

**Abstract**

**ITalian-IsraeLi initiative for the NUTRItional improvement of SOLAnaceous crops  
(IT-IL-NUTRI-SOL)**

The potato is the fourth most important staple food for mankind. Breeding of potatoes for nutritional value is mainly focused on carotenoid, anthocyanin and glycoalkaloid contents. Carotenoids and anthocyanins exhibit antioxidant activity, therefore increasing their level in the tuber is a desirable trait. Glycoalkaloids contribute to the characteristic taste of the potato and have been reported to exhibit anti-cancer activity, but are toxic to humans and their level in the tuber must be regulated carefully. The glycoalkaloids are common constituents of other members of the *Solanaceae* family, such as tomato and eggplant. The levels of the abovementioned secondary metabolites are genetically determined; however, developmental, tissue specific and environmental cues affect their final content.

Breeding of potato has traditionally been slow, due to its tetraploid genetics, inbreeding depression and lack of good genetic maps. The sequencing of the potato genome by an international consortium including one of the partners of the project, as well as the synteny between potato, tomato and eggplant genomes, will facilitate the introduction of molecular markers for the assisted breeding of these traits. The major objectives of the present proposal are (1) to develop advanced tools for breeding high, stable levels of carotenoids and anthocyanins and low levels of glycoalkaloids in tubers for commercial utilization over a range of climates; (2) to identify glycoalkaloid biosynthetic pathway and related genetic markers for breeding of agricultural important Solanaceae crops (potato, tomato and eggplant) with reduced levels of these toxic metabolites. To this end, the following specific objectives will be addressed:

(a) The level of carotenoid, anthocyanin and glycoalkaloid metabolites and their biosynthetic gene expression will be monitored in a panel of potato genotypes, eggplant introgression and recombinant inbred lines and of tomato mapping population, including carotenoid- and anthocyanin- enriched clones and their crosses, and divergent crosses for glycoalkaloid content.

(b) Stability of carotenoid, anthocyanin and glycoalkaloid traits in potato will be measured in selected clones under abiotic stress conditions typical of the Mediterranean region (drought, heat).

(c) Potato, eggplant and tomato lines divergent for their glycoalkaloid content will be subjected to metabolomic and transcriptomic analyses to identify new glycoalkaloid-related genes and QTL for low glycoalkaloid level.

(d) Data from previous objectives will be used to construct transcriptional-metabolic networks to identify key regulators controlling of metabolite levels in the tuber and fruits, and to find potential genetic associations between the pathways.

Identification and quantification of metabolites will be done by HPLC coupled with high resolution MS, and GC-MS analyses; both metabolites and their degradation products will be detected. Gene expression will be monitored by real-time PCR and Illumina RNA-seq to gain an overview of general metabolism in the selected potato, eggplant and tomato genotypes; mapping of glycoalkaloid-associated loci will be identified by QTL analysis using ILs, F2 and RIL populations and exploiting the synteny across these Solanaceous crops.

The present proposal addresses these issues by combining several research groups from Italy and Israel, with expertise in carotenoid, anthocyanin and glycoalkaloid metabolism as well as in genetics, molecular biology, physiology and biochemistry of potato, tomato and eggplant plants.