Theor Appl Genet (1998) 97: 1191–1196

Erratum

D. Bernacchi · T. Beck-Bunn · D. Emmatty · Y. Eshed
S. Inai · J. Lopez · V. Petiard · H. Sayama · J. Uhlig
D. Zamir · S. Tanksley

Advanced back-cross 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 (1998) 97:170–180

Due to a technical error, the tables 1–6 were unfortunately not included in the above-mentioned article.

We apologize for this error and print the missing tables.

Received: 27 October 1997 / Accepted: 25 November 1997

Abstract Improved-processing tomato lines were produced by the molecular breeding strategy of advanced backcross QTL (AB-QTL) analysis. These near-isogenic lines (NILs) contained unique introgressions of wild alleles originating from two donor wild species, *Lycopersicon hirsutum* (LA1777) and *L. pimpinellifolium* (LA1589). Wild alleles targeted for trait improvement were selected on the basis of previously published replicated QTL data obtained from advanced backcross populations for a battery of important agronomic traits. Twenty three NILs were developed for 15 genomic regions which were predicted to contain 25 quantitative trait factors for the improvement of seven agronomic traits: total yield, red yield, soluble solids, brix × red yield, viscosity, fruit color, and fruit firmness. An evaluation of the agronomic performance of the NILs in five locations worldwide revealed that 22 out of the 25 (88%) quantitative factors showed the phenotypic improvement predicted by QTL analysis of the BC_3 populations, as NILs in at least one location. Per-location gains over the elite control ranged from 9% to 59% for brix × red yield; 14% to 33% for fruit color; 17% to 34% for fruit firmness; 6% to 22% for soluble-solids content; 7% to 22% for viscosity; 15% to 48% for red yield, and 20% to 28% for total yield. The inheritance of QTLs, the implementation of the AB-QTL methodology for characterizing unadapted germplasm and the applicability of this method to other crops are discussed.

Key words Molecular breeding · Germplasm · Quantitative traits

---

Communicated by G. Wenzel

D. Bernacchi · S. Tanksley (✉)
Department of Plant Breeding and Biometry, 252 Emerson Hall,
Cornell University, Ithaca, NY 14853-1902, USA
Fax: +1 607 255 6683
E-mail: SDT4@Cornell.edu

T. Beck-Bunn · J. Uhlig
Seminis Vegetable Seeds, 37437 State Highway 16, Woodland,
CA 95695, USA

D. Emmatty
Heinz U.S.A., Agricultural Research Department, P.O. Box 57,
Stockton, CA 95201-3057, USA

Y. Eshed · D. Zamir
Department of Field Crops, The Faculty of Agriculture,
Hebrew University of Jerusalem, Kennedy Lee Building, Room 222,
Box 12, Rehovot 76–100, Israel

S. Inai · H. Sayama
Nippon del Monte Corp., Research and Development,
3748 Shimizu-cho, Numata, Gumma 378, Japan

J. Lopez
Nestlé Research and Development Center, Apartado 435, E-06080,
Badajoz, Spain

V. Petiard
Centre Recherche Nestlé, 101 Avenue Gustave Eiffel,
37390 Notre Dame D'OE, Tours, France

Table 1 Targeted quantitative factors from *L. hirsutum* LA1777 (H) and *L.* pimpinellifolium LA1589 (PM) and corresponding NILs. Targeted QTL are in lower case italics and targeted quantitative factors identified at subthreshold significance are in capitals (trait affected and *marker locus*) (Bernacchi et al. 1997b; Tanksley et al. 1996). Chr = chromosome. NIL = near isogenic line. SSC = soluble solids; BOS = viscosity Bostwick; YDT = total yield; YDR = red yield; BYR = brix red yield; FC = fruit color and FIR = fruit firmness. See Fig. 1 for cM lengths of introgressed fragments

Targeted factor	Chr	Donor	NIL
SSC-TG260/CT267	1	H	TA523
	1	H	TA1257
ssc3.2/BOS-TG417	3	H	TA1276
ydt4.1/YDR-CD59/BYR-CD59	4	H	TA1133
fc4.2/*byr4.1*/BOS-CT50/SSC-TG163/YDR-TG163	4	H	TA517
	4	H	TA1284
BYR-TG574/FIR-TG574/YDR-TG574	4	H	TA1138
fc5.1/BOS-TG441	5	H	TA1116
	5	H	TA1292
	5	H	TA1291
	5	H	TA1293
ssc5.1/FC-TG60/CT138	5	H	TA1118
	5	H	TA1117
	5	H	TA1297
fc11.2	11	H	TA1347
fir3.1	3	PM	TA515
byr3.1/*ssc3.1*	3	PM	TA524
	3	PM	94T872-13
	3	PM	94T868-24
SSC-CT101	5	PM	TA514
vis9.1	9	PM	94T873-30
	9	PM	TA534
FC-TG393	11	PM	TA516

Table 2 Number of QTL/factors for which the corresponding NILs showed the expected phenotypic effect in at least one location. SSC = soluble solids; BOS = viscosity Bostwick; YDT = total yield; YDR = red yield; BYR = brix red yield; FC = fruit color; FIR = fruit firmness

	SSC	BOS	YDT	YDR	BYR	FC	FIR
Total # QTL/factors tested as NILs	6	4	1	3	4	5	2
# showing expected effect at $P \leq 0.1$	4	4	1	2	4	5	2
# showing expected effect at $P \leq 0.05$	4	3	0	1	3	4	2

Table 4 QTL/factors classified according to significance of BC_3 detection and significance of NIL best representing the predicted effects. P = significance level of single point analysis (QTL) and of linear contrast between NIL and control (NIL Δ%). Names of QTL/factors are described in Table 1

Significance of NIL Δ%				
Significance of QTL/factor detection in BC_3	ns	$0.1 \leq P < 0.01$	$0.01 \leq P < 0.001$	$0.001 \leq P < 0.0001$
$0.1 \leq P < 0.01$	*ssc5.1*	SSC-TG260/CT267 *ydt4.1* YDR-CD59 BYR-CD59 BOS-CT50 FC-TG60/CT138 BYR-TG574	SSC-CT101	BOS-TG441
$0.01 \leq P < 0.001$	YDR-TG574	YDR-TG163 FIR-TG574 *fc5.1*	BOS-417 FC-TG393 *byr3.1*	SSC-TG163
$0.001 \leq P < 0.0001$	*ssc3.1*	*fc4.2* *vis9.1*	*ssc3.2* *byr4.1* *fir3.1* *fc11.2*	

Table 3 QTL-allelic effect (Δ%) predicted for the NILs based on BC$_3$ data compared with observed performance of the NILs. Grouped data are QTL/factors statistics from BC3 mapping (first row, in italics) and corresponding NIL/s statistics (subsequent rows). If QTL/factor did not reach the threshold significance in BC$_3$ only the trait affected is described (Bernacchi et al. 1997b). Statistics for QTL are Δ% = percent phenotypic change associated with the *L. hirsutum* (H) or *L. pimpinellifolium* (PM) allele; P = significance of the association (Bernacchi et al. 1997b). Statistics for NIL evaluation are Δ% = percent phenotypic difference relative to *L. esculentum* control E6203; P = significance of contrast NIL-E6203. Markers, in *italics*, are RFLP loci associated with QTL/factor. Introgression indicates the segments of H DNA contained in the NIL. IS = Israel; SP = Spain; CAP = California, Woodland; CAH = California, Stockton and JP = Japan. ns = not significant ($P > 0.1$). na = not available in a given location. Avg. Δ% = average phenotypic effect associated to the H or PM allele, considering only deviations at $P \leq 0.1$ irrespective of the direction of the difference. none sig = none of the contrasts were significant at $P \leq 0.1$. The NILs selected for best performance in the case of QTL/factors represented by more than one NIL are indicated in bold

Trait, QTL (*BC*$_3$) NIL	Donor	*Marker* Introgression	IS		SP		CAP		CAH		JP		Avg. Δ%
			Δ%	P	Δ%	P	Δ%	P	Δ%	P	Δ%	P	
Soluble solids	H	*TG260/CT267*	*6*	*0.03*	*5*	*0.07*	*7*	*0.07*					*6.0*
TA523		TG260-CT190	9	0.01	– 3	ns	– 3	ns	6	0.06	7	0.08	7.5
TA1257		CT190	2	ns	– 4	ns	4	ns	1	ns	4	ns	ns
Soluble solids, ssc3.2	H	*TG417/CT243*	*11*	*0.0009*	*12*	*0.0006*	*5*	*ns*					*11.5*
TA1276		TG417-CT243	5	ns	–1	ns	1	ns	8	0.015	5	ns	8.3
Viscosity (*Bostwick*)	H	*TG417*			*–2*	*0.013*							*– 14.6*
TA1276		TG417-CT243			2	ns	– 9	0.1	– 11	0.013	– 22	no rep	– 9.9
Total Yield, ytd4.1	H	*CD59*	*16*	*0.03*	*20*	*0.078*	*9*	*0.1*					*14.8*
TA1133		CD59	– 12	0.1	– 10	ns	20	0.1			28	0.1	12.0
Red yield	H	*CD59*	*15.4*	*0.09*	*26*	*0.05*	*2*	*ns*					*20.7*
TA1133		CD59	– 14.2	0.02	3.5	ns	20	0.1	19.1	0.04	48.2	0.03	18.2
Brix red yield	H	*CD59*	*17*	*0.03*	*15*	*ns*	*– 5*	*ns*					*17.2*
TA1133		CD59	– 20	0.005	– 5	ns	13	ns	11	ns	42	0.04	10.7
Red yield	H	*TG163*	*– 1*	*ns*	*– 12*	*ns*	*33*	*0.006*					*32.5*
TA517		TG305-CT50-TG163	– 14	0.03	15	0.1	5	ns	– 12	ns	1	ns	0.5
TA1284	H	CT50-TG163	– 1	ns	– 19	0.08	– 32	0.02	– 2	ns			– 25.2
Soluble solids	H	*TG163*	*3*	*ns*	*10*	*0.004*	*5*	*ns*					*9.6*
TA517		TG305-CT50-TG163	9	0.01	10	0.008	6.31	0.014	22	<0.0001	13.8	0.002	12.2
TA1284		CT50-TG163	13	0.001	9	0.01	0.14	ns	5.5	0.1			9.2
Brix red yield, bry4.1	H	*TG163*	*3*	*ns*	*6*	*ns*	*41*	*< 0.0001*					*41.0*
TA517		TG305-CT50-TG163	– 7	ns	267	0.01	13	ns	8	ns	16	ns	26.5
TA1284		CT50-TG163	11	0.1	– 11	ns	– 32	0.02	4.	ns			– 10.2
Fruit color, fc4.2	H	*TG163*	*46*	*0.0003*	*14*	*0.06*	*– 3*	*ns*					*29.7*
TA517		TG305-CT50-TG163	7	ns	0	ns	23	0.05	– 14	0.1	33	0.03	14.0
TA1284		CT50-TG163	– 9	ns	0	ns	– 2	ns	7	ns			ns
Viscosity	H	*CT50*			*12*	*0.04*							*12.1*
TA517		TG305-CT50-TG163			– 4	ns	– 3	ns	– 15	0.001			– 15.3
TA1284		CT50-TG163			– 13	0.02	– 13	0.02	– 6	ns			– 12.8
Red yield	H	*TG574*	*14*	*0.08*	*3*	*ns*	*37*	*0.007*					*26.5*
TA1138		*TG264-TG574-CT50*	– 3	ns	3	ns	16	ns					ns
Brix red yield	H	*TG574*	*12*	*0.08*	*9*	*ns*	*34*	*0.01*					*22.7*
TA1138		TG264-TG574-CT50	– 1	ns	7	ns	24	0.08	12	0.1	13	ns	18.2

Table 3 Continued

Trait, QTL (BC_3) NIL	Donor	*Marker* Introgression	IS		SP		CAP		CAH		JP		Avg. Δ%
			Δ%	P	Δ%	P	Δ%	P	Δ%	P	Δ%	P	
Firmness	H	*TG574*	*– 9*	*ns*	*17*	*0.01*	*13*	*ns*					*17.0*
TA1138		TG264-TG574-CT50	17	0.06	4	ns	2	ns	34	0.04	25	0.1	25.3
Fruit color, fc5.1	H	*TG441*	*42*	*0.01*	*15*	*0.06*	*2*	*ns*					*28.4*
TA1116		TG441-CT167-CD64	7	ns	17	0.04			– 1	ns	8	ns	16.7
TA1291		TG441			0	ns	– 2	ns	– 1	ns			ns
TA1292		TG441			6	ns							ns
TA1293		CD64	7	ns	17	0.04	18	0.1	– 1	ns			17.4
Viscosity	H	*TG441*			*– 12*	*0.05*							*– 11.8*
TA1116		TG441-CT167-CD64			– 3	ns			– 23	< 0.0001			– 22.5
TA1291		TG441			6	ns	5	ns	15	0.001			14.7
TA1292		TG441			– 7	ns							ns
TA1293		CD64			– 11	0.053	1	ns	5	ns			– 10.6
Soluble solids, ssc5.1	H	*TG69*	*12*	*0.01*	*8*	*0.08*	*13*	*0.02*					*11.0*
TA1118		TG69-CT138	3	ns	3	ns	– 2	ns	4	ns	– 1	ns	ns
TA1117		TG69-CT138	1	ns	– 4	ns	– 5	0.03	– 1	ns	– 1	ns	– 5.4
TA1297		CT138	2	ns	– 8	ns	– 5	0.03	3	ns	1	ns	– 5.4
Fruit color	H	*TG60/CT138*	*31*	*0.06*	*5.*	*0.01*	*6*	*0.052*					*14.0*
TA1118		TG69-CT138	– 4	ns	0	ns	13	ns	11	ns	25	0.1	25.0
TA1117		TG69-CT138	7	ns	6	ns	18	0.1	7	ns	8	ns	18.0
TA1297		CT138	– 9	ns	– 11	0.1	3	ns	– 10	ns	8	ns	– 11.1
Fruit color, fc11.2	H	*TG393*	*46*	*0.0002*	*– 3*	*ns*	*2*	*ns*					*46.2*
TA1347		TG393	14	0.02	3	ns	0	ns	– 20	0.02	8	ns	– 2.6
Soluble solids ssc3.1/3.2	PM	*TG129/CD51/TG388*	*7*	*0.04*	*7*	*0.0007*	*7*	*< 0.0001*					*7.1*
TA524		TG246-TG129-CD51-TG388	– 2	ns	– 4	ns	– 8	0.002	– 4	ns	– 1	ns	– 7.9
94T872-13		TG246-TG129-CD51	3	ns	– 11	0.03	na	na	– 3	ns	– 5	ns	– 10.8
94T868-24		TG388	2	ns	– 6	0.1	– 5	0.04	– 3	ns	– 1	ns	– 5.4
Brix red yield, byr3.1	PM	*CD51-TG388*	*5*	*ns*	*18*	*0.001*							*18.2*
TA524		TG246-TG129-CD51-TG388	9	0.1	2	ns	– 8	ns	9	ns	59	0.005	34.1
94T872-13		TG246-TG129-CD51	25	0.001	– 15	ns			0	ns	– 7	ns	24.7
94T868-24		TG388	7	ns	– 3	ns	– 19	0.1	6	ns	8	ns	– 19.4
Firmness, fir3.1	PM	*TG525*	*40*	*0.0001*									*40.0*
TA515		TG114-TG525-CT141-TG66	22	0.01	4	ns	2	ns	34	ns	– 17	ns	22.2
Soluble solids	PM		*– 1*	*ns*	*1*	*ns*	*5.2*	*0.04*					*5.2*
TA514		CT101	2.1	ns	11	0.005			– 7	0.04	5	ns	1.70
Viscosity, vis9.1	PM	*TG421*			*– 13*	*0.0003*							*– 13*
TA534		TG421			– 8	0.1	– 7	0.1	– 3	ns	– 36	no rep	– 7.5
94T873-30		TG421-CT74-TG551			– 3	ns	– 5	ns	– 5	ns	– 28	no rep	ns
Fruit color	PM		*11*	*ns*	*23*	*0.009*	*1*	*ns*					*2.3*
TA516		TG393-I2-TG36-TG546	18	ns	25	0.002	17	0.1	– 15	0.07	25	0.07	12.9

Table 5 QTL/factors classified according to the number of locations of BC_3 detection and the number of locations where corresponding NIL showed the predicted effect (NIL Δ%) ($P \leq 0.1$). Names of QTL/factors are described in Table 1

	Number Loc. significant NIL Δ% in predicted direction				
Number Loc. QTL/factor detection in BC_3	0	1	2	3	5
1		*fir3.1* SSC-CT101 BOS-TG441 *fc11.2* BYR-CD59 *byr4.1*	*byr3.1* YDR-TG163 BOS-CT50 BOS-417 *vis9.1*	FIR-TG574 FC-TG393	SSC-TG163
2	YDR-TG574	*fc5.1* *ssc3.2*	BYR-TG574 *fc4.2*	YDR CD59	
3	*ssc3.1* *ssc5.1*	*FC-TG60/CT138*	*ydt4.1*	SSC-TG260/CT267	

Table 6 Percent phenotypic differences between NILs and the *L. esculentum* control for traits other than those predicted by QTL analysis results. Δ% = percent phenotypic difference. Only the best performing NIL for each target are considered. IS = Israel; SP = Spain; CAP = California, Woodland; CAH = California, Stockton and JP = Japan. FC = fruit color; BYR = brix × red yield; YDR = red yield; FIR = fruit firmness; AFW = average fruit weight; SSC = soluble solids; BOS = viscosity Bostwick; YDT = total yield. Loc = location. The original association between the introgressed markers and any given trait are given under BC_3 association (Bernacchi et al. 1997b) as follows: if a QTL was detected with significance in the BC_3, its name is given as well as the estimated phenotypic effect associated with the wild allele; if an association failing to reach QTL significance was detected, the location in which it was detected is given in brackets, preceeded by a negative sign (−) if the H or PM allele was associated with inferior performance or a positive sign (+) if H or PM allele improved the trait

NIL	Trait	NIL deviations from E6203 at $P < 0.1$								BC_3 mapping
		Loc	Δ%	Loc	Δ%	Loc	Δ%	Loc	Δ%	
TA253	FC	IS	+15							*fc1.3* −33%, (−CAP)
	BYR	CAH	+22	JP	+48					(−CAP)
	YDR	JP	+38							(−IS, −CAP)
	FIR	CAH	+46							
	AFW	CAH	−10	CAP	−20	SP	−22			(+CAP)
TA1276	FC	CAP	−4	JP	−10					(+SP, +CAP)
	FIR	CAH	−23	SP	−12					(−SP)
	YDR	IS	−11							(−IS, −SP, −CAP)
	AFW	CAH	−15	CAP	−12	IS	−15	SP	+11	(−IS, −SP)
TA1133	BOS	CAH	−9	CAP	−8	SP	−20			
	SSC	CAH	−7	CAP	−6	IS	−6	SP	−7	(−CAP)
	AFW	CAH	−14	IS	−15	SP	−18			
TA517	pH	SP	+2	JP	+1.5					(−SP, −CAP)
	YDT	IS	−16							(−SP)
	FIR	SP	−12	JP	−23					
	AFW	CAH	−25	CAP	−21	IS	−21	SP	−20	(−SP)
TA1284	YDT	CAP	−31							
	AFW	CAH	−15	IS	−15	SP	−16			(−SP)
TA1138	BOS	CAH	+12	CAP	+13	JP	+21			(+SP)[a]
	SSC	CAH	+7	CAP	+6					(+SP)[a]
	AFW	CAH	−12	CAP	−12					(−SP, −CAP)
	FC	SP	−8							
TA1116	SSC	CAH	+9	IS	+8					
	FIR	CAH	+53	IS	+22	JP	+25			
	AFW	CAH	−20	SP	−21					
TA1117	FIR	JP	−23	SP	−17					*fir5.1* −32% (−SP)[a]
	BYR	IS	−20	SP	−20					(−IS, −SP)

Table 6 Continued

NIL	Trait	NIL deviations from E6203 at $P < 0.1$								BC_3 mapping
		Loc	Δ%	Loc	Δ%	Loc	Δ%	Loc	Δ%	
TA1347	FIR	CAH	+27							
	BYR	JP	+53	SP	−24					
	YDR	JP	+51							
	BOS	CAH	−15							(−SP)
	SSC	CAP	−7	SP	−7	IS	+5			
	FC	CAP	−21							(+IS)
	AFW	CAH	−11							(−IS, −SP)
TA524	BOS	CAH	+10							(−SP)
	YDR	JP	+60	IS	+11					(+SP)
	FIR	JP	+33							
	AFW	CAH	−15	SP	−16					(−CAP, −IS, −SP)
TA516	BYR	SP	−24							(+IS)
	SSC	CAP	−5							(+CAP, +SP)
	AFW	CAH	−8	CAP	−25	IS	−16	SP	+12	(−CAP, −IS, −SP)
TA514	BYR	IS	+18							
	FC	IS	+36							(+SP)
	AFW	JP	+34							
	FIR	SP	−12	JP	−33					
TA534	YDR	JP	+30	SP	+29					(+ IS)[a]
	BYR	SP	+18							
	FIR	CAH	+34	SP	+13					
	SSC	SP	−8							(−SP)[a]
	FC	CAH	−22	CAP	−16	SP	−11			(−SP)
TA515	FIR	CAH	+53	CAP	−23					(+IS)
	AFW	SP	+20	CAH	−13	CAP	−32			(−IS)

[a] A QTL or a subthreshold association was detected for the RFLP marker adjacent to introgressed segment