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BARD

FINAL REPORT

PROJECT NO. IS-3009-98

**Fine Mapping and Genetic Interactions of Nearly
Isogenic Allelic Series Representing Yield and
Quality QTLs Derived from Wild Tomato Species**

D. Zamir, S. Tanksley

2002

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Project Title: Fine mapping and genetic interactions of nearly isogenic allelic series representing yield and quality QTLs derived from wild tomato species.

Investigators

Principal Investigator (PI):

Dani Zamir

Co-Principal Investigator (Co-PI):

Steve Tanksley

Institutions

The Hebrew University

Cornell University

Keywords *not* appearing in the title and in order of importance. Avoid abbreviations.

Abbreviations commonly used in the report, in alphabetical order:

Budget: IS: \$ 127,500

US: \$ 127,500

Total: \$ 255,000

Dani Zamir

Signature
Principal Investigator

Dr. ERAN VARDI
DIRECTOR
AUTHORITY FOR RESEARCH
AND DEVELOPMENT

Erani Vardi
Signature
Authorizing Official, Principal Institution

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TOTAL P.02

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Publication Summary (numbers)

	Joint IS/US authorship	US Authors only	Israeli Authors only	Total
Refereed (published, in press, accepted)	2	6	4	12
Submitted, in review, in preparation				
Invited review papers				
Book chapters				
Books				
Master theses				
Ph.D. theses		2	1	3
Abstracts				
Not refereed (proceedings, reports, etc.)				

Postdoctoral Training: List the names and social security/identity numbers of all postdocs who received more than 50% of their funding by the grant.

Cooperation Summary (numbers)

	From US to Israel	From Israel to US	Together, elsewhere	Total
Short Visits & Meetings	1	1		2
Longer Visits (Sabbaticals)				

Description of Cooperation:

The cooperation in this project is based on the extensive experience and interest of the participating groups in tomato genetics and by the fact that they have previously collaborated. All the data generated from the mapping project is being fed, in real time, to SGN in a manner that allows efficient access (<http://www.sgn.cornell.edu/>).

Patent Summary (numbers)

	Israeli inventor (s) only	US inventor (s) only	Joint IS/US inventors	Total
Submitted	1			1
Issued (allowed)				
Licensed				

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Title of Project

Fine Mapping and Genetic Interactions of Nearly-Isogenic Allelic Series Representing Yield and Quality QTLs Derived from Wild Tomato Species

Abstract

Wild germplasm represents a rich source of QTLs capable of enhancing productivity of crop plants. Using the molecular linkage map of tomato in conjunction with novel population structures, we have identified QTLs from five *Lycopersicon* species that improve key yield and quality associated traits of processing tomatoes. In this research we employed multi-testing sites for fine mapping analysis of the different components of the affected traits combined with genetic interaction studies. Our results demonstrate that 'exotic libraries', which comprise of marker-defined genomic regions taken from wild species and introgressed onto the background of elite crop lines, provide an important opportunity for improving of the agricultural performance of modern crop varieties. Furthermore, we showed that these genetic resources can also serve as reagents for the discovery and characterization of genes that underlie traits of agricultural value. The results set the stage for using the QTLs in marker assisted programs and for applying map-based cloning of the targeted QTL/genes. The cloning of QTLs revealed genes that control pathways for agricultural yield in tomato that may be common for other crop species.

Achievements

The greatest achievement of the present BARD project is the map based cloning of two yield associated QTLs in tomato. This accomplishment goes beyond the objectives proposed in the original proposal. These QTLs (FW2.2 and Brix9-2-5) are the first QTLs cloned in any organism and open the way to explore the genetic basis of complex trait. Traits like yield, quality and stress response show complex inheritance patterns that result from the segregation of numerous interacting QTLs, the expression of which is modified by the environment. Much of the efforts of the past year were devoted to a more detailed analysis of the two QTL. In addition, this project led to the formulation of concepts and strategies that increase the efficiency of utilization of wild germplasm in plant breeding.

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Publications - Journal Articles

- Zamir D. (2001) Improving plant breeding with exotic genetic libraries. *Nature Review Genetics* 2:983-989.
- Frery A, Nesbitt TC, Frery A, Grandillo S, van der Knaap E, Cong B, Liu J, Meller J, Elber R, Alpert K, Tanksley S 2000. Cloning and Transgenic Expression of *fw2.2*: a Quantitative Trait Locus Key to the Evolution of Tomato Fruit. *Science* 289:85-87.
- Fridman E, Pleban T and D Zamir (2000) A recombination hotspot delimits a wild species QTL for tomato sugar content to 484-bp within an invertase gene. *Proc Natl Acad Sci USA* 97: 4718-4723.
- Lippman, Z, Tanksley 2001. Dissecting the genetic pathway to extreme fruit size in tomato using a cross between the small-fruited wild species *L. pimpinellifolium* and *L. esculentum*, var. 'Giant Heirloom'. *Genetics* 158:413-422.
- Monforte A, Freidman E, Zamir D, Tanksley S 2001. Comparison of a set of allelic QTL-NILs for chromosome 4 of tomato: Deductions about natural variation and implications for germplasm utilization. *Theor Appl Genet* 102:572-590.
- Van der Knapp E, Tanksley S 2001. Identification and characterization of a novel locus controlling early fruit development in tomato. *Theor Appl Genet* 103:353-358.
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- Fulton T M, Grandillo S, Beck-Bunn T, Fridman E, Frampton A, Lopez J, Petiard V, Uhli J, Zamir D, Tanksley S 2000. Advanced backcross QTL analysis of a *Lycopersicon esculentum* x *L. parviflorum* cross *Theor Appl Genet* 100:1025-1042.
- Ku H, Grandillo S, Tanksley S 2000. fs8.1, a major QTL, sets the pattern of tomato carpel shape well before anthesis. *Theor Appl Genet* 101:873-878.
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- Fridman E, Gur A and D. Zamir (2001) Phenotyping, fine mapping and cloning of a wild species QTL that increases horticultural yield in tomatoes. *Proc. Int. Soc. Sugar Cane* 24: 22-28.
- Fridman, E., Y. S. Liu, L. Carmel-Goren, A. Gur, M. Shores, T. Pleban, Y. Eshed and D. Zamir (2002) Two tightly linked QTLs modify tomato sugar content via different physiological pathways. *Mol. Genet. Genomics* 266: 821-826.