



EPSO / EC Workshop  
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Brussels, Belgium



## Preparatory workshop "European Solanaceae genomics consortium" - Summary report -

### Executive summary

The meeting organized by EPSO and hosted by the European Commission, brought together representatives of the Solanaceous research community from all European countries working on Solanaceous genome projects, i.e. France, Germany, Italy, Spain, UK and The Netherlands. The primary objectives of the meeting were to define a "concerted" European contribution to the International Solanaceous Genome Project, and to lay the foundations for a European Solanaceous Genome Project and to explore its possible funding opportunities for a concerted Integrated Project under the European Framework 6 programme.

At this meeting it became absolutely clear that Europe's major asset is its strong and dynamic Solanaceous research community that is highly motivated to contribute towards the international effort to sequence the tomato and potato genomes, and to exploit these resources once they are available (More detailed descriptions of the different national genome programmes are provided below). In particular, the current discussions with the respective national funding agencies indicate that in addition to the ongoing genomics programmes on different Solanaceous species (physical mapping, map-based cloning, SNP marker development, BAC and EST sequencing, QTL cloning, microarray development and TILLING), there are excellent prospects for **a substantial European contribution towards the sequencing of the tomato genome**: at present the indications are that Europe may contribute to the sequencing of two (The Netherlands, UK), possibly four (France, Italy) of the twelve tomato chromosomes. In view of the moderate price tag of the proposed sequencing strategy (BAC by BAC sequencing of the euchromatic chromosome arms) - estimated at 1 to 2 million € for a tomato chromosome -, representatives of some of the other countries felt that it may be possible to convince their funding agencies to join the international effort. In addition to the above, a major contribution to the sequencing of the potato genome is intensively being pursued by The Netherlands and Germany. Beyond the sequencing, the representatives of the European leading centres in plant bioinformatics, expressed their commitment to contribute to the annotation of the tomato genome sequence and to comparative genomics with other sequenced genomes. Finally, the representatives of the European Commission expressed their full support to the participation of Europe to this international initiative, comparing the sequencing of the tomato genome - the model for Solanaceous species - to the very successful international effort to sequence the Arabidopsis genome.

In conclusion, the meeting has highlighted not only Europe's strong motivation and desire to participate in the international project, but also outlined the scope of its concrete contributions to the tomato genome sequencing effort. All participants agreed that the principal deliverable of the tomato genome sequencing project should be a high quality finished sequence of the gene

rich portion of the genome, and unanimously endorsed the BAC by BAC sequencing strategy as the way forward. To underscore the importance of a common European contribution, the participants agreed that in addition to presenting their national genome programmes, the concerted "European Solanaceous Genome Programme" be presented at the Washington meeting on November 3.

With regard to the second objective, exploring the opportunities for a European Solanaceous Genome Project to be funded in FP6 under priority 5 "Food quality and safety", the participants unanimously agreed that the timing for such an initiative is perfect, and that the preparation of a proposal should be actively pursued following the November 3 meeting. The focus of the envisaged Integrated Project proposal will be on the exploitation of the Solanaceous genome platform to improve the nutritional quality of Solanaceous vegetables, in line with the objectives of the priority 5, but will definitely include substantial contributions to the Solanaceous Genome Project. The additional funding by the European Commission will undoubtedly strengthen the integration of the national programmes, and consolidate Europe's position in the International effort. These objectives are perfectly in line with its ERA policy and Europe's efforts to strengthen its competitive position in plant genomics in general.

## National contributions

### **France**

The French tomato genomic network gathers researchers of INRA and Universities. Research objectives concern molecular and genetic bases of fruit quality and plant-pathogen interactions. Several genetic and genomic tools were developed, including genetic maps of genes and QTLs (not only on tomato, but also on pepper, potato and eggplant), ESTs covering specific fruit development stages or specific plant-pathogen interactions, a BAC library of the pepper genome and the resequencing of 12,000 non redundant ESTs of the US collection. The present research concern proteome analysis along fruit development and the establishment of a collection of mutants and TILLING facilities. Most of these resources will be freely available to the international scientific community.

France has the facilities for participating to large sequencing projects in the National Center for Sequencing (Genoscope) but, although INRA supports the project, the extent of the French participation to the tomato genome sequencing will depend on the international and particularly on the European initiative.

### **Germany**

In Germany, there is currently no nation wide Solanaceae genome project. Within the GABI program supported by the German Ministry for Education and Research, there is ongoing research on the potato genome (C. Gebhardt) at the MPI for Plant Breeding Research in Cologne: This centres around physical mapping and genomic sequencing of a hot spot for pathogen resistance, development of an SNP map for potato, construction of function maps for pathogen resistance and tuber quality traits, association mapping, macro-synteny studies between potato and Arabidopsis. Genome analysis in tomato (K. Theres) at the MPI for Plant Breeding Research includes map based cloning of shoot branching genes, and micro-synteny studies between tomato and Arabidopsis. At the MPI for Molecular Plant Physiology, Golm (Departments M. Stitt , L. Willmitzer and T. Altmann) a technology platform for metabolomics and transcriptomics of

tomato/potato has been established to study fruit metabolism and development. In addition, thematic research projects study tomato heat shock proteins (L. Nover, Frankfurt University) and tomato carotenoids and tocopherols (U. Sonnewald, IPG Gatersleben).

Solanaceae research in Germany will greatly benefit from the tomato genome sequence. Facilities for genomic sequencing of selected regions of the potato/tomato genome are available. Our contributions will depend on the availability of European funding in the framework of a successful European initiative.

## Israel

Tomato is the most researched plant in Israel where laboratories with diverse interests are located in The Volcani Institute, The Weizmann Institute, The Technion, The Hebrew University of Jerusalem, Ben Gurion University and Tel Aviv University. Our small and collaborative community has focused in the past years on the development of genetic resources and their utilization in developmental studies, metabolic profiling (with a strong emphasis of carotenoids), disease resistances, stress tolerance and breeding. The genetic resources that were developed in Israel include the MicroTom system for high throughput mutagenesis screens, saturation mutagenesis libraries (Fast Neutron and EMS) in the variety M82 and *L. pennellii* introgressions lines (ILs). Such exotic resources are presently under development for additional tomato species as well as a number of wild pepper species. The launch of The Solanaceae Genome Project will help to stimulate local granting agencies to partake in the international effort.

## Italy

Several projects utilising genomics tools to address biological questions in tomato are under way, or are being finalised. They are financed by the Italian Ministry of Research through its Funds for Strategic Research (project GeneFun), for Basic Research (projects Arabidopsis-tomato genomics, PlantStress and EGEN), for Industrial Research (project ItaLyco) and the ministry of Agriculture (project Ecopom). The main deliverables include macro- and microarray profiling, proteomics, TILLING, Virus Induced Gene Silencing (VIGS), characterisation of traditional Italian ecotypes, metabolic engineering, engineering for pathogen resistance. Phenomena under study include fruit and flower development, photomorphogenesis, plant/pathogen interactions, abiotic stress, carotenoid biosynthesis. Approx 7.3 M€ will go into tomato "-omic" research in the years 2002-2005, 75% of which through the Fund for Industrial Research. In a joint effort with France and the US, sufficient funds have been earmarked in the above-mentioned projects, to re-sequence approx. 12.000 TIGR tomato ESTs. An Italian Plant Genomics Network has been recently set up. The plans are to lobby with the Italian funding agencies to raise approx. 4 additional M€ dedicated to Solanaceous genomics, half of which dedicated to the sequencing of the gene-rich region of one tomato chromosome within the international initiative under discussion. The launch of a European project on Solanaceous genomics will help to put these efforts into a European and international context and to avoid unnecessary duplications of work.

## Spain

Although there are several National projects using genomic tools to address specific questions in Solanaceae, there is no Spanish Solanaceae Programme as such. There are however several genomics projects in Solanaceae currently under review. GenSOL has been submitted to the Spanish Initiative in Genomics and Proteomics (McyT); The major contributions of this proposal

are the generation of normalized and full-length libraries and the generation of stable transgenic RNAi tomato plants for 500 genes -involved in fruits or plant-pathogen interaction, and VIGs for another 650 genes -related to plant-pathogen interaction. A second Solanacea genomic Project BAIInSOL is under review by the Genoma Spaña - Genome Canada where Solanacea research as a priority area. The project addresses the question on how environmental stresses (biotic and abiotic) affect the sink strength in potato tubers/ tomato fruits and uses genomic tools (transcriptomics, proteomics and metabolomics) and reverse genetics on targeted genes. Up to 8 trilateral projects involving up to 15 different Spanish groups have been submitted to evaluation to McyT-GenoPlante-GABI initiative on genomics. All these projects using genomic tools and natural variability in different members of Solanaceae.

## The Netherlands

The Centre for BioSystems Genomics (CBSG), The Netherlands Network for Plant Genomics founded in 2003, aims at improving the environmental and consumer quality of tomato and potato by application of genomics technologies.

To improve the access to valuable potato genes CBSG has started the construction of a physical map based on AFLP fingerprinting of 90.000 individual BACs of *Solanum tuberosum*. To link physical and genetic position of traits this map will be integrated with the existing potato genetic map that consists of 10.000 AFLP markers To identify novel pathways towards pest and disease resistance CBSG started sequencing 200 BACs known to contain resistance gene homologues.

CBSG collaborates with Rod Wing's group at Arizona University, USA to integrate their tomato physical BAC map with a 7000 AFLP tomato genetic marker map constructed by CBSG's partners. To shed light on the structure of tomato chromosomes, sequencing of BACs that span the tip of chromosome 6 has started. Funds are available to sequence in total 7 Mb of chromosome 6 DNA and another 3 Mb of tomato DNA accommodating loci involved in resistance and quality traits.

## United Kingdom

In response to the invitation to the US tomato genome sequencing meeting a grouping of UK researchers called TRUK (Tomato Resources UK) have been drawn together in order to support this initiative. This has been carried out by Graham Seymour (Graham.Seymour@hri.ac.uk) and Gerard Bishop (gdb@aber.ac.uk). TRUK is comprised of a strong research community (around 30 groups) working on Solanaceous crops in the UK. This research is being undertaken in UK Universities, Research Institutes and Industry. TRUK has been able to identify the possible contribution to the International Tomato Sequencing Programme, with the BBSRC being willing to consider a proposal to deliver 25 Mb of sequence for the international community and if funded this would allow the UK to sequence a decent portion of the gene-space on one chromosome. We also have indications that Defra are willing to consider additional financial support, contingent on BBSRC investment. However, the BBSRC investment depends on the US initiative being funded, also on funding from other European partners. Of course the UK tomato and potato communities would also have to make the appropriate case for support. It seems likely that the UK sequencing will be done at Sanger, especially if this is the most cost effective location. The UK also has key experience in handling genomic and genetic resources and has pioneered many Solanaceous-based technologies. The benefits to TRUK of EU participation in the sequencing and downstream genomic technologies will be immense.