Linkage relationships among multiple QTL for horticultural traits and late blight (P. infestans) resistance on chromosome 5 introgressed from wild tomato Solanum habrochaites

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ABSTRACT

When a wild species’ allele at a quantitative trait locus (QTL) conferring a desirable trait is introduced into cultivated species, undesirable effects on other traits may occur. These negative phenotypic effects may result from the presence of wild alleles at other closely-linked loci that are transferred along with the desired QTL allele (i.e., linkage drag), and/or from pleiotropic effects of the desired allele. Previously, a QTL for resistance to Phytophthora infestans on chromosome 5 of Solanum habrochaites was mapped and introgressed into cultivated tomato (S. lycopersicum). Near-isogenic lines (NILs) were generated and used for fine-mapping of this resistance QTL, which revealed coincident or linked QTL with undesirable effects on yield, maturity, fruit size, and plant architecture traits. Subsequent higher-resolution mapping with chromosome 5 sub-NILs revealed the presence of multiple P. infestans resistance QTL within this 12.3 cM region. In our present study, these sub-NILs were also evaluated for 17 horticultural traits, including yield, maturity, fruit size and shape, fruit quality, and plant architecture traits in replicated field experiments over two years. Each previously detected single horticultural trait QTL fractionated into two or more QTL. A total of 41 QTL were detected across all traits, with ~30% exhibiting significant QTL × environment interactions. Co-location of QTL for multiple traits suggests either pleiotropy or tightly-linked genes control these traits. The complex genetic architecture of horticultural and P. infestans resistance trait QTL within this S. habrochaites region of chromosome 5 presents challenges and opportunities for breeding efforts in cultivated tomato.
INTRODUCTION

The value of wild species as sources of genetic diversity for breeding their crop species relatives has long been appreciated, and there are many examples of their use in crop improvement (Labate and Robertson 2012). In modern breeding, introgression of genes controlling useful traits from wild into cultivated species is often facilitated by first associating molecular marker genotypes with trait phenotypes, a process known as gene mapping or quantitative trait locus (QTL) mapping (Collard et al. 2005). Once the chromosomal locations of QTL controlling a particular trait are known, marker-assisted selection (MAS) can be employed to transfer wild alleles with favorable trait effects into a crop species while simultaneously selecting against wild alleles at other loci to create improved varieties (Xu and Crouch 2008). MAS breeding can be particularly effective in the improvement of quantitative traits, traits that are controlled by a few to many genes that may interact with each other and with the environment (St.Clair 2010). However, effective use of QTL alleles from wild species can be complicated by linkages among desired and undesirable trait loci, and/or by interactions of QTL with the environment (Bernardo 2008). Genes controlling a desirable trait may also affect one or more other traits, a phenomenon known as pleiotropy (Chen and Luebberstedt 2010).

Tomato is an important crop worldwide and is the second most valuable vegetable in US production (National Agriculture Statistics Service 2011). Cultivated tomato (Solanum lycopersicum) has limited genetic diversity in comparison with its diverse wild tomato species relatives, primarily due to genetic bottlenecks during domestication (Miller and Tanksley 1990; Park et al. 2004). Wild Solanum habrochaites is an important source of genetic diversity for tomato improvement. Among the traits that can be improved via introgressions from S. habrochaites are horticultural traits such as yield, fruit size, and fruit quality (Bernacchi et al.)
A very desirable trait of *S. habrochaites* is its resistance to *Phytophthora infestans*, the oomycete pathogen responsible for late blight disease of tomato and its close relative potato (Brouwer *et al.* 2004; Foolad *et al.* 2008). Late blight disease causes significant losses in tomato, resulting in approximately $5 billion in crop losses and chemical control costs annually (Judelson and Blanco 2005). Brouwer *et al.* (2004) mapped QTL for quantitative resistance to *P. infestans* from *S. habrochaites* on each of the twelve tomato chromosomes. Brouwer and St.Clair (2004) further refined the locations of three of the QTL (on chromosomes 4, 5, and 11) by fine mapping with near-isogenic lines (NILs). These three resistance QTL were also found to be co-located and/or linked with some QTL having negative effects on horticultural traits such as plant height, plant shape, maturity, yield, and fruit size, suggesting linkage drag.

Our interests in understanding the genetic basis of QTL controlling horticultural traits and their linkage relationships with QTL for resistance to *P. infestans*, as well as in developing material useful for breeding improved tomato varieties, led us to conduct further investigations on the introgressed chromosome 5 region from *S. habrochaites*. In a companion study (Johnson *et al.* 2012) we mapped the chromosome 5 resistance QTL reported in Brouwer and St.Clair (2004) at higher resolution with sub-NILs. We found that the resistance QTL located in a 12.3 cM region subsequently fractionated into two and three QTL groups for foliar and stem resistance, respectively. In the present study we used the same set of chromosome 5 sub-NILs as
Johnson et al. (2012), focusing on mapping loci associated with horticultural traits and determining linkage relationships among these loci and the late blight resistance QTL. Our goals here were to: (1) determine the genetic architecture and environmental stability of QTL controlling horticultural traits within the chromosome 5 introgressed region from S. habrochaites; (2) determine the linkage relationships among loci controlling horticultural and P. infestans resistance traits; and (3) assess the implications of trait genetic architecture, QTL environmental stability, and linkage relationships among QTL for the potential improvement of cultivated tomato via breeding.

**MATERIALS AND METHODS**

**Plant Materials, Genotyping and Marker-Assisted Selection:** We developed a set of sub-near-isogenic lines (sub-NILs) in S. lycopersicum for a chromosome 5 introgression from a P. infestans resistant donor parent, wild tomato S. habrochaites accession LA 2099, via marker-assisted selection during backcrossing and selfing generations, as described in Johnson et al. (2012). Genomic DNA extractions, genotyping with chromosome 5 PCR-based markers (SCAR, CAPS, and SSR), primer sequences, enzymatic reaction conditions, and restriction enzymes used for each marker are described in Johnson et al. (2012).

We genotyped 1589 BC₆S₁ progeny to identify recombinant sub-NIL progeny; a subset of 652 progeny (150 recombinant plus 502 non-recombinant) was used to construct a linkage map for the introgressed region (see Linkage and QTL Mapping, below). Heterozygous recombinant BC₆S₁ individuals underwent self-pollination and progeny were marker-selected to obtain homozygous recombinant BC₆S₂ sub-NILs. These plants underwent self-pollination to obtain ample BC₆S₃ sub-NIL seed for replicated field experiments. We evaluated 58 BC₆S₃ sub-NILs in
the 2009 field experiments. In the 2010 field experiments, a subset of 41 of the 58 sub-NILs was evaluated to allow increased replication per location while reducing genetic redundancy, as explained in Johnson et al. (2012). Graphical marker genotypes for the 58 selected BC$_6$S$_3$ sub-NILs are presented in Table S1.

**Field Experimental Design and Procedures:** BC$_6$S$_3$ sub-NILs and the parental NIL from which they were derived (subsequently referred to as NIL5) were evaluated in replicated experiments at field locations in Salinas, CA (designated as locations 1 and 2) and in Davis, CA (locations 3 and 4) over two years. Summer in Salinas is generally cool and humid, which is conducive to late blight disease development, while Davis summers are warm and dry, typical of processing tomato production areas in California’s Central Valley.

Seedlings were grown in a greenhouse for six weeks and then transplanted into the field locations. Sixty-one genotypes (NIL5, 58 sub-NILs for chromosome 5, and two commercial processing cultivars, E6203 and Hypeel 45), and 44 genotypes (NIL5, 41 sub-NILs, Hypeel 45, and E6203) were included in the 2009 and 2010 experiments, respectively. Experiments were arranged in a randomized complete block design (RCBD). For both years, one plot per genotype per block was included, except for controls for which there were two plots per block. In 2009, three blocks per location were used. In 2010, use of a reduced number of 41 sub-NILs enabled replication to be increased to five blocks in each of locations 1 and 2 and to four blocks in each of locations 3 and 4. At each of the four locations, each plot consisted of 5 plants spaced 0.30 m apart in rows separated by 1.02 m in locations 1 and 2, and by 1.52 m in locations 3 and 4. Border rows and plots with the cultivar E6203 surrounded each experiment at each location. Standard horticultural field practices for processing tomato were used at all locations. Locations 1 and 2 were sprinkler irrigated, while locations 3 and 4 were furrow irrigated, as needed.
**Phenotypic Trait Evaluations:** All traits were evaluated on a per-plot basis. Vegetative horticultural traits were evaluated at all four locations. Late blight disease was only evaluated in Salinas (locations 1 and 2) since this disease did not occur in Davis, as expected, due to typical warm, dry summers. Reproductive traits were only evaluated at Davis (locations 3 and 4) due to logistics of timely sampling of ripe fruit. Vegetative horticultural traits evaluated were plant height (H) and width (W) in cm, canopy density (CD; visual rating scale, 1=very sparse to 5=very dense), and plant habit (HAB; visual rating scale, 1=prostrate to 5=very upright). H, W, CD, and HAB were assessed at locations 1 and 2 at 71 and 46 days after planting (DAP) in 2009 and 2010, respectively. At locations 3 and 4 these traits were evaluated at 80 DAP in 2009 and at 68 (H and W) and 73 (CD and HAB) DAP in 2010. From plant height and width, two secondary traits were derived, plant size (SZ; product of height × width) and plant shape (SH; ratio of height to width). The reproductive horticultural traits measured or scored were as follows. DAP to maturity was evaluated at two stages of maturity: when each plant in the plot had its first ripe fruit (DAP1st), and when 50% of fruit in a plot were ripe (DAP50). Weight of 30 ripe fruit was evaluated when 50% of fruit in a plot were ripe (30Wt). Yield in kg (YLD) was evaluated when 95% of the fruit in a plot were ripe. Ripe fruit were used to obtain the weight of 100 seed (SW), which was measured only in 2009 due to labor limitations. The ripe fruit quality traits pH and Brix (i.e., sugar content or soluble solids) were measured using a pureed sample of 10 whole fruit obtained from plots with 50% ripe fruit using an Oakton pH Testr2 (Oakton Instruments, Vernon Hills, IL, USA) and a Reichert AR200 digital refractometer (Reichert Technologies, Buffalo, NY, USA), respectively. Size traits obtained on ripe fruit were perimeter (FP), width (FW; width at mid-height), and height (FH; height at mid-width). These traits were measured on flatbed scanner images of eight longitudinally-sliced fruit per plot using Tomato Analyzer.
software (Brewer et al. 2006), which refers to fruit length as height and fruit longitudinal circumference as perimeter. From FH and FW, the secondary variable fruit shape (FS; ratio of FH to FW) was obtained. Trait names, abbreviations and brief descriptions are given in Table 1.

In 2009, on September 15th, Salinas locations 1 and 2 were inoculated with a local *P. infestans* isolate per Johnson et al. (2012). In 2010 in mid-September, a natural *P. infestans* infection occurred in both locations, precluding the need for inoculation. As described in Johnson et al. (2012), phenotypic scoring of late blight disease symptoms was performed visually and symptom data were used to calculate area under the disease pressure curve (AUDPC) for foliar and stem disease symptom progression (referred to as LEAF and STEM, respectively). Lower AUDPC values indicate less disease symptom progress, and are therefore indicative of increased disease resistance.

**Statistical Data Analysis:** Data for each trait (Table S2) were tested for normality using the Shapiro/Wilk W statistic in PROC UNIVARIATE in SAS (SAS Institute, Cary, NC, USA) and for homogeneity of variance using Levene’s test. Data for heteroscedastic traits were weighted by the reciprocal of the variance for those terms with significant departure from the assumption of equal variance. Analysis of Variance (ANOVA) for each trait was performed using PROC GLM in SAS with the following linear additive model for a randomized complete block design and multiple locations:

\[
\text{Trait} = \text{Loc} + \text{Block(Loc)} + \text{Genotype} + \text{Loc*Genotype}
\]

where Trait was a given phenotypic trait, Loc was the effect of location, Genotype was the individual sub-NIL or control (NIL5, E6203, Hypeel 45), a * indicated an interaction, and parentheses indicated a nested variable. Block(Loc) was considered a random variable. Significant genotype × location interactions were detected in 2009 for traits LEAF, DAP50,
YLD, FH, FS, FP, 30Wt, Brix, pH, CD, H, W, SH, and SZ, and in 2010 for STEM, DAP1st, DAP50, FH, FW, FS, FP, 30Wt, Brix, pH, H, W, SH, and SZ. For these traits, separate analyses were conducted for each location. PROC MIXED in SAS was used to estimate least squares means (LSMeans), due to missing data for some traits, and to perform means separation with Tukey’s HSD.

Pearson correlation coefficients (r) were calculated for pairwise combinations of all trait genotypic means in 2009 and in 2010 using Proc CORR in SAS. Only significant (P ≤ 0.05) correlations equal to or greater than 0.4 are reported.

**Linkage and QTL Mapping:** A linkage map for the introgressed region was constructed using DNA marker genotype data across 17 loci for 652 BC6S1 progeny (150 recombinants plus 502 non-recombinants). The map was constructed with JoinMap 3.0 (Van Ooijen and Voorips 2001) using the Kosambi mapping function and a 3-LOD significance threshold. After the release of the tomato genome sequence (Sato et al. 2012), we developed additional markers using the SL2.40 genome build (http://solgenomics.net) to help define the physical extent of the chromosome 5 S. habrochaites introgression within NIL5 (see Supporting File S1 for details).

The Composite Interval Mapping (CIM) module in WinQTLCartographer2.5 (Wang et al. 2011) was employed for detection of QTL using sub-NIL means obtained from ANOVA for each trait. QTL mapping was performed using CIM Model 6 (Standard Model) and the forward and backward regression method with a walkspeed of 1 cM and a window size of 2 cM. Trait-specific permuted LOD thresholds (P = 0.05) were empirically established for each trait using 1000 permutations (Churchill and Doerge 1994) in WinQTLCartographer.

A QTL for a trait was considered significant at P ≤ 0.05 if the peak LOD value exceeded the trait-specific permuted threshold. Multiple QTL were declared for a single trait when the
LOD values between significant ($P \leq 0.05$) peaks within the introgressed region decreased below the significance threshold for at least two contiguous markers. Each significant QTL was denoted by trait name, location and year. For example, DAP1st34_2009 is a QTL detected in the analysis of DAP1st trait data from locations 3 and 4 in 2009.

A linkage map showing locations of significant QTL was constructed using MapChart2.1 (Voorips 2002). QTL locations were indicated as 1-LOD bars and 2-LOD whiskers (Figure 1). For purposes of discussion, QTL were assigned to QTL trait groups (delineated as Hort 5-1 through Hort 5-4) based on coincidence of their 1-LOD support intervals. Although a few of the QTL have 1-LOD support intervals that extended beyond the boundary of their assigned group, their peak locations supported their placement in their respective groups.

Comparisons were made among QTL for $P. infestans$ resistance traits (LEAF and STEM; see Johnson et al. 2012) and horticultural traits for QTL coincidence by visual inspection of their chromosomal locations on the linkage map. A statistical test based on the hypergeometric probability distribution (Lin et al. 1995) was used to calculate QTL correspondence, the probability of obtaining the observed number of matching QTL by chance. A QTL match was declared when the one-LOD support intervals overlapped. The number of comparison intervals ($n$) was 7, based on the average size of our resistance and horticultural trait QTL (1.9 cM) and the overall map distance of the $S. habrochaites$ introgression (12.3 cM).

Our QTL locations were also compared to those previously reported for both disease resistance and horticultural trait QTL on chromosome 5 in tomato and in potato, based on common markers as well as genomic sequence data for both crop species. Sources used for QTL location comparisons included the following: tomato (Eshed and Zamir 1996; Bernacchi et al. 1998b; Zhang et al. 2002; Causse et al. 2004; Coaker and Francis 2004; Semel et al. 2006;
Brewer et al. 2007; Jones et al. 2007); potato (Collins et al. 1999; Visker et al. 2003; Visker et al. 2005; Sliwka et al. 2007; Achenbach et al. 2009; Danan et al. 2011); and genomic sequences (http://solgenomics.net; Xu et al. 2011; Sato et al. 2012). When common markers were not available, the Tomato-Expen 2000 map (Fulton et al. 2002b) available on the Sol Genomics Network (http://solgenomics.net; Bombarely et al. 2011) was used to facilitate map alignment.

**Selection of Sub-NIL Breeding Lines:** Truncation selection was applied sequentially for traits LEAF, YLD, FP, 30Wt, and DAP1st in order to identify breeding lines potentially useful for development of tomato varieties with improved resistance to *P. infestans*. Out of 41 sub-NILs evaluated in both years, the first round of truncation removed 7 lines with LEAF values less resistant than control cultivar E6203 in two years or locations. The second round removed 8 lines with YLD < 66% of E6203 in two years/locations, while the third round removed 6 lines with FP < 92% of E6203 in two years/locations. The fourth round removed 6 lines with 30Wt < 80% of E6203 in two years/locations. The final round removed 3 lines with DAP1st > 10 days later than E6203 in two years/locations; however, 5 lines that would have been removed based on this criterion were kept due to their relatively higher levels of foliar resistance to *P. infestans* (i.e., lower LEAF values). At the end of the selection process, 11 lines were chosen.

**RESULTS**

**ANOVA:** In 2009, 61 genotypes (sub-NILs and controls) were evaluated for late blight disease symptom traits (Johnson et al. 2012) and horticultural traits (Table 1). For all traits, genotypes were significantly different (*P* ≤ 0.05, Table 2). Significant genotype × location interactions were detected in 2009 for LEAF, DAP50, YLD, FH, FS, FP, 30Wt, Brix, pH, CD,
H, W, SH, and SZ. As a result, these traits were analyzed separately by location. $R^2$ values per trait ranged from 0.45 to 0.91.

In 2010, 41 genotypes were evaluated for disease symptom traits and horticultural traits (Table 1). For all traits, genotypes were significantly different ($P \leq 0.05$, Table 2). Significant genotype × location interactions were detected in 2010 for STEM, DAP1st, DAP50, FH, FW, FS, FP, 30Wt, Brix, pH, H, W, SH, and SZ. Therefore, these traits were analyzed separately by location. $R^2$ values per trait ranged from 0.43 to 0.89. In general, foliar resistance to *P. infestans* (LEAF) exhibited higher $R^2$ values than stem resistance (STEM), with the exception of location 1 in 2009. Horticultural traits involved with fruit size measurements had higher $R^2$ values than those associated with fruit quality or plant architecture.

**Means separation:** There were significant ($P \leq 0.05$) differences among genotypic means for all traits, except for CD in location 3 in 2009 (Table S1). In general, sub-NILs with *S. habrochaites* alleles at marker loci TG358 and At1g10500 were significantly later maturing (DAP1st and/or DAP50) than control cultivar E6203 in at least one trait and year or location combination and most of these lines also had significantly reduced YLD and 30Wt. Relative to E6203, NIL5 exhibited significantly ($P \leq 0.05$) greater foliar resistance to *P. infestans* (i.e., lower LEAF values), and increased Brix, but also had later maturity (DAP1st and DAP50) and larger plant size (H, W, and SZ). Sub-NILs 08GH5516, -5616, and -5861 also displayed significantly ($P \leq 0.05$) improved foliar resistance (LEAF) and larger plant size, with the latter two also having significantly higher Brix.

**Correlations:** Pearson correlation coefficients ($r$) were obtained for *P. infestans* resistance trait means with horticultural trait means within each year (Table 3). Only significant correlations ($P \leq 0.05$) greater than or equal to 0.4 are discussed here. CD was weakly negatively
correlated with LEAF and STEM ($r = -0.41$, range -0.42 to -0.46, respectively). HAB was positively correlated with LEAF and STEM ($r = 0.41$, range 0.57 to 0.64, respectively), with upright plants having higher AUDPC values (i.e., more susceptible). Maturity traits were negatively correlated with LEAF and STEM only in 2010, although this was influenced by location and time of maturity trait evaluation (DAP1st vs. DAP50). Significant ($P \leq 0.05$) correlations were also found between pairs of horticultural traits (Table S3). Of particular note, YLD was negatively correlated with maturity traits DAP1st and DAP50 in both years (range -0.50 to -0.78), and CD was significantly positively correlated with the maturity traits in both years (range 0.53 to 0.83).

**Linkage Mapping:** The linkage map for the chromosome 5 introgressed region from *S. habrochaites* was 12.3 cM and spanned markers TG358 to At3g55360 (Figure 1). The average marker spacing was 0.7 cM and the largest gap was 2.5 cM between markers At2g39950 and TG23. Using additional markers developed from the SL2.40 *S. lycopersicum* tomato genome sequence build (http://solgenomics.net), we determined that the introgression in NIL5 extended north of TG358 to at least TG318, and south of At3g55360 to at least CT130. Comparison of our genetic map with the SL2.40 *S. lycopersicum* genome sequence also indicated that the order of markers TG69 and At3g55360 were reversed, suggesting an inversion or possibly errors in the reference genome sequence.

The 12.3 cM region from TG358 to At3g55360 corresponds to a physical distance of 2.35 Mbp in the SL2.40 *S. lycopersicum* genome sequence build, while the 12.0 cM region from TG358 to TG69 corresponds to a *S. lycopersicum* physical distance of 2.7 Mbp. However, the physical distances based on *S. lycopersicum* are approximate only since the introgressed region is from *S. habrochaites*, which may have a different physical distance. Based on the physical
distance between markers in the \textit{S. lycopersicum} genome sequence, the physical extent of the \textit{S. habrochaites} introgression beyond the boundaries of our linkage map likely includes at least another 896 kb north of TG358 and at least another 680 kb south of TG69.

**Mapped QTL:** Within the introgressed chromosome 5 region containing resistance QTL \textit{lb5b} (Brouwer and St.Clair 2004), 67 significant ($P \leq 0.05$) QTL were detected for 17 horticultural traits (Figure 1 and Table 4). In 2009, 45 QTL were detected and 22 in 2010. If we consider multiple coincident QTL for the same trait as a single, unique QTL, then a total of 41 unique QTL were mapped across the 17 traits.

**Horticultural Trait QTL Groups:** Based on their location on the linkage map, four major horticultural trait QTL groups (\textit{Hort5-1} through -4) were delineated (Figure 1 and Table 4) as described in Materials and Methods. \textit{Hort5-1} contained QTL for every trait evaluated with the sole exception of fruit width (Figure 1, Table 4). The QTL controlling reproductive traits within this group tended to explain a higher \%PV than those of the other groups. This group includes QTL for days to first ripe fruit, days to 50\% ripe fruit, yield, fruit height, fruit size, and fruit weight. The only QTL detected for pH and seed weight were also located within this group. QTL in \textit{Hort5-1} also controlled the plant architecture traits canopy density, plant habit, plant height, plant width, plant shape, and plant size (Table 4). There was evidence of genotype × environment interaction (G × E) for plant architecture, since the presence of the \textit{S. habrochaites} allele at these QTL produced denser, taller plants in 2009, while it resulted in a smaller, shorter, more prostrate phenotype in 2010. Plants with the wild allele at these QTL also had delayed maturity, reduced fruit size and weight, but slightly higher seed weight and Brix.

The \textit{Hort5-2} QTL group contained QTL for 8 of the 17 horticultural traits evaluated, and included primarily QTL for traits involving fruit size, fruit shape and plant architecture traits.
(Table 4). The *S. habrochaites* allele at the Hort5-2 QTL group resulted in a shorter, more prostrate plant architectural phenotype. The wild allele also increased fruit size and weight primarily as a result of increased fruit width. The Hort5-3 QTL group contained QTL for 8 of the 17 traits evaluated (Table 4). In contrast to the Hort5-2 effect on plant size, the *S. habrochaites* allele at the Hort5-3 QTL group increased plant size, both height and width. Maturity was slightly delayed by the presence of the wild allele in both years, but only in a single location in 2010. The Hort5-4 QTL group contained QTL for 6 of the 17 traits evaluated: fruit shape, fruit size, plant width, plant shape, Brix and canopy density (Table 4). The *S. habrochaites* allele at the Hort5-4 QTL group was associated with a wider, more prostrate, and less dense plant architecture and decreased fruit size.

Plant architecture was influenced by the presence of the *S. habrochaites* introgression at each of the four QTL groups, with Hort5-2 causing a reduction in plant size, Hort5-3 and Hort5-4 causing an increase in plant size, and Hort5-1 having an environmentally-dependent effect. Fruit size was impacted by Hort5-1 and Hort5-4, both reducing fruit size, and by Hort5-2, which was associated with larger fruit. Delayed maturity and increased Brix were caused by Hort5-1 and Hort5-3, while the other two groups had no significant effect on these important traits.

**Horticulture Trait QTL and Linkage with *P. infestans* Resistance QTL:** In our companion study (Johnson *et al.* 2012), we detected two and five QTL groups within the introgressed chromosome 5 region controlling foliar (LEAF) and stem (STEM) resistance to *P. infestans*, respectively, with the QTL groups designated as LFRes5-1, 5-2 and STRes5-1 through 5-5 (see Figure 1). We used markers in common to align the QTL groups and visual inspection. LFRes5-1 and STRes5-1 were co-located with Hort5-1 (Figure 1). STRes5-2 slightly overlapped
Hort5-2. LFRes5-2, STRes5-2, and STRes5-3 were co-located with Hort5-3. STRes5-4 and STRes5-5 were co-located with Hort5-4.

The Hort5-1 QTL group included QTL for 16 of the 17 horticultural traits measured. Most of the horticultural trait QTL within this group mapped within marker interval TG358–T0536, and all shared a peak LOD at TG358 (Figure 1 and Table 4). LFRes5-1 and STRes5-1 each contained only a single QTL spanning the same interval TG358–T0536, also with peak LOD at TG358, thus the horticultural trait QTL and these resistance QTL were co-located.

QTL were detected in the Hort5-2 QTL group for 8 of the 17 horticultural traits measured (Figure 1 and Table 4). The 1-LOD support intervals for the QTL within Hort5-2 and STRes5-2 overlapped slightly and the peaks for H, SH, and SZ QTL comprising this group were at At2g39950 and At3g55800. However, STRes5-2 consisted of only a single QTL with a peak approximately 2.5 cM away at TG23, suggesting that Hort5-2 is only linked to, rather than co-located with STRes5-2.

The Hort5-3 QTL group included QTL for 8 of the 17 horticultural traits evaluated, each QTL with peak LOD either at At2g31970 or in the interval At2g31970–At4g12590 (Figure 1 and Table 4). In contrast, LFRes5-2 was composed of three overlapping resistance QTL with the common lower boundary marker At4g12590, but different upper boundaries of markers At3g17210, At2g31970, and At5g49510 (see Table 4 in Johnson et al. 2012). The uppermost of these three resistance QTL had peak LOD at At5g49510, while the lower two QTL had peaks in the interval At2g31970–At4g12590. Their peak locations suggest a closer linkage of the QTL in Hort5-3 with the lower two resistance QTL in LFRes5-2 than with the uppermost QTL. The two QTL for DAP1st and the YLD QTL in this group were co-located with LFRes5-2, each spanning the interval At5g49510-T1541.
The *Hort 5-4* QTL group included QTL for 6 of the 17 horticultural traits measured, but only for traits related to fruit size, fruit shape, fruit quality, and plant architecture (Figure 1 and Table 4). The co-located resistance QTL groups *STRes5-2* and *STRes5-3* were composed of three QTL spanning interval T1541-At3g55360: one QTL for resistance from the *S. habrochaites* allele with its peak at TG69, and two QTL with opposite allelic effect, with peaks at T1541 and TG69 (see Table 4 in Johnson *et al.* 2012). The horticultural trait QTL and the resistance QTL in this interval all exhibited unstable expression across experimental environments (see next subsection), which precluded a more precise determination of the co-localization of these QTL.

**QTL Stability and QTL × Environment Interaction:** QTL for YLD, fruit size (FH, FP, and 30Wt), and maturity (DAP1st and DAP50) at *Hort5-1* were detected repeatedly over years and locations, indicating stability of QTL expression (Figure 1, Table 4). In contrast, the FS QTL in this *Hort5-1* group were detected in two locations in 2009 but not in 2010, suggesting environmental influence on QTL expression. *Hort5-1* also contained QTL for H, but depending on the year and location, the wild allele had opposite effects on plant height: in 2009 in Davis the presence of the wild allele increased height, and in 2010 in Salinas it decreased height. This difference in allelic effect over years was likely due to the large environmental differences between the locations and years. Within the region represented by this QTL group, Brix, pH, CD, and W were only detected in a single location in a single year, indicating QTL × E interactions.

The significant QTL at *Hort5-2* were all detected only in 2009 in both Davis locations, with the exception of SZ. Therefore, all the QTL in this group exhibited QTL × E interactions.

In general, QTL for architectural traits (HAB, H, and SZ) at *Hort5-3* were stable since they were detected over years and locations. However, differences in allele directionality for W indicated QTL × E effects, possibly as a result of different row spacing used in Salinas versus
Davis. Also, a QTL for SH was detected only in one location in 2009. The QTL for Brix in this group were detected in both Davis locations, but only in a single year, also suggesting QTL × E interactions.

In group *Hort5-4*, QTL for W were detected in one location in 2009 and in two in 2010. The other QTL in this region were only detected in a single year (for SH and SZ) or in a single location (for FS, FP, Brix, and CD), again indicating QTL × E interactions and QTL instability.

**Coincidence of QTL between Horticultural and Resistance Traits:** The hypergeometric probability distribution was used to test the significance of correspondence of QTL for *P. infestans* resistance (reported in Johnson *et al.* 2012) with those for horticultural traits. The correspondence of LEAF QTL with both DAP1st and YLD QTL was significantly different from chance (*P* = 0.047 for each comparison). No other QTL coincidences between *P. infestans* resistance QTL and horticultural trait QTL were significant.

**Selection of Sub-NIL Breeding Lines:** Nine sub-NILs were selected as being potentially useful as breeding lines for development of tomato varieties with improved resistance to *P. infestans*: 08GH5516, -5616, -5861, -6042, -6261, -6288, -6321, -6345, and -6805 (Table S1). We compared these lines with cultivar E6203 to evaluate their potential in breeding. Three lines (08GH5516, -5616, and -5861) had significantly improved foliar resistance (i.e., lower LEAF values) at both Salinas locations in 2010 and had generally lower LEAF values (though not significantly different) in both locations in 2009. 08GH5616 and -5861 had significantly higher Brix in all experiments. 08GH5516, -6288, -6321, and -6805 did not have significantly later maturity and none of the selected lines were significantly taller except 08GH5616.
DISCUSSION

Genetic Architecture of Horticultural Traits: Our higher resolution mapping of horticultural trait QTL within an introgressed chromosome 5 region from *S. habrochaites* revealed a complex genetic architecture for various traits, including maturity, yield, fruit size, shape, and weight, soluble solids, canopy density, and plant size and shape (Figure 1, Table 4). Factors contributing to this genetic complexity include QTL previously detected as single QTL fractionating into multiple QTL for a given trait, tight linkages among QTL for multiple traits, the presence of previously unmapped horticultural trait QTL, and QTL with opposite directionality of allelic effects in different environments.

Brouwer and St.Clair (2004) used near-isogenic lines (NILs) for the chromosome 5 region introgressed from *S. habrochaites* to map late blight disease resistance and horticultural trait QTL for plant height, plant shape (referred to here as plant habit), maturity, yield, and fruit size. In our present study, the single QTL mapped for each trait in Brouwer and St.Clair (2004) each fractionated into multiple QTL upon higher resolution mapping, a phenomenon reported previously in other mapping studies (Chen and Tanksley 2004; Lecomte *et al.* 2004; Edwards and Mackay 2009; Studer and Doebley 2011; Johnson *et al.* 2012). Studies in tomato interspecific populations have found similarly complex genetic architectures for traits such as fruit size and fruit quality when mapping within defined chromosomal regions (Fridman *et al.* 2002; Yates *et al.* 2004). In contrast, some high resolution mapping studies reported only single QTL for traits such as Brix (Fridman *et al.* 2000; Fridman *et al.* 2004), fruit shape (Ku *et al.* 2001), and fruit weight (Alpert and Tanksley 1996; Frary *et al.* 2000).

Tight linkages were identified among multiple QTL controlling horticultural traits in our study. The most complex group, *Hort5-1*, contained QTL for 16 of the 17 traits evaluated and all
were mapped within a single 1.8 cM interval. Coincident QTL for multiple traits have also been
detected within similarly small genetic map distances in other studies of wild species
introgressions in cultivated tomato (Frary et al. 2003; Yates et al. 2004; Gur et al. 2010).

Contributing to the genetic complexity of this chromosome 5 region are the presence of
QTL for canopy density (CD) and plant size (SZ) which remained undetected in the previous
study by Brouwer and St.Clair (2004). This result may be explained by the presence of closely
linked QTL in repulsion with opposite allelic effects upon these traits (Figure 1, Table 4). The
individual effects of these QTL can only be separated upon mapping with additional
recombinants to provide increased resolution (Mackay et al. 2009). Higher resolution mapping
has also allowed detection of QTL controlling stem resistance to P. infestans (STEM, Johnson et
al. 2012) that were previously undetected at lower resolution by Brouwer and St.Clair (2004).

The traits mapped within this region of chromosome 5 from S. habrochaites showed
diverse genetic complexity, each varying in number of QTL and direction of allelic effects
(Figure 1, Table 4). Yield (YLD), maturity (DAP1st), fruit height (FH), and plant habit (HAB)
were each controlled by two QTL with the same direction of allelic effect, while fruit weight
(FW) and canopy density (CD) were each controlled by two QTL of opposite allelic effect. Fruit
shape (FS) and Brix were each controlled by three QTL with the same direction of allelic effect,
while fruit size (FP), plant height (H), plant width (W), and plant size (SZ) were each controlled
by three QTL of varying direction of allelic effect. Plant shape (SH) had the most complex
genetic architecture, being controlled by four QTL with alternating direction of allelic effect.
Similar genetic complexity, including multiple closely-linked QTL with varying direction of
allelic effects, has previously been reported upon higher-resolution mapping of QTL in maize
(Graham et al. 1997), *Drosophila melanogaster* (Pasyukova et al. 2000; De Luca et al. 2003), mice (Mollah and Ishikawa 2011), and rat (Granhall et al. 2006).

Brouwer and St.Clair (2004) originally reported the linkage of *P. infestans* resistance QTL *lb5b* from *S. habrochaites* with QTL controlling plant shape and some reproductive traits. Subsequently, Johnson et al. (2012) described fractionation of this single resistance QTL into multiple QTL. In the present study, we used the same set of sub-NILs for chromosome 5 as Johnson et al. (2012) and mapped horticultural trait QTL linked to *P. infestans* resistance QTL. Other studies have reported linkage of horticultural trait QTL with disease and pest resistance genes or QTL introgressed from wild tomato species (Tanksley et al. 1998; Robert et al. 2001). Close linkage of QTL for disease resistance and horticultural traits has been reported for interspecific populations in other crop species including potato (Visker et al. 2003; Danan et al. 2011). Similar results have also been observed in intraspecific populations in potato (Bradshaw et al. 2004), pepper (Ben Chaim et al. 2001; Barchi et al. 2007), bean (Miklas et al. 2003; Ender and Kelly 2005; Mkwaila et al. 2011), and cacao (Brown et al. 2007). Horticultural traits associated with resistance QTL may be related causally to the resistance, for example traits such as plant height, lodging resistance, and canopy density that affect a plants’ ability to avoid environmental conditions conducive to infection. Alternately, the cosegregation of QTL for horticultural traits with resistance traits may be due to repressed recombination between loci controlling the two traits, particularly in introgressions from wild species.

**Tight Linkage and Pleiotropy:** Co-location of QTL controlling multiple horticultural traits with each *P. infestans* resistance QTL group (Figure 1) may be due either to tight linkage or pleiotropy (Brown 2002; Chen and Luebberstedt 2010). Our results suggest tight linkage between QTL groups controlling foliar resistance to *P. infestans* (LEAF, designated as LFRes;
Johnson et al. 2012) and maturity (Figure 1). This linkage is particularly interesting due to previously reported correlations between these traits and coincidence of maturity and resistance QTL in potato (see *P. infestans* Resistance and Maturity Traits, below). Each of the three horticultural QTL groups coincident with *P. infestans* resistance QTL groups (*Hort5-1*, 5-3, and 5-4) also contain QTL controlling other (non-maturity) traits, suggesting tight linkage to resistance QTL (Figure 1). Alternatively, QTL coincidence may be due to pleiotropy in some cases, but we cannot determine this from our current data as it would require additional studies involving thousands of segregating progeny (Mackay et al. 2009; Chen and Luebberstedt 2010).

Increased mapping resolution in our study revealed that some of the previously identified coincidences among QTL for horticultural and resistance traits in Brouwer and St.Clair (2004) were most likely due to tight linkage, rather than to pleiotropy. QTL within *Hort5-2* and 5-4 had 1-LOD support intervals that did not overlap with the two foliar resistance QTL groups *LFRes5-1* and *LFRes5-2* and their coincident stem resistance QTL groups *STRes5-1* and *STRes5-2*. This result suggests that the *Hort5-2* QTL for plant height, size, and shape are only linked, not pleiotropic, to *LFRes5-1* and *STRes5-1*. Similarly, the *Hort5-2* QTL and the *Hort5-4* QTL for fruit shape, Brix, canopy density, plant width, and plant shape are likely to be linked, not pleiotropic, to *LFRes5-2* and *STRes5-2*. Other studies of coincident QTL controlling different traits in tomato have also found the QTL to be tightly-linked, rather than pleiotropic, when mapped at higher resolution using sub-NILs (Monforte et al. 2001; Lecomte et al. 2004).

**Stability of QTL and QTL × Environment Interaction:** The majority of QTL mapped in our study were stably expressed over environments, detected with coincident or overlapping 1-LOD support intervals over multiple years and/or locations. Our inferences regarding QTL stability are limited to two locations across two years for all other traits because only the plant
architecture traits were evaluated in all four locations (Salinas and Davis). Of the 41 horticultural trait QTL mapped, 29 were stably expressed over multiple environments, including QTL for maturity, yield, fruit size and shape, Brix, and plant size and shape. In all years and locations, in *Hort5-1* QTL were detected for maturity, yield, fruit height, fruit size, and fruit weight, and in *Hort5-3* for plant height. The remaining 12 horticultural trait QTL were only mapped for a single location within a single year.

Inconsistent detection of QTL across environments (years, locations, etc.) may be due to interaction between expression of the QTL and the environments in which it is evaluated, described as QTL × E (Bernardo 2008; Xu and Crouch 2008; Mackay et al. 2009). Such interactions may reduce the efficiency of marker-assisted selection and may ultimately limit the utility of beneficial QTL alleles, depending on the target environments (Xu and Crouch 2008). Traits exhibiting QTL × E in our study included yield, fruit height, fruit shape, fruit size, Brix, pH, canopy density, and plant shape. While many mapping studies conducted across multiple environments report QTL that are stable, QTL instability (i.e., QTL × E) is also common. For example, studies in tomato (Bernacchi et al. 1998b; Frary et al. 2004), potato (Constanzo et al. 2005), and maize (Peng et al. 2011) all identified QTL that were stable across multiple environments and others that exhibited QTL × E interactions.

Comparison of our results to those of other QTL mapping studies in tomato was limited because some studies were conducted in only a single environment (Monforte and Tanksley 2000; Van Der Knaap et al. 2002; Semel et al. 2006) or did not test for or report on genotype × environment interactions (Causse et al. 2007; Mathieu et al. 2009). Consequently, we focused our comparisons to studies that mapped QTL in tomato populations evaluated across multiple locations and/or years and that tested for environmental interactions. In these studies, detection
of QTL in a single environment was observed for 25-50% of mapped QTL, (Frary et al. 2004; Johnson et al. 2012), 10-25% (Bernacchi et al. 1998b), and <10% of detected QTL (Eshed et al. 1996; Eshed and Zamir 1996; Tanksley et al. 1996; Brouwer and St.Clair 2004; Do et al. 2010). Our results (29% of QTL detected in only a single environment) fall within the upper range of these studies.

QTL × E may also explain differences in the direction of allelic effects at QTL in some locations versus others, as exhibited by QTL controlling plant architecture in our study. A QTL in Hort5-1 increased plant height in both Davis locations in 2009 but decreased plant height in both Salinas locations in 2010, and a similar pattern was observed for plant width QTL in Hort5-3 (Table 4). Other studies have reported changes in the direction of allelic effect depending on environment, for example QTL controlling yield, fruit color, and Brix in tomato (Bernacchi et al. 1998a), yield in maize (Bouchez et al. 2002; Moreau et al. 2004) and plant height and kernel weight in wheat (Campbell et al. 2003).

**QTL Comparisons to Previously Mapped QTL in Tomato and Potato:** The map resolution of most previously reported QTL are not sufficient for determining precise locations of QTL. Nonetheless, comparisons based on common markers and informed by genomic sequence data suggested correspondence of some of our QTL with previously reported chromosome 5 QTL for disease resistances and horticultural traits in interspecific tomato populations. Bernacchi et al. (1998b) reported QTL for yield, soluble solids (Brix), and maturity associated with marker TG69 in lines derived from *S. lycopersicum* × *S. habrochaites*. These QTL may correspond to our Hort5-3 group QTL for yield, Brix, and days to first ripe fruit, although the low resolution of their map and single marker regression analysis precluded more precise QTL localization. In lines derived from *S. lycopersicum* × *S. pimpinellifolium*, Brewer et
al. (2007) reported a QTL for heart shaped fruit in the interval TOM152-TG60 that may correspond to QTL we detected for fruit shape in *Hort5-1, 5-2, or 5-3*. They also mapped a QTL for distal blockiness (a trait defined by Tomato Analyzer software) in the interval TG60-TG185 that may be coincident to QTL we detected for fruit shape in *Hort5-3 or 5-4*. Using *S. pennellii* introgression lines (ILs), Causse *et al.* (2004) identified a QTL for pH in IL5-3 that may correspond to our *Hort5-1* group QTL for pH, and QTL in IL5-4 for Brix and other sugar-related traits that may be coincident to our *Hort5-3 and/or 5-4* QTL for Brix. With *S. pennellii* ILs, Eshed and Zamir (1996) detected QTL in IL5-4 for plant weight, Brix, and yield that may be coincident to our *Hort5-3* QTL for plant size, Brix, and yield or to our *Hort5-4* QTL for plant size and Brix. Jones *et al.* (2007) used *S. pennellii* ILs to map *SP5G*, a paralog of the *self-pruning* (*sp*) gene for determinant growth, to interval TG351-TG60, which is coincident to the upper portion our *Hort5-3* group and includes QTL for plant height, plant width, and plant size. The wild allele from *S. pennellii* at the *SP5G* locus delayed the expression of determinacy, which resulted in increased plant height. We observed similarly increased plant height in sub-NILs containing the *S. habrochaites* allele compared to those with the cultivated allele at TG60, which is closely linked to *SP5G*. Semel *et al.* (2006) detected QTL in *S. pennellii* IL5-3 for biomass, Brix, seed weight, and yield that may by coincident with our *Hort5-1, Hort5-2*, and/or *Hort5-3* QTL for plant size, plant height, plant width, Brix, seed weight, and yield.

Previous reports of resistance QTL corresponding to the *lb5b* introgressed region are detailed in Johnson *et al.* (2012). Several studies have described QTL for resistance to *P. infestans* on chromosome 5 of potato, a close relative of tomato. The majority of these studies report a resistance QTL located between potato markers GP21 and GP179 (Collins *et al.* 1999; Visker *et al.* 2003; Visker *et al.* 2005; Achenbach *et al.* 2009; Danan *et al.* 2011). This interval
coincides with the upper extent of the *S. habrochaites* introgression in NIL5, which suggests that the potato QTL at that interval may correspond to *LFRes5-1* and *STRes5-1*. Some of these studies also reported linkage between the QTL for resistance and QTL for delayed maturity (Collins *et al.* 1999; Visker *et al.* 2003; Visker *et al.* 2005). This maturity QTL in potato may correspond to our maturity QTL at *Hort5-1*.

**P. infestans Resistance and Plant Maturity:** *P. infestans* resistance (i.e., lower STEM or LEAF values) was significantly negatively correlated with earlier maturity in the sub-NILs (Table 3), indicating that later maturity was associated with increased resistance. As previously noted, resistance QTL groups were also co-located with QTL for maturity traits (Figure 1). The observed QTL correspondence was found to be unlikely due to chance alone, according to a statistical test based on the hypergeometric probability function. A number of studies in potato have reported a significant positive correlation of increased resistance to *P. infestans* with late maturity (Toxopeus 1958; Collins *et al.* 1999; Bradshaw *et al.* 2004; Danan *et al.* 2009). Linkage of resistance and maturity QTL in potato was noted on chromosome 5, which is syntenic to tomato chromosome 5 (Collins *et al.* 1999; Oberhagemann *et al.* 1999; Visker *et al.* 2003; Bradshaw *et al.* 2004; Visker *et al.* 2005). Overall, our findings agree with others’ observations regarding the correlation of *P. infestans* resistance with maturity and linkage of QTL controlling these traits on chromosome 5.

Alignment of our tomato chromosome 5 map with the potato MetaQTL map (Danan *et al.* 2011) using common markers, facilitated by the Tomato-Expen 2000 map (Fulton *et al.* 2002b) on SGN (<http://solgenomics.net>), suggests that the potato QTL for resistance and maturity that mapped to marker interval GP21-GP179 likely corresponds to our *LFRes5-1*, *STRes5-1* and *Hort5-1* QTL groups, respectively. This QTL coincidence suggests conservation
of gene function and synteny between these closely-related genera for genes controlling these
two traits within this region of chromosome 5. Genome-wide conservation of gene function and
order between these genera are supported by evolutionary studies of the Solanaceae (Grube et al.
2000; Fulton et al. 2002a; Wu and Tanksley 2010), as well as by direct comparisons of the
tomato and potato genome sequences (Sato et al. 2012).

Late plant maturity may contribute to increased resistance to *P. infestans* due to temporal
variation in inoculum production and/or increased susceptibility of plants during the seedling and
reproductive growth phases (Collins et al. 1999). These factors have primarily been investigated
in potato. During an epidemic *P. infestans* inoculum production increases and then decreases as
uninfected host tissue becomes scarce and/or the environment becomes less favorable
(Ferrandino 2012). Young plants tend to be more susceptible, but exhibit increased resistance
during vigorous vegetative growth before becoming more susceptible again during their
reproductive phase (Collins et al. 1999). In our study, earlier maturing lines may have exhibited
greater susceptibility due to the coincidence of favorable environmental conditions for increased
*P. infestans* inoculum production with their more susceptible reproductive growth phase. This
explanation was supported by our observations that, in both years in the field, symptoms of *P.
infestans* infection were first observed while the earlier lines were flowering and setting fruit but
the later maturing lines were still growing vigorously. Additional experiments would be required
to determine whether the observed correspondence between maturity and resistance had a
physiological basis or was merely a coincidence of the planting dates and onset of environmental
conditions favorable to pathogenesis.

**Implications for Tomato Breeding:** Our study revealed a complex genetic architecture
of QTL for horticultural traits and *P. infestans* resistance within an introgressed region of
chromosome 5 from *S. habrochaites*, primarily due to linkage and/or pleiotropy between resistance QTL and horticultural trait QTL and the presence of QTL × E for some traits. This complexity presents challenges for use of wild species QTL alleles in breeding. The beneficial QTL alleles can be useful for tomato breeding if progeny without unfavorable repulsion phase linkages are obtained via recombination. In addition, suitable environments can be targeted for deployment of alleles exhibiting environmental interactions, and complementary genetic backgrounds for expression of these alleles can be identified.

We identified favorable progeny sub-NILs that resulted from recombination between linked QTL with alleles in repulsion, for example, at the *Hort5-3* QTL for Brix (39-45 %PV) and the *Hort5-2* QTL for fruit weight (10-15 %PV) (Table 4). Based on the genotypes and trait phenotypes of the sub-NILs, the beneficial alleles from *S. habrochaites* at these two horticultural trait QTL and at the *P. infestans* resistance QTL group of largest phenotypic effect (*LFRes5-2*, 18-47 %PV; Johnson *et al.* 2012) are linked in coupling and not pleiotropic to the QTL for which the wild allele has the largest negative effects (%PV) upon maturity, yield, fruit height, fruit size and weight in *Hort5-1* (Figure 1 and Table 4). Co-location of these beneficial QTL alleles linked in coupling makes the marker interval TG23-T1541 a particularly desirable target for marker-assisted breeding. It would be helpful to identify other recombinants with additional favorable allelic combinations at linked QTL, particularly if the resistance QTL *LFRes5-1* and *STRes5-2* are to be used to develop cultivars with improved resistance as well as acceptable horticultural trait phenotypes.

Slightly negative phenotypic effects of linkage drag need not preclude the use of QTL in certain breeding situations. For example, the *Fhb1* QTL for resistance to Fusarium head blight (*F. graminearum*) in wheat has been used in MAS breeding, despite the linkage of this QTL to
loci causing a minor delay in heading date (Haeberle et al. 2009). Sub-NILs possessing the wild allele at \textit{Hort5-3}, \textit{LFRes5-2}, and \textit{STRes5-2} QTL, but lacking the wild parent allele at \textit{Hort5-1}, \textit{5-2}, \textit{LFRes5-1} and \textit{STRes5-1} QTL, such as sub-NIL 08GH5516 or -6261, may be more immediately useful for breeding improved tomato cultivars since they possess more favorable horticultural trait phenotypes. MAS breeding for target wild alleles at \textit{Hort5-3} simultaneously with background selection against wild alleles at \textit{Hort5-4} in segregating progeny populations from crosses between these donor lines and other cultivated tomato lines would eliminate the negative effects of wild alleles at \textit{Hort5-4}, producing more useful breeding lines.

Breeders prefer to deploy QTL alleles exhibiting stable expression across a wide range of production environments to maximize applicability for crop improvement. However, the presence of QTL × E does not necessarily impede the use of a QTL in breeding for improved cultivars. QTL for specific environments may be useful if those environments happen to be the major target environments for production of that crop (Paterson et al. 1991; Asins 2002; Paterson et al. 2003). By integrating crop modeling and MAS, QTL with environmental interactions can be exploited in breeding crop ideotypes for particular environments (Yin et al. 2003; Cooper et al. 2009). The favorable QTL identified in our experiments for Brix and fruit weight in \textit{Hort5-3} were detected in both locations in which they were evaluated, but only in one of two years. Further assessment of the stability of these QTL effects in target environments for processing tomato production would determine their value for cultivar improvement.

Truncation selection for multiple traits resulted in the selection of nine sub-NILs that had improved resistance relative to processing tomato cultivar E6203: 08GH5516, -5616, -5861, -6042, -6261, -6288, -6321, -6345, and -6805 (Table S1). In addition, two (08GH5616 and -5861) had significantly higher Brix than their cultivated parent, E6203, in every environment in which
they were evaluated. The selected sub-NILs can be used directly as donor lines for MAS breeding to improve fruit weight, Brix, and *P. infestans* resistance in tomato cultivars (Collard *et al.* 2005; Foolad and Panthee 2012). Additionally, they can be exploited as parents in crosses with other trait QTL donor lines to combine the beneficial effects of QTL alleles for desirable traits via MAS breeding, a technique known as QTL pyramiding (Collard and Mackill 2008; St. Clair 2010; Wang *et al.* 2012). Our most *P. infestans*-resistant sub-NILs with the most acceptable horticultural phenotypes (e.g., 08GH5516 or -6261) could be intercrossed with selected sub-NILs containing late blight disease resistance QTL from chromosome 11 (Johnson *et al.* 2012; J.E. Haggard, E.B. Johnson, and D.A. St.Clair., unpublished results) to breed for improved resistance. Similar efforts could also be pursued for use of beneficial wild alleles at QTL for Brix and fruit weight in breeding for improved horticultural traits in processing tomato.

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FIGURE LEGENDS

FIGURE 1: QTL mapped to a chromosome 5 region introgressed from *Solanum habrochaites* to *S. lycopersicum.*

Horticultural trait QTL and *Phytophthora infestans* resistance QTL groups detected in chromosome 5 sub-NILs evaluated in 2009 and 2010 field experiments, sorted by trait class. Left of linkage map are horticultural trait QTL group names, locations and distances in cM; right of linkage map are *P. infestans* resistance trait QTL groups (*LfRes* and *StRes* refer to LEAF and STEM resistance, respectively; Johnson *et al.* 2012) and QTL detected for horticultural traits, sorted by trait class. Boxes and whiskers show 1-LOD and 2-LOD intervals, respectively. Arrows on QTL bars indicate LOD peak locations. QTL names are given by trait, location(s) and year evaluated (see Materials & Methods). The effect of the *S. habrochaites* allele at a QTL is indicated after the QTL name: a (-) indicates a decrease in that trait value.
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<td>Area under the disease progress curve (AUDPC) for stem symptoms</td>
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TABLE 2: SUMMARY OF ANALYSES OF VARIANCE PERFORMED ON TRAIT DATA.

*F* test values and *R*^2^ values are presented for each analysis by trait, year, and location or combination of locations (see Materials and Methods).

*R*^2^ indicates the fit of the data to the linear additive model for each analysis. Late Blight Resistance results are from Johnson *et al.* (2012).

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* = \( P \leq 0.05 \); ** = \( P \leq 0.01 \); *** = \( P \leq 0.001 \)

--- = not included in model
TABLE 3: TRAIT CORRELATIONS

Pearson correlation coefficients ($r$) among *Phytophthora infestans* resistance traits (LEAF and STEM, data from Johnson *et al.* 2012) and horticultural traits were performed using genotype means. Only significant correlations greater than or equal to 0.4 are presented. Trait names are given by year according to trait and location(s) (see Materials & Methods).

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* = $P \leq 0.05$; ** = $P \leq 0.01$; *** = $P \leq 0.001$
Table 4: SUMMARY OF SIGNIFICANT QTL FOR HORTICULTURAL TRAITS

Group indicates coincident QTL, as defined by coincidence of the 1-LOD intervals. $R^2$ values are the proportion of phenotypic variation explained by the marker-trait association. Allele Direction is the direction of the effect of the *S. habrochaites* allele at that QTL, in terms of the trait being measured. 1-LOD Support Interval positions refer to the cM distances on the linkage map for the introgressed region from *S. habrochaites*. See Johnson et al. (2012) for LEAF and STEM QTL results.

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<td>1 &amp; 2</td>
<td>(-)</td>
<td>3.0-8.7</td>
<td>At2g39950-At4g12590</td>
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<td></td>
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<td>Hort5-3</td>
<td>2009</td>
<td>3 &amp; 4</td>
<td>(+)</td>
<td>7.3-9.4</td>
<td>At5g49510-At4g12590</td>
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<td>2010</td>
<td>3 &amp; 4</td>
<td>(+)</td>
<td>6.3-9.4</td>
<td>At5g49510-At4g12590</td>
</tr>
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Figure 1: Linkage map of chromosome 5 introgressed region from *S. habrochaites, Phytophthora infestans* resistance QTL groups and QTL for horticultural traits from 2009 and 2010 field experiments sorted by trait class. Below linkage map are horticultural trait QTL group locations and distances in cM; above linkage map are resistance trait QTL groups (*LfRes* and *StRes* refer to LEAF and STEM resistance, respectively; Johnson *et al.*, 2012) and QTL detected for horticultural traits. Boxes and whiskers show 1-LOD and 2-LOD intervals, respectively. Arrows on QTL bars indicate LOD peak locations. QTL names are given by trait, location(s) and year evaluated (see Materials & Methods). The effect of the *S. habrochaites* allele at a QTL is indicated after the QTL name: a (-) indicates a decrease in that trait value.