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 $\rightarrow$ severe reduction in $V_G$ $\rightarrow$ limits selection gain

- Wild *Lycopersicon* species $\rightarrow$ 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:
  \[L. \text{esculentum (SC)} \times L. \text{hirsutum LA2099 (SI)}\]
  ↓
  \[♀ L. \text{esc.} \times ♂ \underline{F_1 \text{hybrid}} (\text{SI}) ♀ \times ♂ L. \text{hir.}\]
  ↓
  \[\text{BC}_{1}-\text{E} (n = 213) \quad \text{BC}_{1}-\text{H} (n = 133)\]
  \{clonal propagation of each BC\text{$_1$} 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) → 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 → narrow location of QTL
- Is resistance associated (+/-) with horticultural traits?
- Identify target regions for high-resolution mapping and MAS breeding
LB-susceptible *L. esculentum*  

BC$_4$ NIL for a resistance QTL introgressed from *L. hirsutum*
NIL 11 sub-NIL genotypes and LB resistance means (by trait, location, date), LSD comparisons

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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 \textit{lb5b} and \textit{lb11b}

- QTLs \textit{lb5b} and \textit{lb11b} from \textit{hirsutum} each conferred resistance to \textit{P. infestans} in \textit{L. esculentum} background
  - Indicates QTLs additive in effect
  - Coincidence with horticultural trait loci (+/- linkage drag)

- \underline{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 $F_1$ 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 ($BC_1$) population:
  
  \[
  L. \text{esculentum (SC)} \times L. \text{hirsutum LA1778 (SI)} \]
  
  \[
  \downarrow \quad \♀ L. \text{esculentum} \times F_1 \text{hybrid (SI)} \]
  
  \[
  BC_1 \text{ set 1 (n = 196)} + BC_1 \text{ set 2 (n = 204)} \]

- Evaluated $BC_1$ 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
QTL \textit{stm9} detected consistently across experiments

\begin{itemize}
  \item \texttt{GDist} (cM)
  \item \texttt{Marker}
  \item \texttt{E39M4933}
  \item \texttt{TG254}
  \item \texttt{T758/T1641}
  \item \texttt{E35M5036}
  \item \texttt{T1670}
  \item \texttt{T1673}
  \item \texttt{CT143}
  \item \texttt{T532}
  \item \texttt{TG223}
  \item \texttt{cLET3c15}
  \item \texttt{T1617}
  \item \texttt{E39M4718}
  \item \texttt{E32M6266}
  \item \texttt{TG35}
  \item \texttt{CT74}
  \item \texttt{TG8}
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\begin{itemize}
  \item \texttt{LRTS}
  \item \texttt{Set 1, fall '98}
  \item \texttt{Set 1, spring '03}
  \item \texttt{Set 2, spring '03}
  \item \texttt{Set 2, fall '03}
  \item \texttt{P = 0.05}
\end{itemize}

\textbf{← 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*
Acknowledgements

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Sylvaine Coulibaly
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Glenn Kohler
Liz Jones

*current members

Collaborators:
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Lesley Randall

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