIOLOGICAL ANALYSIS


*) Dipartimento di Scienze del suolo, della pianta, dell’ambiente e delle produzioni animali, Università di Napoli “Federico II”, Via Università 100, 80055 Portici (Na);
**) Istituto per i Sistemi Agricoli e Forestali del Mediterraneo - CNR, Via Patacca 85, 80056 Ercolano (Na)

SNP, tomato, drought, stress tolerance, re-sequencing

Drought stress in plants is one of the resulting effects of climatic change in the world and its consequences cause major yield losses. Most crop plants, including tomato (*Solanum lycopersicum*), are sensitive to drought stress. Substantial genetic variation for Drought Tolerance (DT) exists within the cultivated tomato, as well as in other related wild species. However, the genetic variability in the response to drought stress in tomato species is not well understood to warrant its use for developing drought-tolerant cultivars.

The aim of this work is to identify polymorphisms within genes involved in DT across tomato cultivars and wild species by re-sequencing. The tomato genotypes were tested, belong to different *Solanum* species and to a collection of cultivated varieties and ecotypes. Phenotypic characterization of genotypes was performed at the physiological level by determination of relative water content (RWC) and water loss rate (WLR) after many hours of dehydration. In addition, the effect of the water deficit was also assessed on the photosynthetic performance in leaves of 3 genotypes of tomato grown under a plastic tunnel. Photosynthetic performance of PSII, stomatal conductance, RWC and leaf water potentials in tomato leaf tissues were monitored during application of stress and after recovery watering.

In order to identify Single Nucleotide Polymorphisms (SNPs), specific primers were designed for sequences of 6 putative drought stress-related genes retrieved from GenBank. In particular, sequences annotated as MKP1 (MAP kinase phosphatase), Asr2 (ABA stress ripening), TSW12 (a lipid transfer protein gene), dehydrin TAS14, rd22 (dehydration responsive gene) and STO (putative zinc-finger protein) were analyzed. After amplification, SNPs discovery was achieved by re-sequencing PCR products on a ABI PRISM 3130 GENETIC ANALYZER. An average of 16 SNP and 2 IN/DEL were identified in these gene sequences. The wild species showed many mutations and this was predictable because the reference sequence reported in GenBank was from *S. lycopersicum*.

The identification of polymorphisms associated to the DT may lead to the development of useful molecular markers helping assisted selection programs.