

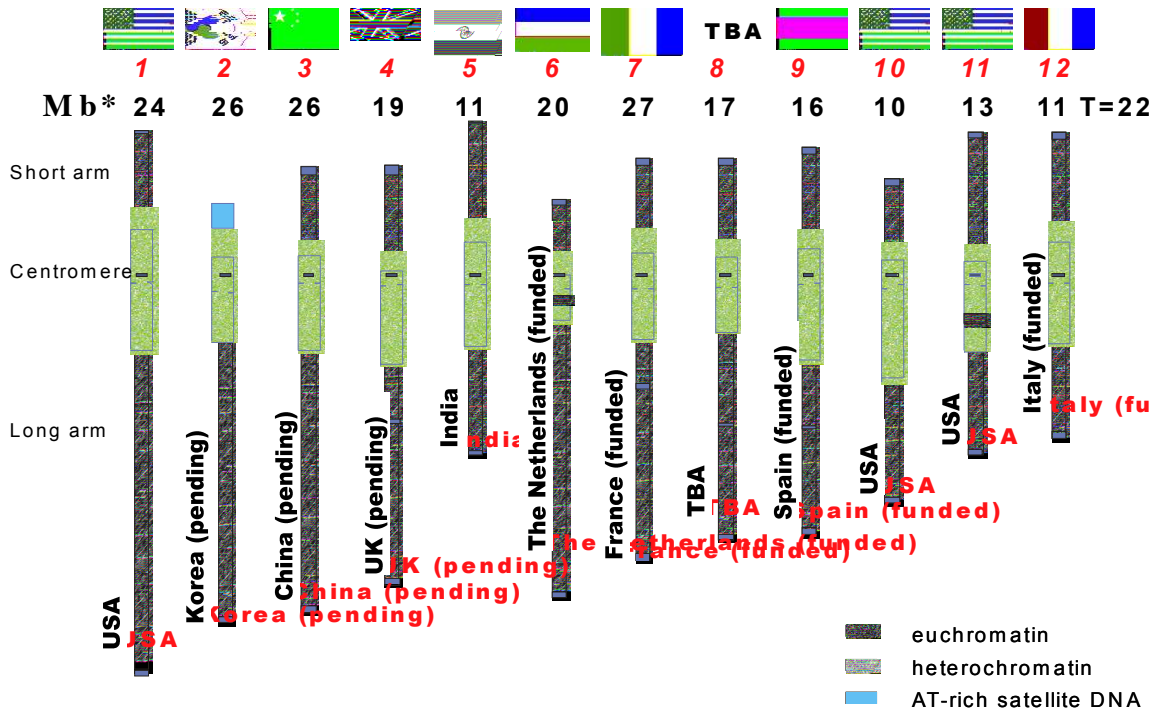
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*STATUS OF SOLANACEAE RESEARCH FROM AROUND THE WORLD*

Scientists from 23 countries provided written summaries of their present Solanaceae research and future grant submission plans. The sequencing of all the euchromatic regions of the tomato genome is being proposed by eight different countries on a chromosome-by-chromosome basis (Figure 10). The vision of SOL, however, goes much beyond the DNA sequence and thus we aim to extend the number of countries that will participate in this 10-year initiative. Some of the projects listed in this White Paper are by nature less expensive than high-throughput genomic undertakings, but are as important, particularly when we aim to explore issues of diversity and adaptation. This will allow many more countries to contribute and participate in the expedition into the higher levels of organization of biological systems.

**Figure 10:** Assignments of chromosome sequencing tasks to 10 countries. The country sequencing chromosome 8 will be announced in Sept 2004 at the first Solanaceae meeting in Wageningen, The Netherlands. The size in Mb is given for the euchromatic portion of each chromosome.



*Solanaceae research in different countries:*

## ARGENTINA

### Centers of Solanaceae research in Argentina

#### Research Institutes

*National Institute for Agricultural Technology (INTA):*

Instituto de Biotecnología CICVyA INTA Castelar, Province of Buenos Aires

Instituto de Recursos Biológicos INTA Castelar, Province of Buenos Aires

EEA INTA Balcarce, Province of Buenos Aires

EEA INTA La Consulta, Province of Mendoza

INGEBI (Instituto Nacional de Investigaciones en Ingeniería Genética y Biotecnología)

IIBL (Instituto de Investigaciones Bioquímicas Leloir)

#### Universities

University of Buenos Aires, Faculty of Sciences

University of Mendoza, Faculty of Agronomy

University of Córdoba, Faculty of Agronomy

The Northwestern part of Argentina ("Puna") belongs both biologically and culturally (southern part of the Inca civilization) to the center of origin and domestication of Solanaceae, particularly in the case of potato.

#### Sources of Support

Most basic research (including some small scale genomic efforts) is supported in part by ANPCyT (Agencia Nacional de Promoción Científica y Tecnológica) and CONICET (both dependent of the Secretary of Science and Technology) and by international funding like INCO-EU. Breeding and conservation of genetic resources are financed by INTA (dependent of the Secretary of Agriculture).

#### Topics of Research

The major topics are:

*Sequencing metabolic genes from wild tomato species (L. pennellii)* (at INTA Castelar, by Hopp E. in collaboration with the group of Fernie A/Willmitzer L, Berlin, Germany)

*Host pathogen molecular interaction between potato and its pathogenic viruses and tomato and its pathogenic bacteria* (at INTA Castelar, IIBL: headed by Dr. Ceriani F.)

*Molecular biology of fruit development and stress resistance in tomato* (University of Buenos Aires, headed by Dr. Norberto Iusem)

*Polen-pistillum molecular interaction in tomato* (INGEBI, headed by Dr. Jorge Muschietti)

*Characterization of genetic resources and breeding:* This research is focused on potato (INTA Balcarce) tomato and pepper (INTA La Consulta). It includes the use of molecular markers (SSR). There is a large germplasm bank which includes a replica of the one in CIP (International Potato Center) at INTA Castelar

*Phylogenetic and genetic diversity studies using molecular markers, sequencing of some*

*markers (ITS, etc.) of Solanum species* (INTA Castelar, University of Córdoba and Mendoza)  
Molecular characterization of protein kinases of *Solanum tuberosum* induced at the onset of tuber development (INGEBI Leded by Dr. Téllez-Iñón)

*Plant propagation and genetic transformation:* Research is focused primarily on potato and tomato transformation for different breeding purposes and development of germplasm maintenance protocols (INTA Castelar).

*Molecular farming.* Research is focused on the development of vaccine products through expression systems in potato (INTA Castelar headed by Dr. M. Borca ).

### **Potential Contribution of Argentina to the Tomato Sequencing Project**

At this time, it is unlikely that major funds are available in Argentina to provide support to a tomato sequencing program. However, basic infrastructure and research facilities and human resources are already available for this purpose due to the ongoing sunflower genomic project. Sequencing metabolically significant region of the wild species *L. pennellii* should allow rapid identification of genetic factors underlying metabolic changes in *L. esculentum* lines harbouring introgressions of this species.

### **Deadlines for Submission of Genomics Submissions**

There is no specific genomic-oriented funding, although it is prioritised among general submission programs. October 2004.

## **AUSTRALIA**

### **Centres of Solanaceae research in Australia**

#### **Research Institutions**

Primary Industries Research Victoria (PIRVic), the research agency of the Victorian Department of Primary Industries (DPI), bears national responsibility for breeding of potatoes through the National Potato Breeding Program (NPBP), to provide cultivars for fresh, crisping and french fry end-uses in the Australian industry. Potatoes were first introduced into Australia with the First Fleet in 1788 and current varieties are predominantly of American origin. As a consequence of declines in productivity due to disease pressures in the 1930s, a research station was established at DPI-Toolangi, outside the main region of cultivation, in 1944. This site provides the base for current activities in potato breeding, and since 2003, is part of the Plant Genetics and Genomics (PGG) Research Platform. This affiliation provides access to facilities and expertise in PIRVic's Plant Biotechnology Centre at La Trobe University, Bundoora, Melbourne, which has world-class infrastructure for high-throughput structural genomics, functional analysis and plant genotyping. PIRVic's Plant Health and Plant Production Research Platforms provides associated expertise in plant pathology, physiology and agronomy.

#### **Universities**

The Tasmanian Institute of Agricultural Research (TIAR) is affiliated with the University of Tasmania campus at Burnie. Coordination of a Potato Processing Research and Development Program is performed by Dr. Rowland Laurence, with contributions from the relevant state agencies and also links to Crop and Food Research New Zealand (CFRNZ). The primary activities are in the area of plant pathology, physiology and agronomy of potatoes.

#### **Breeding Companies**

Because of PIRVic's role on a national basis, no commercial breeding is currently undertaken, but there is close collaboration between industry groups and companies and the National Potato Breeding Program (NPBP). These industry groups and companies provide commercial direction into determining breeding priorities and are involved in evaluation trials and commercialisation of new cultivars.

#### **Background**

The Australian industry produces c. 1.3 million tonnes annually with a farm gate value of over AU\$400 million. The market is split in the approximate proportions 70:30 between processing and fresh products. Processing is performed by companies such as McCains, Arnotts and Simplot. The majority of production (c. 80%) is in south-eastern Australia, with Tasmania, South Australia and Victoria each producing around 25% of total production. A total area of c. 12,000 hectares are cultivated for potatoes in the state of Victoria. Traditional zones of cultivation in these states have been highlands with coolish, wet climates and fertile soils, as compared to sandy or loamy soils in Western Australia. In recent years, cultivation has been extended into lowland regions close to the Murray-Darling river basin, characteristic of hot, dry conditions and deep, sandy soils, and dependent on irrigation.

The Australian industry requires cultivars adapted to shorter growing seasons than those characteristic of the northern hemisphere (120 days compared to 150 days), with enhanced heat

tolerance and resistance to pathogens important to the Australian industry. There is also a competitive advantage for cold chipping/crisping cultivars that may be ground-stored for processing throughout the winter.

### **Sources of Support**

Support for potato breeding and associated sciences has traditionally been provided by recurrent funding from the relevant state agencies, as well as the industry levy funding council, Horticulture Australia Ltd. (HAL), which was formerly known as the Horticultural Research and Development Corporation (HRDC).

### **Major Topics of Research**

- Adaptation to shorter growing seasons
- Adaptation to elevated temperatures
- Tolerance to water stress, particularly uniform tuber formation under fluctuating water levels
- Enhance water use efficiency
- Quality traits such as reduced enzymatic browning, after-cooking darkening and low temperature starch conversion to sugars
- Resistance to endemic pests and pathogens such as tomato spotted wilt virus (TSWV), common scab and powdery scab
- Pre-emptive breeding to biotic stresses such as potato virus Y (PVY) and the *Phytophthora infestans* (late blight) A2 strain.

Implementation of molecular genetic marker-based technologies into the NPBP was a major recommendation of a program review (Brennan, P., Heap, M. and Zerella, C.) commissioned by HAL in 2004. Initial work in this area, based on work directed by Mr. Tony Slater (breeding program leader, DPI-Toolangi) and Prof. John Forster (plant molecular genetics leader, DPI-Bundoora) has used a selection of genomic DNA-derived SSR markers from the public domain to characterise c. 200 accession in the Australian germplasm collection. In parallel, a pair-cross family between parents that are resistant and susceptible respectively to TSWV has been generated for molecular map construction and QTL analysis, in concert with phenotypic data being generated by Dr. Brendan Rodoni (DPI-Knoxfield).

### **Potential Contribution of Australia to the Tomato Sequencing Project**

Highly unlikely: however, PIRVic-PGG is a core partner in the Multinational *Brassica* Genome Project (international *B. rapa* sequencing effort), and contribution to an international potato genome sequencing initiative remains a formal possibility.

### **Deadlines for Submission of Genomics Submissions**

A substantial molecular marker technology component (c. AU\$240,000 per year for the period from 2005-2010) was included in the current NPBP proposal, which is under consideration for funding by HAL.

## BRAZIL

Coffee is the most valuable agricultural commodity in world trade, commanding a turnover of US\$ 10 billion annually. Coffee is the world's most important beverage and upon which the economies of many producing countries from the south depend. Unfortunately, coffee appears as an "orphan crop" at the taxonomic level. The International Solanaceae Genome Project (SOL) is certainly the best opportunity for coffee research network to develop collaborative work in the area of genomics. Coffee belongs to Rubiaceae and is closely related to the Solanaceae family, as these two families are included in the Asterid I class (Figure 1).

### **Coffee genomics in Brazil:**

The Brazilian Coffee Genome Project is funded by three Institutions and programs; Fapesp, CBP&D do Café (Brazilian Consortium for Coffee Research and Development) and Embrapa/Cenargen (Brazilian Agriculture Research Company / Center of Genetic Resources). A total of US\$ 700,000 was invested in the project to date. Most of the infrastructure utilized for sequencing was already set up prior to the initiation of the Coffee Genome Project, by the AEG group (Agriculture and Environment Genomes), funded by Fapesp. This group alone includes 24 laboratories, at several research institutions, each one equipped with an automated sequencer ABIPrism 377. Five central sequencing labs also possess an ABI3700. The CBP&D is also a national consortium of 44 Universities and Public Research Institutes that funds projects related with all aspects of coffee culture. The central coordination of the project is under responsibility of the IAC (Agronomic Institute of Campinas / SP). The Bioinformatic processing and analysis is under the responsibility of Dr. Gonçalo Guimarães Pereira at Unicamp (State University of Campinas/ SP), and the corresponding web page is [www.lge.ibi.unicamp.br](http://www.lge.ibi.unicamp.br).

The project has a goal of 200,000 ESTs to be sequenced, and the deadline for the project is March/04. At present, 85% of all the ESTs were already sequenced. Clustering and annotation of those sequences has also been completed, and Blast searches performed in the database so far can identify genes of all biological categories and functions. Interestingly, the most significant hits are always with species such as tomato, potato and tobacco. Based on this information, we believe that including coffee, as part of the integrated Solanaceae project would represent a major contribution for improving the knowledge of coffee molecular genetics. The inclusion of Coffee as an integral part of SOL will extend the reference yardstick to evaluate issues of diversity and adaptation.

## CANADA

### Centers of *Solanaceae* research:

#### Federal Research Institutions

- AAFC Crops and Livestock Research Centre (Charlottetown-Nappan)
- AAFC Atlantic Food and Horticulture Research Centre (Kentville-Bouctouche)
- AAFC Potato Research Centre (Fredericton)
- AAFC Horticulture Research and Development Centre (Saint-Jean-sur-Richelieu)
- AAFC Food Research Program Centre (Guelph)
- AAFC Southern Crop Protection and Food Research Centre (London-Vineland-Delhi)
- AAFC Greenhouse and Processing Crops Research Centre (Harrow)
- AAFC Lethbridge Research Centre (Lethbridge)
- AAFC Pacific Agri-Food Research Centre (Summerland-Agassiz)

#### Provincial Research Institutions

- Alberta Department of Agriculture, Food and Rural Development Crop Diversification Centre South (Brooks)
- Saskatchewan Department of Agriculture, Food and Rural Revitalization,
- New Brunswick Department of Agriculture, Fisheries and Aquaculture (Bon Accord-Fredericton-Wicklow)

#### Universities

- University of Alberta (Edmonton)
- University of Manitoba (Winnipeg)
- University of Guelph (Guelph)
- University of Waterloo (Waterloo)
- University of Western Ontario (London)
- University of Montreal (Montreal)
- University of Quebec in Montreal (Montreal)
- McGill University (Montreal)
- Laval University (Quebec City)
- Nova Scotia Agricultural College (Truro)
- St. Mary's University (Halifax)

#### Genomics companies

- Solanum Genomics International Inc. (Fredericton)

#### Sources of Support

Most university research is supported in part by NSERC (the Natural Sciences and Engineering Research Council of Canada). Large-scale genomics efforts are funded to a maximum of 50% through Genome Canada, with additional support provided through provincial funding initiatives or other sources.

#### The major topics of research are:

*Production of genetic resources and mapping:* This research is focused on potato (AAFC Fredericton, AAFC Lethbridge) and tomato, petunia (University of Guelph).

*Development and implementation of genomics platforms:* This occurs through the Canadian Potato Genome Project, a Genome Canada-funded project encompassing five institutions (based primarily in Fredericton), and involves EST generation, microarray expression



analysis, activation tagged mutant production and bioinformatics.

*Pre-and post-harvest physiology:* This research is focused on effects associated with processing quality traits (primarily with potato), as well as senescence, aging and the effects of a variety of greenhouse growth conditions on tomato/pepper production. Major efforts for potato exist at AAFC Fredericton, AAFC Charlottetown-Nappan, NSAC Truro, NBDFA Wicklow and University of Alberta. Major tomato and pepper programs exist at University of Guelph, University of Waterloo, AAFC Harrow and AAFC Summerland-Agassiz.

*Metabolism:* This research is focused on carbon metabolism and source-sink relationships. Efforts are geared towards potato starch synthesis (University of Guelph) and starch quality (AAFC Guelph), and carbon metabolism during tomato fruit development (University of Guelph and Laval University).

*Biotic and abiotic stress:* Biotic stress research is focused on plant pest/pathogen interactions, metabolite profiling of these interactions, resistance genes and mechanisms, pest/pathogen screening and control strategies. Major research programs are in progress at several AAFC Centres (Charlottetown-Nappan, Fredericton, Sain-Jean-sur-Richelieu, London-Vineland-Delhi, Lethbridge), as well as University of Guelph, University of Manitoba, McGill University, University of Montreal, Laval University, Alberta Crop Diversification Centre South, NBDFA Wicklow and SGII. Abiotic stress research is focussed on drought, salinity and nutrient stresses, with research programs at AAFC Fredericton, Alberta Crop Diversification Centre South, University of Montreal and University of Quebec in Montreal.

*Plant propagation:* Research is focused primarily on potato organogenesis, somatic embryogenesis, development of germplasm maintenance protocols and nuclear stock production. Programs are in effect at NBDFA Wicklow-Fredericton, AAFC Fredericton and University of Montreal.

*Molecular farming.* Research is focused on the development of vaccine products through expression systems in tobacco and potato. Programs are ongoing at AAFC London-Vineland-Delhi, Laval University and SGII.

*Reproductive development:* Research is focused on self-incompatibility in potato and tomato fruit development. Research programs are in effect at University of Montreal and University of Guelph.

### **Potential Contribution of Canada to the Tomato Sequencing Project**

At this time, it is unlikely that funds are available in Canada to provide support to a tomato sequencing program. Given the importance of potato, and the major potato research efforts in Canada, a contribution towards a potato genome sequencing effort is a more distinct possibility.

### **Deadlines For Submission Of Genomics Submissions**

Funding for the next round of large-scale genomics research via Genome Canada has not yet been confirmed. However, discussions with the upper levels of Genome Canada have indicated an interest in a potato genome sequencing effort for any future rounds of funding. Preliminary discussions have taken place between Canadian researchers and European/American researchers towards this end.

## CHINA

### Highlights of Solanaceae Research in China

The Solanaceae is one of the most economically important crop families in China. There is a large scientific community including breeders, geneticists and molecular biologists with research focused on tomato and potato, the two major Solanaceae species in China.

### Centers of Solanaceae research in China

Institute of Genetics and Developmental Biology in China (IGDB), Chinese Academy of Sciences, Beijing, Beijing Genomics Institute, Beijing

### Sources of Support

Chinese Academy of Sciences, Ministry of Science and technology in China, National Natural Science foundation of China

### Topics of research

#### Tomato as a model to study plant-insect interactions:

This research is aimed at understanding the biochemical and molecular basis of plant resistance to insects, with a long-term goal of developing novel crop protection strategies that rely on the plant's "built-in" resistance capabilities, thereby reducing the use of environmentally damaging pesticides. Wound-inducible proteinase inhibitors in tomato provide an attractive model system to study the signaling pathways that regulate this form of defense. An ever-increasing body of evidence has indicated that the fatty acid derived signal jasmonic acid is an intercellular signal for host defense response, and that the biosynthesis of jasmonic acid is regulated by a peptide signal called systemin (Li et al., 2003; Li et al., 2002). Sequence of tomato genome will greatly facilitate gene identification in the systemin/JA signaling pathway and broadly increase our understanding of induced resistance of plants to insects attack.

#### 2) Using tomato as model to study molecular biology of plant nutrition:

The main consideration to use tomato as a model for this aspect of research is lethal mutants of the root-specific house-keeping genes can be easily rescued and maintained by grafting onto a wild type compared with *Arabidopsis*. Additionally, some genes involved in mineral uptake and metabolism in tomato genome show less genetic and biochemical redundancy compare to those in *Arabidopsis* genome, for example, *CHLN* gene. Dr. Hongqing Ling's group is studying molecular mechanisms of Fe and P uptake and metabolism. In last several years, they have isolated *CHLN* (a gene encoding nicotianamine synthase catalyzing nicotianamine synthesis from methionine in plants. Nicotianamine is a polyamine involved in iron uptake and metabolism), *FER* (a gene encoding a protein containing bHLH DNA-binding domain, it is as a putative transcription factor controlling iron deficiency responses and iron uptake in tomato roots) and *LeFROI* (a gene encoding a Fe<sup>3+</sup>-chelate reductase reducing ferric to ferrous iron on root surface) from tomato genome using map-based cloning and PCR-based homology cloning approaches (Ling et al., 2002, Ling et al., 1999). Additionally, they are trying to isolate new genes involved in iron and phosphate uptake and metabolism using a forward genetic approach.

### **Potential Contribution of China to the tomato and potato sequencing project**

- 1) As proposed before, the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences could do the sequence of the euchromatin region of tomato chromosome 3. We are now actively seeking sources of funds from relevant agencies in China.
- 2) The other major potential contribution of China to the genomics study of Solanaceae is that the Beijing Genomics Institute potentially could sequence the potato genome using a whole-genome shotgun sequencing strategy. If an ordered sequence map can be created for tomato, then other Solanaceous species such as potato could be shotgun sequenced and ordered using the tomato genome as a guide (through synteny). This would also allow fantastic comparative genomics studies. The Beijing Genomics Institute has track record for its sequencing and genomics capability (they completed 1% of the human genome sequencing, the draft sequence of rice genome, and a draft sequence of silkworm genome, etc.)

## COLOMBIA

### Centers of Solanaceae research

#### Research Institutions

Corporacion Colombiana de Investigacion Agropecuaria, CORPOICA  
Corporación para Investigaciones Biológicas, CIB

#### Universities

Universidad Nacional de Colombia  
Universidad de Antioquia  
Universidad Catolica de Oriente

#### Others

Centro virtual de investigacion de la cadena agroalimentaria de la papa, CEVIPAPA

### Centers of coffee research

Centro Nacional de Investigaciones de Cafe, CENICAFE

### Topics of Solanaceae research

*Germplasm collection and characterization.* Mainly conducted at CORPOICA, which is the institution responsible for maintaining the National Germplasm Bank for food and agriculture. At present, there are more than 22000 accessions of plant genetic resources representing more than 75 species. In the case of the Solanaceae family, the germplasm bank comprises 44 species of the genera Capsicum, Lycopersicum, Cyphomandra, Physalis, Nicotiana and Solanum. The Solanum collection is the second largest of the world after the CIP collection in Peru.

CORPOICA has developed a solid ex-situ conservation platform including field, refrigeration, and in vitro conservation systems supported by a complete database. Research efforts are oriented to improve the knowledge of the genetic variability existing in the germplasm banks and to advance in the molecular characterization of these materials (through RFLP, AFLP, SSRs) to adding value to these collections and allowing a sustainable use of these genetic resources. Important information regarding morphological, physiological and biochemical characterization of different accessions is available in CORPOICA's databases. Other sources of Solanaceae germplasm are in the National Colombian Herbarium (COL, Universidad Nacional de Colombia), which comprises 520.000 collections of the Colombian flora. COL exchanges material with national and international herbaria and it is one of the most important sources of information in South America.

*Systematics and taxonomy.* Study of phylogenetic relationships among the most widely distributed groups in Solanum, Cestrum, Lycianthes, and some genera of the subtribe Withanieae through morphological, chemical and molecular systematics (Universidad Nacional de Colombia, Universidad de Antioquia in collaboration with the Natural History Museum, London and the Universidad Central de Venezuela). Future research will include collaboration in a worldwide project whose aim is the creation of a comprehensive inventory of *Solanum* (headed by Lyhn Bohs, Sandra Knaap and Michael Knee and recently funded by the National Science Foundation, NSF (USA).

*Breeding.* Traditional breeding for lulo, tree tomato and potato. Relevant research advances includes the release of a high vitamin C Lulo (*S. quitoense*), the release of a lulo cultivar named "lulo la selva" (*S. quitoense* x *S. hirtum*) showing resistance to nematodes, and the field identification of inter-specific *Cyphomandra betacea* materials tolerant to anthracnose (CORPOICA)

*Tissue culture and genetic transformation.* *in vitro* multiplication, plant regeneration and genetic transformation of potato, lulo and tree tomato (Universidad Nacional de Colombia, CIB, Universidad Catolica de Oriente).

*Integrated pest management.* Formulation of biopesticides -- use of BT toxins for pest control in potato and tomato (CORPOICA, Universidad Nacional de Colombia, CIB).

### **Funding of Solanaceae research**

Maintenance of the germplasm banks of plants, animals and microorganisms is funded by the Colombian Ministry of Agriculture and CORPOICA. Other research is funded by the Instituto Colombiano para el Desarrollo de la Ciencia y la Tecnologia (COLCIENCIAS), CEVIPAPA, the Bolsa Nacional Agropecuaria, and the Universities. However, funds for genomic / molecular studies are needed, particularly for species with potential international commercialization (*C. betacea*, *S. quitoense* and *P. peruviana*). Genomics research conducted on these species will be of great importance for diversity and adaptation studies proposed in the SOL project. Likewise, information derived from the sequencing of the tomato genome and from functional and comparative genomics with other Solanaceae species as proposed in the SOL project will be of great importance for developing a genomics platform for these Andean species.

### **Topics of coffee research**

CENICAFE is the Research Center of the National Coffee Growers' Federation of Colombia, an organization that unifies coffee producers through out the country and brings economic and social development to the coffee zone. Since its creation in 1927, it has funded scientific research, agricultural extension, and diversification programs to support the coffee industry, as well as, physical infrastructure (road building, electrification), education, health, and other services that provide economic and social development for the 4 million people in the coffee growing area. The Federation founded CENICAFE in 1938 with the mission to generate scientific knowledge and technologies to help sustainability of coffee production in Colombia while preserving natural resources in the coffee regions (soil, water, flora, and fauna). CENICAFE's research covers the complete range of coffee production: from genetic studies aimed at development of new coffee varieties right through marketing. In 1991, CENICAFE initiated a collaborative project with Cornell University to train a multidisciplinary team of Colombian scientists in Entomology, Plant Breeding, Plant Pathology and Molecular Biology. This project was funded by the National Coffee Growers Federation of Colombia and has generated the expertise that will now enable CENICAFE to work as a full research partner in coffee genomics with Cornell University to tailor these efforts towards applications to coffee improvement.

*Coffee genomics initiative.* CENICAFE is currently preserving and characterizing one of the largest *Coffea arabica* germplasm collections in the world with more than a thousand accessions (several from Ethiopia, a center of diversity for coffee). Our genomics studies will be oriented toward exploring and characterizing genetic diversity in the genus *Coffea*, in terms of insect and pathogen resistance, quality and yield to use it for CENICAFE's breeding efforts in *C. arabica*. CENICAFE has invested several years in the development of populations for mapping purposes and QTL analysis. The parental genotypes for the crosses were selected based on the diversity studies performed by Moncada (2000). Analysis of the heritable characteristics of quantitative and qualitative type on populations derived with that objective, will allow us to obtain information on the number, chromosomal location, effect and genetic interactions of loci that control the expression of those characters. We are currently funded by the Colombian Ministry of Agriculture to develop a coffee genetic map. Our initial objective is to screen 500 SSR and map those that are polymorphic onto one or more mapping populations. The isolation and characterization of microsatellite markers was initiated in Susan McCouch's laboratory during the joint project between Cornell and CENICAFE. Additional SSR markers are being developed

at CENICAFE. Evaluation of SSR polymorphism in the parents is being conducted at CENICAFE to obtain the most informative markers for population analysis. In addition, 1000 COS markers, developed in collaboration with Steve Tanksley, will be screened and those that are polymorphic will be mapped. The map, including the identity and the order of the markers, will be published. The map will lay the foundation for identifying QTLs associated with traits of interest for coffee improvement and will represent a basic framework for saturation with additional markers in the future. This will be a first step in the process of identifying genes of agronomic importance. Genes of particular interest are those involved in resistance to insects and diseases, in the flowering process, yield, and in cup quality, among others. The specific markers chosen for map construction will provide interspecies links and also provide tools that are easy and inexpensive to use for large scale breeding applications. Both SSRs and COS represent highly informative PCR-based markers that will be efficient for use in both basic genetics research and breeding applications.

## EUROPEAN UNION (EU)

In 2000 Commissioner Busquin launched the European Research Area - ERA – policy aimed at creating a comprehensive set of measures directed at promoting the integration of European research. One of the major objectives has been to identify areas of strategic interest in which integration is to be pursued with high priority. A model for this philosophy has been the steps taken towards the creation of a European Plant Genomics network, under the ERA-NET programme, and the establishment of a Technology Platform for Plant Genomics and Biotechnology. The former initiative is comprised of national science policy makers, representatives of the major funding agencies including scientists and experts. The objective will be to harmonize funding strategies and mechanisms, develop a framework for cross border collaborative research and establish a long-term common European policy for plant genomics. The Plant Genomics ERA-NET is becoming operational on January 1, 2004.

The development of 2025 Plant Genomics Platform is aimed at bringing together all the stakeholders (science, industry, society) to develop a 20 year vision for plant genomics and biotechnology in Europe. This vision will include economic and industrial priorities as well as Europe's role in the global context in a manner that will allow the establishment of a strategic research agenda to meet long-term goals. This Plant Genomics Platform constitutes an important step towards a coherent European strategy for plant genomics and will provide a firm basis for long term funding.

The European Solanaceae Genome Initiative is aimed to bring together a broad scientific base for Solanaceae research. Europe is blessed with a strong and dynamic research community with more than 100 groups that are directly involved in Solanaceae research. The well-structured national programs are reflected in the countries write-ups with excellent complementarity between the groups and already established research alliances. Europe's Solanaceae research community is highly motivated to contribute to the SOL project particularly when the vision of the international project is highly consistent with the views developed in Europe. The plan is to submit an Integrated Solanaceae Project application for funding in FP6. In tomato the European countries are already preparing grant applications to sequence 5 chromosomes. For potato a large number of BACs will be sequenced (The Netherlands, Germany) as a part of an already existing European collaboration. Other topics that are of interest include physical mapping, SNP marker development, EST sequencing, map-based cloning and QTL cloning, microarray development, metabolic profiling technologies, TILLING and a bioinformatics effort that will benefit from the solid European expertise in genome annotation and comparative genomics.

The FP6 funding opportunities for a Solanaceae genome project are in Priority 5 – “Food quality and safety”. This will provide complementary funding for the sequencing of the tomato genome as a first step to support the exploitation of the genome resource to improve the nutritional quality of Solanaceae vegetables. The funding from the European Commission will strengthen the integration of the national programs and consolidate Europe's contribution to the International Solanaceae Genome Project. Europe is highly motivated to participate in the international SOL project and to contribute significantly to the tomato genome sequencing effort as well as follow up biology along the proposed line of research of system biology of diversity and adaptation. A grant proposal integrating the concepts described above will be submitted to the European Commission in 2004 under the European FP 6 program. This initiative is part of a broader drive to integrate Europe's plant biology research where plant genomics has been recognized as a high priority technology area.

## FRANCE

### Centers of *Solanaceae* research in France

#### Research Institutions

INRA Plant Physiology & Biotechnology, Bordeaux  
INRA Genetics and Breeding of Fruit & Vegetables, Avignon  
INRA Genomics and Biotechnology of Fruit, Toulouse  
INRA Horticultural Plant Growing Systems, Avignon  
INRA Safety and Quality of Plant Products, Avignon  
INRA Cell wall Polysaccharides laboratory, Nantes  
CNRS Plasts and Cell Differentiation Laboratory, Grenoble  
INRA Plant Pathology, Antibes  
INRA Plant Pathology, Bordeaux  
INRA Plant Genomic, Evry

#### Universities

University of Bordeaux  
University of Toulouse, National Polytechnic Institute  
University of Grenoble

#### Sources of Support

Research is supported by INRA institutional resources, by grants of the French Ministries of Research and Agriculture, by Genoplante programme and by EU programmes (APOPHYS, DREAM)

#### Major Topics of Research

- *Production of genetic resources, mapping.* Mapping and genotyping research activities on tomato, pepper, potato and eggplant are centred at INRA-Avignon (M. Causse, V. Lefebvre, MC Daunay), partly in interaction with breeding companies. A pepper BAC library was constructed at INRA-Avignon and INRA-Evry (Genoplante). Generation of EMS mutants at INRA-Bordeaux (C. Rothan).
- *Development and implementation of genomics analytic platforms.* INRA-Toulouse (M. Bouzayen) is the source centre for tomato microarrays production and distribution and is in charge of sequencing of the unigene set of tomato ESTs. INRA-Bordeaux (C. Rothan) is setting facilities for implementation of TILLING strategy on the tomato model. Tomato proteome is characterized at INRA-Avignon (M Causse).
- *Metabolomic platform.* Metabolic profiling is analysed through NMR and HPLC at INRA-Bordeaux.

#### Major areas of biological interest are

- *Fruit development and fruit ripening.* The control of fruit development and ripening is addressed through the characterisation of hormone-dependent regulation of gene transcription (INRA-Toulouse). Early stages of fruit development are studied through investigation of the control of cell division and cell enlargement (INRA-Bordeaux). Fruit composition in relation to consumer perception is studied at INRA-Avignon
- *Metabolism, transport, and sink-source interactions.* This research is mainly conducted at INRA-Bordeaux on the tomato.



- *Secondary metabolism.* Research on carotenoid biosynthesis in relation with plast differentiation are developed at CNRS/University Fournier, Grenoble.
- *Fruit cell wall structure and modifications.* Cell wall genes involved in fruit firmness are studied at INRA Avignon and modifications of cell wall structure during fruit development are addressed through biochemical and biophysics approaches at INRA Nantes.
- *Disease Resistance in Solanaceae.* Among the major pathogens studied in several SOL species are potyviruses (INRA-Avignon and Bordeaux), nematodes (INRA-Avignon and Antibes) and Phytophthora (INRA-Avignon)

### **Potential Contribution of France to the Tomato Sequencing Project**

Decision on whether France they will make a major contribution to the tomato genome sequencing project is still under discussion. A proposal will be submitted to CNS (National Centre for Sequencing) in 2004 (likely March/April). An EU funding to support contribution to the tomato sequencing will also be sought and a proposal will be submitted in 2004. Following discussion with INRA national authorities, it is likely that France will strongly contribute to the functional genomics program through the generation of tomato generic resources for high throughput reverse genetics (EMS, TILLING, proteomics).

## GERMANY

### Centers of *Solanaceae* research in Germany

#### Research Institutions

Max Planck Institute for Plant Breeding Research (MPIZ), Cologne  
Max Planck Institute for Molecular Plant Physiology (MPIMP), Golm  
Max Planck Institute for Chemical Ecology (MPICE), Jena  
Institute for Plant Breeding and Crop Plant Research (IPK), Gatersleben  
Institute for Plant Biochemistry (IPB), Halle

#### Universities

University of Halle  
University of Cologne  
Technical University Munich/Weihenstephan (TU Weihenstephan)  
University of Hannover

#### Breeding Companies

Germany has several, strong potato breeding companies, which are organized in the Gesellschaft für Pflanzenzüchtung e. V. (GFP), Arbeitsgruppe 13 (Kartoffeln).

#### Agrochemical companies

Plantech (Bayer Crop Science)

#### Sources of Support

Research is supported by grants from the German Ministry for Research and Education (BMBF, e.g. the GABI programme), by the Deutsche Forschungsgemeinschaft (DFG, e.g. a “Sonderforschungsbereich” SFB in Halle), the European Union (e.g. the EuDicot and APOPHYS projects) and by institutional resources of the Max Planck society and the two Leibniz Institutes (IPB and IPK).

#### Major Topics of Research

*Production and molecular characterization of genetic resources, mapping of agronomic traits, marker development, analysis of gene activation in response to biotic and abiotic stress.* This research focuses on potato. It is centered at MPIZ-Cologne and at the TU Weihenstephan, partly in interaction with breeding companies.

*Positional cloning, physical and comparative mapping and genomic sequencing in potato and tomato.* This type of research is carried out at MPIZ-Cologne.

*Development and implementation of genomics analytic platforms.* This occurs in particular at MPIMP-Golm (expression arrays, metabolomics) and at IPK-Gatersleben and IPB-Halle (metabolomics, in the latter case, especially secondary metabolism).

#### Major areas of biological interest are:

*Genome analysis.* Research on the potato genome started 1986 at MPIZ-Cologne (C. Gebhardt) with the construction of molecular maps and proceeded with the localization of genetic factors controlling resistance to pathogens and tuber traits. This work led to the molecular cloning of the *R1* gene for resistance to late blight and the *Gro1* gene for resistance to the root cyst nematode *Globodera rostochiensis*. Major interests are (1) the molecular basis of QTL for quantitative

resistance and QTL for traits related to carbohydrate metabolism (tuber starch and sugar content, cold sweetening), (2) population genetics (LD mapping, haplotyping, natural variation) of breeding pools and wild potato species, (3) comparative function maps.

*Metabolism, transport, and sink-source interactions.* This research was initiated in the early 1990's, profiting from the possibility for routine transformation of Solanaceae species. Initial work was often in tobacco, but quickly potato and tomato became the major species used. The work includes detailed analysis by reverse genetics of many major pathways in central carbon and nitrogen metabolism, also analysis of transport protein families. A particular area of research was the pathway of starch synthesis, resulting in the ability to radically alter the structure and properties of starch. Major centers for this research include the MPIMP-Golm, IPK-Gatersleben and the Universities of Cologne (Prof. Flügge) and Hohenheim (Prof. Von Wiren; The biotech company Plantech - now part of Bayer Crop Science) was a product of these research activities. Recent developments include studies of hormonal signals and of bacterial pathogenic factors that influence sink growth and cell functions (MPIZ-Cologne, IPB-Halle, University of Halle, IPK-Gatersleben).

*Secondary metabolism.* The IPB-Halle in particular has a long-standing expertise in the analysis of phenylpropanoid and alkaloid metabolism in *Solanaceae* spp.

*Biotic and abiotic stress.* This on the one hand encompasses the mapping of resistance genes (MPIZ-Cologne, University of Hannover, TU Weihenstephan), and on the other hand the analysis of stress responses with genetic, biochemical and genomics tools (in particular at the IPB-Halle, the University of Halle, the University of Frankfurt (Prof. Nover), TU Weihenstephan (Prof. Wenzel).

*Chemical Ecology.* Research on Solanaceae spp. plays a central role in the molecular analysis of plant-insect interactions at the MPICE-Jena, in particular in the work of Profs Gershenzon and Baldwin.

*Plant architecture.* The origin of axillary meristems, shoot branching and apical dominance is studied at the molecular level in tomato at MPIZ-Cologne (K. Theres)

#### Potential Contribution of Germany to the Tomato Sequencing Project

At this time, it is unlikely that funds are available in Germany to provide significant direct support to a Solanaceae sequencing program (see below).

The major potential contribution of Germany to a potential tomato sequencing program would be to provide strong support for follow-up activities to ensure effective use of the information contained from the tomato genome sequence. In particular:

In providing resources and programs to allow transfer of the results from tomato into potato breeding programs. Tomato breeding and cultivation is not a major activity in Germany, whereas potato is an important crop. It is also an important crop in some of the new members to the EU (e.g., Poland).

In providing centers with a strong analytic infrastructure to allow analysis of genetic diversity in potato, tomato and other Solanaceae. In addition to basic research, this directly addresses topics related to the nutritional and health value of crops, and therefore provides a strong support for breeding programs. These are already being used, for example, in an in-depth analysis of tomato introgression lines to identify loci that produce major shifts in metabolism. The possibility of

attracting large funding for a systematic study of metabolite levels in several crops including potato and tomato, in order to provide a database of food composition, a background for assessment of substantial equivalence, and a background for breeders to use in breeding in the future.

### **Deadlines For Submission Of Genomics Submissions**

The framework and aims of the second phase of the GABI programme have already been implemented and the reviewing process for projects in the second phase is completed, and does not include this aim. The DFG is not really able to support activities on this scale, but concentrates instead on funding focused biological projects.

However, in parallel with attempts to raise international support for Solanaceae research and more specifically for tomato genome sequencing, it will be possible in Germany to seek sources of money internally for the development and application of these tools.

## GREECE

### NATIONAL AGRICULTURAL RESEARCH FOUNDATION (N.AG.RE.F.)

#### Centers of Solanaceae research:

1. National Agricultural Research Foundation (N.AG.RE.F.)  
Agricultural Research Center of Macedonia - Thrace  
(i) Department of Vegetable Crops  
(ii) Greek Gene Bank  
570 01 Thermi, Thessaloniki, Greece
2. National Agricultural Research Foundation (N.AG.RE.F.)  
Vine and Vegetable Institute  
Gastouni, Greece, GR-273 00
3. National Agricultural Research Foundation (N.AG.RE.F.)  
Institute of Viticulture, Vegetable Crops and Floriculture  
713 07, Heraklion, Crete, Greece

#### Sources of support

- N.AG.RE.F.
- Ministry of Agriculture
- E.U. (RESGEN)
- General Secretary of Research and Technology - Hellas

#### Major topics of research

##### Tomato

- Introduction of indigenous and exotic germplasm of tomatoes, and development of selected material by conventional and marker assisting breeding for creating new cultivars.
- Evaluation of Greek genetic resources of tomato to abiotic stress (drought, etc.), using morphological and/or physiological parameters, and molecular markers.
- Germplasm screening for morphological and agronomic traits, and adaptation studies.

##### Eggplant

- Management, Conservation and Valorization of Genetic Resources of eggplants (*Solanum melongena* L.).
  - Regeneration and description of 100 *Solanum* species.
  - Evaluation of resistance in *Verticillium dahliae* of 100 *Solanum* species.
  - Exploitation of *Solanum* genetic resources as stocks for eggplant to control soil-borne diseases (graft compatibility tests, influence of rootstock to scion yield and quality, etc.).
- Development of resistant eggplant cultivars to *Verticillium dahliae* by exploiting the wild species *Solanum torvum* and *S. sisymbriifolium*.
- Development of resistant eggplant cultivars to spider mites by exploiting the wild species *S.*

- macrocarpon.
- Conservation of genetic integrity of eggplant cultivars.

### **General**

1. Collecting expeditions of Greek tomato, pepper and eggplant germplasm.
2. Regeneration, multiplication and phenological characterization of greek germplasm of tomato, pepper and eggplant, and their wild relatives.
3. Conservation of genetic integrity, maintenance and seed production of greek solanaceous cultivars.
4. Development of new cultivars of tomatoes, pepper and eggplant, both table and processing, well adapted to low input and/or biological horticulture.

### **Agricultural University of Athens (AUA)**

Agricultural University of Athens (AUA)  
Faculty of Crop Science and Production  
Dept. of Plant Breeding and Biometry  
Iera Odos 75, Athens, Greece, 118 55

#### Sources of support

1. AUA (own funds)
2. Graduate Studies Program
3. Pythagoras

#### Major topics of research

1. The development of tomato cultivars for the greek market both table and processing.
2. The isolation and study of bioactive metabolites and their use for the study of biodiversity of local varieties of tomato.
3. Evaluation of local tomato varieties to salinity by in vitro tests.

### **Mediterranean Agronomic Institute at Chania**

Dept. of Horticultural Genetics Biotechnology  
PO BOX 85, Alysion Agrokipiou  
73100 Chania

#### Sources of support

- In house funding

#### Major topics of research

##### Tomato

1. Molecular basis of hypoxia and anoxia stress
2. Characterization of the physiological role of tomato fruit prolyl-4-hydroxylases (P4H) (Identification of the P4H cDNAs expressed during tomato fruit development, characterization of their expression profiles and use of P4H pharmacological agents to inhibit

enzymatic activity).

### **Aristotle University of Thessaloniki**

Department of Pharmaceutical Sciences  
Division of Pharmacognosy-Pharmacology  
Laboratory of Pharmacognosy  
Group of Biotechnology of Pharmaceutical Plants  
541 24 Thessaloniki, Greece

#### Sources of support

General Secretariat of Research and Technology – Hellas (ministry of Development of Greece)  
Ministry of Education of Greece  
European Union  
In house funding

#### Major topics of research

##### Tobacco

- Ascorbate involvement in abiotic and biotic stress

##### Tomato

1. Ascorbate biosynthesis, metabolism and oxidation. Ascorbate involvement in abiotic and biotic stress.
2. Molecular basis of hypoxia and anoxia stress in tomato fruit.
3. Biosynthesis and genetic manipulation of arginine, citroulline and ornithine.

### **University of Crete**

Dept. of Biology  
Vasilika Vouton, P.O.Box 2208  
71409 Heraklio, Crete,  
Greece,

and

### **Institute of Molecular Biology and Biotechnology**

FORTH, Vassilika Vouton  
P.O.Box 1527  
GR 711 10 Heraklion, Crete  
GREECE

#### Sources of support

- European Union
- General Secretariat of Research and Technology - Hellas
- Ministry of Education

#### Major topics of research

1. Viroid-host interactions, characterization of host factors interacting with viroid RNA
2. Virus -host interactions (tobacco, potato)-resistance through posttranscriptional gene silencing

3. Mechanisms of posttranscriptional gene silencing
4. Regulation of gene expression by miRNA and target gene identification

**Center for Research and Technology Hellas  
Institute of Agrobiotechnology**

6TH km Charilaou-Thermis Rd. PO Box 361  
570 01 Thermi, GREECE

Sources of support

- European Union
- General Secretariat of Research and Technology - Hellas
- Ministry of Education
- Private Companies

Major topics of research

General

1. RNA trafficking in grafted vegetables
2. Epigenetic mechanisms: DNA methylation, micro RNAs and RNA interference in gene regulation and plant development
3. Bioinformatics tools for microRNA identification
4. Oxidative stress and stress tolerance mechanisms in plants
5. Flower development
6. Molecular diagnostics and molecular markers for crop improvement
7. Phospholipid mediated signal transduction mechanisms
8. Insect resistance mechanisms

Pepper

1. Regeneration and transformation of red pepper
2. Development of edible vaccines in red pepper

Tomato

1. Development of grafting techniques to combine micropropagation and micrografting



## HUNGARY

### Research Institutions

Agricultural Biotechnology Center (ABC)

### Universities

University of Veszprém, Georgikon Faculty of Agriculture, Potato Research Center

### Companies in Hungary with commercial interests in Solanaceae

Solanum Ltd, Berzence

Solum Corp., Komárom

Haladás Agric. Corp., Dunaegyháza

### Industry related organisations

Potato Marketing Board, Budapest

### Sources of Support

Hungarian Scientific Grant (OTKA), National Research and Development Programme (NKFP), European Union Framework Programme 5, Ministry of Agriculture and Regional Development  
Ministry of Education

### Topics of Research

- *Virology*

Production of transgenic virus resistant potato, tobacco and pepper (potato virus Y, cucumber mosaic virus and tomato spotted wilt virus)

Study the mechanisms of plant virus resistance

Developing efficient transformation and regeneration techniques for potato and pepper by using different *Agrobacterium* strains and vectors without markers for selection

- *Stress and tuber development*

Studying the function of the SNF1-related protein complex in potato

Drought tolerance mediated by trehalose phosphate synthase in potato

- *Optimising nutritional quality of potato*

Production of transgenic potatoes with increased methionine and cysteine content

- *Conventional (sexual crossing) breeding*

Development of potato varieties resistant to the most important pests (viruses, common scab, late blight, potato cyst nematode)

Developing breeding lines containing Ry<sub>sto</sub> and/or Ry<sub>hou</sub> and/or Ry<sub>adg</sub> genes in heteromultiplex manner

- *Application of biotechnological methods in the breeding programme*

Somatic hybridisation: *S. brevidens* (PLRV, PVY and *Erwinia* resistance) + *S. tuberosum*, *S. bulbocastanum* (late blight resistance) + *S. tuberosum*

- *Genetic modification of potato*

Used genes: aldose-reductase, superoxide-dismutase, ferritin (in collaboration with the Biological Research Center, Szeged)

· *Plant pathology*

Investigation of potato genotypes for virus and late blight resistance

Virus epidemiological investigations (occurrence and spreading of potato viruses)

**Participants:**

*Agricultural Biotechnology Center*

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## INDIA

### Centers of *Solanaceae* research in India

#### Research Institutions

Indian Institute of Vegetable Research (IIVR), Varanasi  
Indian Agricultural Research Institute (IARI), New Delhi  
Central Potato Research Institute (CPRI), Shimla  
Indian Institute of Horticultural Research (IIHR), Bangalore  
National Center for Plant Genome Research (NCPGR), New Delhi  
National Bureau of Plant Genetic Resources (NBPGR), New Delhi  
Bose Institute (BI), Calcutta  
Central Coffee Research Institute (CCRI), Chikmagalur  
International Center for Genetic Engineering and Biotechnology (ICGEB), New Delhi

#### Universities

University of Delhi, South Campus (UDSC), New Delhi  
University of Hyderabad (UH), Hyderabad  
Kerala Agricultural University (KAU), Thrissur  
Punjab Agricultural University (PAU), Ludhiana  
University of Agricultural Sciences (UAS), Bangalore

#### Breeding Companies

India has several tomato and potato breeding companies, which are providing seeds to farmers

#### Sources of Support

The research in area related to SOL at the University and Institutions is mainly supported by grants from Dept of Biotechnology, New Delhi and Indian Council of Agricultural Research, New Delhi. In addition Dept of Science and Technology, Council of Scientific and Industrial Research, Dept of Atomic Energy and University Grants Commission also support research in the area of SOL.

#### Topics of Research

The major topics are

*Production of genetic resources and mapping:* Several germplasm lines of tomato (1052), brinjal (350) are maintained by IIVR. Similarly IIHR has germplasm collection of chili and capsicum (1586), brinjal (557) and tomato (600). Both IIVR and IIHR have developed several hybrids of brinjal and tomato for higher yield and quality, resistance to bacterial wilt and drought tolerance. IIVR also has six wild relatives of tomato and their accessions. The wild relatives are being utilized in breeding to transfer the resistant genes from wild to cultivated varieties of tomato. IIVR is also working on molecular mapping and marker assisted breeding for TLCV, fusarium wilt and bacterial wilt resistance in tomato. The narrowing genetic diversity in Indian tomato varieties using RAPD techniques was demonstrated by NBPGR. IIVR is also developing RILs

using contrasting parents for QTL mapping in tomato.

*Pre-and post-harvest physiology:* Several groups (IARI, BI, NCPGR, UDSC) are developing transgenic tomato plants for regulating tomato fruit ripening and quality. Current approach uses ACC synthase4 gene and Le-MADS-Rin gene in antisense direction (BI, UDSC, IARI) that causes delay in fruit ripening (IARI, BI). The group at BI is over-expressing SAM decarboxylase under the control of fruit ripening specific promoter to enhance the level of spermidine. It is also characterizing E8 promoter of tomato. The IARI group is also working on characterizing fruit ripening specific promoter for LeExp1 from tomato.

*Ripening specific genes:* The group at UDSC identified the sequences of 156 ripening related genes from tomato on searching databases. The tomato cDNA libraries were generated from different stages of fruit ripening. So far more than 50 genes have been cloned. These genes fall into following categories: genes encoding ethylene receptors, expansins, heat-shock proteins, ethylene responsive proteins, transcription factors, kinases, 14-3-3 like proteins, lipoxygenases, cell wall enzymes, enzymes of carbohydrate metabolism, pigment synthesis and various other miscellaneous ripening regulated proteins.

*Biotic and abiotic stress:* Several centers in India are studying the viruses, bacteria and fungal pathogens infecting tomato and develop varieties to control the viral diseases (KAU, UAS, IIHR, IIVR). These universities and institutions have released several resistant lines to bacterial wilt and viral diseases. The group at NCPGR has generated transgenic tomato lines with oxalate decarboxylase gene that are resistant to pathogen infection. The group at ICGEB is developing resistant lines against bacterial and viral pathogens.

*Molecular farming:* The investigators at UDSC in collaboration with other partner Institutions have expressed genes for *ctxB*, *tcpA* and *acfA* antigens of *Vibrio cholerae* in tomato. Feeding of transgenic tomato fruits expressing cholera toxin B subunit (CTB) has been found to elicit production of IgA antibodies against this antigen in mice.

*Development of EMS, gamma radiation and T-DNA insertion population in tomato:* The research on mutagenesis of tomato is performed at the UH. The EMS-mutagenized and gamma-radiated lines are currently used for mutant screening in tomato and in future would be used for TILLING. At UH transformation of tomato is carried out for T-DNA insertional mutagenesis using *Agrobacterium*.

*Mutant isolation/characterization:* The group at UH has isolated several mutants, which are novel in nature and may have arisen due to mutation in important regulatory genes. A dominant mutant has been obtained that is defective in phototropism. The polycotyledon mutant of tomato has been related to enhanced-polar auxin transport. Several mutants have been isolated that display delay in fruit ripening in tomato. The genetic regulation of root development in tomato is examined using isolated short root mutant, profuse branching root mutant and lateral root less mutant.

*Photomorphogenesis in tomato:* At NCPGR working is carried on the cloning of *ZBF1* gene from tomato. It is followed by raising transgenic tomato plants overexpressing *ZBF1* gene to analyze the role of light in regulation of tomato development

### **Potential Contribution of India to the Tomato Sequencing Project**

India would contribute to SOL in three specific area using tomato as a model system.

1. Sequencing of a part of tomato genome
2. Saturation mutagenesis of tomato using TILLING and T-DNA insertional mutagenesis.
3. Functional genomics of tomato for fruit ripening, improvement of fruit quality and disease resistance in tomato

### **Deadlines For Submission**

The Dept of Biotechnology (DBT) is the major funding body for supporting research in area related to SOL. It has invited proposals for funding in the areas related to SOL for tomato genome sequencing, functional genomics and high throughput reverse genetics (TILLING and insertional mutagenesis) by the end of August 2004.

## ISRAEL

### Centers of *Solanaceae* research in Israel

#### Research Institutions

Agricultural Research Organization (ARO), The Volcani Center  
MIGAL Research Institute  
The Weizmann Institute of Science  
The Technion Israel Institute of Technology

#### Universities

Tel Aviv University  
The Hebrew University of Jerusalem  
Ben-Gurion University of the Negev

### Sources of Support

The research is supported in part by national foundations (Ministry of Science, Ministry of Agriculture, Israeli Science Foundation) and by bi-national foundations (BARD, GIF, DIP, BSF).

### Major tools of Research

1. *Introduction of exotic germ plasm, marker assisted breeding and cloning of important agronomical traits as well as analysis of synteny.* This research, which focuses on tomato and pepper, is performed at the ARO, the Hebrew University and the Weizmann Institute of Science.
2. *Development of EMS, Fast Neutron Ds transposon insertion population in tomato.* This research is performed at the ARO, the Hebrew University and the Weizmann Institute of Science.
3. *Development and implementation of genetic and genomics platforms.* This research is performed at most institutes and universities.
4. *Development and implementation of trans-activation system in Tomato and tobacco.* This research is performed at the Weizmann Institute (Yuval Eshed).

### Major areas of biological interest

- a. *Molecular biology and metabolism of fruits.* This research is performed on the model plant tobacco as well as on tomato and pepper. The studies include isolation and analysis of promoters and genes expressed in early stages of fruit development, identification of genes, regulatory elements and enzymes that modulate various traits such as sugars, amino acids, secondary metabolism (vitamins, flavonoids, carotenoids, aroma), hormones, cuticle development, fruit size and shape, pungency, color, fragrance, aroma, texture, amino acids. There is great emphasis in the research on the carotenoids biosynthesis pathway where a number of the key genes were isolated and characterized.

Major centers for this research include the ARO, MIGAL Research Institute and The Weizmann Institute of Science and the Hebrew University of Jerusalem.

b. *Biotic and abiotic stresses.* The research on plant pathogen interactions includes pathogen stresses as well as salt draught stresses. Methodologies include identification of genes associated with disease-resistance, signal transduction of stress responses including reactive oxygen species response, genes and networks controlling stress responses in relation to growth and development. Breeding programs, including development of molecular markers, includes tomatoes for resistance to TYLCV resistance, pepper for resistance to TMV, CMV, TSWV and powdery mildew, root knot nematodes. The research on abiotic stresses includes the role of small heat shock proteins in the protection against extreme temperature stresses (tomato), the genetics of water loss and drought stress (tomato and pepper) and the functions of aquaporins in draught and salt stresses (tomato). Major centers for this research include the ARO, The Weizmann Institute of Science, the Hebrew University of Jerusalem and Ben-Gurion University.

c. *Control of plant physiology and development.* This research includes phloem genomics, as well as molecular, genetic and genomics studies on the role and function of specific xanthophylls in photosynthesis, organ morphogenesis, leaf polarity, polar morphology, lateral expansion of plant organs, the control of the transition from vegetative growth to flowering, flowering time as well as flower and fruit development, is studied using genetic and molecular tools, such as mutant analysis, and identification of important genes. Expression patterns and functions of crucial genes are characterized. In addition, circadian clock and its relation to flowering time are studied. Mutant analysis, genetic mapping and molecular analysis is used to study the genetics of development in tomato, in particular meristem function, plant architecture and leaf shape. GA signal transduction and response are studied in petunia. Major centers for this research include the Weizmann Institute of Science, the Hebrew University of Jerusalem and the Technion Institute of Technology, Haifa.

## Resources

1. cDNA libraries of tomato flower and young fruit, subtracted cDNA from parthenocarpic fruit. cDNA library of pepper fruit, genomic library of *L. hirsutum*. Pepper mapping populations: *C. frutescens* introgression lines (under construction), *C. chinense* introgression lines (some chromosomes), F2 intra-specific *C. annuum*, BC2 inter-specific *C. annuum* x *C. frutescens* (The ARO).
2. -EMS population: ~1000 families in Micro-Tom.
  - Insertion lines with a Ds transposon: ~3000 lines out of which only 800 were recently propagated, the rest of the seeds is ~8 years old. (Avi Levy, The Weizmann Institute).
  - 6000 EMS and 8000 Fast Neutron mutants in the variety M82 (The Hebrew University - 'The genes that make tomatoes' a saturated phenotypic database <http://zamir.sgn.cornell.edu/mutants/>). Seventy six *L. pennellii* introgression lines in M82 are distributed by the Tomato Genetics Resource Center in Davis, CA. <<http://tgrc.ucdavis.edu/>>

## ITALY

### Centers of *Solanaceae* research in Italy

#### Research Institutions

National Agency for New technologies, Energy and the Environment (ENEA),  
Biotechnology Unit (Rome, Matera)  
National Research Council (CNR), Institute of Plant Genetics (Naples, Bari)  
Stazione Zoologica (SZN), Naples

#### Universities

University of Viterbo  
University of Naples  
University of Bari  
University of Siena  
University of Florence

#### Companies

Metapontum Agrobios  
Farmen SnC  
Biogen Srl

#### Sources of Support

The research is supported by the Italian Ministry of Research and the Italian Ministry of Agriculture.

#### Major topics of Research

*EST sequencing and re-sequencing.* This is mainly performed at ENEA and by a group coordinated by C. Bowler. The goal is to re-, within June 2004, 12.000 Cornell ESTs.

*Transcriptional profiling* Several groups are using arrays bought from TIGR (potato, Univ. of Naples) and Cornell (tomato, ENEA/ CNR Naples/ SZN). SZN has developed a “boutique” macroarray and ENEA a “boutique” microarray, comprising mainly genes for light signal transduction/carotenoid biosynthesis. Several groups are using differential display and cDNA-AFLP as profiling tools.

*Mutant isolation/characterization:* The group of G.P. Soressi (Univ. of Viterbo) has a large collection of mutants for fruit colour/quality and plant architecture.

*Virus-induced gene silencing* It is being used at ENEA as a functional genomics tool (M. Tavazza/ G. Giuliano) using PVX and blue light photoreceptors. Constructs are now being developed in TRV.

*Bioinformatics:* Tomato promoter analysis using bioinformatic tools is being developed at the University of Florence (M. Buiatti).



## **Major areas of biological interest are**

*Carotenoid biosynthesis/fruit quality in tomato.* Transcriptional regulation/metabolic engineering studies are conducted at ENEA (C. Rosati/G. Giuliano). Some metabolic engineering is also conducted at Metapontum Agrobios (F. Cellini). QTLs for fruit carotenoid content are being mapped in Naples (S. Grandillo/L. Monti). A large mutant collection is available at the University of Viterbo (A. Mazzucato-G.P. Soressi)

*Photomorphogenesis in tomato.* The group of C. Bowler (Stazione Zoologica di Napoli) focuses mainly on phytochrome signal transduction, while the ENEA group (G. Perrotta/G. Giuliano) focuses mainly on cryptochromes.

*Biotic and abiotic stress.* Main stresses under study comprise fungi (oidium), for which a monogenic recessive resistance has been mapped at the University of Bari (L. Ricciardi); viruses (TYLC, CMV) for which transgenic resistant lines have been developed at ENEA (M. Tavazza) and Metapontum Agrobios (F. Cellini); insects, for which genetic engineering is ongoing at the University of Naples (L. Monti); salinity/drought, for which mutant studies/transcriptional profiling are ongoing at Naples (S. Grillo/L. Monti) and ENEA Trisaia (A. Maggio); cold and soft rot in potato, for which interspecific hybridization is ongoing at the University of Naples (L. Frusciante).

*Profiling of local ecotypes.* This is being performed using a combination of traditional (biochemical and sensory profiling) and molecular techniques (transcriptional profiling, development of molecular markers) at several institutes, including CNR, ENEA and SZN.

*Reproductive biology.* The main centers are at the University of Siena (M. Cresti, biology of pollen), University of Viterbo (G.P. Soressi/A. Mazzucato, parthenocarpy), and University of Naples (L. Frusciante, meiotic mutants in potato).

## **Potential Contribution of Italy to the Tomato Sequencing Project**

Although it is unclear, at the present moment, if Italy will contribute to the genomic sequencing effort, plans are being put in place for applying for funds for the sequencing of the euchromatic portion of a chromosome (approx 20 Mb). The actual sequencing would be performed at the University of Padua and at ENEA.

## **Deadlines For Submission**

A first deadline will be at the end of 2003/beginning of 2004, with further deadlines in 2004.

## **JAPAN**

### **Places of Solanaceae research in Japan**

#### **Research Institutions**

Kazusa DNA Research Institute, Chiba  
National Institute of Vegetable and Tea Science (NIVTS), Mie  
Chiba Prefectural Agriculture Research Center, Chiba  
National Institute of Genetics, Mishima  
RIKEN, Yokohama

#### **Universities**

Tsukuba University  
University of Tokyo  
Tohoku University  
Hokkaido University  
Tokyo University of Agriculture and Technology  
Nagoya University

#### **Companies in Japan with commercial interests in Solanaceae**

Sakata Seed Corporation  
TAKII & Co., LTD.  
SUNTRY Ltd.  
KAGOME CO.,Ltd.  
Nippon Del Monte Corporation

#### **Sources of Support**

In Japan, research is supported by grants from Ministry of Education, Culture, Sports, Science and Technology (MEXT)\_the Japan Society for the Promotion of Science (JSPS)\_Ministry of Agriculture, Forestry and Fisheries (MAFF) and The New Energy and Industrial Technology Development Organization (NEDO). Unlike other institutions, Kazusa DNA Research Institute is supported by the grant from the Chiba local state government.

#### **Major Topics of Research**

\_ EST, full-length cDNA sequencing  
37,000 ESTs from 5' end of cDNA clones prepared from fruits and leaves of a dwarf tomato, MicroTom were sequenced. PCR products of independent 11,000 EST clones were spotted on Nylon filters for macroarray analysis.  
Full-length cDNA libraries of MicroTom are ordered.

- \_ Metabolomics
- \_ Disease resistance
- \_ Fruit development and ripening
- \_ Plant development and hormone biology
- \_ Tobacco BY2 cell biology
- \_ Eggplant breeding

### **Potential Contribution of Japan to the Tomato Sequencing Project**

We have not yet discussed about how we contribute to tomato genome sequencing itself. However, we will contribute an important part of the Tomato Sequencing Project, sequencing of tomato full-length cDNA clones, especially those specific to tomato. As shown in the full-length cDNA sequencing projects of Arabidopsis (RIKEN, Seki et al., *Science* 296: 141-145, 2002) and rice (MAFF, Kikuchi et al., *Science* 30: 376-379, 2003), to which Japanese research groups have contributed substantially, full-length cDNA sequence information is crucial to determine the transcribed and spliced sequences from the genome nucleotide sequences, especially those of previously unknown genes. We plan to sequence at least 1,000 full-length clones within one year. If we have a grant of full-length cDNA sequencing, we will increase the number of clones accordingly.

## KOREA

### Centers of *Solanaceae* Research in Korea

#### Research Institutions

Korea Research Institute of Bioscience and Biotechnology (KRIBB), Taejon  
National Institute of Agricultural Biotechnology (NIAB), Suwon  
National Horticultural Research Institute (NHRI), Suwon  
National Alpine Agricultural Experiment Station, Pyungchang

#### Universities

Seoul National University, Seoul  
Korea University, Seoul  
Kyungbook National University, Taegu  
Chungbook National University, Cheongjoo  
Kangwon National University, Chuncheon

#### Breeding Companies

Nongwoo Bio. Co., Yeujoo  
Heungnong Seed Co. (Seminis Inc.), Seoul  
Joongang Seed Co. (Seminis Inc.), Seoul  
more than 10 small seed companies are selling pepper and tomato seeds.

#### Sources of Support

The research could be supported by CFGC (Crop Functional Genomics Research Center, a 21st Frontier Research Program of Ministry of Science and Technology), Biogreen 21 program of Rural Development Administration and by institutional resources of each institute. Individual grants are also from KOSEF (Korea Science and Engineering Foundation).

#### Major Topics of Research

- *Molecular mapping and BAC library construction for pepper genome.* This research is performed in CPMGBR (Center for Plant Molecular Genetics and Breeding, funded by KOSEF) in Seoul National University (Dr. B.D. Kim) and focused on pepper. The research areas include molecular cloning of disease resistance and quality traits, pepper BAC library construction, development of various plant transformation vectors and detection of QTLs for agronomically important traits.
- *EST, Microarray and construction of platforms for functional genomics of pepper.* This occurs in particular at the Plant Genomics Lab. of KRIBB (Dr. D. Choi). The research topics include generation of pepper EST (currently around 30,000 EST), development of microarray using generated EST, development of bioinformatics tools and pepper expression profile DB. This project is currently funded by CFGC (Crop Functional Genomics Research Center) and PDRC (Plant Diversity Research Center) both are 21st century frontier research programs of ministry of science and technology.

#### Major areas of biological interest are

- *Plant-microbe interactions.* Four major labs in Korea are focused in this research. Functional genomics of pepper transcription factors which responded to pathogen is

performed using microarray, over-expression in model plants and VIGS techniques (Dr. D. Choi in KRIBB). Molecular mapping and cloning of hot pepper resistant locus for *Xanthomonas campestris* pv. *vesicatoria* and *Phytophthora capsici* are performed using molecular genetics approach (Dr. B.D. Kim in Seoul National University). Characterization of genes involved in systemic acquired resistance of pepper and studies on signaling network of disease resistant are also performed (Dr. K.H. Paek and Dr. B.K. Hwang in Korea University). Marker assisted selection for breeding of pepper multiple disease resistance are also performed (Dr. H.K. Park in Seoul National University). Development of multiple disease resistant pepper root stocks is performed using classical breeding techniques (Dr. B.S. Kim in Kyungpuk National University).

- *Functional genomics using VIGS*. Virus-induced gene silencing is a powerful tool for studying functions of a number of genes. VIGS of selected *Nicotiana benthamiana* genes for plant development and signaling is performed by Dr. H.S. Pai in KRIBB.
- *Metabolic engineering*. Generation of small scale EST and metabolic engineering of potato for lignans production are performed by Dr. J.H. Jeon in KRIBB.
- *Abiotic stress*. Functional characterizations of pepper genes involved in environmental stresses and studies on functional genomics of osmosensors in pepper are performed by funding from CFGC (Drs. C.B. Hong and Y.N. Hong in Seoul National University). Signal transduction studies on cold stressed pepper using cDNA microarray are also performed (Dr. H.B. Kwon in Sunmoon University).
- *Transformation technology development*. Pepper has extremely low frequency of transformation using currently available techniques. There are two government-funded research projects are performed by private company (Dr. C.H. Harn in Nongwoobio Co. and Dr. Y.S. Kim at Kumho Co.)

### **Potential Contribution of Korea to the Tomato Sequencing Project**

As shown in this write-up, *Solanaceae* genomics researches in Korea are mainly focused on hot pepper plant. Even though *Solanaceous* plants are important crops in Korea (2.2 billion US\$ per year), tomato is a minor crop among them. Subsequently, there is no research project on tomato genomics in Korea at this moment. Research scientists in *Solanaceae* genomics area could agree with the importance of tomato genome sequencing as a reference genome of *Solanaceae* plants but we still have long way to persuade the funding agency and plant research community in Korea.

Following is the potential contribution of Korea to the Solanaceae Genome Initiatives program in conditions of separate funding is available from our government:

- Participate in sequencing of one tomato chromosome (hopely chromosome No. 2 and up to 20 Mb).
- Parallel sequencing of portion of pepper chromosome (linkage group No. 2)
- Shotgun sequencing of euchromatin region of pepper chromosome (up to 50,000 random sequences for two years term).
- Extending of pepper EST to 100,000 (currently we have about 30,000 EST from 8 different cDNA libraries) using more dissected cDNA libraries.

In best case, we can perform all of above. However, in worst case, we may only perform shotgun sequencing of euchromatin region of pepper chromosome and ESTs.

### **Deadlines for Submission of Grants Proposal**

There are two possible funding sources in Korea for this project. One is BioGreen21 Program operated by Korean Rural Development Administration (RDA) and the deadline for the submission of grant proposal is February 2004. The other is Crop Functional Genomics Center (CFGC), the 21<sup>st</sup> century frontier research program operated by Ministry of Science and Technology (MOST) and the deadline for research proposal will be July 2004.

However, the framework and aims of the both programs have already been implemented and we need discuss about the importance of the Solanaceae genome initiatives with them before we submit our proposal.

## MÉXICO

### Highlights of Solanaceae Research in Mexico

The three most economically important Solanaceae crops for Mexico are Tomato, Potato and Chili Pepper. Most of the research is focused in Chili Pepper, mainly on breeding, tolerance to biotic and abiotic stress and secondary metabolism.

### Centers for Solanaceae Research in México

Research Institutes

Cinvestav – Unidad Irapuato

Colegio de Posgraduados

Instituto Politécnico Nacional (IPN)

Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP)

### Universities

UNAM

UACH

### Sources of Support

CONACYT

### Potential Contributions of Mexico to the SOL project

Capsicum sp. EST libraries

Physalis sp. EST libraries

Lycopersicon BAC sequencing

### NOTES

A search on ISI web of Science (<http://isi1.isiknowledge.com/>) for references related with Solanaceae and including at least one author with address in Mexico but excluding New Mexico [TS=(Solanaceae OR Tomato OR Lycopersicom OR Potato OR Solanum OR Pepper OR Capsicum) AND AD=(Mexico) NOT AD=(New)] results into 376 references.

The following table presents the number of references per Research Center or University (found in the “Author Address” field of the reference).

Number of Solanaceae references per research center		
Number	Research Center or University	
70	Cinvestav UI	Ctr Invest & Estudios Avanzados, Unidad Irapuato
31	UNAM	Univ Nacl Autonoma Mexico
28	CP	Colegio Postgrad
24	IPN	Inst Politecn Nacl
17	INIFAP	Inst Nacl Invest Forestales Agrícolas & Pecuarias
16	UAC	Univ Autonoma Chapingo
13	CIBN	Ctr Invest Biol Noroeste

10	UAQ	Univ Autonoma Queretaro
9	UACH	Univ Autonoma Chihuahua
8	UANL	UNIV AUTONOMA NUEVO LEON
8	UV	UNIV VERACRUZ
8	UAM	Univ Autonoma Metropolitana
8	UG	Univ Guanajuato
7	UM	UNIV MICHOACANA
6	IMSS	Inst Mexicano Seguro Social
5	ITC	Inst Tecnol Celaya
5	UAAAN	Univ Autonoma Agr Antonio Narro
4	UAC	Univ Autonoma Coahuila
4	CICY	CTR INVEST CIENT YUCATAN
4	UASLP	Univ Autonoma San Luis Potosí
3	UAY	Univ Autonoma Yucatan
3	CFS	Colegio Frontera Sur
2	UAG	Univ Autonoma Guadalajara
2	UAA	Univ Autonoma Aguascalientes



## PALESTINE

### **Research Centres in Palestinian Territories:**

#### **\* Universities:**

- (1) Hebron University.
- (2) An-Najah University.
- (3) Al-Quds University.
- (4) Ber Zeit University.
- (5) Bethlehem University

#### **Research centres**

BETCEN (Bethlehem University) and NARC (National Agricultural Research Centre)

#### **Sources of Support:**

Funds depend totally on international grants such as USAID-MERC, DFG-Germany.

#### **Major Research Interest areas:**

The following are the main research interest areas related to the Solanaceae Family:

- (1) Conservation of the local Solanaceae species (Dr. Ayed Mohammad, Hebron University).
- (2) Ongoing research at Hebron University about the identification and mapping genes that confer tolerance to drought and salt stress in tomato in terms of fruit yield, in order to develop cultivars for production under marginal conditions of water availability and salinity. These tolerance characters are polygenic and are derived from wild tomato species where the objective is to fine map the QTLs and to identify candidate genes (Dr. Ayed Mohammad, Dr. Bilal Ghareeb, Molecular Biology, Hebron University).
- (3) Proper cultural practices for tomato, eggplant, pepper, and potato (planting dates, density, fertilization, irrigation etc.).
- (4) Traditional techniques of sun-drying tomatoes at an industrial level. This represents a good example of how traditions can be resuscitated to meet our current consumption tendencies and at the same time the economical needs of our farmers.
- (5) Biological control of diseases, weeds and insect pests of tomato, eggplant, pepper, and potato (Dr. Radwan Barakat, Dr. Abdul- Jaleel Hamdan, Hebron University).
- (6) Suppression of soil borne diseases of tomatoes (Hebron University).
- (7) Disease resistance. An example on this topic can be cited from a current research work that is being conducted at Bethlehem University on TYLCV. Few approaches are being tried to confer resistance for this virus to tomato cultivars including transgenesis (Dr. Na'em Iraqi).

## PERU

The situation of the Andes as the space for evolution of several genera and species of Solanaceae should be considered. In addition to Peru, Ecuador and Colombia might be included as participating countries to represent Andean diversity (and developing countries). These countries' national programs conduct conservation, evaluation and breeding research on Andean fruits (tree tomato, *S. quitoense*).

### Peru/CIP- Potato

1. Germplasm: extensive ex-situ genebank of wild and cultivated potato species held and researched in trust at CIP under FAO auspices.
2. References: Potatoes of Peru, Ochoa; Potatoes of Bolivia, Ochoa- both books fully illustrated with habitats and suggestions for use of the gene pools
3. Institutions: Univ. Nacional Agraria (La Molina); Univ. Nacional (Cuzco)- hybrid populations and scientific capacity and genetic resources for crop improvement, but scarce economic resources

### Peru- Tomato

1. Germplasm: 6 wild species are native; no *ex situ* genebanks are supported (desperately needed for building national capacity and for global research).
2. Institutions: No breeding/scientific program of any kind; only about two people in Peru would agree that they dedicated part time (20%) work to this group.
3. Status: The collection and documentation has finished the exploration phase. The challenge is to find the biological, logistical, and utilitarian reasons to continue collection/evaluation. Rick's thesis of potentials from ecological observations used by E. Vallejos, in finding chilling injury "genes" in *Lycopersicon hirsutum* close to 3,000 msnm is a proper model.
4. Opportunities: promote field-work especially for systematic collection, conservation, evaluation and use. E.g. *L. parviflorum*- 3500 m. resistance to cold temperatures and insects; *L. pimpinellifolium*; *cercaeifolium* - direct exploitation for market and home use; use in breeding. Experienced individuals can help by reducing the chances of reinventing the wheel, providing complementary information that may be usefully integrated into current data bases (e.g. the correct spelling of collection sites). "Gray literature" papers should also be scanned for info.

### Andean countries: Solanaceae fruits

Ecuador and Colombia's national programs conduct conservation, evaluation and breeding research on Andean fruits (tree tomato, *S. quitoense*).

### CIP Research Interests:

1. Phenotypic, histological (cell level) and eventually genetic description of the Phytophthora - Solanum interaction via a systems approach - i.e., comparing pathogenicity and adaptation of the pathogen to diverse hosts, infection/resistance process, and virulence across host genera.
2. Functional characterization of allele series for host-pathogen interaction: viruses and fungi that affect multiple Sols.

## Overview of CIP Activities in Genomics

A) CIP is currently applying sequence- expression-based strategies to characterize genes and regulatory systems related to disease resistance and carbohydrate metabolism in potato and sweetpotato, through a combination of in-house and collaborative arrangements. Gene function-based strategies are being explored and anticipated to be of much utility in the near future.

1. *Consensus and functional maps of disease resistance in potato* (late blight) (Collaborative with CU, CIAT, CRP-CU, UCB, UW, MPI)
  - a. Construction of candidate gene collection and sequence databases for hypothesis testing from comparative biology (resistance and defense; heterologous source).
  - b. Comparative QTL analysis, candidate gene mapping and cladistic analysis of resistance trait architecture (Solanaceae).
  - c. Association genetics in genebank accessions and bred stocks
  - d. Expression profiling (cDNA-AFLP) and function assignment toward identification of candidate genes for general resistance/defense.
  - e. BAC library Construction from CIP-bred source of general resistance for characterization of clustered gene families (R genes, osmotin) and applications of structural genomics to gene discovery
2. *Search, visualization and analytical tools for applications of comparative biology to primary traits of potato and sweetpotato* (Collaborative with NCGR; CGIAR; CU)
  - a. Participation in design of a comparative genomic map viewer on the basis of ISYS.
  - b. Upgrading of potato genetic maps with function and position-based tomato-Arabidopsis COS (EST).
  - c. Development of software prototype to visualize genomic maps and overlay marker, genes/ESTs, similarities, and QTLs to produce customizable graphics with hyperlink functionality.
  - d. Establishment of web-site to manage in-house bioinformatics databases, software and documentation based on open source and free technology, providing interfaces to Perl and Java and running under Windows or Linux/Unix.
3. *Gene discovery and diversity analysis for starch and sugar metabolism in sweetpotato and potato* (Collaborative with AAFC, NCSU and ARCS)
  - a. Development of ESTs from storage and fibrous root core libraries
  - b. Expression profiling and function assignment toward identification of candidate genes for root bulking and starch synthesis.
  - c. Trans-species phylogeny and clustering of starch gene sequences/organization
  - d. Assessment of diversity and discovery of superior alleles in germplasm by SNP
  - e. Development of allele-specific detection systems (SNP)
  - f. Mapping and QTL analysis with candidate genes for carbohydrate metabolism and storage root development
  - g. Diversity assessment and candidate gene expression in post harvest challenged native Andean potatoes resistant to cold sweetening
4. *Assembly of candidate gene collection and genomic tools to characterize stress response in colored Andean potatoes* (Collaborative with VTI, USDA/ARS)
  - a. Biochemical, phenotypic and GxE analyses of Andean potato varieties for nutraceutical production and stress response
  - b. Amplification, purification and full-length sequencing of candidate potato ESTs for stress tolerance, pigment and nutrient production, for construction of a “stress chip” microarray.
  - c. Expression profiling (microarray) under stress challenges and integrated databases for phenotype, sequence, expression and mapping data concerning stress response in Andean potato.
  - d. Characterization of diversity for micronutrient contents (Fe, Zn, vitamins, etc.); GxE and

genetics for use

**B) Expected Outputs:**

A Consortium or Challenge Program on Root and Tuber Crop Genomics or Solanaceae Genomics would greatly enhance rates and achievements in the improvement of mandate species. The availability of improved varieties better suited to local needs and requiring fewer external inputs, will improve opportunities for the poor through higher availability of diversity, contributing to poverty alleviation and protection of the environment. The following practical outputs relevant to the goals and objectives of the CGIAR are envisioned.

- a. Significant, rapid amplification of the available genetic resource base for crop improvement through access to a wider range of genetic information, leading to improved opportunities for breeding and variety development.
- b. More basic and practical precise knowledge about genetic structures of important traits across taxa, and tools to orient and facilitate breeding, especially of complex and lesser-known species.
- c. Minimal duplication of public and private research efforts and accelerated progress through crop, disciplinary and institutional synergies.
- d. Databases, molecular and software tools and new varieties in the public domain, important vehicles for transfer the benefits of science research, conservation and improvement efforts to resource poor farmers.

**Potential contribution to the tomato sequencing project:**

The major support would consist of logistical and research orientation for *in situ* experimentation and interdisciplinary collaboration toward the discovery of adaptive genes/allele series within and across genera;

Can contribute well-characterized germplasm collections (potato); herbaria (web-accessible), and possible regional coordination of research of specific topics –e.g. Phytophthora-Solanum interactions

Full program to use genomic information and tools in breeding (potato; other species.); Education, technology transfer/outreach program in crop and social science related to agricultural development, environment and health.

Consortium member of Challenge Program “Unlocking Genetic Diversity in Crops for the Resource Poor” (Director R. Zeigler) and “HarvestPlus” (Biofortification of staple crops; Director Howie Bouis)

Facilities, logistics for international exchange of germplasm; alliance with competent authorities at national and regional levels (global).

**Deadlines for submission of Genomics proposals.**

The Challenge Program “Unlocking Genetic Diversity in Crops for the Resource Poor” will call for competitive proposals for applications of comparative biology in early 2004. Case study: abiotic stress; alternative topics: resistance; partitioning; nutrition; quality.

## POLAND

### Centers of *Solanaceae* Research in Poland

#### Universities

Agricultural University of Krakow, Department of Genetics, Plant Breeding and Seed Science (AUK)

Warsaw Agricultural University, Department of Plant Genetics, Breeding and Biotechnology (WAU)

#### Research Institutes

Plant Breeding and Acclimatization Institute, Młochów Research Center (IHAR)

Research Institute of Vegetable Crops; Department of Genetics, Breeding and Biotechnology (IWarz)

#### Companies

PNOS Ożarów, Polan, Spójnia Nochowo, Legutko, PHRO Krzeszowice, PlantiCo Zielonki  
PlantiCo Gołębiew

#### Major sources of support

Ministry of Agriculture and Rural Development, Poland

The State Committee for Scientific Research, Poland

#### Major topics of research

##### AUK

- Use of SCAR markers for the genes *Mi* and *Sw-5* against nematodes and *Tomato spotted wilt virus* (TSWV) in tomato, respectively
- Identification of DNA markers linked to the gene *Ve* for resistance to various strains of *Verticillium dahliae* in tomato

##### WAU

- Interspecific crosses of tomato and pepper germplasms
- Transformation and cell culture systems for genetic research of tomato and pepper.
- Functional genomic analysis of tomato using reverse genetics
- Tomato and pepper genome improvement for practice breeding
- Development of novel tools/methods for tomato and pepper improvement useful for practice breeding
- The research on resistance to nematode in tomato and against TSWV in tomato and pepper
- A male sterility systems in pepper
- Application of expression profiling and RNAi technology to obtain pest/pathogen resistant tomatoes

##### IHAR

- Mapping of resistance genes and quantitative trait loci against disease pathogens in potato: *Phytophthora infestans*, *Erwinia* ssp., *Potato virus S*, *Potato virus Y*, *Potato virus M*, *Potato leafroll virus*
- Detection of PCR-based markers of disease resistance useful for marker-assisted

- selection in potato
- Detection of DNA markers for the loci *Ph-1* and *Ph-2* to speed up selection of tomatoes with increased resistance to *P. infestans*

IHAR's research is performed in collaboration with Max-Planck Institute for Plant Breeding Research, Cologne, Germany and Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Warsaw, Poland.

## **IWarz**

- Breeding of tomato lines, F<sub>1</sub> hybrids and cultivars with high yielding ability and superior appearance and quality
- The research on resistance to *Tomato mosaic virus*, *Fusarium oxysporum* f.sp. *lycopersici*, *Verticillium albo-atrum*, *Fusarium oxysporum* f.sp. *radicis-lycopersici*, *Cladosporium fulvum*, *Pseudomonas syringae* pv. *tomato*. The program currently emphasizes the identification of new genes for disease resistance and their incorporation into advanced breeding lines
- Detection of DNA markers for disease resistance selection (*Fusarium oxysporum* f.sp. *lycopersici*, *Pseudomonas syringae* pv. *tomato*), male sterility (*ps*, *ps-2*) and variety purity

## SPAIN

### Centers of *Solanaceae* research in Spain

#### Research Institutions

Centro Nacional de Biotecnología (CNB), Madrid  
Centro de Edafología y Biología Aplicada del Segura (CEBAS), Murcia  
Estación Experimental La Mayora (EELM), Málaga  
Estación Experimental del Zaidín (EEZ), Granada  
Instituto de Biología Molecular y Celular de Plantas (IBMCP), Valencia  
Servicio de Investigación Agroalimentaria, Zaragoza

#### Universities

Universidad de Almería  
Universidad de Barcelona  
Universidad de Málaga  
Universidad Politécnica de Cartagena  
Universidad Politécnica de Valencia

#### Breeding Companies

Spain has strong seed and production breeding companies. They are mostly located in Almería and Murcia.

#### Sources of Support

The research is supported by the Ministry of Science and Technology (MCYT), by Genome Spain (Dependent of the MCYT and Ministry of Health), by the Instituto Nacional de Investigaciones Agrarias (INIA, MCYT) and by regional governments.

#### Topics of Research

Due to the importance of production in Spain of several *Solanaceae* crops there are many topics covered. They are mainly based on small projects that are related to many biological aspects such as development, flowering, architecture, fruit formation and ripening, resistance to biotic and abiotic stresses, hormonal control of tuber formation, etc.

Recently, many labs have joined in the search for funds in order to generate genomic tools in *Solanaceae*. Tomato is one of the most important horticultural crops and Spain is the first producing and exporting country of tomato for fresh market. We pretend to develop genomic tools required for functional analysis of economically important genes. This proposal (GEnSOL) will support the following objectives: **(1)** Generation of cDNA libraries of complete transcripts (tomato), two hybrid system libraries (tomato), ESTs (tomato, pepper and potato) and DNA chips (tomato and pepper). **(2)** Gene expression profiles of tomato and pepper. **(3)** Set the conditions for proteomic analysis of tomato chromoplast. **(4)** Generation of tomato mutants by EMS mutagenesis. **(5)** Functional genomic analysis of tomato using genetic reverse techniques (VIGS, RNAi and TILLING (Targeting Induced Local Lesions In Genomes)). **(6)** Genetic analysis of natural variability of tomato and pepper.

The genomic tools developed in this project will be used for genome-wide analysis, mainly for functional characterization of genes expressed during fruit development, ripening and during responses of tomato plants to pathogen infection. Most importantly, this project represents the best way to collaborate in an international consortium (USA and European

groups) dedicated to the genomic analysis of tomato, the most economically important horticultural crop in our country.

### **Potential Contribution of Spain to the Tomato Sequencing Project**

At this time, the major opportunity to provide significant direct support to a Solanaceae sequencing in Spain comes from Genoma España and regional governments. For this purpose some members of the Spanish genome initiative will have a meeting with the persons responsible in Genoma España and legal representative of regional governments. Another potential contribution of Spain to a tomato sequencing program would be to provide support for follow-up activities to ensure effective use of the information contained in the genome sequence. Thus, there are several genomics projects in Solanaceae currently under review. GenSOL. As previously mentioned, has been submitted to the Spanish Initiative in Genomics and Proteomics (McyT).. A second Solanaceae genomic Project BAIInSOL is under review by the Genoma España – Genome Canada where Solanaceae 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.

### **Deadlines For Submission Of Genomics Submissions**

The possibility of submission of genomics proposal is closed as such. However the mission of Genoma España is to promote research in *genomics* and proteomics. Its aim is that Spain be an active partner in the search for new knowledge and the development of new applications. Because they look private investors and have autonomy as public investors there is not deadline as such.



## SWEDEN

### Places of *Solanaceae* Research in Sweden

#### *Research institutions and breeding companies*

Plant Science Sweden  
Svalöf Weibull AB

#### *Universities*

Umeå Plant Science Centre, Umeå University  
Swedish University of Agricultural Sciences at Alnarp, Skara, Uppsala and Umeå  
University of Skövde

### Sources of Support

Research is supported by the Swedish Research Council for Environment, Agricultural Sciences and Spatial Planning (FORMAS), and the Swedish Research Council (VR).

### Topics of Research

*Plant propagation and genetic transformation:* Research includes breeding of vegetative-propagated crops as well as potato transformation for different breeding purposes. Recent progress includes developing a high-starch potato cultivar, which has become the first genetically modified crop approved for commercial cultivation in Sweden.

*Pre- and postharvest physiology:* The research is focused on optimising production and growth conditions mainly for potato but also to some extent tomato. It also involves developing methods for quality selection in extensive breeding material, as well as methods for studying storage disease resistance. This is achieved by chemical analyses of nutritional value, the incidence of anti-nutritional substances and factors having influence on colour, texture, taste and storing capacity. The influence of different growth substances on pests and microorganisms causing storing rots is also studied.

*Development of potato cultivation.* This includes continuous development of the technology for traditional potato cultivation, such as preparation of soil, nutrition, water and weed control, as well as developing systems for ecological cultivation using environmentally friendly methods.

*Biotic and abiotic stress:* This research focuses on establishing the relation between the crop, pest and diseases as well disease resistance and the impact of environmental factors, such as frost and drought. Pathogens studied include Phytophthora, the potato cyst nematodes and the potato mop-top virus (PMTV).

*Genetic variation and pathogens of coffee,* focusing on genetic variation in coffee and its fungal pathogens.

Tobacco and potato are also used as model systems to study topics such as hormone interactions and metabolism.

## SWITZERLAND

### Centers of Solanaceae research in Switzerland

#### Universities

Institute of Plant Sciences, University of Bern  
Institute of Plant Sciences, University of Fribourg  
Institute of Biochemistry, University of Neuchâtel  
Institute of Plant Sciences, ETH Zürich

#### Agronomical Research Institute

RAC Changins

### Sources of support

Research is supported by Swiss National Science Foundation, European Union, and other sources

### Major topics of research

#### Plant development

This research is centered at the University of Bern and involves both tomato and petunia Plant-microbe interactions

Research on petunia-mycorrhiza interaction involves laboratories at the universities of Fribourg and ETH Zürich. Petunia-Phytophthora interactions are studied at the RAC Changins in collaboration with the University of Bern.

#### Plant-insect interactions

Research on the interactions between wild petunia species and insects, both pollinators and herbivores is carried out at the Universities of Bern and Neuchâtel.

### Major areas of biological interest

#### Petunia as a model system.

Research on petunia started in Bern in 2000. Collections of transposon insertion lines were developed that can be used for both forward and reverse genetics. In addition recombinant inbred lines between the two wild species *P. axillaris* and *P. integrifolia* with the high transposition line *P. hybrida* W138 were obtained. Most of this work was done at the Institute of Plant Sciences, University of Bern (C. Kuhlemeier).

#### Interactions between plants and other organisms

This work involves interactions between petunia and mycorrhizal fungi, with emphasis on developmental aspects (D. Reinhardt, Fribourg) and phosphate acquisition (M. Bucher, ETH Zürich), as well as Petunia and pollinators (hawkmoths, bees, hummingbirds: C. Kuhlemeier, Bern) and herbivores (beetles: C. Kuhlemeier, Bern; T. Turlings, Neuchâtel). In addition, interactions between potato and nematodes are being studied (P. Malnoë, Changins).

#### Transport processes and sink-source interactions.

Areas of interest are the uptake of phosphate (M. Bucher, ETH Zürich) and translocation of nitrogenous compounds (D. Rentsch, Bern).

### **Potential Contribution of Switzerland to the Tomato Sequencing Project**

At this time no immediate plans. However, Switzerland is working towards a Swiss national Plant genomics Platform headed by W. Gruissem (ETH Zürich) and F. Kessler (U. Neuchâtel), which could include solanaceae sequencing.

## THE NETHERLANDS

### Centres of Solanaceae research in The Netherlands

#### Universities:

Wageningen University  
University of Amsterdam  
University of Nijmegen

#### Research Institutes:

Plant Research International  
Agrotechnology and Food Innovations (formerly ATO)

#### Breeding companies:

Potato: Agrico Research BV, Averis Seeds BV, HZPC Holland BV, C. Meijer BV, Van Rijn BV  
Tomato: ENZA seeds, De Ruiter Seeds, Nickerson-Zwaan BV, Rijk Zwaan, SVS Holland BV, Syngenta Seeds BV

#### Potato processing industry:

AVEBE

#### Genomics company:

Keygene NV

The Centre for BioSystems Genomics (CBSG; [www.cbsg.nl](http://www.cbsg.nl) ) is the Netherlands network of plant genomics research. It links plant genomics research groups from Wageningen University, Utrecht University, University of Amsterdam and Catholic University of Nijmegen, the research institutes Plant Research International and Agrotechnology and Food Innovations, and the major Dutch agro-industrial parties in potato and tomato breeding and processing, in a scientific research programme with a strong market focus. The research has a strong focus on potato and tomato.

### Sources of support

The research is supported in part by the Ministry of Economic Affairs and Ministry of Agriculture, Nature and Food Quality, the Netherlands Organisation for Scientific Research (NWO), The Dutch Technology Foundation STW. The Centre for BioSystems Genomics that focuses on genomics research is financed by the Netherlands Genomics Initiative, which is also part of NWO. In addition there are bilateral grants between the knowledge institutes and industry sometimes in collaboration with STW.

### Topics of research

Biological research:

- **Plant-Pathogen Interaction:**

potato: Wageningen University and Plant Research International

tomato: Wageningen University, University of Amsterdam

- **Plant Quality:**

potato: Wageningen University

tomato: Wageningen University, Plant Research International, Agrotechnology and Food Innovations

- petunia: University of Amsterdam, University of Nijmegen
- **Plant Genome:**
  - potato: Wageningen University, Plant Research International, Keygene NV
  - tomato: Wageningen University, Plant Research International, Keygene NV

**Platforms:**

- Genetics resources:  
Centre for Genetic Resources, The Netherlands, Wageningen University, University of Nijmegen
- Mapping agronomics traits:  
Wageningen University, Plant Research International, Keygene NV
- Genome Sequencing:  
Greenomics, Plant Research International
- Micro-arrays, Proteomics and Metabolomics:  
Plant Research International

**The Netherlands contribution to the Solanaceae Genome Sequencing Initiative**

**Tomato:**

- CBSG funds research to integrate Keygene's genetic AFLP map of tomato and the physical map consisting of BAC clones build by Rod Wing's group.
- CBSG funds sequencing a tilling path of BAC clones forming the top of chromosome 6
- CBSG funds sequencing of BAC clones located on chromosome 6 in regions involved in resistance and quality traits.
- NWO and CBSG fund bioinformatics research focused on tomato.

**Potato:**

- CBSG funds sequencing of 200-250 BAC clones located in region of the genome accommodating loci involved in resistance and quality traits.
- The Dutch Technology Foundation, STW and EU Framework Programme 5 fund the construction of a physical BAC map of potato that is expected to be released in summer, 2004.
- A ultra high density map of potato (>10.000 markers) was constructed with amongst others EU funding, and this genetic map is being integrated with the physical map.
- NWO and CBSG fund bioinformatics research focused on potato.

**Deadlines for submission of genomics research project applications**

The Netherlands Genomics Initiative (NGI) started funding the Centre for BioSystems Genomics in 2003. The projects involved in Solanaceous genome research have started.

In parallel NGI and CBSG have formulated a proposal to sequence the potato genome and are searching for funding such a project by (inter)- national agencies.

Also grant proposals are formulated by the CBSG partners to raise additional funds for Solanaceae research. Granting agencies may be NWO, Ministries, Technology Foundation STW, EU and industry.

## TAIWAN

### Centers or Institutes of *Solanaceae* research in Taiwan

TW-SOL-tomato is an initial joint team of graduate institute of Plant Biology in Taiwan University, Asian Vegetable Research and Development Center (AVRDC) and Known-You seed Co. LTD to focus on tomato studies. TW-SOL will be broadened in the coming years with *Solanaceae* research scattered in Academia Sinica, governmental institutes, universities and companies.

### Sources of Support

Research is supported by Council of Agriculture (COA), National Science Council (NSC) and Asian Vegetable Research and Development Center (AVRDC).

### Major topics of research

As for systems approach to diversity and adaptation, Taiwan locates in both tropic and subtropic areas and has diverse environments and species. Tomato occasionally incurs poor growth and fruit setting under hot-dry or hot-wet season in the tropics and sub-tropics. Therefore, AVRDC (<http://www.avrdc.org/>) has been breeding and collecting unique and substantial tomato germplasm, especially of "heat-tolerance" and "multiple diseases resistance" over the past 30 years. The consequent research is related.

1. *Production of genetic resources and mapping.* The germplasm of disease resistance, heat tolerance and other major horticultural traits are continuously collected by breeding program. Mapping of targeted genes follows.
2. *Improvement of fruit setting and production under high temperature.* Along with many tropical diseases, high temperature is the major bottleneck impeding fruit setting and summer production. We will focus on mining and studying "heat-stable" resistant genes against diseases such as bacterial wilt, bacterial spot, *fusarium* wilt and those caused by root-knot nematodes, and several viruses based on heat-tolerant tomato lines.
3. *Functional genomic analysis in tomato under heat-tolerance* Profiling the regulation of gene expression by heat-shock treatment in tomato is studied, especially those of lycopene related genes, genes involving heat-shock protein synthesis and heat-stable *R* genes.
4. *Comparative analysis* The heat-tolerance related comparative studies within *Solanaceae* family are proceeding.

### Potential contribution of Taiwan to tomato sequencing project

Although Taiwan has finished sequencing rice chromosome 5, it is unlikely that funds are available in Taiwan to support tomato genome sequencing at this time. Nevertheless, any sequencing project related to heat-tolerant genotype and follow-up research activities will be strongly supported.

### Deadlines for submission of genomics proposals

Council of Agriculture (COA) now guarantees the funding of these projects for this year. The 10-year-run TW-SOL proposal in the international SOL project is under discussion in National Science Council (NSC) and Council of Agriculture (COA), though both have been supporting ongoing relevant research for years.

## TURKEY

### Centers of Solanaceae Research in Turkey

#### Research Institutions

Citrus and Greenhouse Research Institute-Antalya  
Aegean Agricultural Research Institute  
Blacksea Agricultural Research Institute

#### Universities

Çukurova University-Adana  
University of Trakya-Edirne  
University of Suleyman Demirel-Isparta  
Akdeniz University-Antalya  
University of Ankara-Ankara  
University of Gaziosmanpasa  
University of Harran-Urfa  
Mustafa Kemal University-Hatay (MKU)  
Ege University-Izmir (EGE)  
Uludag University-Bursa  
Yeditepe University-Istanbul  
Izmir Institute of Technology (YTE)-Izmir

### Sources of Support

Research is supported by grants from the State Planning Organization (DPT), National Science of Foundation of Turkey (TUBA), the Scientific and Technical Research Council of Turkey (TUBITAK), University Research Foundation and, to a limited extent, by the private sector.

### Main Topics of Research

- \*Germplasm screening and adaptation studies for tomato, pepper, eggplant and potato (by many research institute and universities)
- \*Development of genetic resources and mapping in tomato, pepper and eggplant (by İYTE)
- \*Analysis of eggplant genome and comparative mapping with other solanaceae species (By İYTE)
- \*Determination of genetic diversity in eggplant and its wild relatives (by İYTE)
- \*Genetic control of biotic stress tolerance including viral, fungal, bacterial, nematode and insect resistance in tomato, pepper and eggplant (by MKU, İYTE, YEDİTEPE, EGE)
- \*Genetic control of abiotic stress tolerance including drought and salinity in eggplant and tomato (by İYTE, EGE)
- \*Analysis of secondary metabolites in eggplant (by İYTE)
- \*Analysis of antioxidant content in pepper, tomato, eggplant (by İYTE)

### Potential Contribution of Turkey to the Tomato Sequencing Project

National funds are not available for large scale sequencing projects in Turkey. However, it may be possible to obtain national or international grants for a smaller project targeted at eggplant. Eggplant is one of the most important vegetable crops in Turkey which ranks third in worldwide production. This project will focus on refining RFLP based molecular genetic linkage map by the addition of AFLPs, ESTs and microsatellite markers mapped in tomato.

In addition, methyl filtered BACs will be sequenced to determine synteny between eggplant and tomato genomes.

**Datelines for Submissions**

An EU and national support for eggplant genome project will be pursued in 2004.



## UNITED KINGDOM

### Places of *Solanaceae* research in UK

#### Research Institutions

Horticulture Research International	(HRI)
John Innes Centre	(JIC)
Kew	
Natural History Museum	(NHM)
Sainsbury Laboratory	(SL)
Scottish Crops Research Institute	(SCRI)

#### Universities

Many independent groups in various institutions (see list below)

Aberystwyth  
Bangor  
Glasgow  
Lancaster  
London  
Nottingham  
Oxford  
UEA  
Sheffield  
Southampton  
York

#### Companies in the UK with commercial interests in *Solanaceae*

ATC  
Unilever  
Syngenta

#### *Industry related organisations*

The British Tomato Growers Association  
British Potato Council

#### Sources of Support

In England and Wales research is mainly supported either by Biotechnology and Biological Sciences Research Council (BBSRC) or Department for Environment, Food and Rural Affairs (defra). Horticultural Development Council (HDC), fund development of near market research for UK horticulture. In Scotland the Scottish Office fund research via Scottish Executive Environment and Rural Affairs Department (SEERAD).

#### Topics of Research

- *Disease resistance and VIGS technology*
- *Fruit development and ripening*
- *Plant development and hormone biology*

- *Taxonomy and comparative genomics*
- *Key independent research areas*

### **Disease resistance and VIGS technology**

The UK is world leading in Solanaceous research in disease resistance and has many pioneering laboratories working on Virus Induced Gene Silencing. Groups working in these areas are focused in the JIC and SL research institutions with many other important laboratories present in other research institutes and universities.

#### *Fruit development and ripening*

Historically work on fruit ripening using tomato has been of central importance in UK's Solanaceae research community. Much of the initial work in this area has been focused at Nottingham University, which continues to be a centre of excellence along with other significant groupings including those at Warwick-HRI, those in London and those in industry.

#### *Plant development and hormone biology*

There are many UK based research groups taking advantage of the unique features of Solanaceous sp in studying plant growth and development. This includes both study of meristems, leaf development and hormonal control of plant development. There are many world class groups working in this research at UK institutions and universities.

#### *Taxonomy and comparative genomics*

Of fundamental importance in obtaining the tomato genome sequences will be to utilise this knowledge in comparative genomics. This will be extremely useful to those working in the world-class centres at Kew and NHM on taxonomy and to other researchers studying comparative genomics.

#### *Key independent research areas*

One of UK's strengths in Solanaceous research are the numerous groups working on specific unique features of solanaceous sp. This is highlighted in the numerous research groups shown below. Of those research areas not already highlighted are those focusing on metabolomics and those working towards enhancing the production of key metabolites with potential health benefits.

### **Potential Contribution of UK to the Tomato Sequencing Project**

Current discussions with BBSRC and defra are encouraging with the UK aiming to sequence ~25Mb of the gene rich regions of Chr4. We also intend to annotate this sequence and generate a mirrored portal for web based access to this data.

### **Deadlines For Submission Of Genomics Submissions**

BBSRC next deadline is January 19 2004.

## UNITED STATES

### Centers of *Solanaceae* research in the US

#### Research Institutions

USDA-ARS, Berkeley, CA  
USDA-ARS, Ithaca, NY  
Boyce Thompson Institute for Plant Research, Ithaca, NY

#### Universities

University of California, Berkeley  
University of California, Davis  
University of Florida, Gainesville  
University of Utah, Salt Lake City  
University of Arizona, Tuscon  
University of Wisconsin, Madison  
Colorado State University  
Cornell University, Ithaca, NY  
New Mexico State University  
North Carolina State University  
Ohio State University

(Note: the above lists of research institutions and universities are not inclusive of all laboratories involved in *Solanaceae* research in the US. Researchers working on or with *Solanaceae* can be found at most every US university with a major plant/agricultural research program. Indicated are those institutions with programs emphasizing *Solanaceae* genomics and/or *Solanaceae* genome utilization.)

#### Seed Companies and Processors

A number of important seed companies and processors (some based in the US and some not) are either directly involved in *Solanaceae* breeding or have an interest in *Solanaceae* improvement in the US and include:

Seminis Seed  
Heinz  
Hunt-Wesson  
Lipton Foods  
Unilever  
Frito-Lay

#### Agrochemical and biotechnology companies

Syngenta  
Monsanto  
Exelixis  
Mendel

#### Sources of Support

The majority of Solanaceae genomics research in the US is supported by the NSF (National Science Foundation) -Plant Genome and USDA-NRI Plant Genome programs. Additional support is provided by the Department of Energy (DOE), the National Institutes of Health (NIH) and industry including those companies mentioned above.

## **Major Topics of Research**

- *Development of genetic resources.*
- *Analysis of Solanaceae genomes and their evolution.*
- *Genomic tool kit development - ESTs genomic libraries and physical maps.*
- *Expression, protein and metabolite profiling.*
- *Bioinformatics*

### ***Major areas of biological interest are:***

- *Genome organization and evolution*
- *Pathogen response and resistance*
- *Abiotic stress - e.g. temperature, water, nutrient, heavy metal*
- *Primary and secondary metabolism*
- *Chemical ecology*
- *Hormone signaling and response*
- *Fruit development and ripening*
- *Development and architecture*

## **Potential Contribution of the US to the Tomato Sequencing Project**

The diversity of ongoing Solanaceae genomics programs position the US well for substantial contributions to tomato genome sequencing. 90,000 tomato BACs have been fingerprinted (Arizona) and are currently being anchored to the genetic map (Cornell/USDA). ESTs collections have been developed for tomato (Cornell/BTI/USDA) and potato (Berkeley) which will facilitate genome annotation. Comparative maps of potato, eggplant, and pepper anchored to tomato (Cornell) will facilitate extension of genome information to the broader Solanaceae, as will ongoing potato physical mapping efforts (Berkeley). Cytogenetic analysis of Solanaceae genomes (Colorado) and analysis of organelle genome sequence integration into the nuclear genome (Rutgers) will further enhance analysis of genome organization and refine sequencing strategy and data analysis. Bioinformatics (Cornell, NC State) and evolutionary genetics (Utah) specialists are in place to assist with genome sequence and cross-species comparative analysis and breeders are poised to implement downstream sequence information into DNA marker systems (Davis, New Mexico, Cornell, Florida, Texas, Ohio).

The US group plans to submit a proposal to the NSF-Plant Genome Program in July of 2004 to request funding for sequencing of six tomato chromosomes or approximately, one half of the tomato genome, and corresponding appropriate informatics support. The US

group has some preferences for target chromosomes but specific chromosomes to be sequenced will be determined once we have ascertained the interests of our international collaborators to minimize overlap and insure that those able to do only one chromosome can target the one most likely to result in funding from their respective granting agency..

As indicated by numerous international collaborators at the November 3, 2003 workshop in Washington, DC, funding in their respective countries is likely but contingent on successful efforts by other countries to insure that in the end their respective investments will be realized by a full tomato gene-space sequence. A significant effort undertaken in the US will insure the highest probability of funding for our international collaborators.

### **Deadlines For Submission Of Genomics Proposals**

NSF-Plant Genome Program

January 24, 2004

USDA-NRI Plant Genome Program

January 9, 2004