

## ION UPTAKE AND YSL1 GENE IDENTIFICATION IN TOMATO

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Tomato breeder are using wild tomato relatives, even non-cross compatibles ones, in order to obtain cultivars with highly commercial values bearing new traits. However, the introgression of a wild genome into the cultivated one produces a new gene combinations that may lead to the expression of undeliverable traits, perhaps not so easy to recognise; even more, phenotypic variations may escape during the selection procedure when minor genes or non-abnormal phenotypes are involved. In the frame of the “GenoPom” project funded by MIUR, we have focused our interest on the alteration of heavy metals uptake from the soil and their loading into edible organs in commercial lines coming from *Solanum* interspecific crosses. Our final aim is to put together data coming from ion homeostasis and gene expression analyses, thus obtaining a ionic map of tomato. To pursue our goal, we have started to study the cv M82 of *Solanum lycopersicon*, the wild relative *Solanum pennelli* and their introgression lines IL. Regarding the experiments on ion homeostasis, *S. lycopersicon* M82 and the introgression line IL 6-4-2 were grown in hydroponics under controlled environmental conditions. Twenty day-old plants were left to grow for 10 days in the presence of non-toxic concentration of Cd (10 mM), Pb (3 mM), Zn (100 mM) given separately or combined. Control and treated roots and leaves were then harvested and stored at -80°C for ionic and gene expression analyses. Ions analysis of *Solanum lycopersicon* M82 and IL 6-4-2 showed that traits correlated to ionic homeostasis is significantly modified in response to all metals and to the genotype. The analysis of ions data, obtained by ICP-MS, give a pictures of the different responses performed both to different stress and to combined stress, probably correlated to the up-regulation and/or down regulation of metal uptake proteins. Performed experiments demonstrate that the introgression of the wild genome into the cultivated one produces a new phenotype, perhaps due to the expression of traits linked to uptake, translocation and accumulation of useful and/or toxic metal into plant tissues and organs.

Regarding the functional genomics approach for gaining insight into gene networks involved in mineral-ion accumulation in tomato plants, in literature has been reported that at least 25 major family genes are involved for metal homeostasis in plants. Among them, the genes *ysl*, *hma*, *mtp*, *znt*, *zrt* have been already studied at least in the plant species *Arabidopsis thaliana*, *A. halleri* and *Thlaspi caerulescens*. So far, no such genes have been reported to be cloned in *Solanum* species. We have focused our study on the genes YSL1, ZNT1 and MTP1 responsible for uptake, translocation and accumulation of metal such as zinc, cadmium, and iron into plant compartment. For all of them, consensus sequences from nucleotide multialignment have been obtained. Then, each of those were blasted in a *Solanum* EST collection databank and an assembled UniGene

sequence was obtained.. Finally, we have designed primers and performed PCR analysis on *S. lycopersicon* and *S. pennelli* genomic DNA. So far, we have cloned a putative *ys11* sequence from tomato, that has shown that a very high percentage of identity (92%) with whole *ys11* gene of *Nicotiana tabacum*; the *in silico* translated sequence of this sequence has shown a 89% of identity with the same tobacco protein.