BARD

FINAL REPORT

PROJECT NO. US-2427-94

**Development and Testing of a Method for the
Systematic Discovery and Utilization of Novel QTLs in
the Production of Improved Crop Varieties: Tomato as
a Model System**

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**DEVELOPMENT AND TESTING OF A METHOD FOR THE SYSTEMATIC
DISCOVERY AND UTILIZATION OF NOVEL QTLS IN THE
PRODUCTION OF IMPROVED CROP VARIETIES: TOMATO AS A
MODEL SYSTEM**

Dani Zamir and Steve Tanksley

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Evaluation of Research Achievements:

The objective of this research was to develop and test a new method for systematic discovery and utilization of QTLs from wild germplasm in the production of improved crop varieties using the tomato as a model system.

Modern cultivated varieties carry only a small fraction of the variation present in the gene pool. The narrow genetic basis of modern crop plants is a result of genetic bottlenecks imposed during early domestication and modern plant breeding. The wild ancestors of most crop plants can still be found in their natural habitats and Germplasm Centers have been established to collect and maintain this material. These wild and unadapted resources can potentially fuel crop plant improvement efforts for many years into the future (Tanksley and McCouch 1997). Unfortunately, scientists have been unable to exploit the majority of the genetic potential warehoused in germplasm repositories. This is especially true as regards to the improvement of quantitative traits like yield and quality. One of the major problems is that much of the wild germplasm is inferior to modern cultivars for many of the quantitative traits that breeders would like to improve.

Our research, focusing on the tomato as a model system, has shown that despite their inferior phenotypes, wild species are likely to contain QTLs that can substantially increase the yield and quality of elite cultivars (de Vicente and Tanksley 1992, Eshed and Zamir 1994, Eshed et al. 1996). Using novel population structures of introgression lines (ILs; Eshed and Zamir 1995) and advanced backcross lines (AB; Tanksley and Nelson 1996, Tanksley et al. 1996) we identified and introduced valuable QTLs from unadapted germplasm into elite processing tomato varieties. Populations involving crosses with five *Lycopersicon* species (*L. pennellii* (Eshed and Zamir 1994; Eshed et al. 1996; Eshed and Zamir 1996), *L. hirsutum* (Bernacchi et al. 1998), *L. pimpinellifolium* (Tanksley et al. 1996), *L. parviflorum* (unpub), *L. peruvianum* (Fulton et al. 1997) have been field and laboratory tested in a number of locations around the world. QTLs from the wild parent were identified that improve one or more of the key quantitative traits for processing tomatoes (yield, brix, sugar and acid composition and earliness) by as much as 10-30%. Nearly isogenic lines (QTL-NILs) have been generated for a subset of these QTLs. Each QTL-NIL contains the entire genome of the elite cultivated parent except for a segment (5-40 cM) of the wild species genome corresponding to a specific QTL.

Description of Cooperation:

This proposal is part of a long term BARD supported collaboration of the two laboratories to characterize different aspects of the tomato genome as they relate to genetics and plant breeding. The

true nature of the collaboration is reflected by a number of joint publications of the true groups and by the continuing collaborative research that is presently being conducted.

Conclusions

The genetic material and information that was developed in this program is presently used by American and Israeli seed companies for the breeding of superior varieties. We expect that in the next few years these varieties will make a difference in the marketplace.

Publications:

Paran I, I Goldman, SD Tanksley and D Zamir (1995) Recombinant inbred lines for genetic mapping in tomato. *Theor Appl Genet* 90:542-548.

Eshed Y and D Zamir (1995) An introgression line population of *Lycopersicon pennellii* in the cultivated tomato enables the identification and fine mapping of yield associated QTL. *Genetics* 141:1147-1162.

Goldman I, I Paran and D Zamir (1995) Quantitative trait locus analysis of a recombinant inbred line population derived from *Lycopersicon esculentum* x *Lycopersicon cheesmanii* cross. *Theor Appl Genet* 90:925-932.

Alpert, Kevin B. and Steven D. Tanksley. 1996. High-resolution mapping and isolation of a yeast artificial chromosome contig containing fw 2.2: A major fruit weight quantitative locus in tomato. *Proc. Natl. Acad. Sci.* 93:15503-15507.

Grandillo, S. and S.D. Tanksley. 1996. QTL analysis of horticultural traits differentiating the cultivated tomato from the closely related species *Lycopersicon pimpinellifolium*. *Theor. Appl. Genet.* 92:935-951

Eshed Y, G Gera and D Zamir (1996) A genome-wide search for wild-species alleles that increase horticultural yield of processing tomatoes *Theor Appl Genet* 93: 877-886.

Eshed Y and D Zamir (1996) Less than additive epistatic interactions of QTL in tomato. *Genetics* 143:1807-1817.

Fulton, Theresa M., James C. Nelson, Steven D. Tanksley. 1997. Introgression and DNA marker analysis of *Lycopersicon peruvianum*, a wild relative of the cultivated tomato, into *Lycopersicon esculentum*, followed through three successive backcross generations. *Theor. Appl. Genet* 95:895-902

Bernacchi and Steven D. Tanksley. 1997. An interspecific backcross of *Lycopersicon esculentum* x *L. hirsutum*: Linkage analysis and a QTL study of sexual compatibility factors and floral traits. *Genetics* 147:861-877.

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- Tanksley SD and SR McCouch (1997) Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* 277: 1063-1066.
- Chunwongse, J., S. Doganlar, C. Crossman, J. Jiang, and S.D. Tanksley. 1997. High resolution genetic map of the *Lv* resistance locus in tomato. *Theor. Appl. Genet.* 95:220-223.
- Brommonschenkel, S.H. and S.D. Tanksley. 1997. Map-based cloning of the tomato genomic region that spans the Sw-5 tospovirus resistance gene in tomato. *Mol Gen Genet* 256:121-126
- Bernacchi, D., T. Beck-Bunn, Y. Eshed, J. Lopez, V. Petiard, J. Uhlig, D. Zamir and S. Tanksley. 1998. Advanced backcross QTL analysis of tomato. I. Identification of QTL for traits of agronomic importance from *Lycopersicon hirsutum*. *Theor. Appl. Genet* 97: 381-397
- Doganlar, Sami, Jeff Dodson, Brad Gabor, Teresa Beck-Bunn, Curt Crossman and Steven D. Tanksley. 1998. Molecular mapping of the *py-1* gene for resistance to cork rot (*Pyrenochaeta lycopersici*) in tomato. *Theor Appl Genet* 98: 784-788.
- Bernacchi, D., T. Beck-Bunn, d. Emmatty, Y. Eshed, S. Inai, J. Lopez, V. Petiard, H. Sayama, J. Uhlig, D. Zamir and S. Tanksley. 1998. Advanced backcross QTL analysis of tomato. II: Evaluation of near-isogenic lines carrying single donor introgressions for desirable wild QTL-alleles derived from *Lycopersicon hirsutum* and *L. pimpinellifolium*. *Theor. Appl. Genet* 97:170-180. 97:1191-1196.
-) Tanksley SD, D Bernacchi, T Beck-Bunn, D Emmatty, Y Eshed, S Inai, J Lopez, V Petiard, H Sayama, J Uhlig and D Zamir (1997) Evaluations of yield and quality on a pair of processing tomato inbreds nearly isogenic for the *Tm2a* gene for resistance to the tobacco mosaic virus. *Euphytica* 99:77-83.

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Project Title: DEVELOPMENT AND TESTING OF A METHOD FOR THE SYSTEMATIC DISCOVERY AND UTILIZATION OF NOVEL QTLs IN THE PRODUCTION OF IMPROVED CROP VARIETIES: TOMATO AS A MODEL SYSTEM

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Affiliated Institution:

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Signature:
Principal Investigator

Signature:
Officer of the Affiliated Institution

FINAL REPORT

DEVELOPMENT AND TESTING OF A METHOD FOR THE SYSTEMATIC DISCOVERY AND UTILIZATION OF NOVEL QTLs IN THE PRODUCTION OF IMPROVED CROP VARIETIES: TOMATO AS A MODEL SYSTEM

Dani Zamir and Steve Tanksley

OBJECTIVES: The objective of this research was to develop and test a new method for systematic discovery and utilization of QTLs from wild germplasm in the production of improved crop varieties using the tomato as a model system.

Summary of the Results

Modern cultivated varieties carry only a small fraction of the variation present in the gene pool. The narrow genetic basis of modern crop plants is a result of genetic bottlenecks imposed during early domestication and modern plant breeding. The wild ancestors of most crop plants can still be found in their natural habitats and Germplasm Centers have been established to collect and maintain this material. These wild and unadapted resources can potentially fuel crop plant improvement efforts for many years into the future (Tanksley and McCouch 1997). Unfortunately, scientists have been unable to exploit the majority of the genetic potential warehoused in germplasm repositories. This is especially true as regards to the improvement of quantitative traits like yield and quality. One of the major problems is that much of the wild germplasm is inferior to modern cultivars for many of the quantitative traits that breeders would like to improve.

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improve one or more of the key quantitative traits for processing tomatoes (yield, brix, sugar and acid composition and earliness) by as much as 10-30%. Nearly isogenic lines (QTL-NILs) have been generated for a subset of these QTLs. Each QTL-NIL contains the entire genome of the elite cultivated parent except for a segment (5-40 cM) of the wild species genome corresponding to a specific QTL.

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Publications

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Eshed Y and D Zamir (1995) An introgression line population of *Lycopersicon pennellii* in the cultivated tomato enables the identification and fine mapping of yield associated QTL. *Genetics* 141:1147-1162.

Tanksley SD and JC Nelson (1996) Advanced backcross QTL analysis: a method for simultaneous discovery and transfer of valuable QTLs from unadapted germplasm into elite breeding lines. *Theor. Appl. Genet.* 92:191-203.

Tanksley SD, S Grandillo, TM Fulton, D Zamir, Y Eshed, V Petiard, J Lopez and T Beck-Bunn (1996) Advanced backcross QTL analysis in a cross between an elite processing line of tomato and its wild relative *L. pimpinellifolium*. *Theor Appl Genet* 92:213-224.

Eshed Y, G Gera and D Zamir (1996) A genome-wide search for wild-species alleles that increase horticultural yield of processing tomatoes *Theor Appl Genet* 93: 877-886.

Eshed Y and D Zamir (1996) Less than additive epistatic interactions of QTL in tomato. *Genetics* 143:1807-1817.

Grandillo S, HM Ku and SD Tanksley (1996) Characterization of fs8.1, a major QTL influencing fruit shape in tomato. *Molecular Breeding* 251-260.

Alpert, Kevin B. and Steven D. Tanksley. 1996. High-resolution mapping and isolation of a yeast artificial chromosome contig containing fw 2.2: A major fruit weight quantitative locus in tomato. *Proc. Natl. Acad. Sci.* 93:15503-15507.

Fulton TM, T Beck-Bunn, D Emmatty, Y Eshed, J Lopez, J Uhlig, D Zamir and SD Tanksley (1997) QTL analysis of an advanced backcross of *Lycopersicon peruvianum* to the cultivated tomato and comparison of QTLs found in other wild species. *Theor Appl Genet* 95:881-894.

Tanksley SD, D Bernacchi, T Beck-Bunn, D Emmatty, Y Eshed, S Inai, J Lopez, V Petiard, H Sayama, J Uhlig and D Zamir (1997) Evaluations of yield and quality on a pair of processing tomato inbreds nearly isogenic for the *Tm2a* gene for resistance to the tobacco mosaic virus. *Euphytica* 99:77-83.

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Brommonschenkel, S.H. and S.D. Tanksley. 1997. Map-based cloning of the tomato genomic region that spans the Sw-5 tospovirus resistance gene in tomato. *Mol Gen Genet* 256:121-126

Chunwongse, J., S. Doganlar, C. Crossman, J. Jiang, and S.D. Tanksley. 1997. High resolution genetic map of the Lv resistance locus in tomato. *Theor. Appl. Genet.* 95:220-223.

Doganlar, Sami, Jeff Dodson, Brad Gabor, Teresa Beck-Bunn, curt Crossman, and Steven D. Tanksley. 1997. Molecular mapping of the *py-1* gene for resistance to corky root rot (*Pyrenochaeta lycopersici*) in tomato. *TAG (In Press)*.

Fulton, Theresa M., James C. Nelson, Steven D. Tanksley. 1997. Introgression and DNA marker analysis of *Lycopersicon peruvianum*, a wild relative of the cultivated tomato, into *Lycopersicon esculentum*, followed through three successive backcross generations. *Theor. Appl. Genet* 95:895-902

Tanksley, Steven D. and Susan R. McCouch. 1997. Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* 277:1063-1066.

Bernacchi D, T Beck-Bunn, Y Eshed, S Inai, J Lopez, V Petiard, J Uhlig, D Zamir and SD Tanksley (1997) Advanced backcross QTL analysis of tomato: I. Identification of QTL for traits of agronomic importance from *Lycopersicon hirsutum*. *Theor Appl Genet* (in press).

Bernacchi D, T Beck-Bunn, D Emmatty, Y Eshed, S Inai, J Lopez, V Petiard, J Uhlig, D Zamir and SD Tanksley (1997) Advanced backcross QTL analysis of tomato: Evaluation of near-isogenic lines carrying single donor introgressions for desirable wild QTL alleles derived from *Lycopersicon hirsutum* and *L. pimpinellifolium*. *Theor Appl Genet* 97:170-180.

Zamir D and Y Eshed (1998) Tomato genetics and breeding using nearly isogenic introgression lines derived from wild species. in: *Molecular Analysis of Complex Traits*. ed. AH Paterson. CRC Press Inc. Fl. (in press).