

UC-Davis Tomato Breeding and Genetics Research Program

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Tomato (*Lycopersicon* species)



Wild tomato species: Source of genetic diversity (V_G) for agricultural traits

- Cultivated tomato (*L. esculentum*)
 - domestication bottlenecks → severe reduction in V_G → limits selection gain
- Wild *Lycopersicon* species → rich source of V_G
 - Resistance to biotic stresses (pathogens, pests)
 - Resistance to abiotic stresses (cold, heat, drought, salt)
 - Nutritional and fruit quality traits

Improving Quantitative Traits in Plant Breeding

- Target selected beneficial QTLs from wild tomato species for marker-assisted (MAS) breeding
- Issue: undesirable linked genes (linkage drag)
- *Ultimate target for MAS: Genes underlying QTLs that control the trait phenotype*
- *Selection for target genes to minimize linkage drag & enhance crop improvement*

Phytophthora infestans (Late Blight): Infects Tomato and Potato



Symptoms: water-soaked lesions, tissue necrosis on leaves, stems, fruit → can spread rapidly → plant death

- Cultivated tomato (and potato) lack resistance
- Wild species are resistant to *P. infestans*

Genetic resistance to *P. infestans*

- Resistance present in wild species:
 - qualitative (controlled by dominant ‘*R*’ genes)
 - quantitative (QTLs)
- *R*-genes: exhibit classic ‘gene-for-gene’ relationship with pathogen *Avr* loci
- New isolates quickly overcome single *R*-genes
- Quantitative resistance: longer lasting, ‘durable’?

QTL Mapping of Quantitative Resistance to Late Blight in Tomato: Approach

- Reciprocal backcross populations:

L. esculentum (SC) × *L. hirsutum* LA2099 (SI)



♀ *L. esc.* × ♂ *F₁ hybrid* (SI) ♀ × ♂ *L. hir.*



BC₁-E (n = 213)



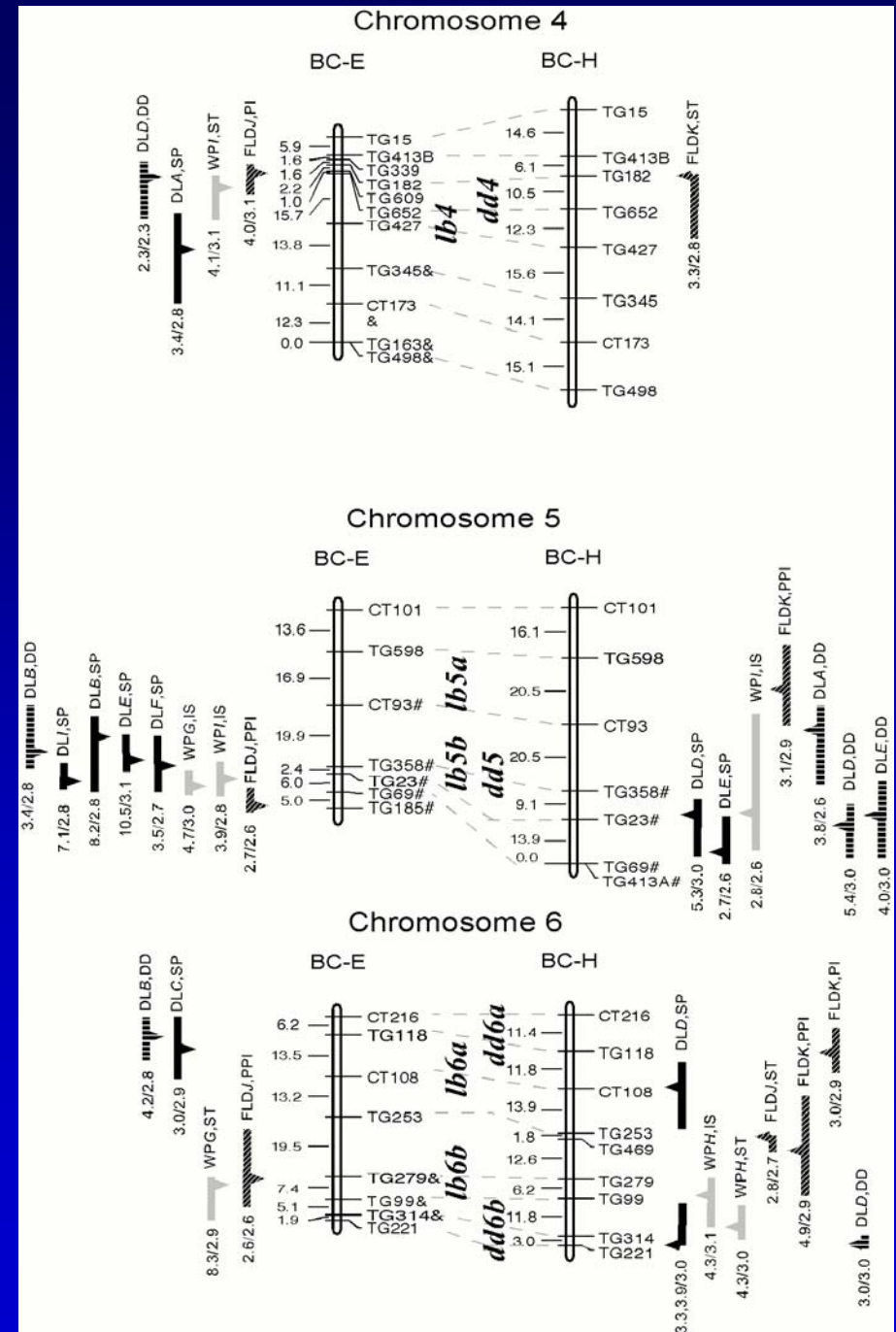
BC₁-H (n = 133)

{clonal propagation of each BC₁ plant}

- Disease phenotyping: field, whole plants, leaflets
- Replicated experiments over 2 years

Late blight resistance QTLs mapped in reciprocal BC₁ *L. esculentum* × *L. hirsutum* populations

Chromosomes 4, 5, & 6



Mapping of LB Resistance QTLs in *L. esculentum* × *L. hirsutum*: Results

- QTLs detected across experiments and assays:
QTLs lb1a, lb2a, lb3, lb4, lb5b, lb6ab & lb11b
 - % phenotypic variation per QTL: 7% to 27%
 - No coincidence with locations of *Ph1, Ph2, Ph3* (known tomato *P. infestans* qualitative *R* genes)
- These QTLs represent a novel source of resistance to *P. infestans* in tomato

Fine mapping of LB resistance QTLs: *lb4, lb5b, lb11b*

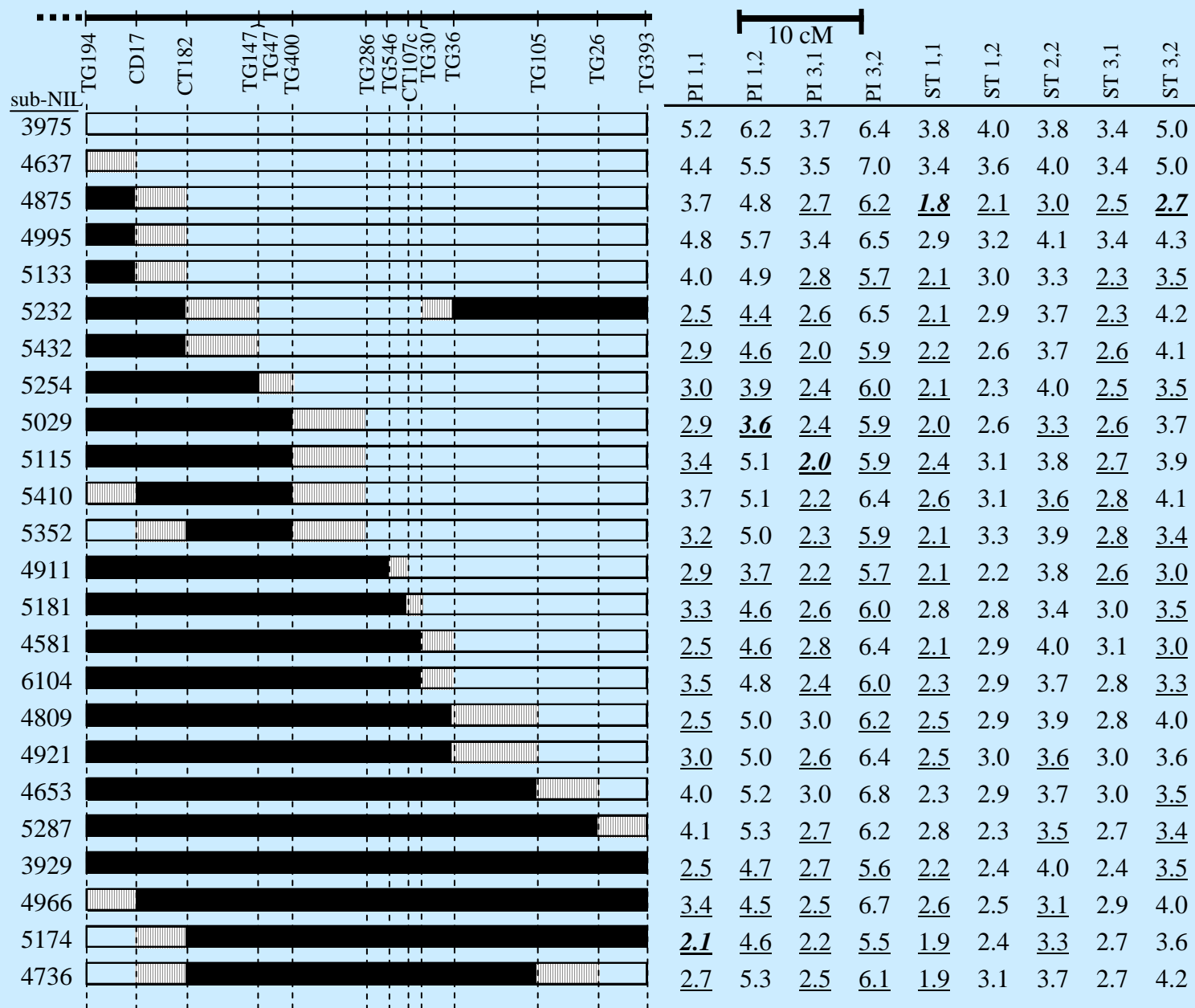
- QTL regions are large (> 25 cM) \rightarrow Refine position by fine-mapping
- Recombinant sub-near-isogenic lines (sub-NILs) for each single QTL region in an *L. esculentum* background used to perform fine mapping \rightarrow narrow location of QTL
- *Is resistance associated (+/-) with horticultural traits?*
- *Identify target regions for high-resolution mapping and MAS breeding*

LB-susceptible *L. esculentum*

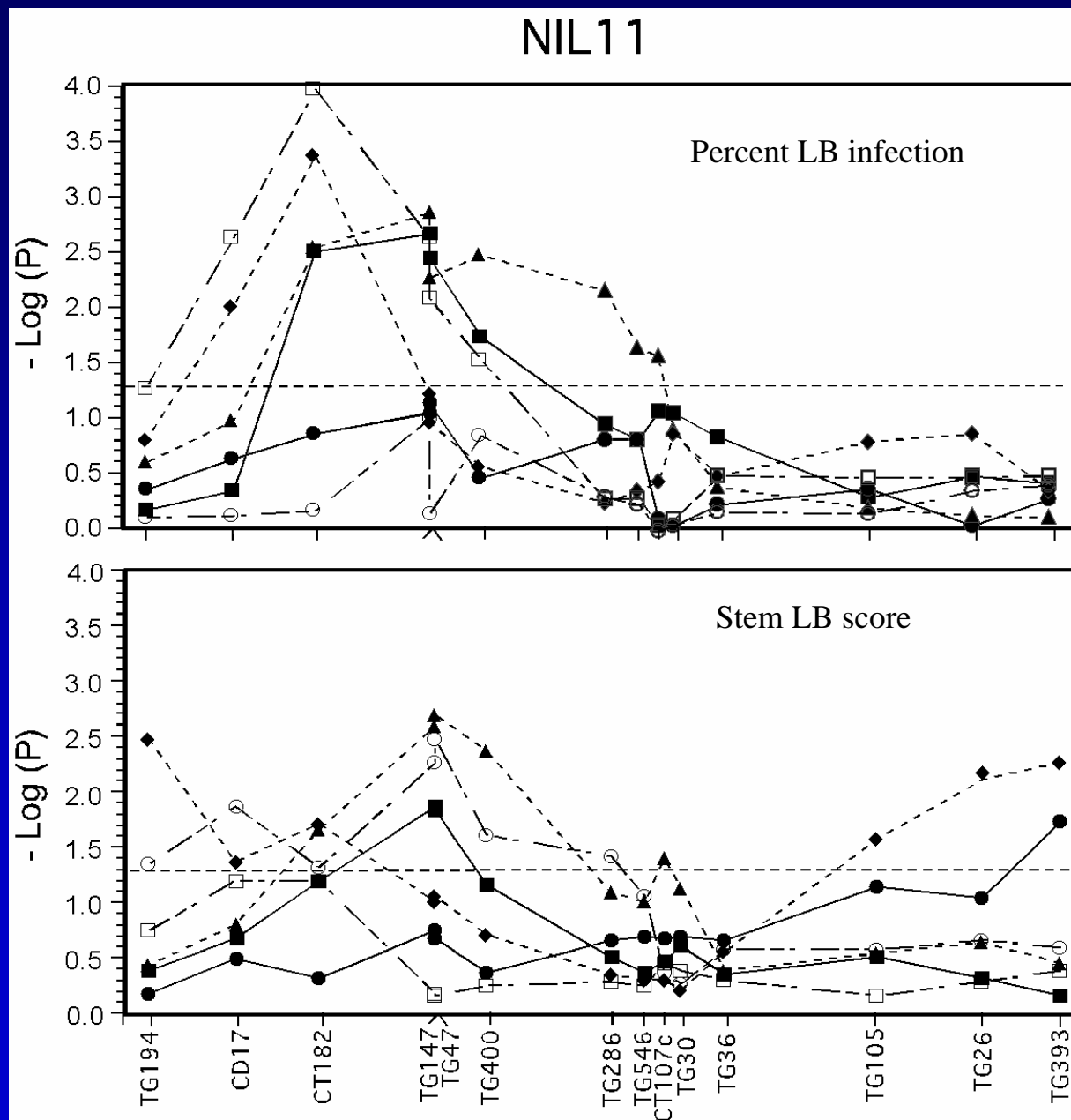
BC₄ NIL for a resistance QTL
introgressed from *L. hirsutum*



NIL 11 sub-NIL genotypes and LB resistance means (by trait, location, date), LSD comparisons



NIL11 sub-NILs marker-genotype mean *t*-tests: LB resistance



Fine mapping of LB resistance QTLs

lb4, lb5b, lb11b: Results

- Tomato QTLs *lb4, lb5b, lb11b* mapped to 5 - 9 cM intervals:
 - All 3 coincide with potato LB resistance QTLs
 - *Lb5* and *lb11* coincide with several horticultural traits
 - *Lb5b* coincides with Solanaceae pathogen/pest R-genes or R-gene clusters
- *QTL/QTL and QTL/R-gene coincidence suggests functional conservation in Solanaceae*

High-resolution mapping of LB resistance QTLs *lb5b* and *lb11b*

- QTLs *lb5b* and *lb11b* from *hirsutum* each conferred resistance to *P. infestans* in *L. esculentum* background
 - Indicates QTLs additive in effect
 - Coincidence with horticultural trait loci (+/- linkage drag)
- Refine LB resistance QTL locations by high-resolution mapping with recombinant sub-NIL progeny
- Evaluate potential beneficial alleles and linkage drag for horticultural traits

Identification of sub-NIL recombinants for late blight resistance QTLs using marker-assisted selection



High resolution mapping of LB resistance QTLs *lb5b* and *lb11b*

- Sub-NIL recombinant lines for QTLs *lb5b* and *lb11b* marker selected and advanced to homozygosity
 - BC5S4 families: ~ 60 per QTL
 - Replicated field trials (Salinas and Davis) in 2009
- Evaluate LB resistance and horticultural traits of recombinant families in field trials
- Use trait data to map trait QTLs and determine linkage among loci

LB resistance QTLs: Next Steps

- Complete high-resolution mapping (*lb5b* & *lb11b*)
- Combining ability study with selected recombinants in F₁ hybrid combinations with commercial inbreds

Future:

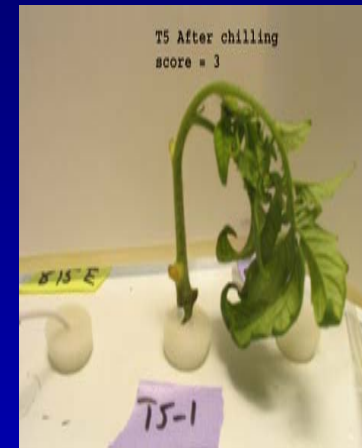
- ID candidate genes for QTL via genomic sequence analysis
→ do functional tests → *identify gene(s) underlying QTL that control the resistance phenotype*
- Determine relationship of resistance QTLs to *R*-genes → comparative genomics within Solanaceae
- MAS transfer of *lb* QTLs for breeding tomato

Chilling Injury and Temperature-Induced Water Stress in Tomato

- Temperatures below 10°C damage cultivated tomato, cause crop loss and shortened production season
- Wild *Lycopersicon hirsutum* LA1778 originates from high altitudes (10,000 feet) and thrives at chilling temperatures that damages cultivated tomato
- What is genetic and physiological basis of resistance to chilling and temperature-induced water stress?

Root chilling reduces water transport to shoots & leaves, causing water stress

- If roots are chilled (4-6°C):
 - Shoots of cultivated tomato wilt because stomata stay open, causing water loss.
 - Shoots of *L. hirsutum* LA1778 maintain normal water content by closing stomata, preventing water loss. Root-to-shoot signaling is involved.



QTL Mapping of Shoot Turgor Maintenance under Root Chilling

- Interspecific backcross (BC₁) population:

L. esculentum (SC) × *L. hirsutum* LA1778 (SI)



♀ *L. esculentum* × F₁ hybrid (SI)



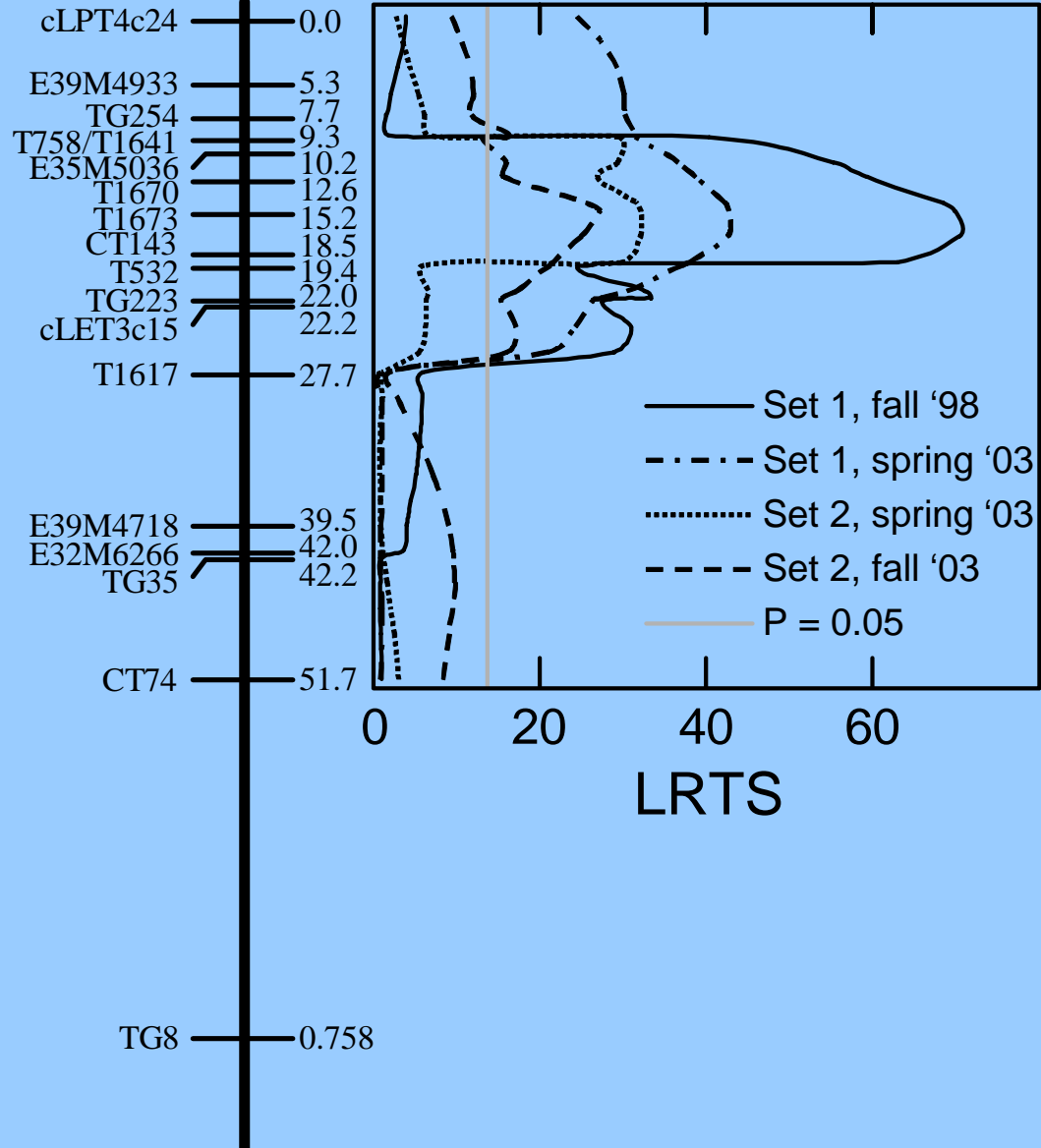
BC₁ set 1 (n = 196) + **BC₁ set 2** (n = 204)

- Evaluated BC₁ population sets for shoot turgor maintenance after 2 hr root exposure to 4°C in chilled nutrient solution in replicated experiments
- Major QTL on chr 9 (*stm9*) detected consistently

Ch9

QTL *stm9*
detected
consistently
across
experiments

Marker Dist. (cM)



← peak

QTL *stm9*: Physiology and Genetics

- NILs confirmed positive phenotypic effect of *hirsutum* alleles at *stm9*
- Fine-mapping with sub-NILs located *stm9* to ~2.7 cM region on chr 9
- Recombinant sub-NILs being generated for high-resolution mapping of *stm9*
- *Future goal: ID candidate gene(s) for stm9*

QTL *stm9*: Physiology and Genetics

- Reciprocal root-shoot grafted plants with various genotypes for *stm9* alleles indicated root-shoot communication involved in stomatal closure to preserve shoot turgor
- Characterizing physiological traits of sub-NILs differing for alleles (H versus E) at *stm9*
- Analyzing xylem sap with proteomics and metabolomics to determine signaling molecules
- *Future goal: Role of *stm9* in recovery from water stress episodes under field conditions*

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