

Black Shank Resistance and Leaf Surface Chemistry of Flue-Cured Breeding Lines Nearly-Isogenic for QTLs of Beinhart 1000 Origin

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Objectives

- Identified sources of quantitative or partial resistance to black shank
- Developed near-isogenic lines
- Evaluated two quantitative trait loci (QTLs) conferring black shank resistance
- Evaluated leaf surface chemistry traits co-segregating with QTL on linkage group 15 (*Phn15.1*)

Outline

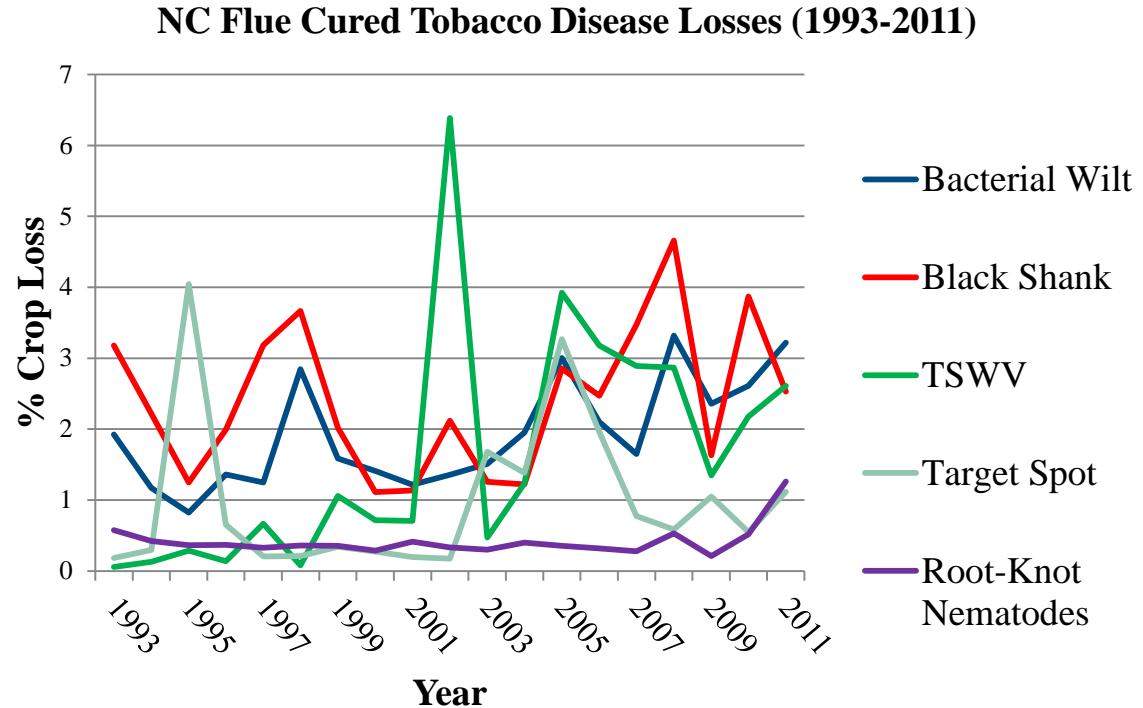
- Background
- Development of Near-isogenic lines
- Evaluation of Near-isogenic lines
 - Black shank resistance
 - Leaf surface chemistry
- Continuing research

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Black shank is the most important flue-cured tobacco disease in the U.S.

- Causal organism:
Phytophthora nicotianae





Black shank symptoms in NC71

Controlling black shank with genetics

- Single gene resistance
 - *Ph* gene ineffective against Race 1 isolates
 - *Wz* lines being evaluated
- Quantitative sources of partial resistance
 - Non-race specific
 - Polygenic

Beinhart 1000 x Hicks Mapping population

Beinhart 1000

- Cigar-type variety
- High levels of polygenic resistance

Hicks

- Flue-cured variety
- Highly susceptible

1. Doubled haploid (DH) population developed with 117 lines
2. Genotyped with SSR markers
3. Mapped genomic regions contributing to black shank resistance

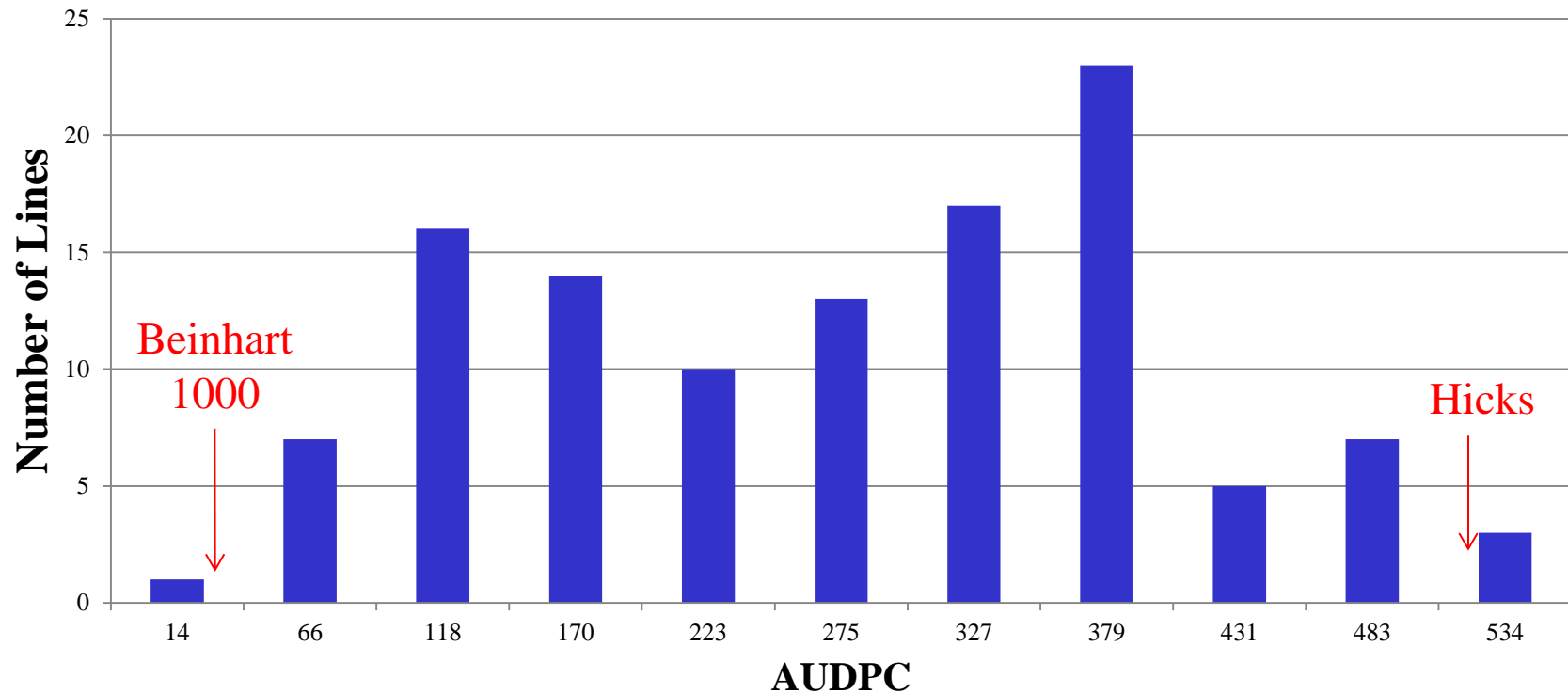


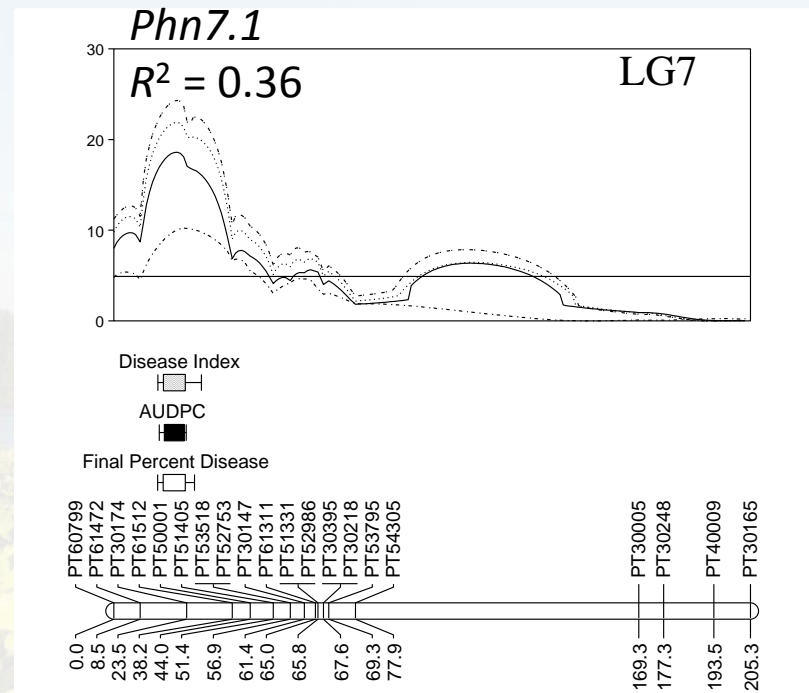
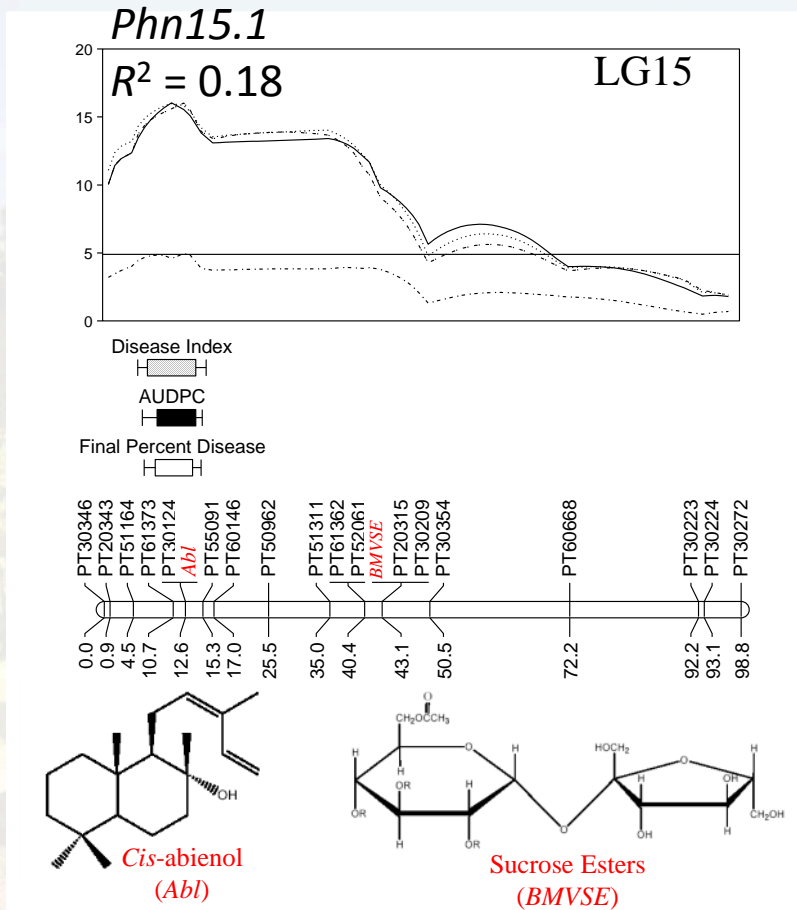
DH line

Beinhart 1000

Work by V. Vontimitta and Patrick McCachren

AUDPC Distribution for Beinhart 1000 x Hicks Doubled Haploid Lines



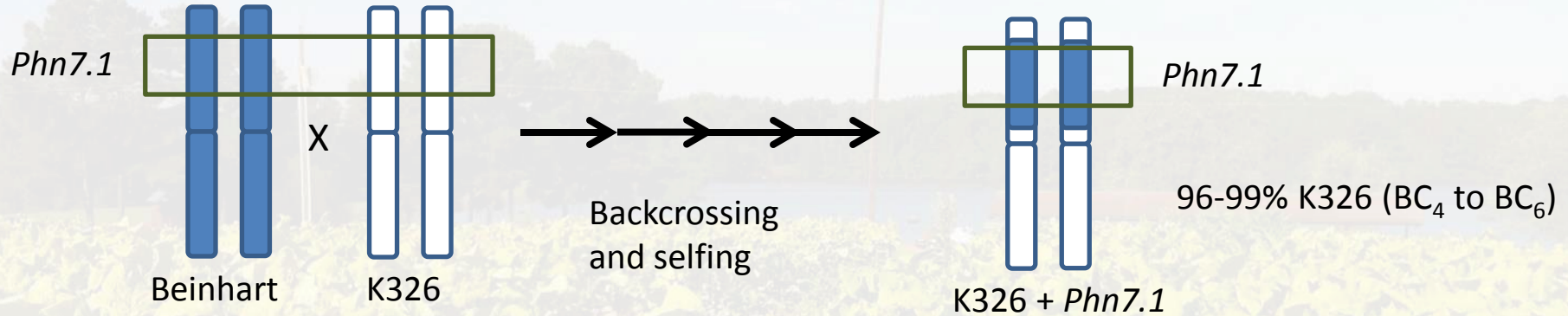


- Major QTL in *Phn7.1* interval also identified in Hicks x Florida 301
- Same or related QTL present in K326

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Near-isogenic lines



- **Donor alleles:** *Phn7.1* and *Phn15.1* QTLs
- **Recurrent backgrounds:** Hicks and K326
- **Marker-assisted backcrossing:**
 - Flanking markers, spaced ~20 cM apart

Development of Near-isogenic lines

- Hicks
 - Hicks + *Phn7.1*
 - Hicks + *Phn15.1*
 - Hicks + *Phn7.1* + *Phn15.1*
- K326
 - K326 + *Phn7.1*
 - K326 + *Phn15.1*
 - K326 + *Phn7.1* + *Phn15.1* in development

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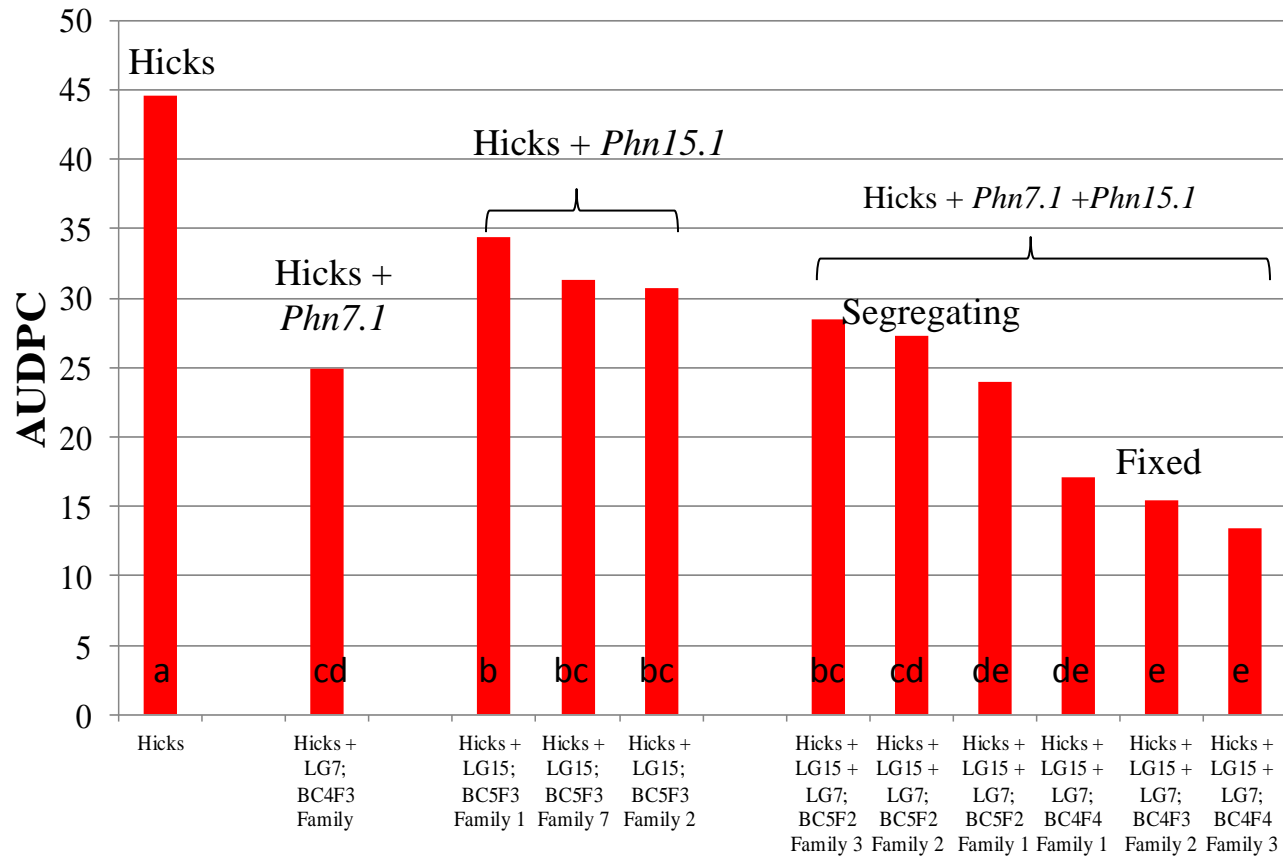
Black shank
resistance of
Hicks NILs



Hicks

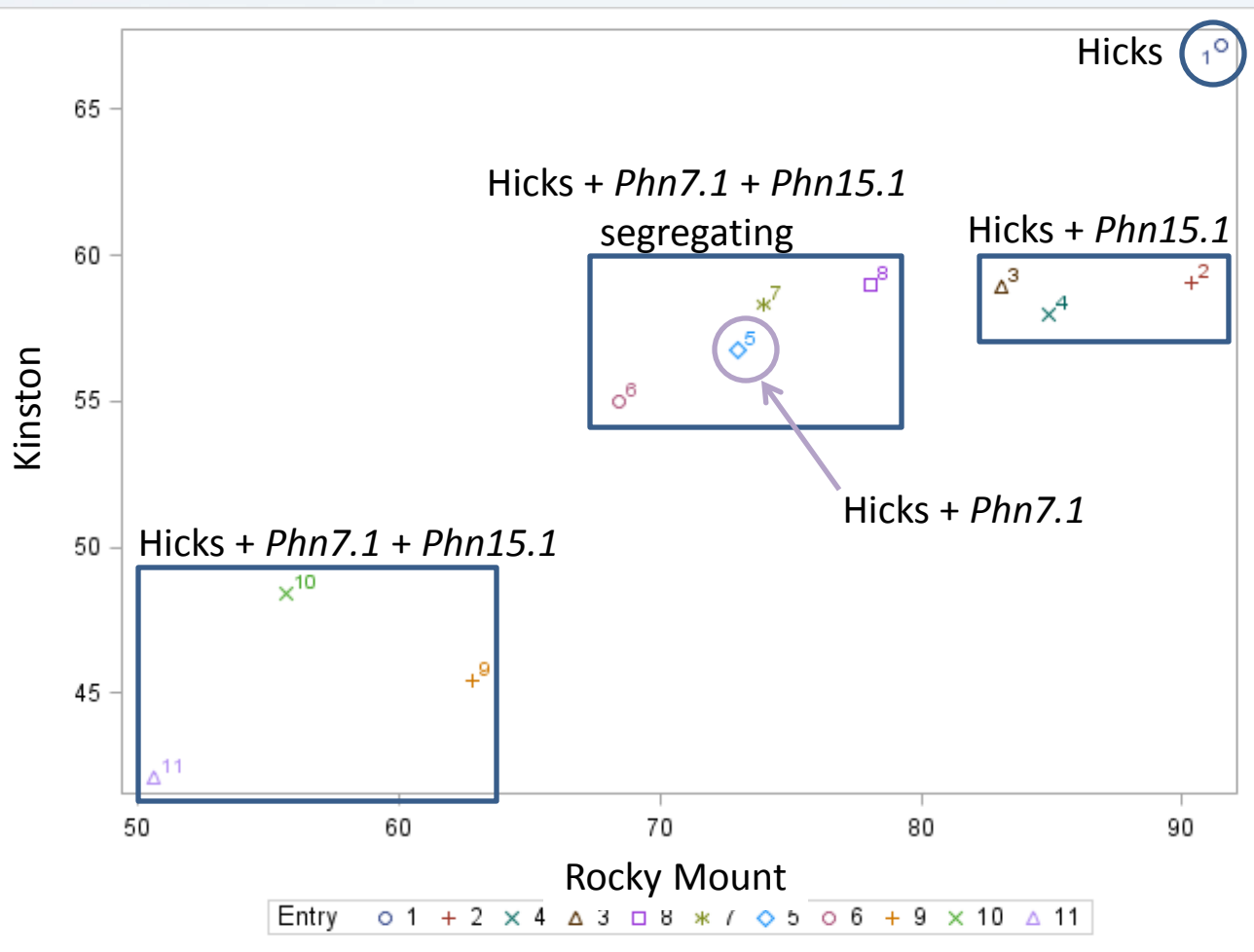
Hicks + *Phn7.1*
+ *Phn15.1*

Hicks NILs



Variability within
NIL classes

- Other Beinhart alleles?



Main trends are consistent across years and environments

Black shank
resistance of
K326 NILs

K326 + *Phn7.1*

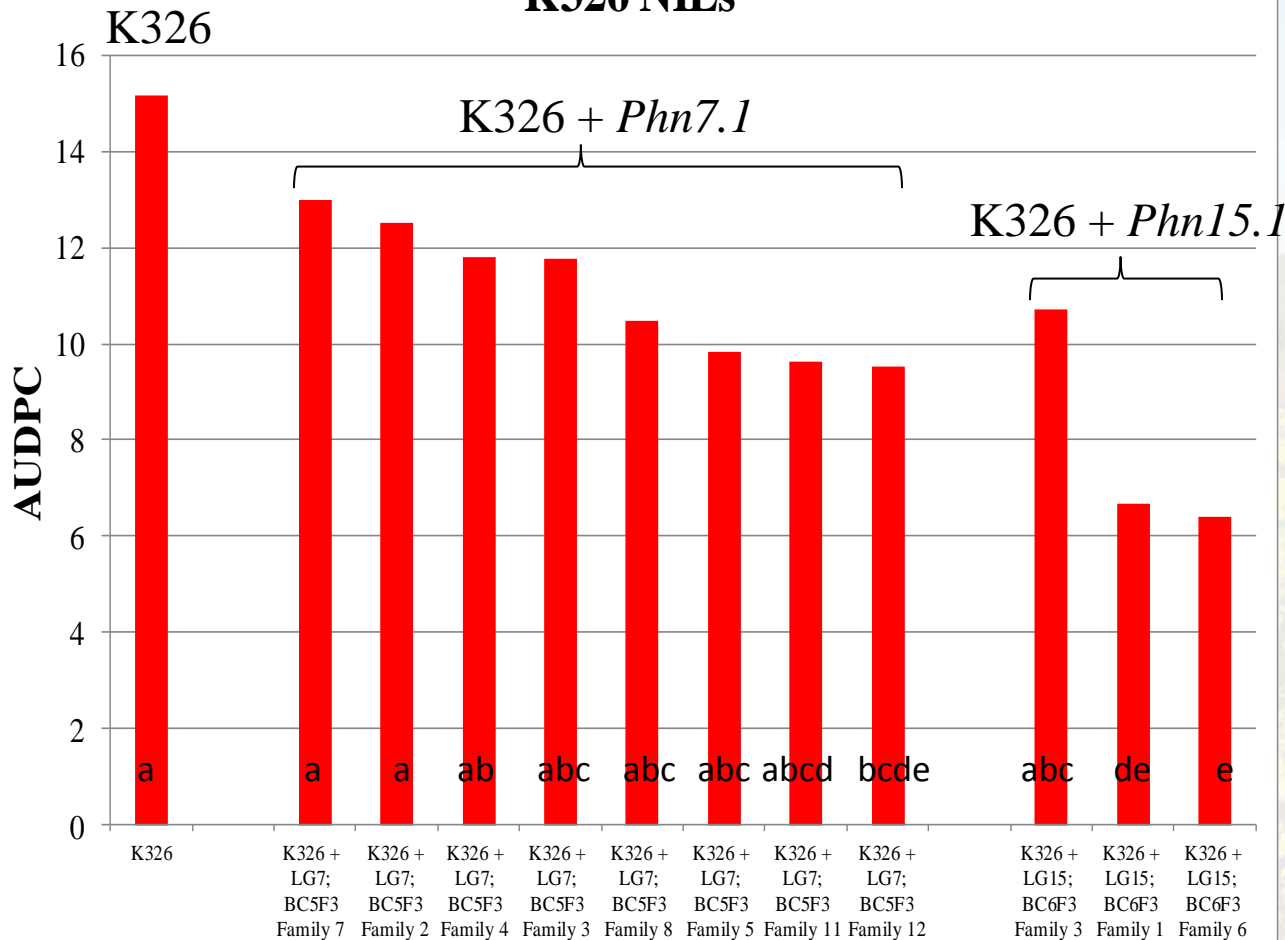
K326

K326 + *Phn15.1*

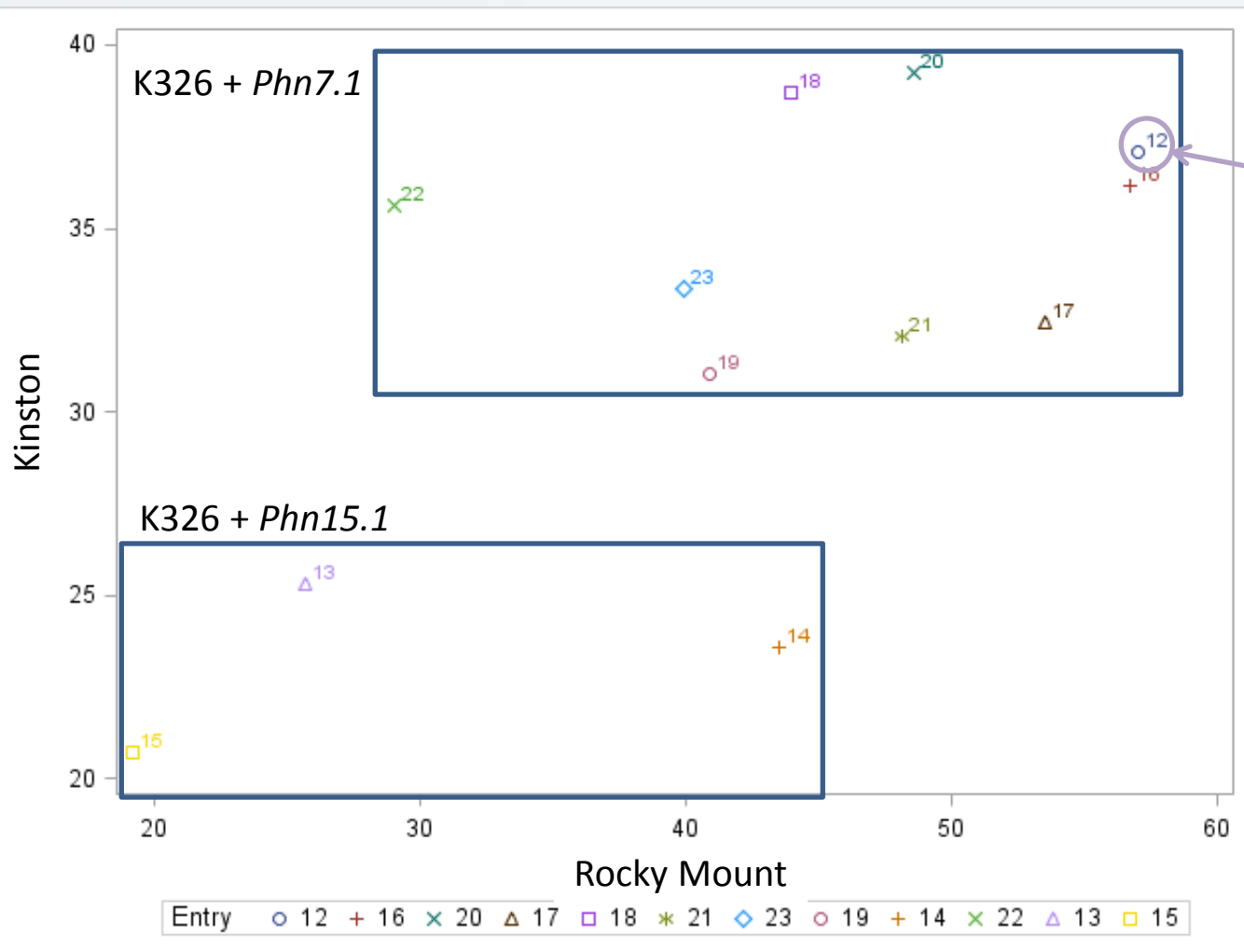
2.5 months after transplanting



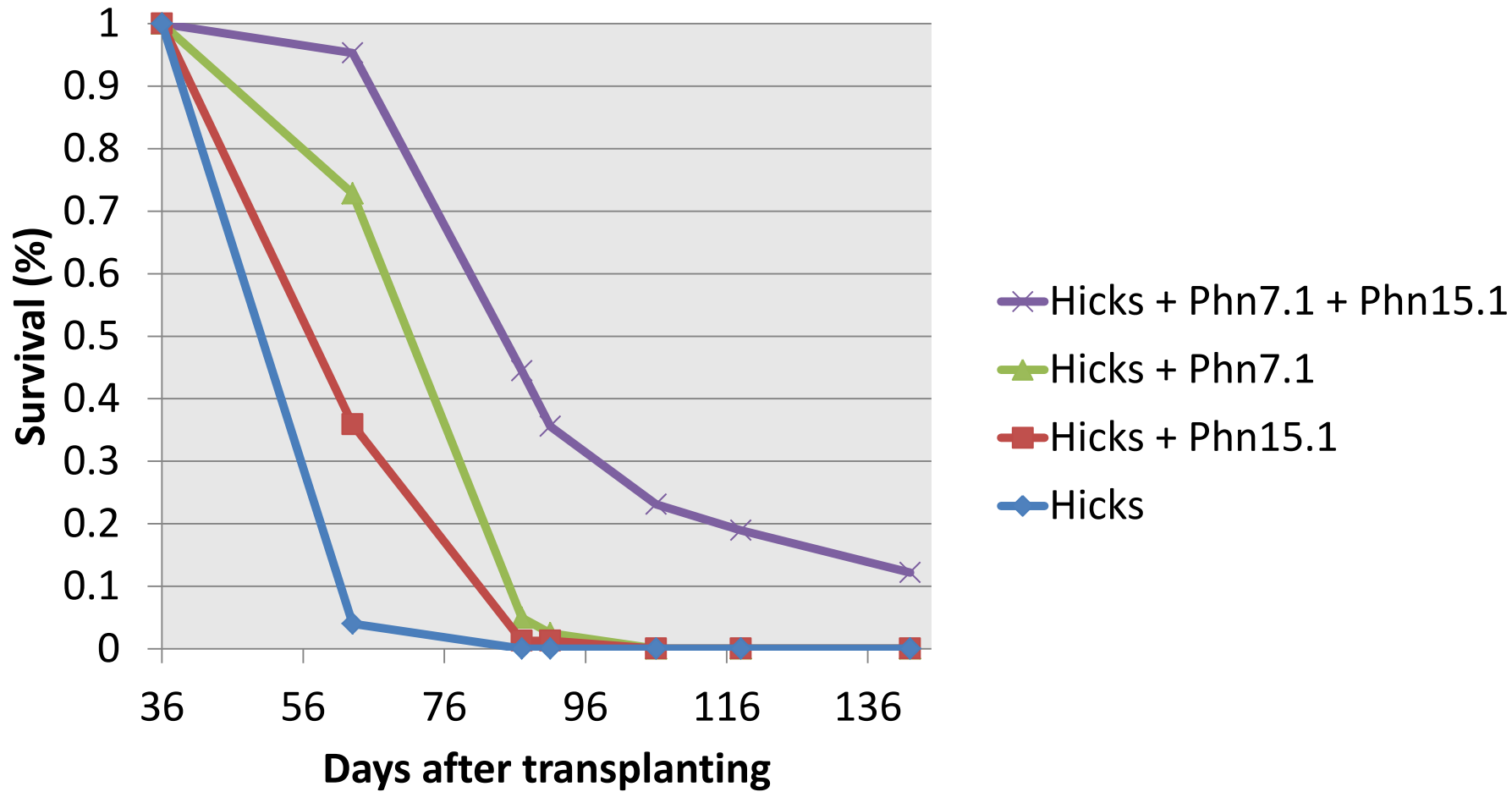
K326 NILs

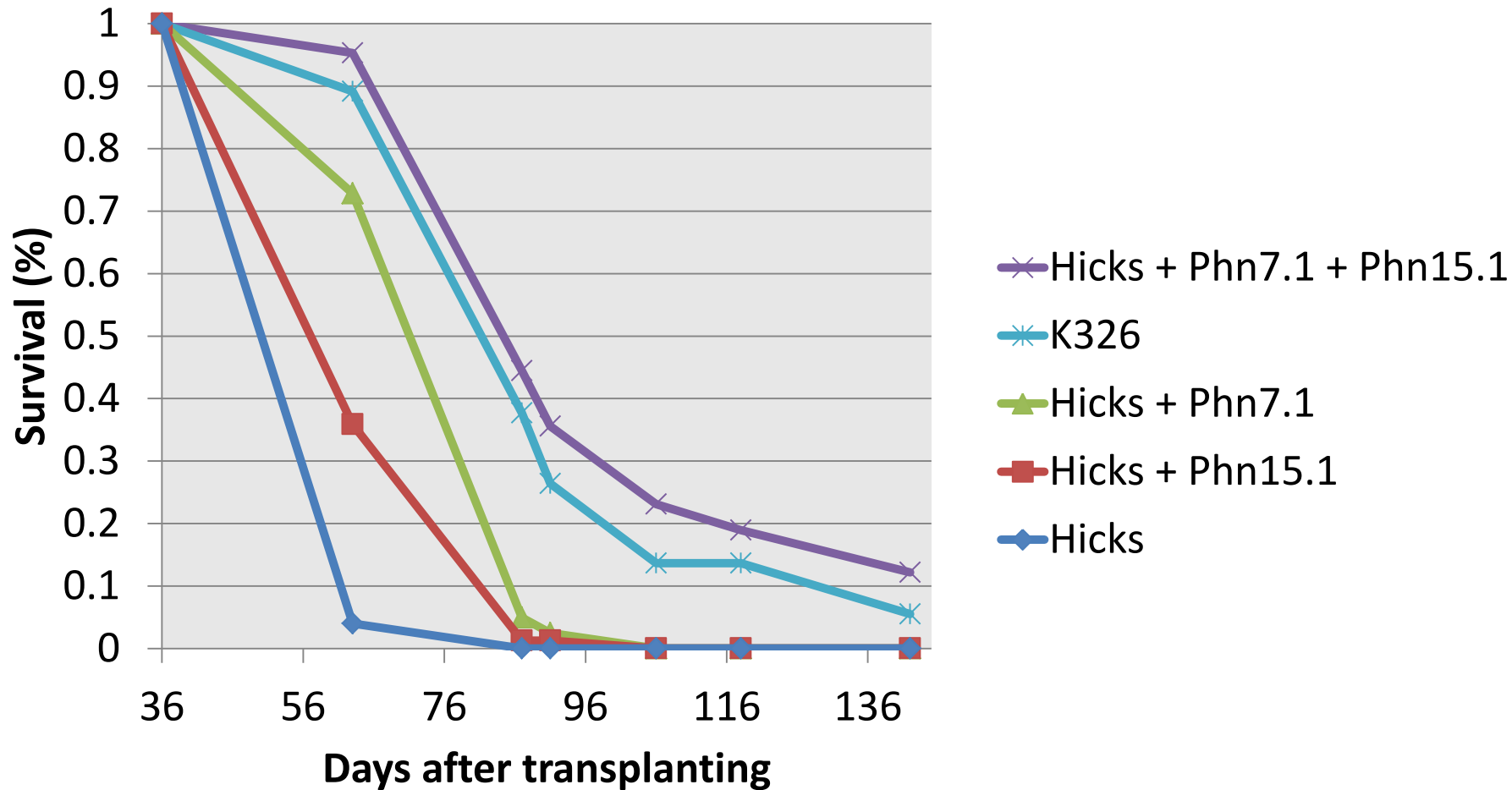


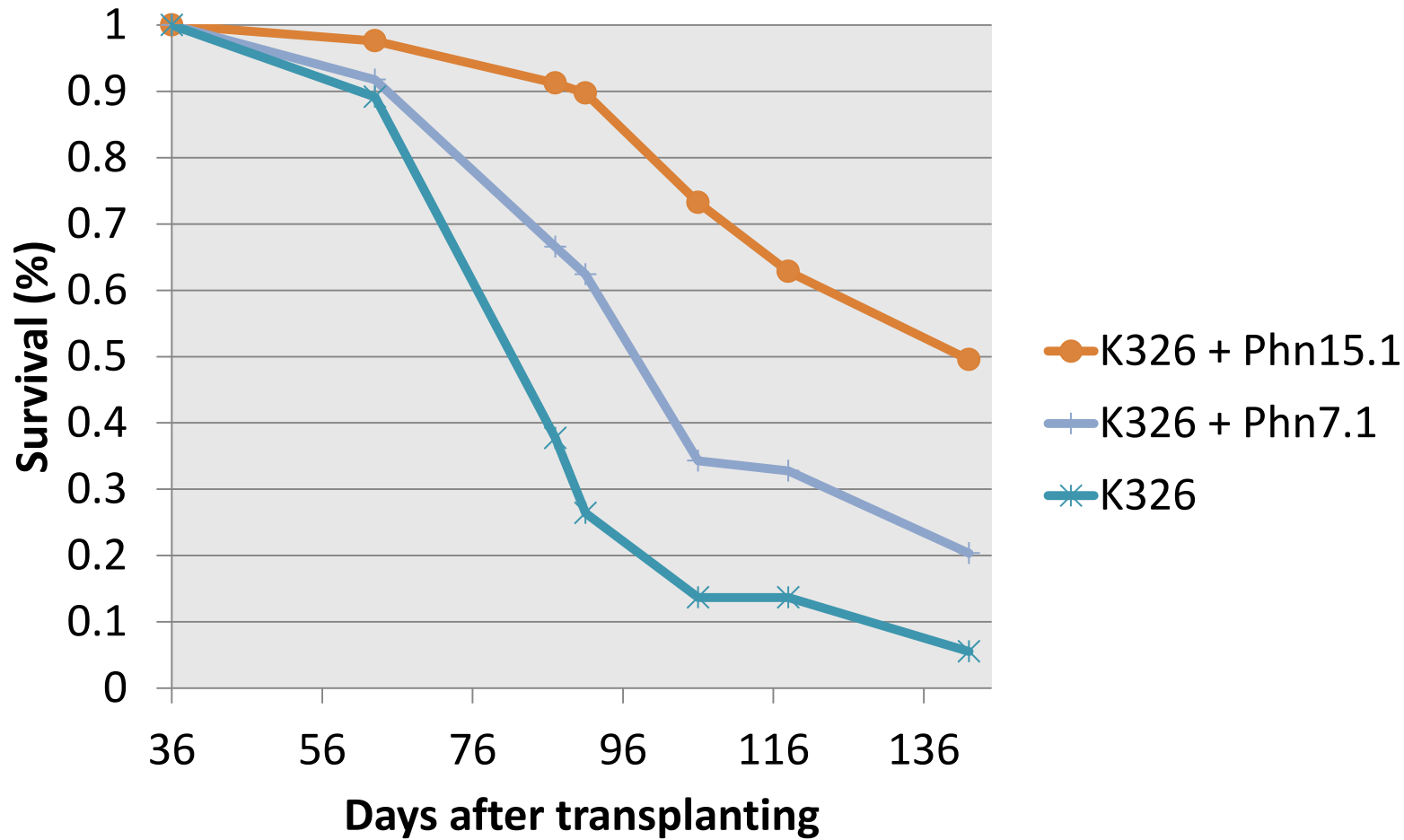
- Unlike Hicks, the addition of *Phn15.1* outperforms *Phn7.1*
- *Phn7.1* likely displaces existing K326 resistance allele

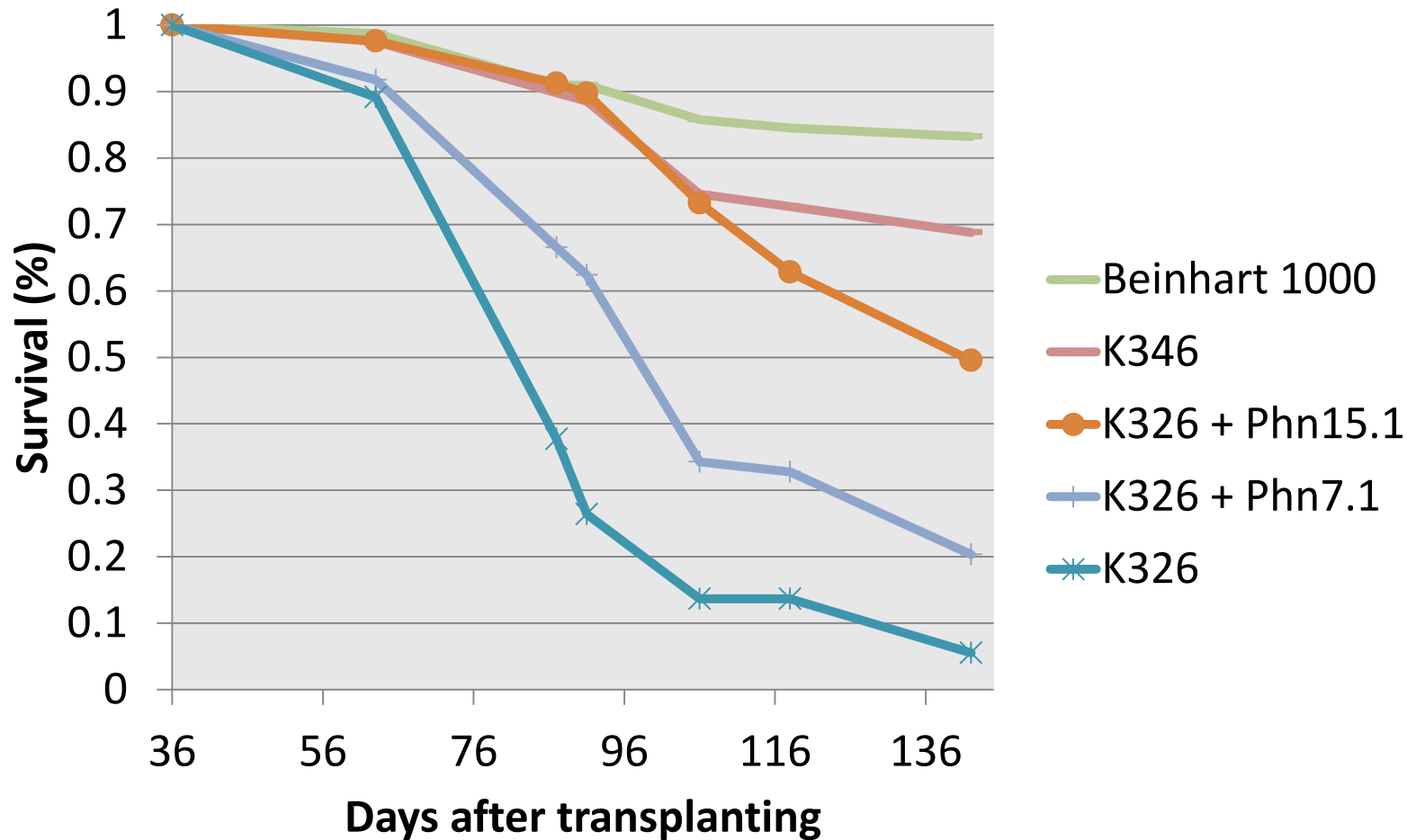


Main trends are consistent across years and environments





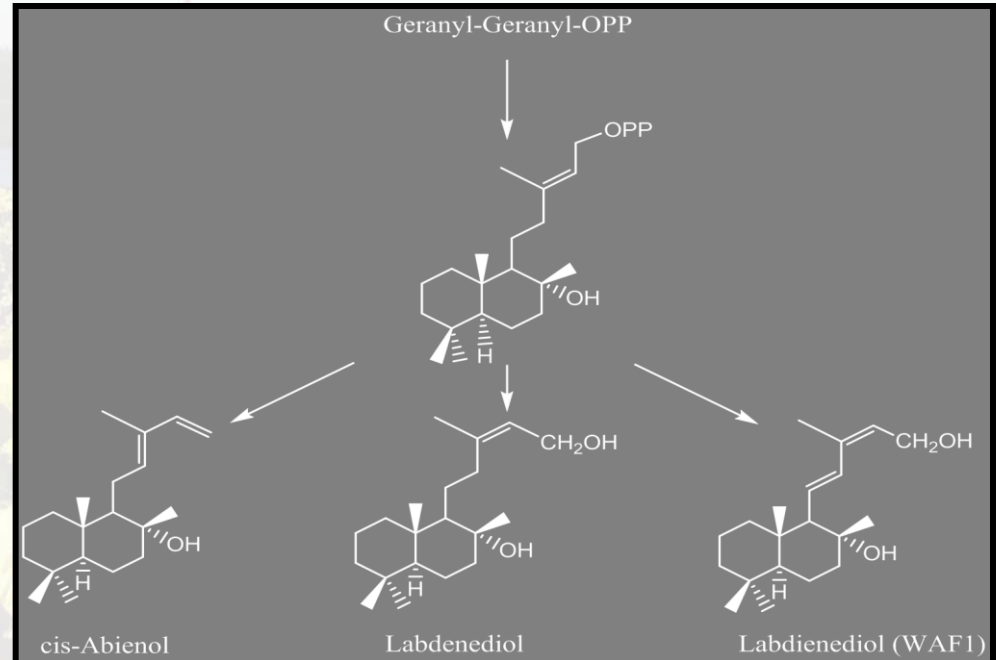
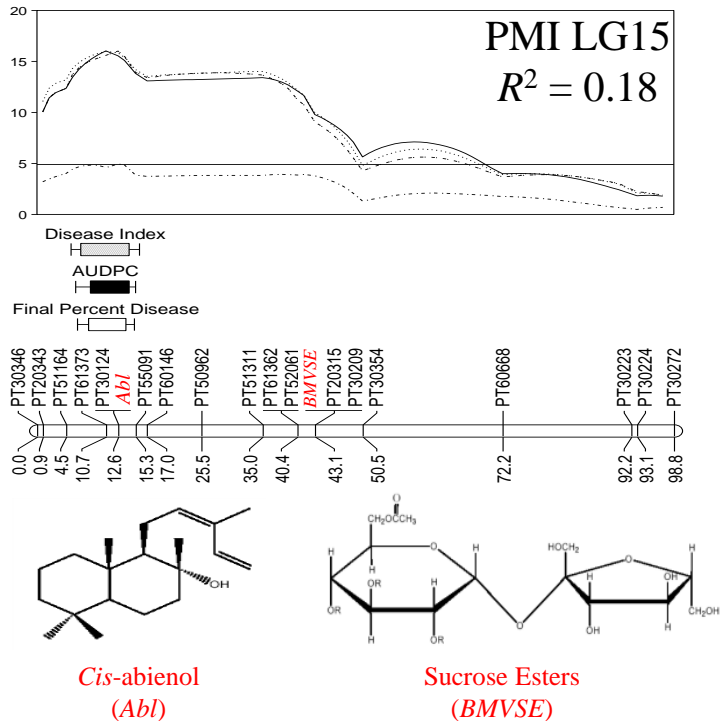




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Leaf surface chemistry genes from Beinhart 1000 co-segregates with *Phn15.1*



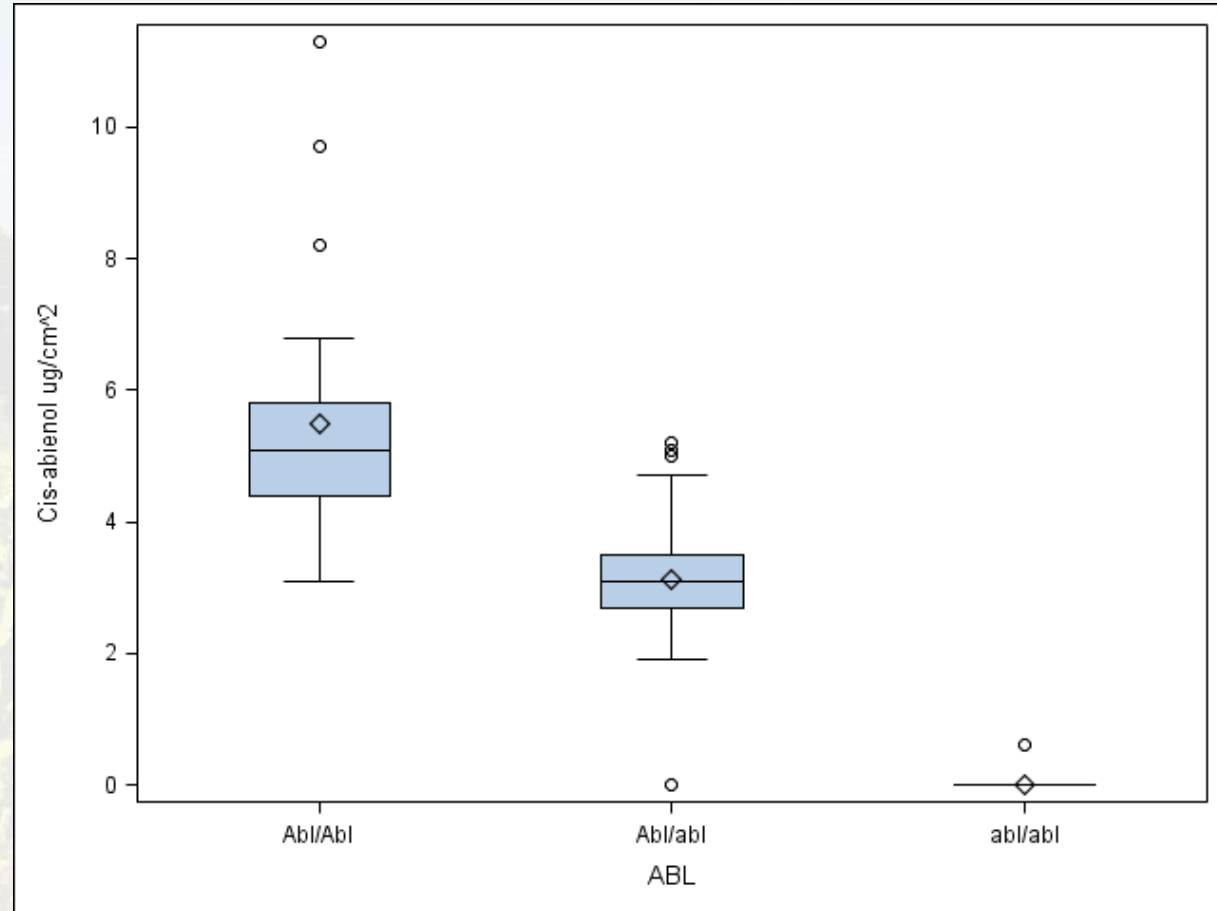
Evaluating Leaf Surface Chemistry

- Measurement of *cis*-abienol and sucrose esters
 - Leaf punch
 - Gas chromatography (GC)
- Determine of gene action
 - Segregating 1:2:1 (*PP:Pp:pp*) Hicks + *Phn15.1*
- Comparison of background effects
 - Stable homozygous and heterozygous families (*PP:Pp*)
 - Hicks and K326 + *Phn15.1*



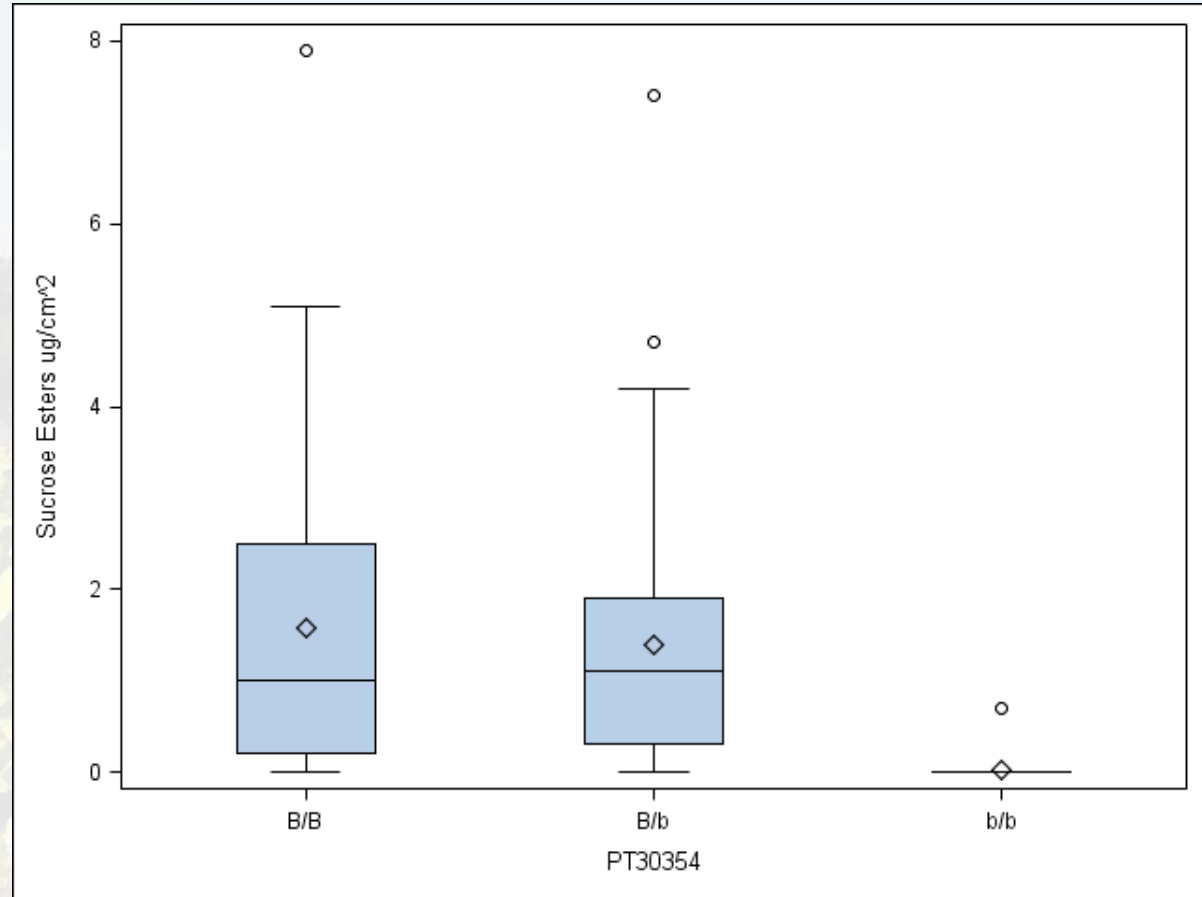
Cis-abienol

- $R^2 = 0.810$
- Additive gene action
 - Additive (a) = 2.764
 - Dominance (d) = 0.389
- Possible modifier genes
 - Significant family effects



Sucrose Esters

- $R^2 = 0.214$
 - Less heritable
- Complete dominance
 - Additive gene action (a) = 0.778
 - Dominance gene action (d) = 0.619
- Like cis-abienol, possible modifier genes
 - Significant family effects
- “*BMVSE*” gene is *unknown!*



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Continuing Research

- Develop additional markers to fine-map QTLs
- Develop additional NILs
- Disentangle linkage between leaf surface chemistry traits and QTLs
 - Fine-map *BMVSE*
- Verify reported results, more precisely estimate effects
- Evaluate any interaction between QTLs, including existing K326 resistance QTL at *Phn7.1* interval
- Evaluate effect of QTLs on yield and quality
- If effective, deploy QTLs in breeding populations using marker-assisted selection (MAS)

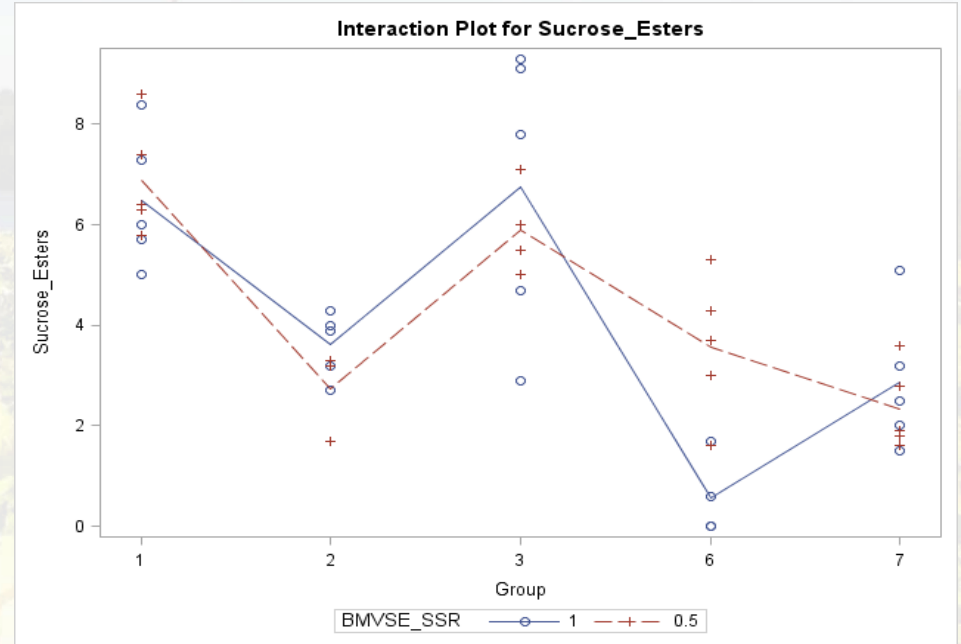
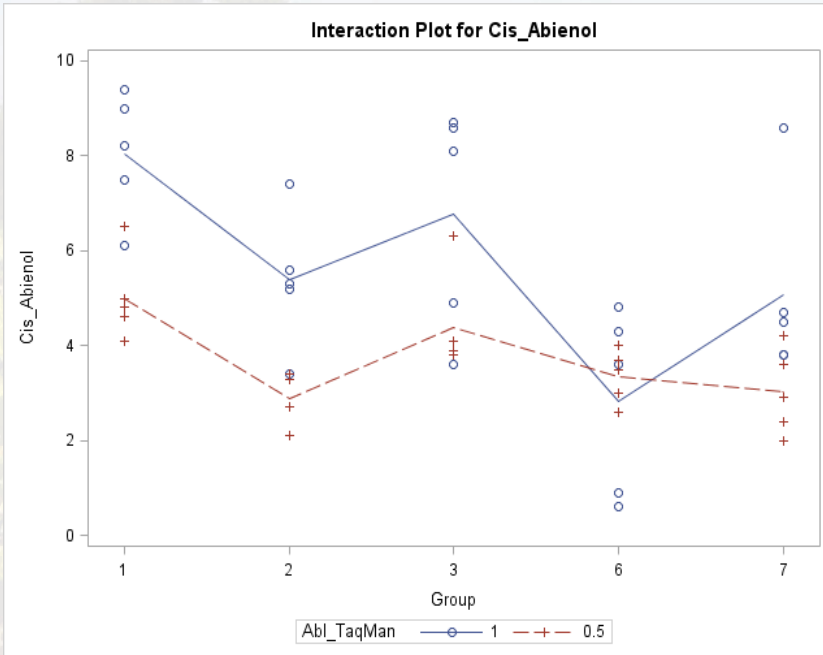
Summary

- Previously identified QTLs conferring black shank resistance in a Beinhart 1000 x Hicks mapping population
- Developed NILs for two largest effect QTLs in Hicks and K326 backgrounds
- QTLs provide moderate levels of resistance, and can be combined
- Leaf surface chemistry traits, *cis*-abienol and sucrose esters co-segregate with QTL on linkage group 15 (*Phn15.1*)
- *Cis*-abienol gene (*Abl*) displays additive gene action
- Unknown sucrose ester gene (*BMVSE*) displays complete dominance



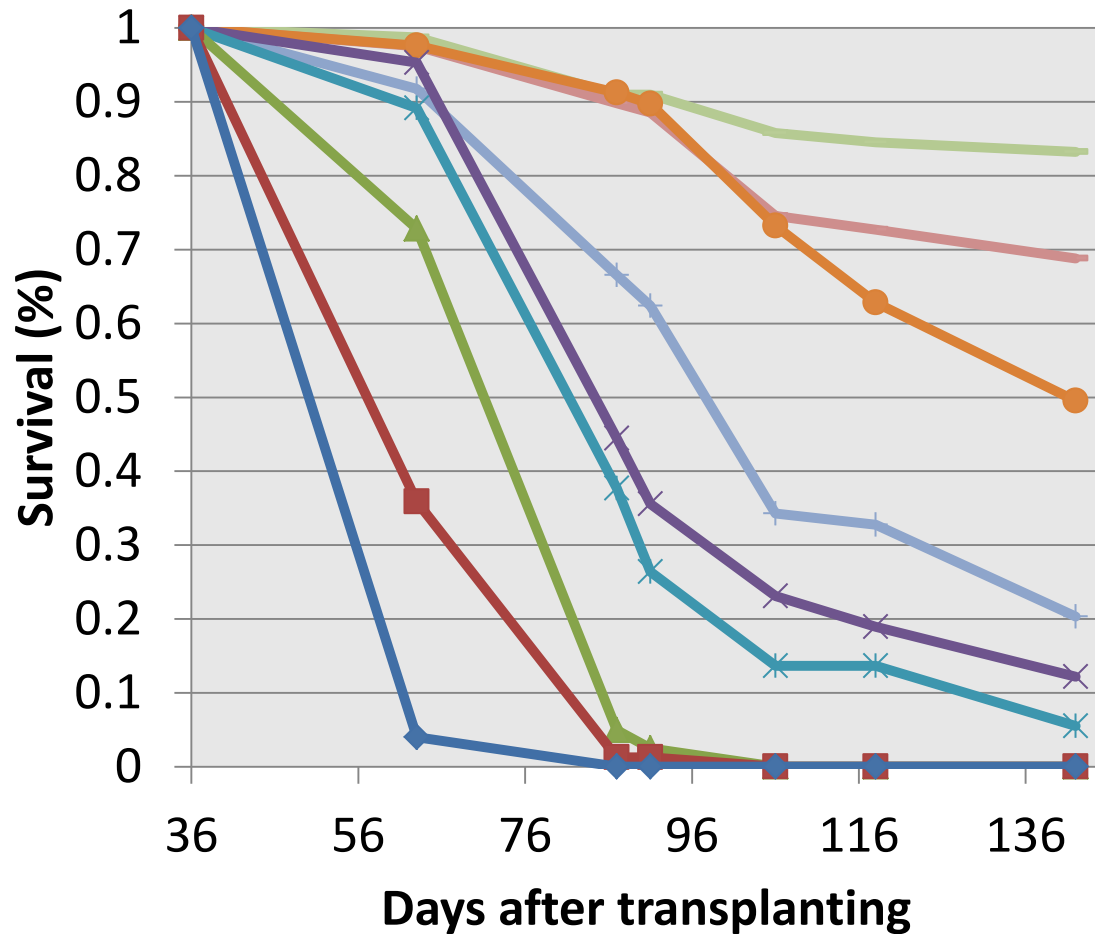
Thank you!

Appendix



2,7 = Hicks

1,3,6 = K326



- Beinhart 1000
- K346
- K326 + Phn15.1
- K326 + Phn7.1
- Hicks + Phn7.1 + Phn15.1
- K326
- Hicks + Phn7.1
- Hicks + Phn15.1
- Hicks