



**SIXTH FRAMEWORK PROGRAMME  
PRIORITY 5  
Food Quality and Safety**

***Publishable Executive Summary period 1-3 (month 1 – 36)***

Project acronym: **EU-SOL**

Project full title: **High Quality Solanaceous crops for consumers, processors and producers by exploration of natural biodiversity.**

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## Executive summary

EU-SOL is a network of plant scientists from universities, research institutes and industry within the EU, EU partner country Bulgaria, Israel, USA and INCO countries Westbank, Argentina, Brazil and South-Africa that focuses on the development of high quality and healthy tomato and potato varieties with improved consumer-, processor- and producer-directed traits. Quality and wholesomeness of food and food products are two issues addressed prominently by society especially in relation to obesity (and atherosclerosis), the most important cause of cardiovascular disease, age-related diseases, such as cancer and diabetes and to the increasing preference of consumers for ‘regional’ and ‘niche’ food specialties. Additionally producers are challenged by constraint in plant architecture and development such as fruit set and tuberisation.

### **Strategic objectives addressed by EU-SOL are:**

1. To extract the under-exploited natural biodiversity present in Solanaceae to improve consumer-driven and environmentally-directed quality of tomato fruits and potato tubers.
2. To map, isolate and characterise genes responsible for quality traits and to dissect the molecular mechanisms underlying these trait by application of state-of-the-art knowledge and innovative technologies.
3. To assemble these genes within new elite genotypes to boost our knowledge and provide a blueprint for novel high quality varieties to be developed by EU breeding companies.
4. To coordinate and integrate breeding research for quality traits, to provide training in innovative technologies, to disseminate the results and to transfer knowledge and technologies to industry.
5. To participate in the international tomato genome sequencing initiative that will tie European Solanaceae research and innovation into the full global activities in this area. This is of pivotal importance for Europe.
6. To create a model for how world-wide scientific collaboration can lead to innovative research that can set the road map on how to improve global food security related to a wide variety of other crop plants.

The **strategic objectives** of EU-SOL are to understand the factors that affect consumer-driven and environmentally-directed quality of the two most important vegetable products in the EU, tomato fruits and potato tubers, both belonging to the Solanaceae. To this end, EU-SOL will attempt to dissect the genetic and molecular components that control these quality traits by applying state-of-the-art knowledge and technologies. EU-SOL particularly focuses on mapping, isolation and characterization of genes responsible for traits important for consumers and processors (health, nutrition, flavour, fragrance, soluble solids, texture, colour, shelf-life, starch, chipping quality) as well as for producers (plant architecture, fruit set and tuberisation), and the mechanisms underlying these traits (control of gene activity, regulatory networks). Important goals are to understand the factors that affect tomato and potato architecture and fruit and tuber composition, to acquire knowledge of carbon and nitrogen acquisition, partitioning and allocation during fruit and tuber development, and to identify the key genes involved. Assembly of these genes within new genotypes will boost our knowledge of the factors that control quality and provide a blueprint for novel high quality varieties to be developed by EU breeding companies using efficient and rational breeding strategies based on marker-assisted breeding and genetic engineering that exclusively use natural plant genes.

To accomplish these objectives EU-SOL will explore and exploit the **natural biodiversity** related to these quality traits that are largely unexplored and hardly used in current commercial varieties. Natural biodiversity is an **under-exploited sustainable**

**resource** that can enrich the genetic basis of cultivated plants with novel alleles that improve productivity, quality and adaptation. This genome-wide project, which is undertaken within a framework of genetically diverse germplasm, will result in a far more profound and comprehensive understanding of the underlying biology as multiallelic effects will be captured. It will provide characterized tomato genetic resources that will be distributed to EU-SOL researchers for exploring traits related to organoleptic quality, consumer health and producer agrotechnical traits.

The activities within EU-SOL are organised into 8 Modules each comprising of related activities carried out in a total of 28 work packages. The strategic objectives are addressed within 4 plant-oriented research Modules (Module 1-4), two Modules addressing state-of-the-art Technology Development (Module 5) respectively Bioinformatics (Module 6), a Module aimed at Management of the Consortium and dissemination of knowledge to the public (Module 7) and a Module focussing on the exploitation of knowledge and results by industry and communication with society (Module 8).

The progress made in the first 36 months of the EU-SOL project is reported in the following concise Module summaries.

Within **Module 1** the “**Organoleptic Quality: Biological Bases of Tomato Fruit and Potato Tuber Quality Perceived by Consumers**” is the focal point. To characterize the preferences of European consumers a large experiment to determine tomato fruit sensory profiles has been performed and completed. The experiment consisted in characterizing in 3 countries (Italy, Netherlands and France) a sample of 18 tomato cultivars corresponding to the diversity available on the market at 3 levels: sensory profiles with trained panels, consumer tests and instrumental measurements. The analysis of data was then done first at a country level, then a comparison among countries was performed. Analysis of the data allowed the identification of major traits for improving the organoleptic quality of tomato fruit. Identification of the most relevant sensory tomato quality traits can subsequently be used by breeding companies to tune their tomato breeding efforts to the wishes of the consumers. To introduce these traits in commercial tomato varieties easy to use molecular markers that are closely linked to these traits are needed. Such markers make the breeding process much more efficient and rationalize the selection process of the best progeny by the breeders. To develop these markers the traits first have to be located on the tomato genome. For that purpose QTL for traits related to tomato flavour, aroma and texture and potato aroma have been genetically mapped in several populations and during three years to determine the influence of environmental factors. Most QTL mapping experiments now have been completed and further fine mapping is underway for several traits to be able to develop molecular markers that are so tightly linked that they are of real value to the breeder.

In addition to genetic approaches such as QTL mapping, two other genomics approaches have been pursued to identify genes involved in fruit quality. These methods used either similarity based bioinformatics approaches or a combination of proteomics and transcriptomics which resulted in the identification of a set of genes involved in tomato fruit development, aroma production, tomato fruit ripening and texture. Functional analysis by reverse genetics of several of these genes is in now progress and transgenic plants for several genes of interest have been obtained. Isolation of these genes also enabled the identification of regulatory DNA elements involved in gene expression during early fruit development. Such DNA elements will be valuable for the spatial and temporal control of the activity of transgenes.

Within this Module all research is on target and most deliverables due have been .

Within **Module 2** “**Health-based Consumer Quality Traits in Tomato and Potato**” a metabolomics technology platform has been established to test a diverse set of tomato and potato materials for the presence of antioxidants and other health related nutraceuticals such as flavonoids, phenylpropanoids, carotenoids, vitamin E and minerals. The aim is to identify the genes responsible for the formation and accumulation of these nutraceuticals and to unravel the regulatory mechanism underlying their biosynthesis, accumulation and degradation.

The main achievements have been the analysis of antioxidant profiles in populations of tomato carrying introgression from wild species and mapping of QTL in these populations. Progress has been made towards the isolation of candidate genes for carotenogenesis in potato and vitamin C in tomato. *Solanum pennellii* introgression lines were subjected to metabolite profiling approaches in order to determine qualitative and quantitative changes in phytochemicals conferring health based quality traits. The profiling technologies targeted the following molecules; (i) **carotenoids**: components of the complete pathway from phytoene to lutein have been determined; (ii) **tocopherols**: principally  $\gamma$  and  $\alpha$ -tocopherol; (iii) phenylpropanoids and **flavonoids**: including *p*-coumaric acid (plus derivatives) chlorogenic acid (plus isomers), rutin and naringenin chalcone. To establish the influence of developmental and environmental conditions on the levels of antioxidants, carotenoids and tocopherols were analysed in five selected *Solanum pennellii* ILs plus the M82 wild type at seven time points during fruit development and ripening.

The most robust QTLs for health-related traits that were independent of environmental growth conditions were identified. These QTLs have been recommended for further study to confirm the relevance for breeding industry.

A diversity microarray analysis of a tomato population segregating for carotenoids/vitamin C content has been carried out. Also the tomato *sunred* gene involved in hyper responsiveness to light and increased phytonutrient production has been cloned. Additionally the mode of inheritance of the phytonutrients of the ascorbate pathway has been fully evaluated. Also the whole tomato carotenoid pathway from phytoene synthase down to beta-carotene hydroxylases (Psy1, Psy2, Pds, Zds, CrtISO, Lcy-b, Beta, Lcy-e, Chy1 and Chy2) as well as the three tomato Cryptochrome genes and the two functional tomato CONSTANS-like genes have been mapped using ILs and sequenced. Several hundred mutations have been identified in both non coding regions (promoter, UTS, introns) and CDS.

Also, good progress was made in elucidating the carotenoid pathway in potato. A number of candidate genes resulted from a micro-array experiment using the POCI array. These candidates will be tested for co-localization with know carotenoid QTL.

The research on the regulatory mechanisms controlling nutraceutical formation yielded very promising results. Transgenic approaches targeting specific genes have been successfully used to modulate vitamin, polyphenol and carotenoid content. General increases in all these compounds have been observed in fruits from transgenic tomato plants in which CRY and DET1 genes have been targeted, and extremely detailed analyses of transcriptional and metabolic changes in these fruits have been performed. In potato "golden" tubers with highly increased provitamin A content have been obtained which also have been subjected to detailed metabolic and transcriptional profiling.

The work in this module is slightly delayed due to the availability of plant materials, which should be corrected however within the next reporting period.

Within **Module 3** the focus is on “**Producer and Processor Traits in Tomato and Potato**”. The presence of natural variation for traits of interest in the gene pool of tomato and potato is used to characterize genetic and molecular factors underlying plant architecture, soluble solids content and composition in tomato fruit, the response of tomato to temperature stress and the development and composition of the potato tuber.

Several hundred tomato QTL were identified in populations derived from crosses between cultivated tomato and wild species like *S. pennellii* and *S. chmielewsko*. QTL for metabolite and enzyme activity including many related to quality, yield and physiological traits under temperature stress were often found to co-localize in biological meaningful manner. Currently, 14 candidate genes have been clones and are selected for functional analyses in order to gain evidences about their involvement on the identified quantitative metabolic traits.

To get further insight into tomato plant architecture rapid progress is made in genotyping and phenotyping of various populations generated by a the cross between *S. lycopersicum* lateral

suppressor or blind mutants and *S. pennellii* for novel architecture QTLs. A new *S. lycopersicum* x *S. chmielewski* population was phenotyped for temperature and salt stress and genetic variation for these traits has been documented.

A number of segregating potato populations has been created and analyzed in the field for a number of tuber quality traits including diversity in vitamin, protein levels and alkaloid content. A considerable breakthrough was the validation of the BSA transcriptomics method for identifying candidate genes associated to a particular quality QTL. Candidate genes for both tuber flesh color, starch gelling and free methionine content have been identified and genetic markers for these traits have been developed for breeding purposes.

The unique selling point of potato is that it produces tubers. How tuberization happens is still a black box while knowledge of this process is of great importance to potato breeders. Moreover scientifically it is a challenge to unravel the developmental process that leads from a stolon which is a modified stem, to a tuber. Therefore a search was initiated for candidate genes involved in the control of tuber initiation, tuber development and sprouting. Significant progress has been achieved in understanding the molecular mechanisms controlling these processes by comparative analysis of gene expression data. Expression profiles were obtained during different stages of potato tuber life cycle as well as from other tissues of potato plants. This has enabled us identifying a number of genes which are specifically expressed in certain tissues and/ or involved in controlling of different developmental processes.

By reverse genetic approaches for several of these candidates it has been shown that they influence the tuberization process itself and also traits like tuber starch content. A major advance was the identification of a potato protein that is orthologous to Arabidopsis FT that is involved in induction of flowering. The potato FT ortholog is probably mobile and involved in the control of tuberization in a photoperiod-dependent manner.

Overall this Module is well on line to meet the objectives for the entire period of EUSOL. In addition some tasks have been re-defined well in advance following consultation between the companies involved.

**Module 4** that focuses on “**Tomato Genetic Resources**” has the task to characterize tomato genetic resources both at the phenotypic level and their marker genotypes and to make this data available to other interested EU-SOL teams. From the start of the project interspecific populations involving the tomato species *Solanum pennellii*, *S. neorickii*, *S. chmielewskii*, *S. habrochaites* and *S. cheesmaniae* and potato *Solanum tuberosum* have been available as well as unpublished RFLP data and phenotypes from at least two years of trials. During the third reporting period a common set of ~ 120 COSII markers has been used to complete the genotyping of the *S. pennellii*, *S. chmielewskii* and *S. habrochaites* IL populations and of the *S. neorickii* BIL population in order to develop a common anchored map. Also, marker surveying for the *S. cheesmaniae* RI population is underway. In addition, the potato genetic map was linked to the tomato genetic map with the use of 139 COS markers.

Another important resource forms a population of 100 mapped tomato mutants which recently allowed the cloning of the gene underlying the compound inflorescence mutation. Several fruit colour mutations currently are in the stage of fine-mapping.

The most significant genetic resource that was constructed is a tomato core collection (CC) consisting of ~7000 accessions collected from multiple sources. The phenotyping for a set of minimal 10 traits was achieved and is viewable on the web via a search engine. The genetic analysis of the population structure of the Core Collection has started with the selection and validation of a set of SNPwave markers. For approx. 4500 plants DNA has been isolated already and the large scale mapping by SNP-wave will start next reporting period.

Also, the interest of the seed company partners is picking up rate. This is reflected by their willingness to support the screening of the expanded CC and their involvement in germplasm phenotyping and seed production. The addition of new seed companies as partners in the Consortium is an illustration of the value and availability of EU-SOL germplasm.

There are no major changes in the module program and work is proceeding on track

**Module 5** has as task to set up our “**Solanaceae Technology Platforms**” that provides a range of state-of-the-art genomics resources for all partners in EUSOL and prevents duplication of effort constructing technology platforms in independent work packages. A main achievements is the development of the 12K EU-TOM1 microarray which is now public and is a reference transcriptional profiling platform for the entire tomato community. In addition, EU-TOM2 has now been released which is a 90K Combimatrix oligoarray, representing the current TIGR tomato gene. An efficient Real Time platform for 1051 transcription factors has been set up and their expression profiles in 11 tissues determined. The results of these experiments have been uploaded on the EU-SOL website and are available for other consortium members. It is expected that in the next year the platform will become high throughput with development of lab-on-chip technology. Furthermore an excellent TILLING resource based around three independent populations has been developed. More than 30 genes have been TILLED following requests from 12 EUSOL partners. The identity of the mutations was obtained by sequencing. The main outcomes of these screens are the identification of mutant lines with improved carotenoids contents (*LeDET1* mutants), shelf life (ACO, DHS, EXP mutants) and fruit colours (CRTISO mutants).

A large number of Gateway-based clones for gene expression, and RNAi or amiRNA-base silencing have been generated and distributed within the consortium. Proof-of-principle experiments demonstrated that reporter genes are expressed as expected in the fruit parts and within the developmental time window characteristic of the promoters of the *SITPRP*, *AtCRC*, *SIPPC2*, *SIPG* and *SIIMA* genes.

Fruit-specific VIGS has been obtained both by GeneLab (with TRV) and by the laboratory of T. Granell (CSIC-VAG). To overcome the irregular distribution of the effects of VIGS, which hampers the identification and quantification of non-visual phenotypes, the latter laboratory has developed a visually traceable VIGS system

This module also facilitates the partners contributions to the international Tomato Genome Sequencing Project. In the past reporting period, from within EU-SOL an initiative was launched to include Next Generation Sequencing Technology in the ongoing Tomato Genome Sequencing Project. The role of EU-SOL will be primarily focused on the assembly and annotation of the next gen sequences and for this reason, part of the sequencing work in module 5 has been re-routed to Module 6 (Bioinformatics). Finally the sequencing of the tomato mitochondrial DNA has been almost completed and an estimated 100 gaps remain to be closed. A first annotation of the MT genome has been released to GenBank.

The work within this Module proceeds on track however a major deviation from the work plan is the introduction of Next Gen Sequencing technology in the EU-SOL sequencing program.

**Module 6** focuses on “**Bioinformatics and integrated Solanaceae research**”. This Module has the aim to integrate and make easy accessible all data produced by the EUSOL consortium. For the analysis of the tomato genome sequences produced by the International Tomato Genome Sequencing Consortium iTAG, the international tomato annotation group set up a pipeline and linked with management tools and data repository maintained by the SOL Genomics Network for optimal coordination. A training set for *ab initio* gene prediction was built and the annotation software tool Eugene also used for gene prediction in Medicago is being optimized as Solanaceae gene finder. During the third year of the project, we have continued to develop the pipeline. New developments include extension of EuGene, including the ability to handle next-generation transcript sequencing data, SIFTER-X, a phylogenomic tool for automatic function prediction that integrates multiple functional attributes, and BOGAS, a system for manual curation of annotations.

Databases and management systems for genome annotation, germplasm, mapping, trait, phenotype, transcriptomics, metabolomics and proteomics data including analysis and visualization tools have been set up. Examples are the transcriptomics database BASE,

proteomics databases ProicDB, the EU-SOL Germplasm database and metabolomics database for GC-MS. Also tools for statistical analysis, e.g. correcting for intensity related errors in LC-TOF-MS data as well as visualization tools have been developed. Data analysis has started and is exemplified by the integrative analysis of data of HPLC-PDA experiments on health related phytochemicals in introgression lines as produced within Module 2.

A public portal under [www.eu-sol.net](http://www.eu-sol.net) serves as a single point of entry to databases. The web portal provides access to fifteen databases and tools from ten EU-SOL partners as well as to documentation, dissemination and outreach, and project-internal exchange.

After delays due to slow availability of tomato genome sequence in the first three years of the project, Module 6 is getting ready for a new, large effort to support the assembly and annotation of next generation sequencing data.

**Module 7** deals with “**Management and Coordination**” of EUSOL.

All management structures have been installed and currently are up-and-running. In June the Annual Reports and Detailed Implementation Plans are sent to the Commission. These documents describe the work performed in the previous 12 months of the project as well as the plans for the next 18-month period. In addition, all required financial reports and management reports are included.

Twice a year, in May and in November, meetings of the Executive Committee are held to evaluate the progress of the EU-SOL. Also in November, the annual EU-SOL Project meetings are organised. At these meetings, also the Scientific Committee and the Scientific Advisory Group convene.

In cooperation with WP8.1 the EU-SOL consortium has been enlarged by the addition of 3 novel partners; Nunhems Netherlands B.V., Gautier Semences and Semillas Fito. For this, the EU-Contract and the Description of Work have been amended and all required forms have been completed and sent to the Commission. An amendment to the EU-SOL Consortium Agreement has been drafted to regulate the entrance of the new partners into the Consortium.

Good progress has been made towards the implementation of the public EUSOL website ([www.eu-sol.net](http://www.eu-sol.net)). The design of the public forum for the consortium research needs more discussion and design alteration, but too is on target for completion. Translation of website content has begun, as well as the development of a school package geared at Mendelian genetics.

To offer training opportunities for researchers, employees of industrial partners and other potential users of EU-SOL knowledge a Training Committee has been installed and a fellowship and workshop program set up. Till now, a total number of 8 fellowships and 2 on-site visits have been offered and 6 workshops have been organized.

**Module 8** has as task the “**Dissemination of knowledge and transfer of technology to industry**”. Additionally it focuses on the “**Interactive consumer approach**”.

Via the EUSOL access-protected intranet website a system has been set-up to ensure a fast evaluation by the Industry Evaluation Panel (IEP) of all manuscripts (and other outreach activities) that will be submitted for publication. Through this system, 79 different manuscripts or poster abstracts already have been evaluated and released for publication.

Patent discussions are starting up and it is expected that more patent applications that are interesting for industry partners will emerge in the last part of the program. The integration of new companies in the consortium was facilitated. As result of this complicated process a protocol was established on how to deal with requests of other companies that want to enter in the EU-SOL program. MTA's for transfer of material between EU-SOL partners have been developed and are available at the EUSOL website. Several MTA's for the transfer of industry material to EU-SOL members have been signed. Further access to the tomato Core Collection has been facilitated by making agreements with the original owners of the plant material so that transfer of the plant material within EU-SOL can be executed by the leader of Module 4.

A preliminary report on consumer perceptions, preferences and opinions has been published. During the third reporting period two editions of the newsletter were edited and published on the

EU-SOL public website. A further edition will be finalised and distributed electronically at the start of the next reporting period. Additional plans for distribution were discussed with partners. Module 8 is well on target in relation with its objectives.

## Plan for using and dissemination of knowledge

Currently, the EU-SOL project has released information and results on the project website and in the form of scientific publications, seminars, poster abstracts, newsletters and other outreach activities:

### **Project web-site:**

At the very start of the EU-SOL project, a public facing web-site was launched ([www.eu-sol.net](http://www.eu-sol.net)). On this site general information about the project is given, as well as a listing of all publications. Furthermore, the site contains contact information of all work-package leaders involved. On specific request of the participating companies in EU-SOL, the web-site also contains an advertisement section where announcements regarding vacant positions can be posted.

### **Outreach:**

The following outreach activities were realized (in part) with funding from the EU-SOL project:

## **Outreach**

### **Articles in reviewed journals**

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## Posters:

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Asis R, Urias U, Milstein D, Kamenetzky L, Fernie AR, Van Sluys MA, Rossi M e Carrari F.(2007): Development of rapid strategies for testing of candidate crop QTLs. 58° Congresso Nacional de Botânica. São Paulo, SP, Brasil.

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Caruso G<sup>1\*</sup>, M Pocovi<sup>1</sup>, E Gilardón<sup>1</sup>. Laboratorio de Marcadores Moleculares, Facultad de Cs. Naturales, Universidad Nacional de Salta, Argentina. ASSESSING GENETIC VARIABILITY IN TOMATO GERMPLASM. Annual Congress of the Argentine Genetics Society

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Kamenetzky, L; Asís, R; Gonzalez, V, Fernie, AR; Van Sluys, MA, Giovannoni, JJ, Rossi, M, Carrari F. Development of rapid strategies for testing of candidate Solanaceae QTLs. Meeting of the American Society of Plant Biologists 26/6-1/7, Mérida, México.(2008)

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Kanellis, A. K. Biosynthesis and Oxidation of Vitamin C in Ripening Fruit. Workshop on “Health promoting compounds in fruit and vegetables: biosynthesis, metabolism, availability and human health: FROM PLANT TO HUMAN GENES”, Prague, Research Institute of Crop Production November 27-28, 2006

Kanellis, A. K. V. Fotopoulos, M.S. Kalamaki, I. Pateraki, E. Ioannidi, M. Sanmartin, and F. Chatzopoulou. Plant ascorbic acid biosynthesis and metabolism. International Conference “Effects of pre- and post-harvest factors on health promoting components and quality of fruit and vegetables”. May 22 –23, 2006, Skierniewice, Poland.

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Lemaire-Chamley M, Mounet F, Montfoulet C, Moing A, Rothan C (2008) Functional characterization of a tissue specific PIN auxin efflux transporter during tomato fruit development, 3rd EUSOL Workshop. 13-16 November 2008, Toulouse. France

LEPICIER M, C COIRET, C FRIGUET, S LÊ, B NAVEZ, M CAUSSE (2008) Comparing Sets of Consumer Preferences from Different Countries: Application to Tomatoes liking. 10th edition of the European Symposium on Statistical Methods for the Food Industry, Louvain-la-Neuve, Belgium, Jan 23-25th 2008

Mathieu E., Gévaudant F., Mouras A., Hernould M., Chevalier C. (2007) Molecular mechanisms governing tomato fruit size: functional analysis of the CCS52 genes during tomato fruit development. EMBO Conference "From basic genomics to systems biology". May 2-4 2007. Gent, Belgium

Minoia, S., Piron, F., Mosca, G., Petrozza, A., Cellini, F., Carriero F., and Bendahmane, A. TILLING in Tomato: A reverse genetic approach for tomato crop improvement. The 4th Solanaceae Genome Workshop 2007, Jeju, Korea

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Mounet F, Moing A, Petit J, Maucourt M, Garcia V, Deborde C, Rolin D, Rothan C, Lemaire-Chamley M (2006) Contribution of tomato fruit tissues to the acquisition of the fleshy trait. XV FESPB Congress, 17-21 July 2006, Lyon, France

Mounet Fabien, Annick Moing, Johann Petit, Michaël Maucourt, Virginie Garcia, Stéphane Bernillon, Catherine Deborde, Cécile Cabasson, Philippe Gallusci, Dominique Rolin, Christophe Rothan, Gwénaëlle Legall, Ian Colquhoun, Marianne Defernez, and Martine Lemaire-Chamley (2007) Cell expansion in tomato mesocarp and locular tissues: integration of transcriptome and metabolome data. Metabolomics Society 3rd Annual Conference. Manchester, UK, 11-14 June 2007

Philippot Murielle, Frasse Pierre, Delalande Corinne, Regad Farid, Zouine Mohamed, Vautrin Sonia, De Tarragon Laurence, Berges Helene, Szinay Dora, deJong Hans, Coriton Olivier, Bouzayen Mondher. The french contribution to the international tomato genome sequencing program. 4th Solanaceae Genome Workshop 2007, September 09th-13th, Jeju Island, Korea

Piron, F., Minoia, S., Bres, C., Just, D., Causse, M., Rothan, C., Cellini, F., Carriero, F. and Bendahmane, A. TILLING Genes in Tomato: From data mining to characterisation of mutant phenotypes. The 4th Solanaceae Genome Workshop 2007, Jeju, Korea

Prasad N, Pirrello J, Mila I, Zhang W., Zhang L, Zouine M., Regad F. and Bouzayen M. Structural and Functional Characterization of Ethylene Response Factor Gene Family in Tomato. 4<sup>th</sup> Solanaceae Genome Workshop 2007 – Jeju Island, Korea September 09-13

Sanseverino W, Maria Raffaella Ercolano, Luigi Frusciante, Yves Van de Peer, Stephane Rombauts. A plant genome Annotation Pipeline for Disease Resistance genes" SOL2008, Cologne.

Sinesio F, Cammareri M, Moneta E, Navez B, Peperario M, Silvertand B, Causse M, Grandillo S (2008) Sensory quality of fresh market tomatoes: studies of Italian preferences. Convegno della Società di Genetica Agraria Padova 14-17 Settembre. ISBN 978-88-900622-8-5

Sinesio F, Cammareri M, Moneta E, Peperario M, Causse M, Grandillo S (2008) Biodiversità del pomodoro: qualità organolettica e preferenze dei consumatori. II Convegno Nazionale SISS. Milano, 30 Giugno – 1 Luglio 2008, p 60.

Steinhauser MC, Semel Y, Zamir D, Stitt M. Quantitative Trait Loci Analysis Of Primary Metabolism In Interspecific Tomato Crosses By Enzymatic Assays .5th Solanaceae Genome Workshop 12/10/08-16/10/08, Koln, Germany. (2008):

Tripodi P, Mäurer S, Di Dato F, Seekh S, Haaren M, Mohammad A, Tanksley SD, Zamir D, Gebhardt C, Grandillo S (2008) A common map for potato and a set of tomato “exotic libraries” based on COSII anchor markers. 5th Solanaceae Genome Workshop. Cologne, 12-16 Ottobre: p 280.

Tripodi P, Mäurer S, Seekh S, van Haaren MJJ, Mohammad A, Tanksley SD, Zamir D, Gebhardt C, Grandillo S (2008) A common anchored map based on a framework of COSII markers for potato and a set of tomato “exotic libraries”. 52° Convegno Annuale Padova 14-17 Settembre. ISBN 978-88-900622-8-5.

UK tomato genome consortia. Sequencing progress of tomato Chromosome 4. 5th SOL- Genome Workshop, Cologne 2008.

Urias U, Milstein D, Van Sluys MA, Carrari F, Rossi M (2007): Characterization of candidate genes associated with metabolic and quality QTLs of *Solanum pennellii* fruits. I Simpósio Brasileiro de Genética Molecular de Plantas. Natal, RN, Brasil.

Urias U, Milstein D, Van Sluys MA, Carrari F, Rossi M (2006). Identificação de genes candidatos ligados a QTLs para mudanças metabólicas e de qualidade de frutos de tomate Simpósio Internacional de Iniciação Científica da Universidade de São Paulo (SIIC). Ribeirão Preto, 13 de novembro.

Viron N. , Fernandez A., Alhag Dow M., Karimi M., Seymour G., Hilson P., Rothan C. and Lemaire-Chamley M. (2009) Expression analysis of tomato fruit-specific promoters. 8e colloque national SFBV, 8 - 10 juillet 2009 Strasbourg, France

Wang H, Hernould M, Huang Y, Chaabouni S, Bouzayen M (2007) Fine Tuning of the Expression of *IAA9*, an Auxin Response Regulator, Is Instrumental to the Triggering of Fruit Set in Tomato. Poster. *The 4<sup>th</sup> Solanaceae Genome Workshop*, Septembre 9-13, Jeju Island, Korea

Wang H, Pierre Frasse, Mohamed Zouine, Alain Latché, Jean-Claude Pech, and Mondher Bouzayen . Combined Transcriptomic & Reverse Genetics Analyses Define Major Involvement of Auxin Signaling during Fruit Set in Tomato. "Auxine" 2008, October 4<sup>th</sup>-9<sup>th</sup>

Wang H, Schauer N, Frasse P, Zouine M, Latché A, Pech J, Fernie A and Bouzayen M (2007) Combined Transcriptomic & Metabolomic Analyses Define Specific Signaling & Metabolic Pathways Associated with Fruit Set in Tomato. Poster. *The 4<sup>th</sup> Solanaceae Genome Workshop*, Septembre 9-13, Jeju Island, Korea.

Zouine M, Anne-Laure Chateigner-Boutin, Isabelle Mila, Hua Wang, Sophie Poles, Alain Latche, Jean-Claude Pech and Mondher Bouzayen. Identification, annotation, transcriptional activity and expression profiling of the tomato Auxin Response Factor gene family. "Auxine 2008", October 4<sup>th</sup>-9<sup>th</sup>

## Seminars

Bourdon. M., Coriton, O., Cheniclet, C., Brown, S., Chevalier, C., Renaudin, J.-P., Frangne, N. (2008). Endopolyploidy in tomato fruit : endomitosis versus endoreduplication ? "Cytogenetics and polyploidy" workshop, Genetics and Plant Breeding Department of INRA, April 2-4, 2008; Angers, France.

Bovy A. Strategies to improve the polyphenolic composition of crop plants. Invited lecture at XXIVth Conference on polyphenols, Salamanca, Sp, July 8-11, 2008.

Bovy A. Metabolomics applications in plant breeding. Invited lecture at the Nederlandse Vereniging voor Planten Weefselweek. Wageningen, March 20, 2009

Bovy A.G. et al. Metabolomics as a tool to screen the biochemical diversity in tomato. Oral presentation at the XVIth Eucarpia meeting, Wageningen May 12-16, 2008.

Bovy A. Indosol with special emphasis on metabolomic tools. Invited lecture at The 4th Indonesian Biotechnology Conference. Bogor August 5-7, 2008.

Bovy A. *The purple tomato: development of extra-healthy fruits and vegetables*. Lecture on Exhibition "Gezond leven 2009", Jaarbeurs, Utrecht, Jan. 23-25, 2009.

Bovy A. Metabolomics applications in plant breeding. Invited lecture at the Nederlandse Vereniging voor Planten Weefselweek. Wageningen, March 20, 2009

Bovy A.G. et al. Metabolomics as a tool to screen the biochemical diversity in tomato. Oral presentation at the XVIth Eucarpia meeting, Wageningen May 12-16, 2008.

Bowler, C. Invited lecture at the University of Minnesota on the role of DET1 during tomato fruit development.

Bowler, C. Invited lecture at the Society of Experimental Biology, UK on the role of DET1 during tomato fruit development.

Broglia, V. Martín Montiel, D. Isola, M. y Gilardón, E. Análisis histológico de cutícula de frutos de tomate en líneas de premejora. XXI Jornadas Argentinas de Botánica. Corrientes. 21 al 24/9/07. (Histological analysis of tomato fruits cuticles in prebreeding lines).

Bryan GJ et al. Analysis of sensory and volatile traits in potato. Division of Primary Industries / La Trobe University , Melbourne, Australia, 8th October 2007.

Bryan GJ et al. Analysis of sensory and volatile traits in potato. Department of Agriculture and Food Western Australia, Australia, 16th October 2007.

Bryan, GJ 2007 Understanding complex resistance and quality traits in potato Department of Primary Industries, La Trobe, Bundoora, Australia (Invited seminar).

Bryan, GJ 2007 Understanding complex resistance and quality traits in potato Department of Agriculture and Food Western Australia (DAFWA), Perth, Australia (Invited seminar).

Campbell, R., Taylor, M., McKenzie, G., Bryan, G. and Ramsay, G. The genetics of carotenoid levels in potato tubers. The 5th Solanaceae Genome Workshop, 12-16th October 2008, Cologne, Germany

Carrari F and Valle E: Assimilate metabolism and metabolomics (Symposium). XIII meeting of the Latin American Plant Physiologists. Rosario, Argentina. August, 2008.

Carrari F. LAT-SOL, Argentina – “Development of rapid strategies for testing of candidate Solanaceae QTLs. Plant Biology 2008. ASPB annual meeting. Mérida, México. April, 2008

Causse M (2009) Genetic and genomic approach for the improvement of sensory quality in tomato Seed Biotechnology center 10<sup>th</sup> Anniversary collaborative symposium. Davis 11-12 May 2009 Invited communication

Causse M, Prudent M, Bertin N, Génard (2009) Integrative approach of size and composition of tomato fruit combining ecophysiology, genetic, genomic and metabolomic analysis. Japan SOL meeting, Mie, March 11-12 2009

Causse M (2008) Genetic and genomic approach for the improvement of sensory quality in tomato. UK SOL meeting, London, 19 decembre 2008 Invited Communication

Causse M, Prudent M, Bertin N (2008) Genetic, genomic and ecophysiological dissection of fruit size and sugar content in tomato. Tomato Eucarpia Workshop, Wageningen, 12-15 May 2008. Invited communication

Cheniclet C. (2008) Endoreduplication and tomato fruit growth. EU-SOL Module 1 meeting, Bordeaux, 3-4 avril 2008 (communication orale).

Chevalier C . Altering the cell cycle towards endoreduplication contributes to the regulation of cell size and final fruit size in tomato. Japan SOL meeting. December 14-15, 2007. Shizuoka, Japan (Invited Conference).

Chevalier C . Altering the cell cycle towards endoreduplication contributes to the regulation of cell size and final fruit size in tomato. University of Tsukuba, Japan. December 17, 2007. (Invited Seminar).

Chevalier C. (2008) Endoreduplication : an engine for fruit growth? EU-SOL meeting, November 14-16, 2008 ; Toulouse, France.

Ducreux, L.J.M, Morris W.L., Shepherd, T., Bryan, G.J., Hedley, P.E., Taylor, M.A. Quality trait dissection in potato tubers using comparative metabolite and transcript analysis. Oral presentation The 5th Solanaceae Genome Workshop, 12-16th October 2008, Cologne, Germany

Diretto G, Scossa F, Taylor M, Hedley P, Stewart D, Giuliano G: Comparative transcriptomic and metabolomic analyses of transgenic “golden” potato tubers over accumulating beta-carotene. SOL 2008, Cologne, October 2008

Falcone G, Fantini E, Chetelat R, Giuliano G: Evolution of fruit quality and flowering traits in cultivated tomato and its wild relatives. SOL 2008, Cologne, October 2008

Faurobert M., J. Chaïb, S. Muños, I. Marty, \*M. Causse\* (2008) X-omic approach of tomato fruit quality. First Symposium on Horticulture in Europe, Vienne, Austria Feb 18-20, 2008. Invited communication

Gilbert L, M. Alhag Dow, A. Monier, C. Rothan and P. Baldet. (2009) Role of ascorbic acid in tomato fruit colour. Journée de l'école doctorale de Bordeaux, 8 avril 2009, Arcachon

Gilbert L, M. Alhag Dow, A. Nunes-Nesi, F. Guillon, M. Lahaye, A.R. Fernie, C. Rothan and P. Baldet. (2008) GDP-mannose-3,5-epimerase (GME), a key enzyme at the crossover between vitamin C and cell wall polysaccharide biosynthesis pathways. 6ème Congrès Jeunes Chercheurs de la Société Française de Biologie végétale. 2-4 Juillet 2008, Tours

Gilbert L, M. Alhag Dow, A. Nunes-Nesi, F. Guillon, M. Lahaye, A.R. Fernie, C. Rothan and P. Baldet. (2008) GDP-mannose épimerase (GME), carrefour entre la voie de biosynthèse de la vitamine C et des parois. Journées du réseau français des parois, 26-28 mars 2008, BousSENS.

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Gilardón E. Agriculturally important genes derived from tomato wild species. (Genes de importancia agronómica provenientes de especies silvestres de tomate). Participant in the roundtable Genetic resources in Solanaceae and their use in crop breeding. . XXXVI Congress of the Argentine Genetics Society. Pergamino, Argentina. 23 to 26/9/07

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Taylor, MA 2007 Analysis of gene expression associated with quality traits in *S. tuberosum* Group Phureja versus *S. tuberosum* Group Tuberosum (Oral presentation). Potato Oligo Chip (POCI) Workshop. 27th - 28th March 2007, WICC Wageningen, Netherlands.

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Zamir, D. The SOL vision. SOL India – Hyderabad, India (Nov 2006).

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Zamir, D. Breeding by design – high throughput phenotyping. The 2nd International Conference of Plant Molecular Breeding: From Genomics to Plant Improvement (March 2007)

Zamir, D. Improving plant breeding using exotic genetic libraries. Aaronsohn-ITMI International Conference, Tiberias, Israel (April 2007)

Zamir, D. A systems approach to complex phenotypes. The Heyne Lecture – Kansas State University (April 2007)

Zamir, D. Introgression line resolution of complex traits in tomato. John Innes Friday Seminar – UK (May 2007)

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Zamir, D. Overdominance for yield in tomato. The International Conference on Polyploidy, Heterosis and Epigenetics – Beijing China (May 2007).

Zamir, D. Systems approach to complex phenotypes. TeMasek Life Sciences Laboratory, Singapore. Biotechnology: Innovative applications from basic research. January 2008:

Zamir, D. Where have all the QTL gone?Molecular Mapping & Marker Assisted Selection in Plants. Vienna, Feb 2008.

### **Web resources**

Partner WU-PSG contributed to a Dutch education website on genomics (<http://www.watisgenomics.nl>) with an article explaining the research implemented.

Partner INTA. The tomato mitochondrial genome site (<http://www.mitochondrialgenome.org/>) available for the consortium members.

Partners NHM, MPIZ, WUR and Lis: EU-SOL L3-Portal (<http://www.eu-sol.net>)

### **Non-reviewed papers and reports:**

Besson Florian Etude de la variabilité de la qualité gustative chez la tomate (*Lycopersicum esculentum*) dans les segments cerise et cocktail. Report for Institut National d’Horticulture (AGROCAMPUS OUEST site d’Angers)

Klein Lankhorst, RM. (2007) Back to the roots of tomatoes and potatoes. Wageningen Update 3/07, p.p. 12-13.

Reports distributed to the Tomato experimenters meeting 15-16 October 2008 (led by Ctifl)

- a. TOMATE 2008, Physical, chemical and sensorial characteristics of “ancient” types.
- b. TOMATE 2008: Physical, chemical and sensorial characteristics of "classical" types, clusters, round, elongated.
- c. TOMATE 2008, Characterization of "Cherry" and "Cocktail" tomatoes, 2 tests, winter and spring
- d. TOMATE 2008, Sensorial Characteristics of "Cherry" and "Cocktail" tomatoes and study of their appreciation by consumers.

**Newsletters:**

EU-Sol Newsletter one (Sept 07)

Includes interviews with the Project leader, information on quality traits as perceived by consumers and key technology in EU SOL.

EU-Sol Newsletter two (May 08)

Includes an interview with Hazera Genetics on the role of a pre-breeder in EU-SOL and Graham Seymour explains the importance of ripening in determining fruit quality.

EU-Sol Newsletter three (Nov 08)

An overview of the project at the half way stage.

**Other outreach activities:**

Benard Marianne, EU-SOL Interactive Approach Stakeholders, LIS Consult, June 2008

Bisschop G. Organizer of 4th annual UK-SOL meeting meeting at Imperial College London (December 08)

Bovy A. NOS Journaal Radio 1. Interview with respect to the purple tomato. November, 2008  
Arnaud Bovy. Op uw gezondheid. Special about lycopene. Television broadcast Ned 3, November 2008

Bovy A. Op uw gezondheid. Special about lycopene. Television broadcast Ned 3, November 2008

Bovy A. Schooltelevision: News from nature. The purple tomato. Television broadcast Ned 3, November 2008

Bovy A. Internet TV: Amazigh TV. The purple tomato. November 2008

Carrari F. The 21<sup>st</sup> century tomato. Using systems biology to model the metabolic networks in tomato fruit. Development. Press release, EUREKAAlert.

Carrari F. Scientific Workshop of Cooperation Argentine-The Netherlands in Plant Biotechnology. 16 lectures from both countries, 3 scientific sections, about 60 participants. Buenos Aires, October, 2008.

De Vriend H. Contribution to the organisation of the Bioexploit/Eucarpia Workshop about Marker Assisted Selection in breeding varieties for Organic Agriculture, Wageningen Februari 25-27.

Zamir D. National Agricultural Exhibition AGRA

## Total Completed Deliverables till Period III (30-06-2009)

Deliverable No	Deliverable name	WP No	Lead Participant	Estimated indicative person-months	Nature <sup>1</sup>	Dissemination level <sup>2</sup>	Delivery date (proj. month)
D1.1.1	Characterisation of a tomato cultivar set for consumer score, sensory profile and instrumental quality, preference map in Italy	WP1.1	27, CNR-IGV	28	R	CO	18
D1.1.2	Characterisation of a tomato cultivar set for consumer score, sensory profile and instrumental quality, preference map in France	WP1.1	13, CTIFL	9	R	CO	18
D1.1.3	Characterisation of a tomato cultivar set for consumer score, sensory profile and instrumental quality, preference map in the Netherlands	WP1.1	16, A&F	7	R	CO	18
D1.1.4	A comparison of preference maps among the 3 countries	WP1.1	4, INRA-A	2	R	CO	18
D1.1.9	Characterisation of a cultivar set for sensory profiles map in Italy	WP1.1	27, CNR-IGV	33	R	CO	30
D1.1.10	Characterisation of a cultivar set for sensory profiles in France	WP1.1	13, CTIFL	3.8	R	CO	30
D1.1.11	Characterisation of a cultivar set for sensory profiles in the Netherlands	WP1.1	16, A&F	4.5	R	CO	30
D1.2.1	A map of QTLs for tomato fruit size and sugar content at two fruit loads	WP1.2	4, INRA-A	6	R	CO	18
D1.2.2	Cytological Characterization of tomato fruit development in IIs and mutants	WP1.2	4, INRA-B	7	R	CO	18
D1.2.4	Seeds of hybrids between tomato lines carrying several QTLs for fruit size and sugar content	WP1.2	4, INRA-A	5	O	CO	18
D1.2.5	A precise location and characterization of a sugar QTL in cherry tomato lines	WP1.2	4, INRA-A	7	R	CO	18
D1.2.6	Collection of tomato fruit orthologs to cell cycle genes (20 genes)	WP1.2	4, INRA-B	2	R	CO	12
D1.2.7	Collection of tomato fruit orthologs to gibberellin pathway (5 genes)	WP1.2	10, CSIC-V	2	R	CO	12
D1.2.8	Collection of tomato fruit orthologs to TCA cycle genes (5 genes)	WP1.2	5, MPIMP	2	R	CO	12
D1.2.9	Collection of tomato transcription factors	WP1.2	2, PRI	2	R	CO	18
D1.2.10	Collection of candidate genes regulated during early fruit development	WP1.2	2, PRI	4	R	CO	18
D1.2.11	Collection of candidate genes regulated in different tissues from early developing fruit	WP1.2	4, INRA-B	8	R	CO	18
D1.2.12	Collection of candidate genes regulated in the fruit in response to gibberellins	WP1.2	10, CSIC-V	10	R	CO	18

Delivered in time

<sup>1</sup> R=report, P=prototype, D=demonstrator, O=other

<sup>2</sup> Dissemination level: PU=public, PP=restricted to other programme participants (including the Commission Services), RE=restricted to a group specified by the consortium (including the Commission Services), CO=confidential, only for members of the consortium (including the Commission Services)

D1.2.13	Primary transformants with down-regulated or overexpressed target genes involved in cell cycle regulation during fruit development (minimum 6 lines obtained from D.1.2.6; RNAi or over-expression)	WP1.2	4, INRA-B	14	R	CO	18
D1.2.14	Primary transformants with down-regulated or overexpressed target genes involved in transcriptional regulation during fruit development (minimum 5 lines obtained from D.1.2.6; RNAi or over-expression)	WP1.2	2, PRI	4	R	CO	18
D1.2.15	Primary transformants with down-regulated or overexpressed target genes involved in gibberellin regulation of fruit set and development (minimum 6 lines obtained from D.1.2.6; RNAi or over-expression)	WP1.2	10, CSIC	16	R	CO	24
D1.2.16	Primary tomato transformants with down-regulated or overexpressed target genes involved in TCA cycle (minimum 5 lines obtained from D.1.2.6; RNAi or over-expression)	WP1.2	5, MPIMP	4	R	CO	18
D 1.2.17	Mutants affected in fruit growth and/or composition by altering expression of genes encoding transcription factors	WP 1.2	2, PRI	8	O	CO	36
D1.2.19	Mutants affected in fruit growth and/or composition by altering expression of genes encoding cell cycle genes (mutants from minimum two different constructs obtained from D1.2.15). (24 m) (INRA B)	WP 1.2	4, INRA-B	2	R	CO	24
D 1.2.20	Detailed morphological and molecular characterization and determination of effect on regulation of early fruit development of the mutants obtained from D1.2.19	WP 1.2	4, INRA B	24	R	CO	36
D1.3.1	Metabolite profiles for all introgression lines, based on 1 <sup>st</sup> year's trial	WP1.3	2, PRI	1	R	CO	13
D1.3.2	Database containing volatile, and QTL data. Map of QTLs for volatiles	WP1.3	1, WU-PSG	2	R/O	CO	18
D1.3.4	Preliminary phenotypic/genotypic characterisation of <i>above</i> populations as well as <i>S. phureja</i> core collection	WP1.3	21, SCRI	9	R	CO	18
D1.3.5	Preliminary expression data of LOX and AAT genes in ripening mutants and in response to environmental conditions. Initial correlation of expression with volatile production	WP1.3	25, UNOTT	16	R	CO	24
D1.3.6	Expression pattern of ERF gene family members in tomato	WP1.3	15, INP-T	8	R	CO	6
D 1.3.7	Gene constructs for reverse genetics approaches	WP 1.3	15, INP-T	12	R/O	CO	30
D 1.3.11.	Preliminary marker (200-300 AFLPs, >20 SSRs) and linkage map data on at least one population segregating for volatiles and sensory characters.	WP 1.3	21, SCRI	9	R/O	CO	24
D.1.3.13	Global volatile compound profile and target gene expression data of tomato ripening mutants and in response to environmental conditions (UNOTT, month 31).	WP1.3	25, UNOTT	7.5	R	CO	31
D.1.4.1	Texture attributes (firmness, mealliness, juiciness) characterised across <i>Solanum chmielewskii</i> ILs.	WP1.4	4, INRA-A	4	R	CO	24
D.1.4.2	Texture attributes (firmness, mealliness, juiciness) characterised across <i>Solanum pennellii</i> ILs	WP1.4	25, UNOTT	12	R	CO	24
D1.4.4	Fine mapping of texture QTLs from cherry tomato and ILs underway	WP1.4	4, INRA-A	5	R	CO	24

D1.4.5	Fine mapping of texture QTLs from <i>S. pennellii</i> ILs underway (where appropriate)	WP1.4	25, UNOTT	6	R	CO	24
D1.4.6	Identification of chemical and physical attributes linked to texture QTLs in tomato	WP1.4	4, INRA-N	13	R	CO	30
D1.4.7	Identification of transcriptome and proteome attributes linked to texture QTLs in tomato.	WP1.4	4, INRA-A	5	R	CO	24
D2.1.3	Generation of data on phytonutrient content to facilitate identification and characterisation of genes underlying QTLs in potato and tomato	WP 2.1	20, RHU	5	R	CO	24
D2.2.1	Tomato populations ( <i>S.lycopersicon</i> x <i>S.pennellii</i> and <i>S.lycopersicon</i> x <i>S.hirsutum</i> ) segregating for carotenoids and vitamin C content	WP 2.2	4, INRA-A	4	R/O	CO	18
D2.2.2	Potato ( <i>S.tuberosum</i> ) populations segregating for carotenoid content	WP 2.2	21, SCRI	12	R/O	CO	18
D2.2.3	Mapping of DDB2 and COP10 (month 36, ENS)	WP 2.2	14, ENS	6	R	CO	36
D2.2.4	Fine mapping of mutations fcd-2 in tomato	WP2.2	18, HUI	4 (2)	R	CO	36
D2.2.5	Identificaton of genes with altered expression in fruits of Vit C mutants of tomato	WP 2.2	12, UMA	8	R/O	CO	18
D2.2.6	Novel mutants/variants in tomato candidate genes controlling carotenoid formation/light responsiveness	WP 2.2	28, ENEA	10	R	CO	36
D2.2.7	A diversity microarray of tomato populations segregating for carotenoids / vitamin C content	WP 2.2	44, UP	11	R/O	CO	18
D2.2.9	Mapping of known candidate genes from potato that underpin identified QTLs for carotenoid content	WP 2.2	21, SCRI	8	R	CO	24
D2.2.10	Novel genes involved in the regulation of carotenogenesis revealed by microarray analysis.	WP 2.2	21, SCRI	8	R	CO	24
D2.2.12	Proof of concept of tomato Diversity array markers	WP2.2	44, UP	9	R	CO	30
D2.2.13	Transgenic potato lines with down-regulated expression of a carotenoid cleavage dioxygenase	WP2.2	21, SCRI	10 (1')	O	CO	36
D2.2.14	Construct a genetic map of <i>S. cheesmanii</i> RI population using DArT and other markers	WP2.2	44, UP	9	R	CO	36
D2.3.1	Function of photoreceptors and downstream signalling components in controlling responses to light in tomato	WP2.3	14, ENS	6	R	CO	31
D3.1.1	F2 populations from crosses between known branching mutants and wild accessions ( <i>S.pennellii</i> and <i>S.chmielewskii</i> ) and between different wild tomato accessions ( <i>S.pennellii</i> and <i>S.chmielewskii</i> ).	WP3.1	5, MPIMP	18	R/O	RE	18
D3.1.2	Identification of the QTL mechanism underlying the changes in metabolite composition underpinning Bx in tomato	WP3.1	5, MPIMP	5	R	CO	18
D3.1.4	Fine mapping of introgressed regions in tomato ILs carrying metabolic QTLs.	WP3.1	43, GATE-USP	9	R	CO	18

D3.1.5	<i>lateral suppressor</i> and <i>blind</i> mutants containing chromosome segments of wild tomato accessions.	WP3.1	6, MPIZ	9	R,O	CO	36
D3.1.8	Physical map for selected introgressed regions in ILs carrying metabolic QTLs	WP3.1	42, INTA	1.5	R	CO	36
D3.1.9	Characterization of <i>S. pennellii</i> and <i>S. lycopersicum</i> alleles for the identified candidate genes	WP3.1	43, GATE-USP	9	R	CO	18
D3.2.1	Genes encoding MYB transcription factors in the tomato.	WP3.2	6, MPIZ	4	R/O	RE	6
D3.2.2	Genes encoding auxin-response transcription factors in the tomato.	WP3.2	15, INP-T	4	R/O	RE	6
D3.2.3	Complete expression patterns of selected tomato MYB genes obtained by real-time PCR.	WP3.2	6, MPIZ	1	R	RE	6
D3.2.4	Expression patterns of selected tomato auxin-response factors obtained by real-time PCR.	WP3.2	15, INP-T	4	R	RE	6
D3.2.5	Vectors for RNAi or dominant negative suppression of selected (at least 10) MYB genes, Aux/IAA genes and auxin-response factors of tomato	WP3.2	15, INP-T	4	R/O	RE	12
D3.2.6	Primary tomato transformants containing RNAi or dominant-negative constructs of selected candidate genes ( MYB genes, Aux/IAA genes and auxin-response factors of tomato)	WP3.2	6, MPIZ	2	R/O	RE	12
D3.2.7	Primary tomato transformants of over-expressing lines containing selected candidate genes ( MYB genes, Aux/IAA genes and auxin-response factors of tomato) .	WP3.2	15, INP-T	6	R	CO	12
D3.2.8	Preliminary characterisation of transgenic tomato lines altered in MYB genes and selection of suitable lines with modified traits related to architecture patterning, fruit yield and fruit quality (sugar content)	WP3.2	6, MPIZ	2	R	CO	18
D3.2.9	Preliminary characterisation of transgenic tomato lines altered in auxin transcription factors and selection of suitable lines with modified traits related to architecture patterning, fruit yield and fruit quality (sugar content)	WP3.2	15, INP-T	6	R	CO	18
D3.2.10	Functional characterization of Aux/IAA and ARF genes to uncover their ability to regulate auxin-responsive promoters.	WP3.2	15, INP-T	24	R	CO	36
D3.2.11	Characterised transgenic lines showing altered MYB gene expression	WP3.2	6, MPIZ	7	R	CO	36
D3.3.1	List of specific tomato traits of agronomic interest, like yield, soluble solids and abiotic stress, to support WP 3.1 and 3.2	WP3.3	34, Keygene	1	R	CO	18
D3.4.1	Populations of diploid potatoes segregating for tuber quality traits	WP3.4	49, AR	18	RO	PU	20

D3.4.2	Harvest and Post harvest data (yield, metabolites, RNA, starch) on potatoes populations segregating for tuber quality traits.	WP3.4	50, AVE	2	R	PU	36
D3.4.3	QTLs for 4 major tuber quality traits in potato	WP3.4	1, WU-PSG	1	R	PU	28
D3.4.4	Identification of 3 candidates genes from the BSA underlying tuber quality QTLs in potato	WP3.4	1, WU-PSG	1	R	PU	30
D3.4.5	DNA markers for at least 3 of the candidates genes/QTLs for tuber quality traits in potato	WP3.4	1, WU-PSG	1	R	PU	30
D3.4.6	Description of allelic variation of the candidate genes for tuber quality traits in potato	WP3.4	1, WU-PSG	1	R	PU	30
D3.4.7	Transcript profiles from tubers of at least 80 genotypes of C x E	WP3.4	1, WU-PSG	1	R	CO	30
D3.4.8	Vitamin C, B5 and B6 profiles in parental genotypes for 2008	WP3.4	32, ABC	1	R	CO	30
D3.4.10	Genetic analysis of transcript profiles in C x E	WP3.4	1, WU-PSG	2	R	CO	36
D3.4.11	Vitamin content Determination of subset of individuals from the population showing the highest variation in parental clones	WP3.4	32, ABC	9	R	CO	30
D3.4.12	Harvest and Post harvest data on populations for 2008 growing season	WP3.4	49, AR	3	R	CO	30
D3.4.13	Harvest and Post harvest data on populations for 2008 growing season	WP3.4	50, AVE	2	R	CO	30
D3.5.1	Dormancy-related cDNA libraries from potato	WP3.5	7, FAU	3	O,R	CO	9
D3.5.2	Dormant bud specific expression profiles from potato	WP3.5	7, FAU	2	R	CO	12
D3.5.3	Molecular marker genes relevant for tuber dormancy in potato	WP3.5	7, FAU	1	R	CO	18
D3.5.4	Transgenic potato plants modified in expression of dormancy-related transcripts	WP3.5	7, FAU	6	O,R	CO	30
D3.5.5	Post-harvest validation of transgenic potato tubers carrying dormancy-related transcripts	WP3.5	7, FAU	6	R	CO	30
D3.5.6	Detailed insights of changing plasmodesmata function during sink-source transition of potato tubers	WP3.5	7, FAU	2	R	CO	12
D3.5.7	Transgenic potato plants modified in expression of viral proteins	WP3.5	7, FAU	3	O,R	CO	24
D3.5.9	Leaf/stolon specific expression profiles during stolon to tuber transition in potato	WP3.5	10, CSIC	4	O,R	CO	9
D3.5.10	Gene expression profiles in developing potato tubers in response to hormonal treatments	WP3.5	1, WU-PSG	4	R	CO	9
D3.5.11	Photoperiod control genes from potato	WP3.5	10, CSIC	4	R	CO	12

D3.5.12	Molecular marker genes relevant to the tuberization switch	WP3.5	10, CSIC	2	R	CO	18
D3.5.13	Transgenic potato plants with modified levels of expression of the tuberization-related transcripts	WP3.5	10, CSIC	4	O,R	CO	24
D3.5.14	Evaluation of transgenic lines altered in expression of genes regulating tuberization with respect to tuber number and tuber yield	WP3.5	10, CSIC-M	6	P, R	CO	30
D3.5.15	Transgenic potato plants with altered growth characteristics and tuberization behaviour	WP3.5	1, WU-PSG	3	O,R	CO	30
D3.5.16	Transgenic potato plants with altered expression of viral protein interacting host factors	WP3.5	7, FAU	5	O,R	CO	24
D3.5.17	Cassette for heterologous expression of genes during stolon induction	WP3.5	10, CSIC-M	3	R	CO	24
D3.5.20	Transgenic potato plants with modified levels of expression of putative FT effectors	WP3.5	10, CSIC-M	6	O	CO	32
D3.5.21	Validation of the roles of FT partners/downstream-regulated genes in tuberization transition	WP3.5	10, CSIC-M	6	R	CO	36
D3.6.1	List of specific traits in potato of agronomic interest to support WP 3.4 and 3.5	WP3.6	51, HZPC	1	R	CO	18
D3.6.2.2	Final list of traits and genes which show most promise in further application oriented research	WP3.6	1, WU-PSG	2	R	CO	30
D3.6.2.3	Final list of traits and genes which show most promise in further application oriented research	WP3.6	49, AR	2	R	CO	30
D3.6.2.4	Final list of traits and genes which show most promise in further application oriented research	WP3.6	50, AVE	2	R	CO	30
D3.6.2.5	Final list of traits and genes which show most promise in further application oriented research	WP3.6	33, BIOPLANT	2	R	CO	30
D4.1.1	A common PCR marker based framework, ensuring whole genome coverage, for the interspecific tomato IL populations involving <i>S. pennellii</i> , <i>S. chmielewskii</i> , <i>S. habrochaites</i> and <i>S. neorickii</i>	WP4.1	27, CNR-IGV	50	R	PU	24
D4.1.2	Linking the tomato and potato maps by PCR-based mapping of 100 common reference markers on the potato mapping populations, and by <i>in silico</i> anchoring	WP4.1	6, MPIZ	2 (1.5)	R	PU	30
D4.1.6	A common anchored map based on a framework of approximately 120 COSII markers, for the <i>S. pennellii</i> (Partner HEBAM), <i>S. chmielewskii</i> , <i>S. habrochaites</i> and <i>S. neorickii</i> interspecific ILs	WP4.1	27, CNR-IGV	14	R	CO	30
D4.2.1	A tomato Core Collection (CC) of 1000 varieties	WP4.2	18, HUIJ	9	R	PU	6
D4.2.2	An optimized protocol for 20-30-plex SNPWave	WP4.2	34, Keygene	4	R	CO	30

D4.3.1	Phenotyping of ILs, RI and core collection	WP4.3	18, HUIJ	25	R	PU	24
D4.3.1.1	Phenotyping of ILs, RI and core collection; <i>Solanum cheesmanii</i>	WP4.3	31, MVC	18	R	CO	24
D4.3.5.1	Phenotypes of <i>S. chmielewskii</i> ILs (I)	WP4.3	52, Syngenta	4	R	CO	32
D4.3.5.2	Phenotypes of <i>S. chmielewskii</i> ILs (II)	WP4.3	53, RZ	3	R	CO	32
D4.3.5.3	Phenotypes of <i>S. chmielewskii</i> ILs (III)	WP4.3	54, DRS	1.5	R	CO	32
D4.3.5.4	Phenotypes of <i>S. chmielewskii</i> ILs (IV)	WP4.3	55, VIL	1.5	R	CO	32
D4.3.8.1	Phenotypes and seed increase of CC lines in the glasshouse (I)	WP4.3	54, DRS	1.5	R	PU	36
D4.3.8.2	Phenotypes and seed increase of CC lines in the glasshouse (II)	WP4.3	55, VIL	1.5	R	PU	36
D4.3.8.3	Phenotypes and seed increase of CC lines in the glasshouse (III)	WP4.3	48, SVS	3	R	PU	36
D5.1.1	Laboratory Information Management System (LIMS) for microarray production and traceability	WP5.1	15, INP-T	7	O	CO	6
D5.1.2	List of oligonucleotides (70 mer long) corresponding to 14000 individual genes (14K) that compose the unigene collection of tomato ESTs. Oligo set corresponding to the core version	WP5.1	28, ENEA	12	P	PU	6
D5.1.3	Tomato 14K DNA chip (EU-TOM1).	WP5.1	15, INP-T	12	P	PU	6
D5.1.4	Efficient microarray hybridisation and data analysis platform available for use by the EU-SOL partners	WP5.1	28, ENEA	8	O	CO	24
D5.1.5	First set of hybridization data. Determination of oligonucleotides giving absent or marginal hybridization signals.	WP5.1	28, ENEA	4	R	CO	24
D5.1.6	Data mining of the tomato expression data (link to Module 6)	WP5.1	15, INP-T	7	R	PU	18
D5.1.7	Primer combinations for RT-PCR of 150 TF genes of tomato, chosen among those giving marginal or absent hybridization in microarray experiments.	WP5.1	2, PRI	13	P	CO	18
D5.1.8	Efficient protocol for HTP real time PCR on transcription factor genes of tomato	WP5.1	2, PRI	2	R	CO	18
D5.1.10	(Affy) DNA chip (EU-TOM2)	WP5.1	28, ENEA	18	P	PU	36
D5.1.11	Primer combinations for RT-PCR of 750 TF genes	WP5.1	2, PRI	2	RO	CO	30
D5.1.12	Primer combinations for RT-PCR of 1000 TF genes	WP5.1	2, PRI	3	R,O	CO	36
D5.2.5	TILLING Genes of agronomic importance in MicroTom (INRA-B) and in RedSetter and M82 mutant populations	WP5.2	4, INRA-E & 38, Agrobios	18 & 9	R	CO	31

D5.3.1	Core set of tomato driver lines for regulated trans activation using two-component system.	WP5.3	19, WIS	4	O	PU	17
D5.3.2	GATEWAY based vectors for ectopic trans activation, RNAi and VIGS.	WP5.3	3, VIB	9	P	PP	17
D5.3.3	GATEWAY based vectors for directed cloning of promoter fragments with either functional cDNAs or hairpin based RNAi (STGs).	WP5.3	3, VIB	9	P	PP	17
D5.4.2	DNA sequence analysis (Phase III) and assembly of up to ~40 BAC clones from tomato chromosome 6	WP5.4	1, WU-PSG	4.2	R	PU	30
D5.4.4	Identification, verification, and send for DNA sequence analysis and assembly of up to ~40 BAC clones from chromosome 9.	WP5.4	10, CSIC-V	12	R	PU	30
D5.4.5	Approx. number of 25 finished tomato BACs using DACS technology	WP5.4	28, ENEA	2	R	PU	24
D5.4.6	Draft version of the DNA sequence of the tomato mitochondrial genome	WP5.4	37, Genomex	18	R	PU	18
D5.4.8	BACs selected on basis of AFLP fishing	WP5.4	42, INTA	9	R	PU	18
D5.4.9	BACs selected on basis of AFLP fishing	WP5.4	34, Keygene	1	R	PU	18
D5.4.10	New markers assigned to each chromosome	WP5.4	15, INP-T	5	R	PU	18
D5.4.11	New seed BACs anchored to specific chromosomes	WP5.4	15, INP-T	2	R	PU	18
D5.4.12	FISH data for the new seed BACs	WP5.4	1, WU-PSG	8	R	PU	24
D5.4.13	FISH data for approximately 70 new seed BACs, mainly from chromosomes 7, 9 and 12	WP5.4	1, WU-PSG	4.2	R	PU	36
D5.4.20	Protocols and Bioinformatics scripts for Long PET pyrosequencing of tomato BACs	WP5.4	37, Genomex	10	R	RE	30
D6.1.1	Web interface to collect finished BAC sequences from the different sequencing centres	WP6.1	8, GSF-MIPS	4	P	PU	1
D6.1.2	A general gene prediction system for Solanaceae. Web interface to access the full featured EuGene gene predictions	WP6.1	3, VIB	16	P	PU	18
D6.1.3	Data exchange format and procedures	WP6.1	8, GSF-MIPS	4	R	CO	6
D6.1.4	In silico pipeline for the automatic detection of transposable elements in plant genomes	WP6.1	3, VIB	4	P	CO	24
D6.1.5	Repeat resolution and assembly quality assessment modules implemented in assembly platform and transfer of expertise on assembly pipelines between sequencing partners	WP6.1	2, PRI	4	P	RE	18
D6.1.6	An accessible set of HOW-TOs, procedures and protocols	WP6.1	3, VIB	0	R	PU	6, 12, 18
D6.1.7.1	A web-based interface to a gene prediction system trained for <i>Solanaceae</i>	WP6.1	3, VIB	4	R	PU	13
D6.1.7.2	A web interface to an automated function prediction system	WP6.1	6, MPIZ	13	R,O	PU	13
D6.1.8	Procedures and check lists for homogeneous curation of gene annotation.	WP6.1	24, ICL	10	R	PU	21

D6.1.11	Improved Eugene based pipeline, integrating more data into the models	WP6.1	4, INRA-T	15 (8)	R	CO	36
D6.1.12	Asses the possibility to use the tomato iTAG pipeline for the potato.	WP6.1	3, VIB	9 (4)	R	CO	30
D6.2.1	Databases for storage and management of functional genomics data for tomato and potato	WP6.2	15, INP-T	7	P	CO	18
D6.2.2	Local implementations of LIMS for metabolomics data	WP6.2	5, MPIMP	4	P	CO	36
D6.2.4	New tools for statistical analysis of metabolomics data	WP6.2	5, MPIMP	3	P	CO	36
D6.2.5	Algorithms and tools for analysis of mass spectral data, data reduction, alignment, and compound and pathway identification	WP6.2	2, PRI	12	P	CO	24
D6.2.7	QTL and metabolic pathway analysis tools	WP6.2	20, RHU	7 (2)	R	CO	30
D6.2.9	Local implementations of LIMS for proteomics data	WP6.2	4, INRA-A	8	R	CO	24
D6.2.10	Web interfaces for access to proteomics data by EU-SOL users	WP6.2	4, INRA-A	6.7	O	CO	30
D6.3.1	Database for storage and management of germplasm and sample passport data for tomato and potato	WP6.3	1, WU-PSG	3	P	CO	13
D6.3.2	User and analysis interface to germplasm and sample passport data	WP6.3	1, WU-PSG	3	P	PU	18
D6.3.3	Database for storage and management of mapping data	WP6.3	1, WU-PSG	3	P	CO	6
D6.3.4	User and analysis interface to mapping database	WP6.3	1, WU-PSG	3	P	PU	18
D6.3.5	Web portal that links all EU-SOL web resources	WP6.3	6, MPIZ	10	P	PU	18
D6.3.7	Tools that enable distributed plant genome annotation through experts	WP6.3	6, MPIZ	6	P	RE	6
D6.3.8	Toolkit for implementation of webservices and distributed access	WP6.3	6, MPIZ	10	P	PU	18
D6.3.9	Tutorial for distributed annotation of tomato and potato sequences	WP6.3	6, MPIZ	8	R	PU	24
D6.3.11	Provide interface to interact with expert annotation, and synchronize corrections with AFAWE (MPIZ), EUSOL tomato genome database (MIPS) and SGN	WP6.3	3, VIB	4,75 (7.5)	O	PU	30
D6.3.14	EUSOL group on <a href="http://www.myexperiment.org">www.myexperiment.org</a> for workflow management	WP6.3	6, MPIZ	5 (1)	O	CO	25
D6.3.15	Web service for automated protein function prediction	WP6.3	6, MPIZ	5	O	CO	25
D6.3.16	EUSOL Moby Central	WP6.3	6, MPIZ	6	O	CO	26
D6.3.19	Basic web services for access to the germplasm and phenotype database	WP6.3	1, WU-PSG	2	O	CO	30

D6.3.20	A system to track seed distribution and growing of germplasm (in interaction with module 7)	WP6.3	1, WU-PSG	2	O	CO	30
D7.2.1	Needs survey of EU-SOL partners for public dissemination	WP7.2	26, NHM	4	R	CO	10
D7.2.2	Prototype website for public-facing information and interaction	WP7.2	26, NHM	2	P,O	CO	14
D7.2.3	Live website for public-facing information	WP7.2	26, NHM	3	O	PU	19
D7.2.4	Live website for public interaction	WP7.2	26, NHM	3	O	PU	19
D7.2.5	Completed on-line education resource about history of tomato and potato agriculture	WP7.2	26, NHM	16	O	PU	25
D7.2.6	Generic public event formats delivered to consortium members	WP7.2	26, NHM	5.7	O	CO	30
D7.2.7	Content on minor solanaceous crops completed and on website	WP7.2	26, NHM	5.7	O	PU	30
D7.2.8	Report on broadscale commonalities and cultural differences in Mendelian genetics teaching across consortium pilot countries	WP7.2	26, NHM	5.7	R	CO	31
D7.2.9	First 6 monthly review of EU-SOL state-of-the-art on website	WP7.2	36, LIS	0.19	O	PU	30
D7.2.10	Preliminary evaluation of teacher needs for schools pack	WP7.2	26, NHM	5.7	R	CO	36
D7.2.11	Second 6 monthly review of EU-SOL state-of-the-art on website	WP7.2	36, LIS	0.19	O	PU	36
D7.3.3	Operational Short-term Fellowship Programme for the period month 25-42	WP7.3	15, INP-T	0.5	R/O	CO	25
D7.3.4	Operational program of on-site visits for the period month 25-42	WP7.3	15, INP-T	0.5	R/O	CO	25
D7.3.5	Second EU-SOL Workshop planned and organized	WP7.3	1, WU-PSG	0.3	R/O	CO	24
D8.1.1	Material transfer agreements (MTA's) related to in-kind contributions to EU-SOL in place	WP8.1	34, Keygene	1	R	CO	1
D8.1.2	A standard protocol for the protection and release of EU-SOL-derived results	WP8.1	11, SZN	1	R	CO	3
D8.1.3	An Industry Evaluation Panel	WP8.1	34, Keygene	1	O	PU	3
D8.2.1	First analysis of consumer perceptions, preferences and opinions concerning tomatoes and different production methods in the European Union	WP8.2	36, LIS	1	R	PU	18
D8.2.2	Electronic newsletter about the progress of the project and related developments in science and society, three editions	WP8.2	36, LIS	2	O	PU	17, 22 & 27
D8.2.3	A list of target groups, a methodology and a first, global survey	WP8.2	36, LIS	1	R	PU	24
D8.2.4	Statements concerning consumer organisations' demands for new tomato and potato varieties to be discussed in interviews	WP8.2	36, LIS	0.84	R	PU	25

D8.2.7	Report of discussion with project partners	WP8.2	36, LIS	0.83	R	CO	33
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## Contractors involved

*Wageningen University (WU), **Coordinator***  
*Plant Research International B.V. (PRI)*  
*Flanders Interuniversity Institute for Biotechnology (VIB)*  
*Institut National de la Recherche Agronomique (INRA)*  
*Max Planck Institute of Molecular Plant Physiology (MPG.MPIMP)*  
*Max Planck Institute for Plant Breeding Research (MPG.MPIZ)*  
*Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU)*  
*Helmholtz Zentrum München German Research Center for Environmental Health GmbH (GSF)*  
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