

Chestnut Mapping— markers, populations and traits— Genes for Engineering and Tools for Breeding

Forest Health Initiative (FHI)

9-10 August 2012

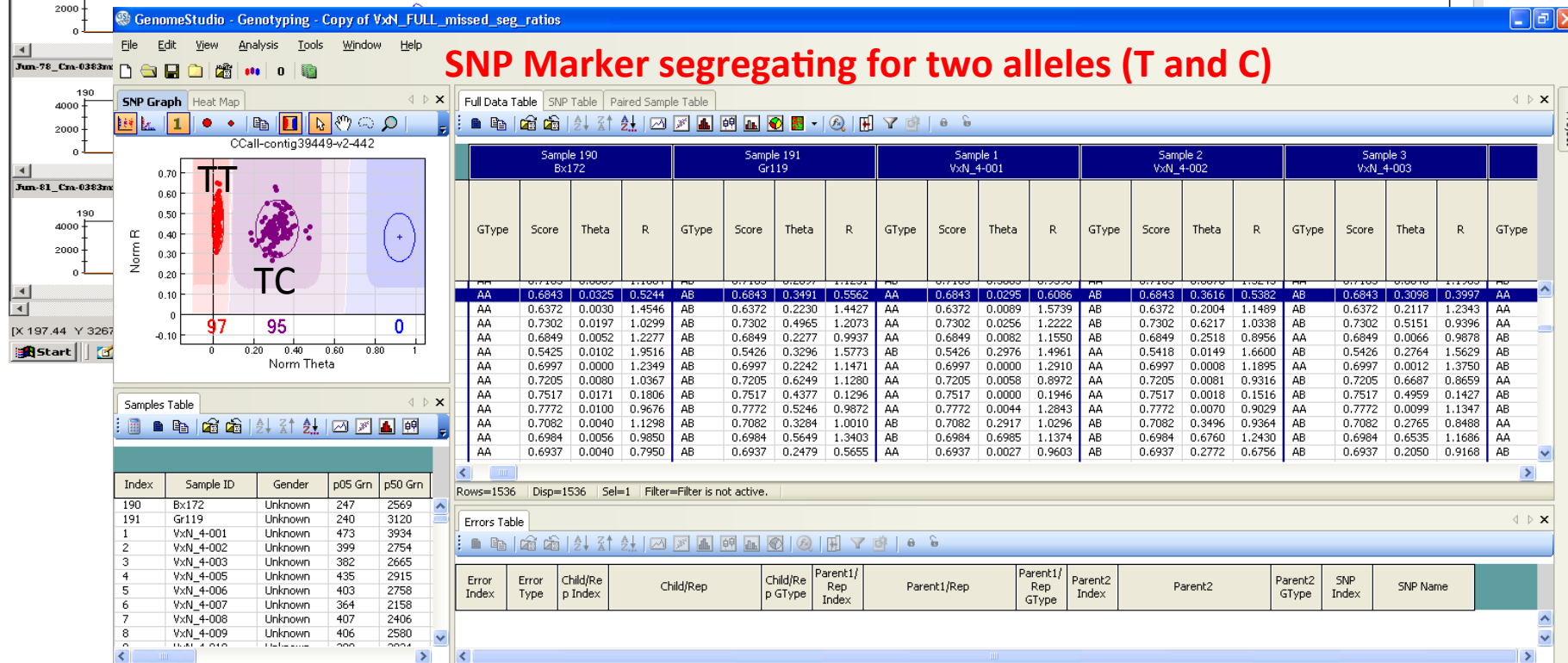
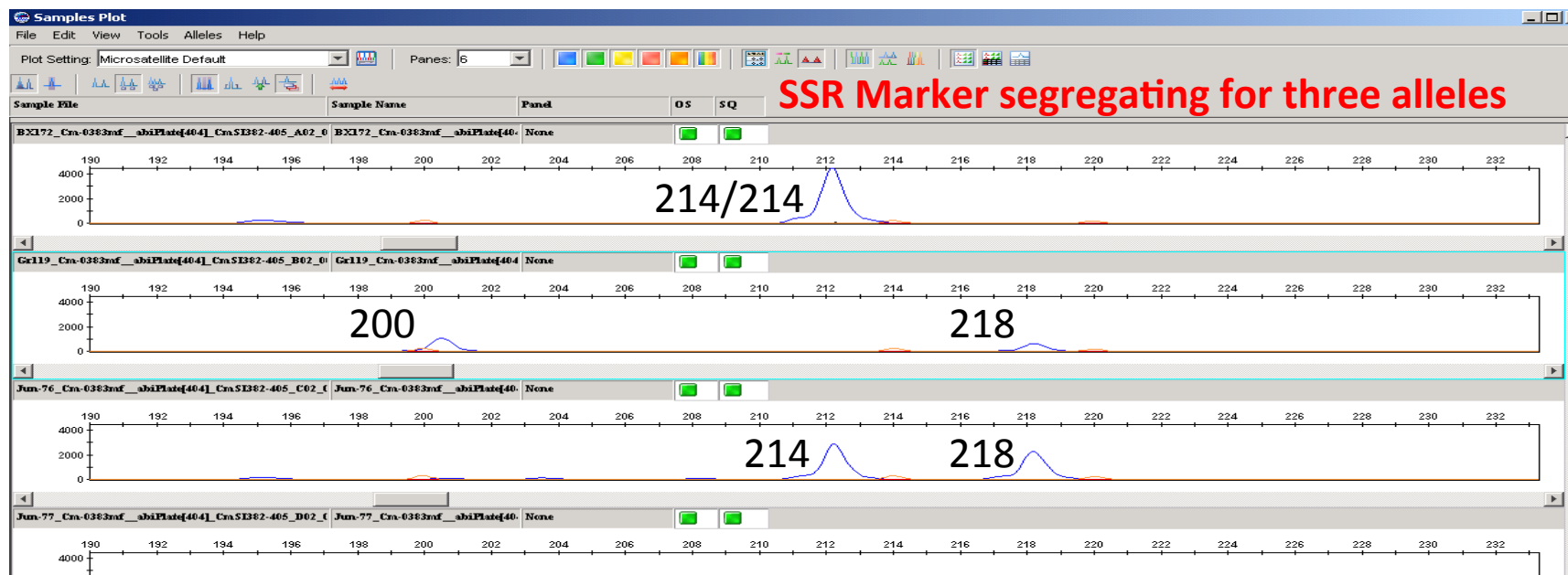
Annual Meeting

Goals

- Develop dense maps for high resolution trait mapping, integrate maps and sequences
 - Map density– increase number of markers
 - Mapping resolution– increase population sizes (more progeny per cross)
- Use integrated maps to
 - Assist in identifying candidate genes for engineering and breeding resistance
 - Assist in selecting for recurrent background (American alleles) in backcross breeding

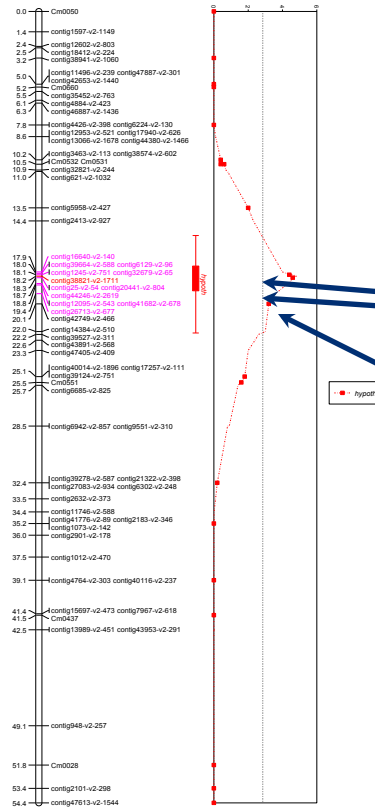
Markers and Maps

- 1156 markers on reference map, manuscript in press with TGG (Kubisiak, Nelson, Staton, et al.)
 - Full set of supplemental files with marker and map information -- Fully integrated with physical map
- ~2500 SNP markers scored on larger populations
 - Graves B1 population in PA, 724 individuals
 - Mahogany F2 population in VA, 214 individuals

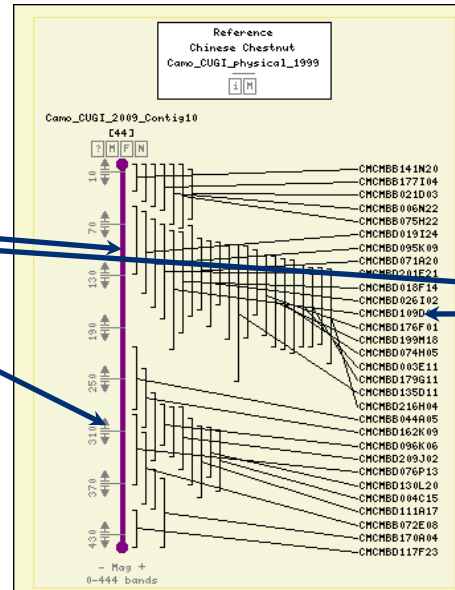


Integrated mapping necessary for finding and validating candidate genes

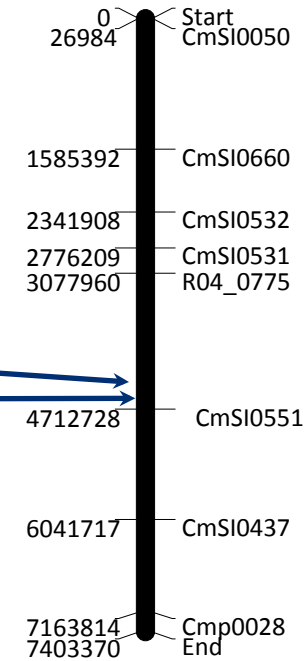
Mahogany_F2_LGB



Genetic mapping
QTL mapping



Physical mapping
BAC contigs



Genome Sequence
contigs/scaffolds

Graves B3 test planting and blight inoculations in Pennsylvania

Planting at age 2

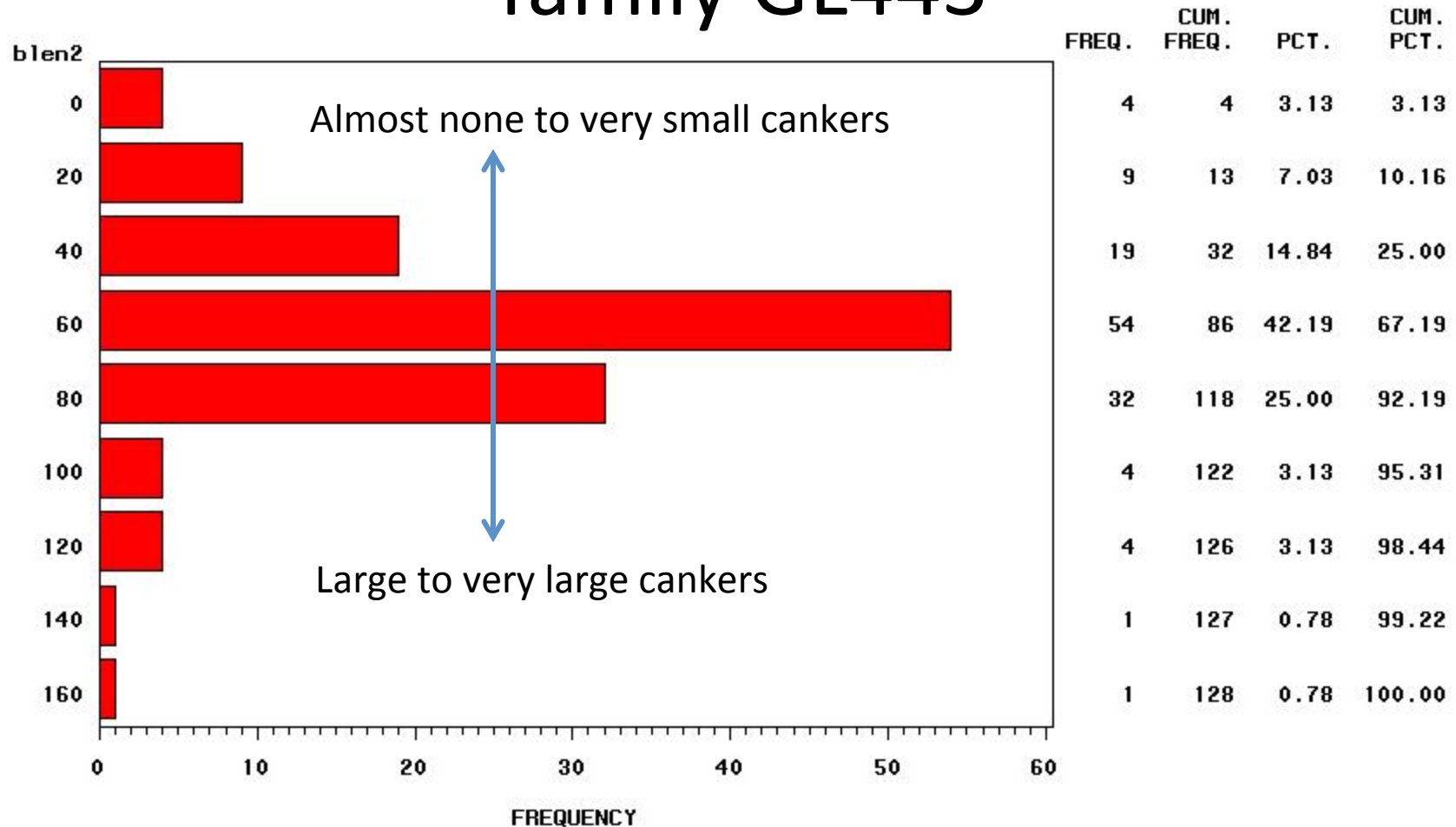
Inoculations at age 6

SG2-3

EP155

Measure canker sizes,
late summer, age 6

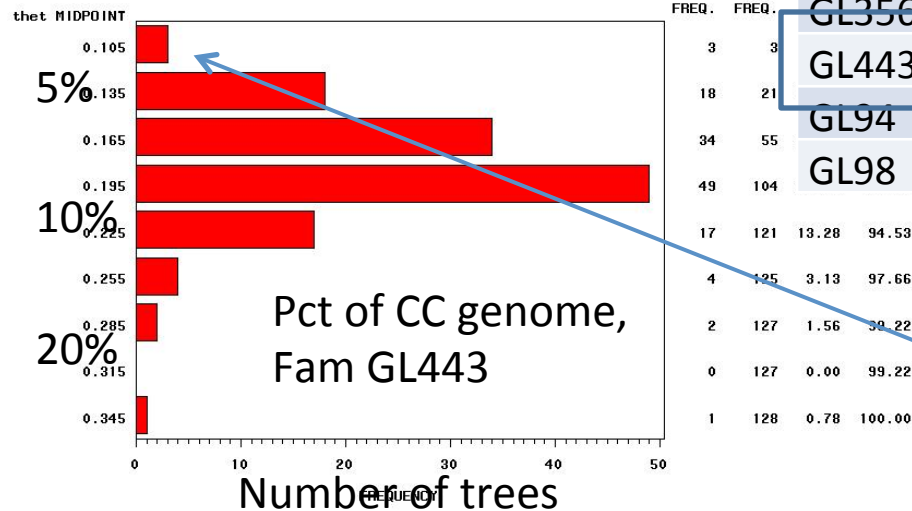
Range of blight response, canker length at time 2, family GL443



Graves B3 population

- Population
- Traits
- Markers per family

Fam	Planted	Inoc'ed	% Planted Inoc'ed	genotyped
AB171	66	23	35%	21
AB247	11	6	55%	6
AB248	193	107	55%	104
AB419	156	88	56%	79
BE134	82	31	38%	31
BE138	267	124	46%	119
GL185	132	40	30%	32
GL239	301	128	43%	115
GL356	75	33	44%	33
GL443	230	136	59%	128
GL94	61	26	43%	24
GL98	147	36	24%	33



Choose most resistant tree with least amount of CC genome

Other populations being analyzed

- All phenotyped for blight resistance
 - ‘Mahogany’ B1, n=56
 - ‘Nanking’ B1, n=102
 - ‘Clapper’ B2, n=95
- Ready for DNA marker genotyping
 - AdairKY1 x GL158
 - GL158 is a B1 tree from ‘Nanking’
 - Phenotyped for Phytophthora root rot (PRR) resistance
 - Two new populations ready for PRR mapping

Summary & Conclusions

- Excellent group of researchers and technicians working together on a great scientific and societal problem
 - Outstanding progress made over 3 years in all phases of the scientific program
- Genomics, Germplasm, Clonal Propagation, Transformation and Screening resources greatly enhanced and extensively integrated
 - Sets up the team for continued progress
 - especially moving from the plantable- to the landscape-tree

Next Steps, Issues

- Funding going forward is key issue
 - Main needs are in maintaining, propagating and evaluating plantable trees in the pipelines at SUNY and UGA
 - Otherwise continued science needed to better understand mechanisms of resistance– genetics/genomics and interaction with environments
- Science coalition/consortium continuing
 - Proposal generating meeting held last week at Clemson University (18 people, 6 institutions)
 - Prof. Albert Abbott (Clemson) is committing to lead on new proposals for the consortium
 - Large integrated USDA proposal best, but will develop plan that can be funded in pieces by any sponsor(s)

Germplasm and Mapping Team

special thanks

- Bert Abbott, Clemson University
 - Tatyana Zhebentyayeva
 - Meg Staton and Bode Olukolu (now NC State University)
- Fred Hebard, The American Chestnut Foundation
 - Laura Georgi
 - Sara Fitzsimmons, Paul Sisco, Joe James
- Dana Nelson, USDA Forest Service, Southern Research Station
 - Tom Kubisiak, now retired
 - Chuck Burdine, Dennis Deemer, Kristel Davis, Ben Bartlett, Daniel Smith

Bringing back
American chestnut—
one tree,
one person,
one population,
one community
at a time.



Photo courtesy Bill Powell