SolCAP

Solanaceae Coordinated Agricultural Project

Dedicated to the Improvement of Potato and Tomato

Executive Commitee :

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Supported by the National Research Initiative Plant Genome Program of USDA's Cooperative State Research , Education and Extension Service

In Solanaceae There is a Major Gap Between Genomic Information and Breeding

- Traits
  - Carbohydrate and sugar metabolism (processing traits)
- Germplasm
  - Elite germplasm, Breeder driven; Appropriate outgroups
- Tools
  - Fund existing facilities to SNP genotype germplasm panels
- Flexible funding
  - genotyping additional populations for validation or additional traits
  - marker conversion
- Data mining and management
  - SGN, SolCAP websites
- Extension
  - eXtension; partner with other CAPs
- Education
  - Curriculum development; breeder workshops, graduate course

SolCAP Education and Extension Objectives

- Team-taught distance-learning graduate level course in translational genomics
- Annual workshops for breeders to integrate genotype-based breeding strategies with elite germplasm
- Use eXtension.org to develop a Community of Practice for plant breeders across all CAPs

Research Objectives

- Collect standardized phenotypic data across multiple environments for tomato and potato.
- Develop extensive sequence data of expressed genes, and identify SNP (1536/7600 proposed) markers associated with candidate genes for CHO and vitamin biosynthetic pathways.
- Establish centralized facilities for SNP genotyping germplasm panels in tomato and potato.
- Address regional, individual program and emerging needs through a small grants program.
- Create integrated, breeder-focused resources for genotypic and phenotypic analysis by leveraging existing databases and resources at SGN and MSU.

Germplasm panels

Collect standardized phenotypic data across multiple environments for tomato

480 lines

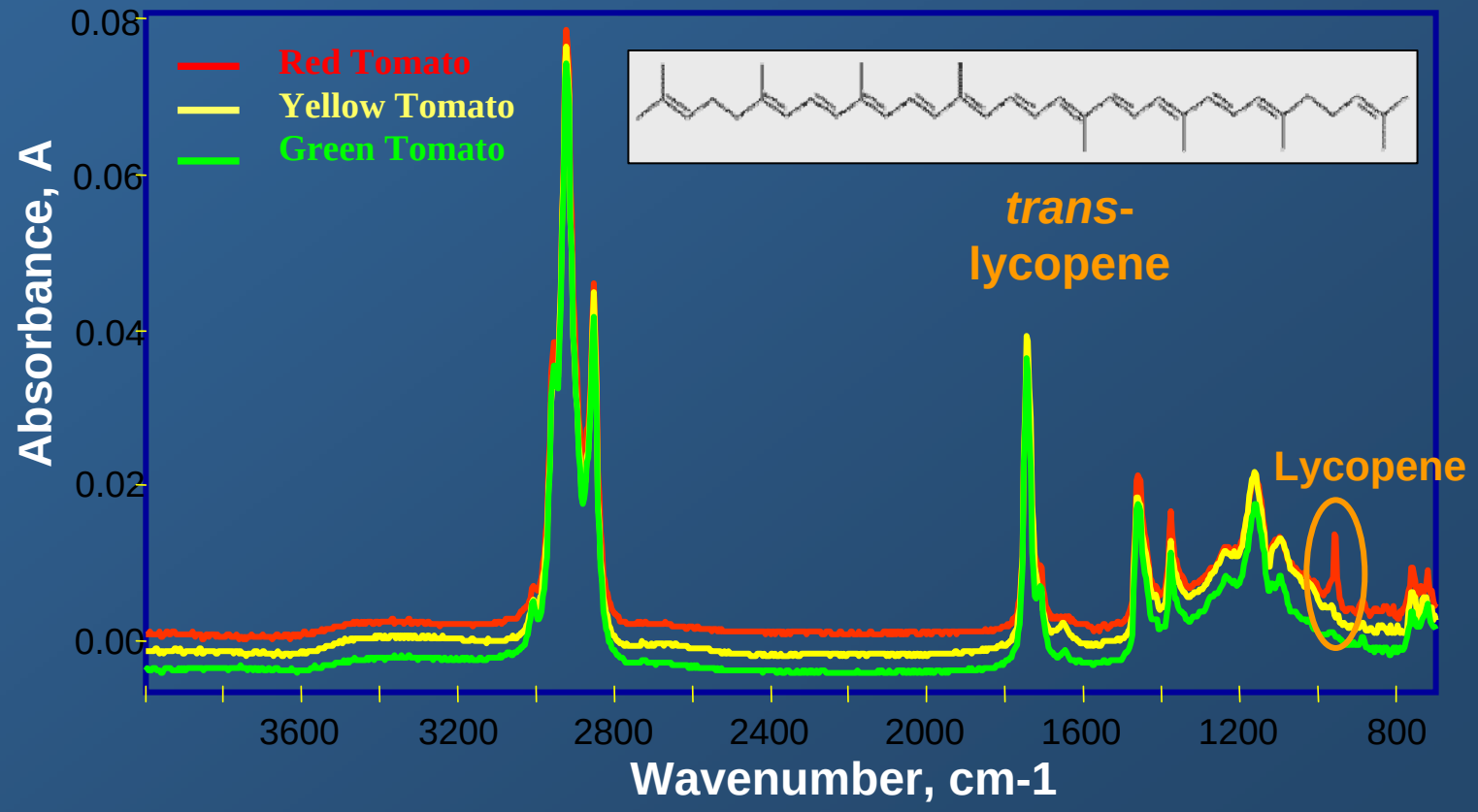
- 144 fresh market
- 144 processing
- vintage lines
- *S. lyc.* cerasiformae
- *Other Solanum*

Trial locations

- Processing
  - California: Campbell's
  - Ohio: OSU
- Fresh Market
  - California: UC Davis
  - North Carolina: NC State
  - Florida: UF
- Vintage lines
  - North Carolina: NC State
  - Ohio: OSU
  - New York: Cornell

High throughput analysis of carotenoids, sugars, and acids using IR Spectra

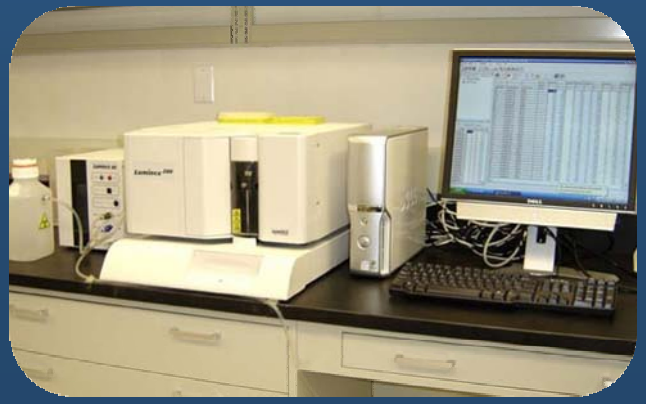
(Luis Rodruiguez-Saona, D. Francis, OSU)



Marker Discovery

- Develop extensive sequence data of expressed genes, and identify Single Nucleotide Polymorphism (SNP) markers
  - 1) associated with candidate genes for sugar, carbohydrate, and vitamin biosynthetic pathways,
  - 2) genome wide

- Catalog allelic variation in structural and regulatory genes and subsequently explore correlation with corresponding traits.



SNP Identification Using Transcript Assemblies (Existing ESTs to date)

- Search page for eSNPs available with frequency statistics

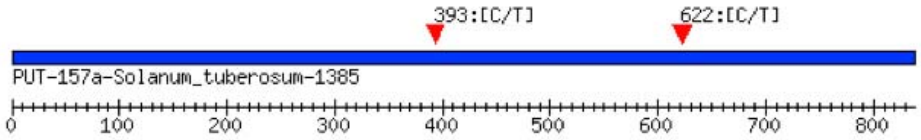
Search for Solanaceae SNPs

SNP Report for PUT-157a-Solanum_tuberosum-1385

EST Assembly PUT-157a-Solanum_tuberosum-1385 Summary

Scientific Name	*Solanum tuberosum*
Assembly ID	PUT-157a-Solanum_tuberosum-1385
Length	838
Num. of Components	23

EST Assembly PUT-157a-Solanum_tuberosum-1385 SNPs



SNP Location	Reference	SNP
393	C (12)	T (7)
622	C (19)	T (2)

- Linking eSNPs with validated SNPs (on-going)
- Adding annotation based search for SNPs

Current SNPs and insilico SNPs

Tomato

Total # of Transcript Assemblies: 48,945
Total # Transcript Assemblies with putative SNPs: 5,198
Total # of putative SNP positions:16,531

Intron SNPs: 1,487 from 302 loci (Van Deynze, Francis et al. 2007)

TA496 ESTs with SNPs VS H1706 BAC sequences							
		n = 1	n = 2	n = 3	n = 4	n = 5-10	n > 10
Total	806	596	106	34	22	38	10
Where EST Coverage = Allele Coverage							
		n = 1	n = 2	n = 3	n = 4	n = 5-10	n > 10
Total	127	not tested	64	22	11	23	7
Proportion	0.16		0.60	0.65	0.50	0.61	0.70

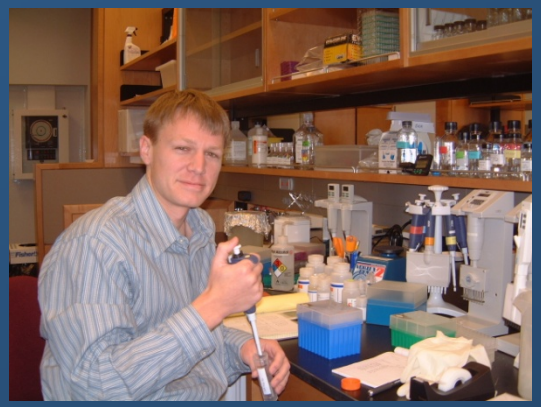
cDNA Libraries for Sequencing

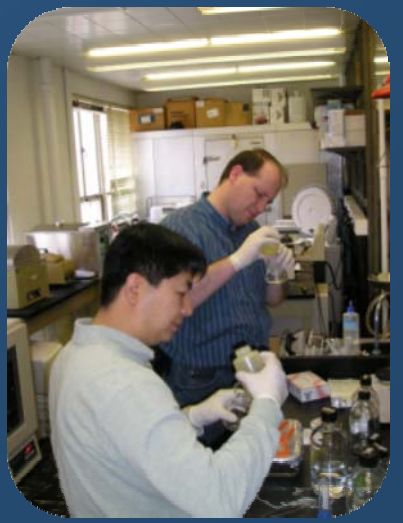
Using Illumina Genome Analyzer (Solexa) at UC Davis

- T5 (CA fresh-market)
- FL7600 (Florida fresh-market)
- NC84173 (NC fresh-market)
- OH9242 (Ohio processing)
- PI114490 (wild cherry tomato)
- PI128216 (wild current tomato)

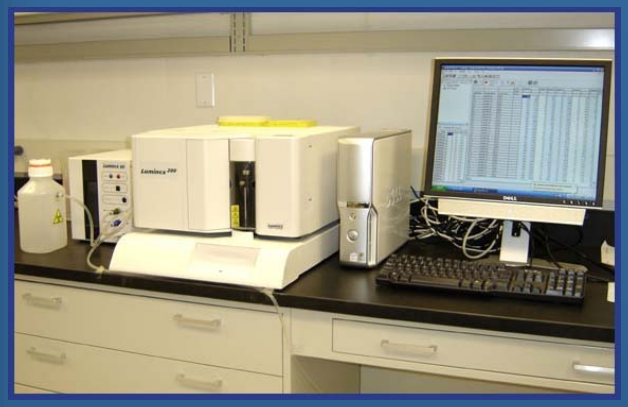
Root
Leaf
Flower
Fruit
Callus

- H1706 (Midwest Processing; Genome sequence)
- TA496 (CA Processing; EST sequence)





Genotyping



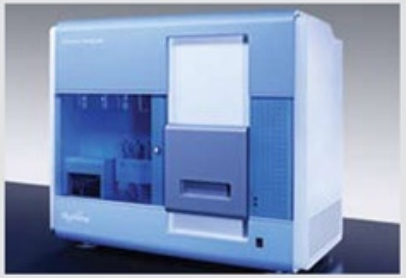
Illumina Golden gate 1,536 SNPs

75% genome wide, 25% traits

- 480 lines

Luminex/Bead express

- Mapping populations

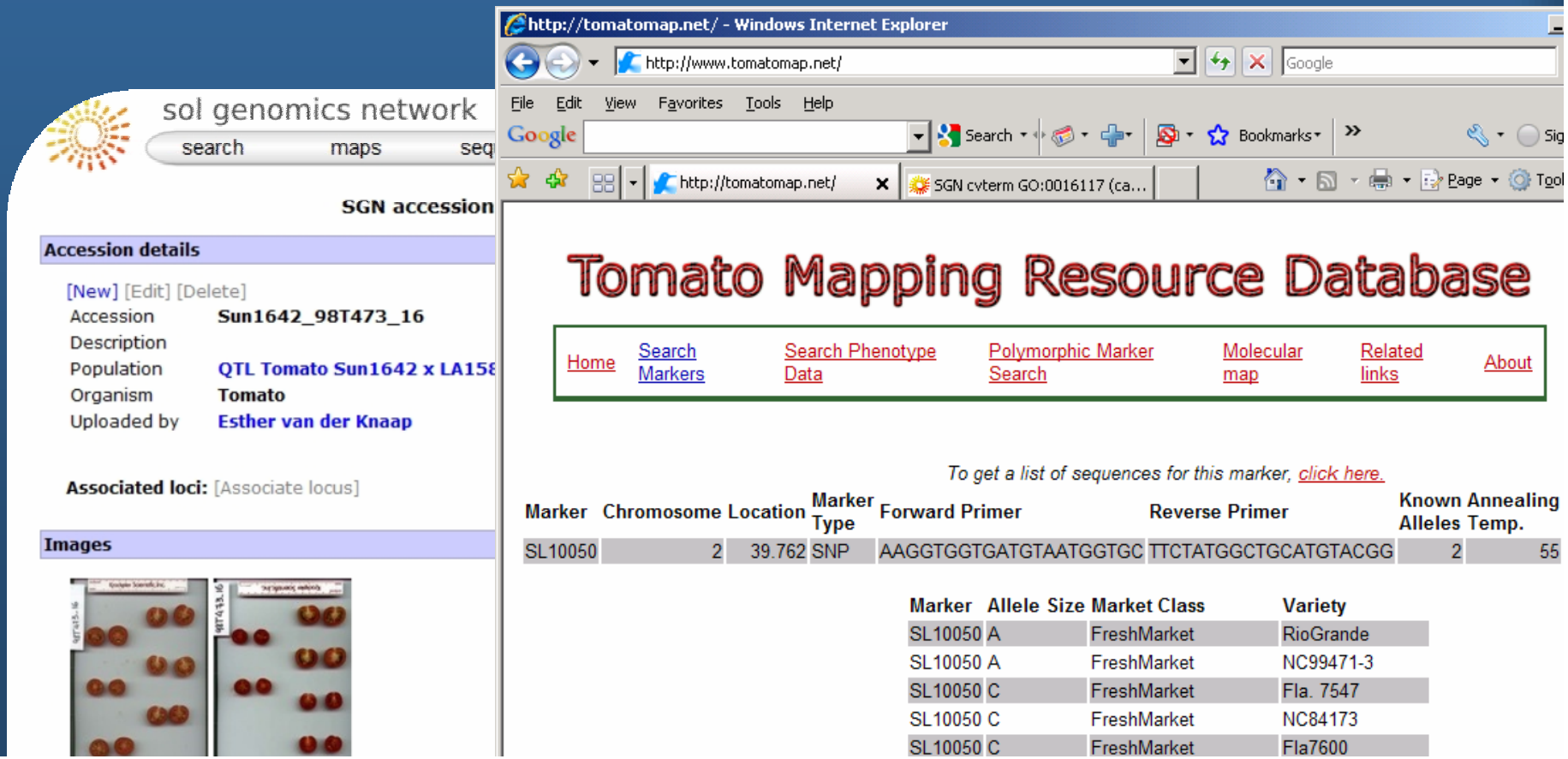


Small Grants Program

- Address regional, individual program and emerging needs within the Solanaceae community through a small grants program.
- Six key areas we intend to allocate resources to are:
  - Genotyping mapping populations in the core facilities requested by the greater breeding community
  - Marker conversion – developing SNP markers linked to QTL into easily assayed (e.g. CAPs or dCAPs) markers that end-users can readily apply in their own research programs
  - QTL validation and MAS
  - Population development to address emerging needs
  - Extension or education special projects
  - New directions not envisioned at the time of proposal submission.

Databases and Resources

- Create integrated, breeder-focused resources for genotypic and phenotypic analysis by leveraging existing databases and resources at SGN and MSU.



Outcomes for Breeding from SolCAP

A genome-wide set of markers and bioinformatic tools accessible by breeders

Better understanding of the allelic variation influencing CHOs

- Parental selection based on genotypes
- design crosses complementary for QTL and traits, and then use MAB in GS.
- Make better use of breeding values through incorporation of information on population structure and kinship
- Use objective means to increase variation in breeding populations.

Visit us at
http://solcap.msu.edu