

EUREKA PROJECT E!2110 - SOLIMAP

1. General description

Project	E! 2110 - SOLIMAP	Status	Announced - 29-JUN-1999
Title	Solanacea Functional Genome Product		
Class	Project	Technological area	Medical and Biotechnology
Start date	09-JUL-1999	End date	09-JUL-2003
Duration	48 months	Total cost	7.3 Meuro
Partner sought	No		
Summary	The Main Objective Is To Create A Strong Molecular Basis For Efficient Functional Genomics In Tomatoes. Tools And General Information That Form This Basis Will Be Used To Study A Number Of Traits By Forward And Reverse Genetic Approaches.		

Budget and duration

Phase	Budget(Meuro)	Duration (Months)
Implementation phase	7.3	48
Total	7.3	48

Member contribution

Member	Contribution	Position	Since
The Netherlands	67.00%	Contact Member	23-DEC-1998
France	33.00%	Participating Member	29-JUN-1999

Participants

Company	Country	Type	Role
KEYGENE N.V.	THE NETHERLANDS	SME	Main
ENZA ZADEN, DE ENKHUIZER ZAADHANDEL B.V.	THE NETHERLANDS	SME	Partner
RIJK ZWAAN ZAADTEELT EN ZAADHANDEL B.V.	THE NETHERLANDS	Large company	Partner
VILMORIN CLAUSE & CIE S.A.	FRANCE	Large company	Partner
DE RUITER ZONEN C.V.	THE NETHERLANDS	SME	Partner

2. Project outline

Project description

The Solanaceae Functional Genome Project aims at creating the required knowledge and tools to apply forward and reverse genetic approaches in Solanaceae species with *Lycopersicon* as the central crop. This will create the possibility to obtain much more detailed knowledge of the molecular basis of some of the well known physiological processes in tomato plant development. Furthermore, the molecular knowledge will help dissect the information obtained related to more complicated traits of which the underlying physiological processes are less well understood.

In forward genetics, genes are identified on the basis of a functional observation (e.g. a phenotype), after which the genomic location of the genes is established. Tools that will be created for the forward genetic approach therefore include a high density genetic map of the tomato genome and YAC and BAC libraries for the creation of an integrated physical/genetic map that is essential for positional cloning experiments.

Reverse genetics start with the identification of a genomic sequence. Novel technologies, such as the cDNA-AFLP(R) technology, will be used to follow the expression of genes in different tissues and developmental stages of the plant. The expression profiles and sequence analysis of transcript tags form the basis for functional studies on gene sequences. The synergy between the forward and reverse genetic approaches proposed in this project warrant the identification of a large number of genes and genetic loci that are directly connected to traits of interest.

Keywords: tomato, functional genomics.

Technological development envisaged

1. The construction of a high resolution genetic map and the YAC and BAC libraries, which together make it possible to construct an integrated physical/genetic map of any region of the tomato genome that is of interest for a specific trait.
2. The production of different back-cross libraries and the corresponding BAC libraries, for the discovery and isolation of new QTL (Quantitative Trait Loci) for traits that are of interest to the participating tomato breeding companies.
3. The production of a transcript database and cDNA libraries. Based on sequence information, a functional analysis of the transcript will help the interpretation of the transcript imaging results obtained in experiments designed to study a specific trait and will make the connection to available public databases.

Markets application and exploitation

The partners in this project represent an important part of the international vegetable seed business, whereas KEYGENE

has a good reputation in the field of DNA marker technology. The cooperation between these parties will generate information about the genetics of agriculturally important features, which will contribute to an more efficient approach of market-oriented breeding of new varieties. This will enable the seed companies to strengthen their market positions. KEYGENE will broaden its technological basis as well as its patent portfolio. In the competitive field of genome research, all partners will not only be able to use the technology and genetic information in tomato crops but can also apply new genes in other agriculturally important crops.

Project codes

BSI

AK	research
ESK	plant genetics
HB/HV	agriculture

NACE

01	Agriculture, hunting and related service activities
73	Research and development

3. Main participant

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Organisation type SME
Participant role Main

Contribution to project

Will perform all the molecular work described in the project work plan. This includes AFLP(R) analysis for genetic mapping, cDNA-AFLP analysis for transcript analysis and the making of genomic and cDNA libraries.

Expertise

4. Partner

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Organisation type SME
Participant role Partner

Contribution to project

Input of breeding expertise. Input of elite germplasm. Own breeding facilities in the NETHERLANDS, SPAIN, FRANCE and TURKEY.

Expertise

4. Partner

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Organisation type Large company
Participant role Partner

Contribution to project

Plant breeding, plant growing, seed production, crossing plants, germ plasm, screenings, field trials in TURKEY and SPAIN, phytotron experiments.

Expertise

4. Partner

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Organisation type Large company
Participant role Partner

Contribution to project

Input of breeding expertise. Input of elite germplast.

Expertise

4. Partner

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Organisation type SME
Participant role Partner

Contribution to project

Will produce genetic material that will be used in this study. Also, phenotypic evaluation of several traits on this material will be carried out.

Expertise