

Genetics of New Varieties and Source of Cercospora Susceptibility

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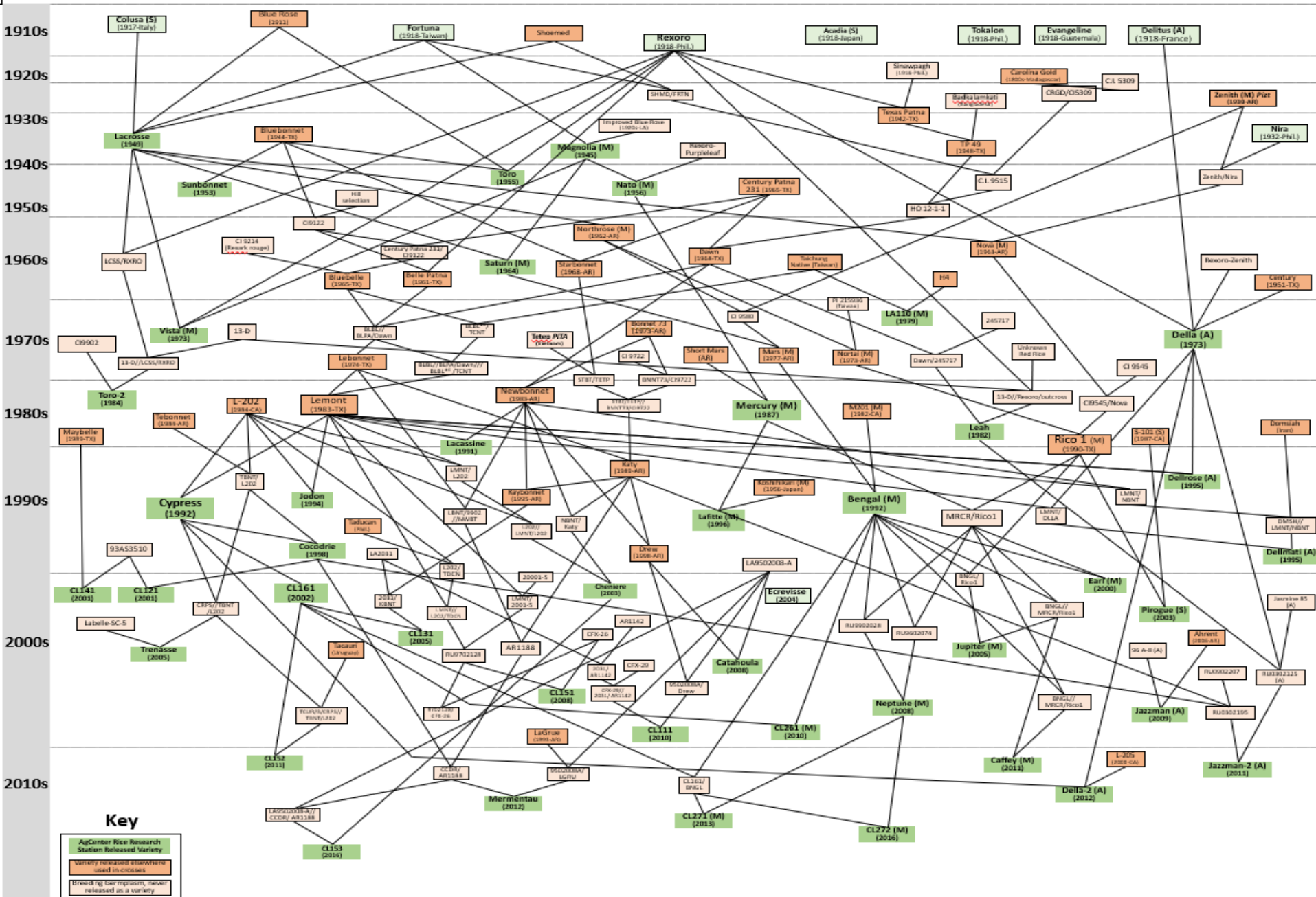
*Rice
Research
Board*



Outline

- Germplasm and New Traits
 - Key lines and genetics of new traits/genes
- Breakdown of trait genetics
 - Semi-dwarf
 - Blast resistance
- Narrow Brown Leaf Spot case study
 - Discovery, Validation, Deployment in applied context

LSU AgCenter Rice Variety Pedigrees: Variety Releases and Founding Germplasm

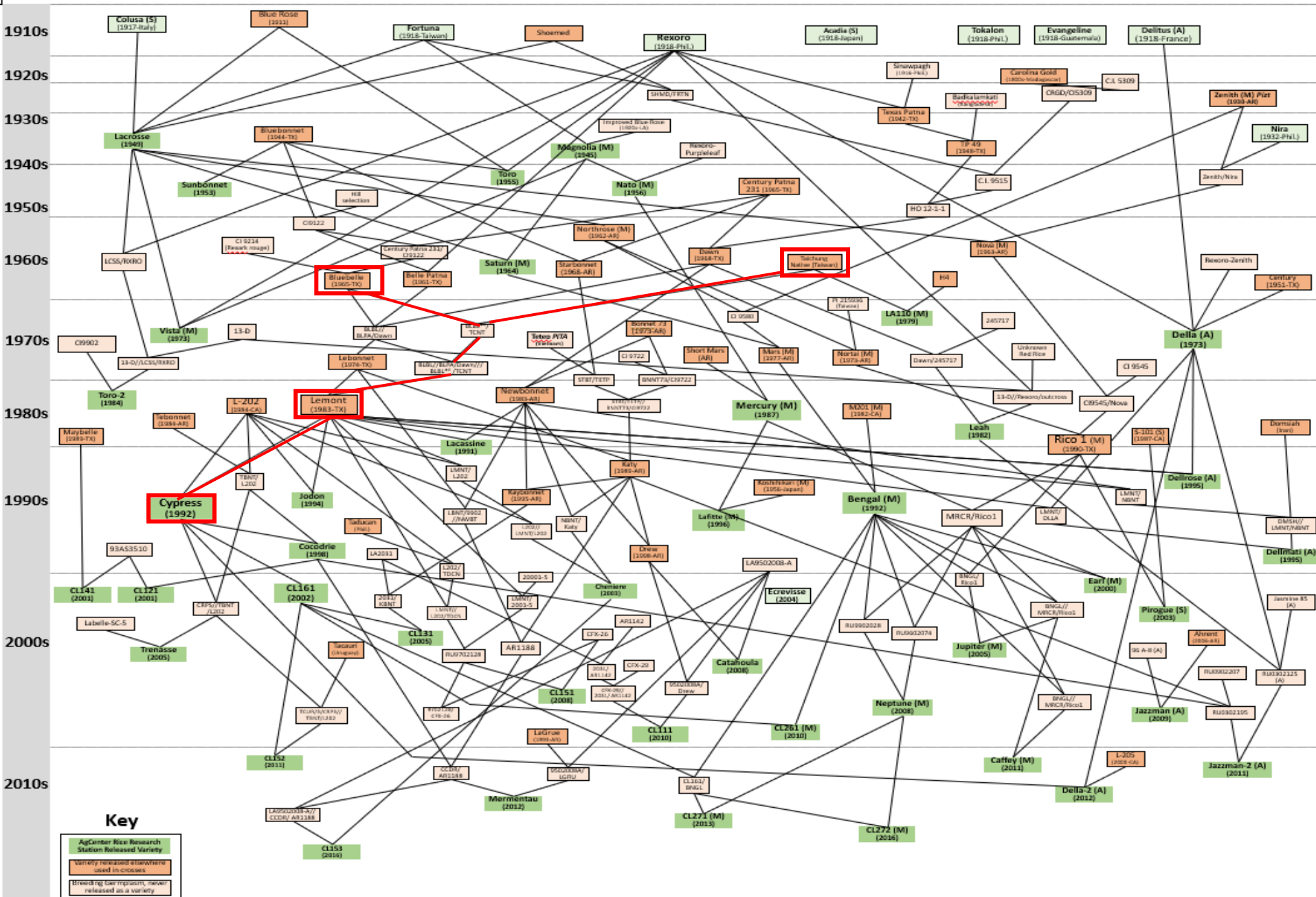


Plant Height- *sd1* gene

- *sd1* is the “green revolution” gene
- Semi-dwarf trait incorporated into wheat and rice

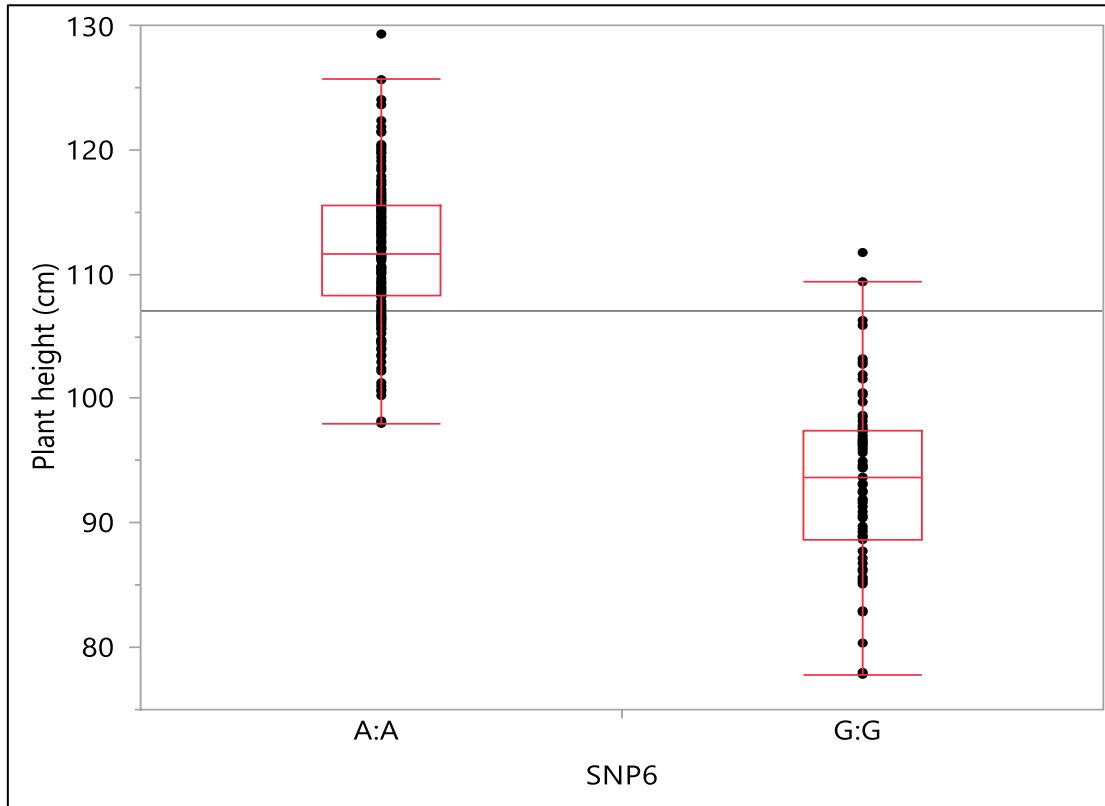


LSU AgCenter Rice Variety Pedigrees: Variety Releases and Founding Germplasm



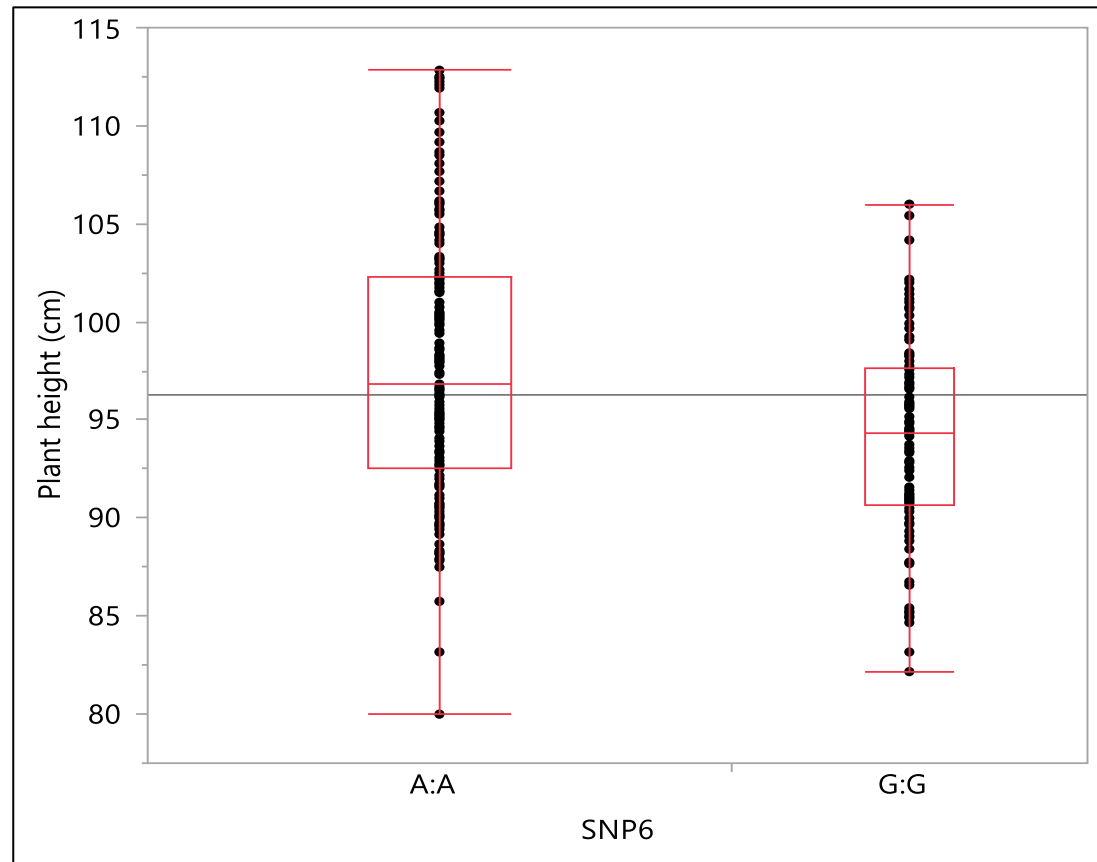
Plant Height- *sd1* gene

sd1 gene in Long Grains

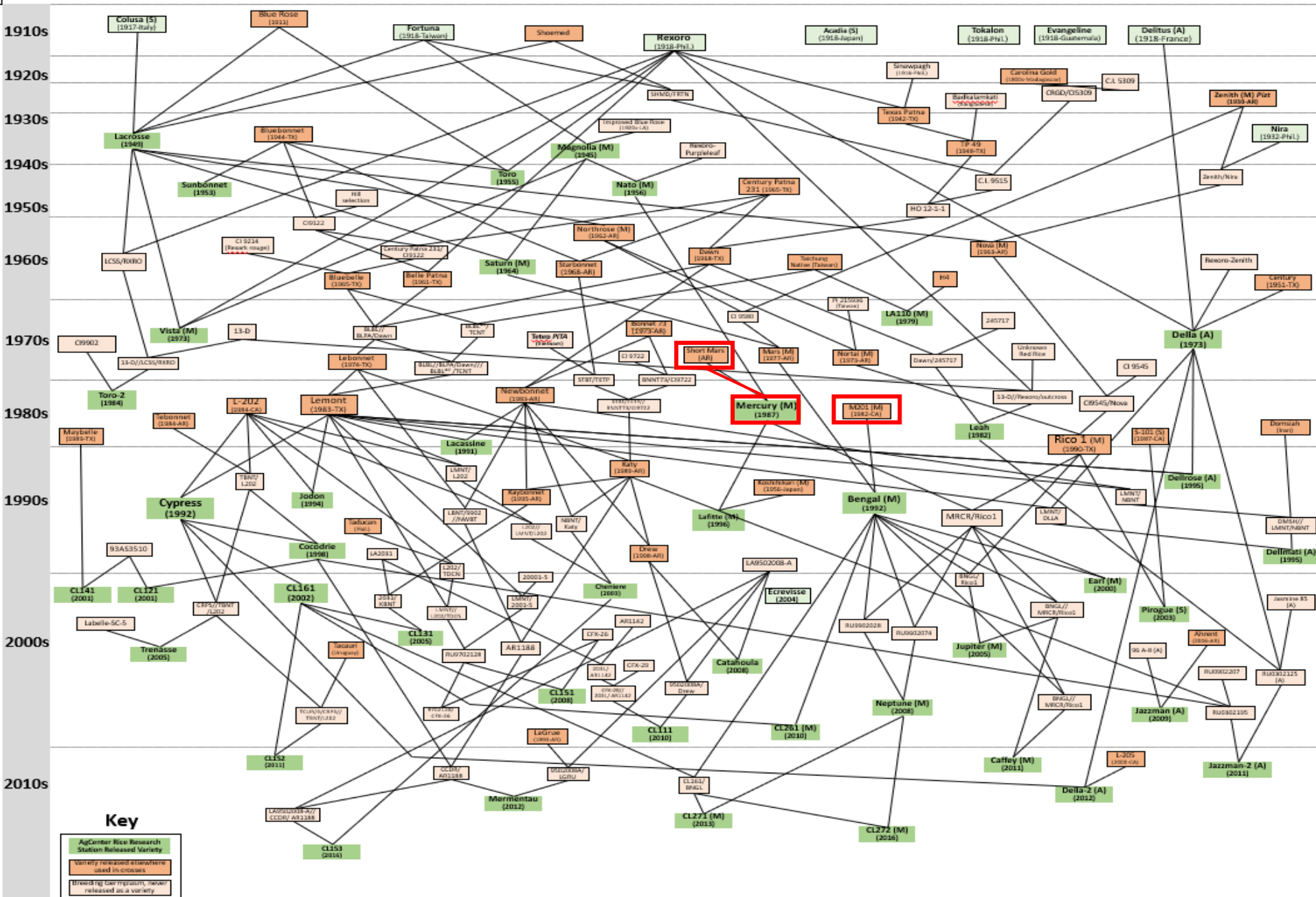


Plant Height- *sd1* gene

***sd1* gene in Medium Grains**

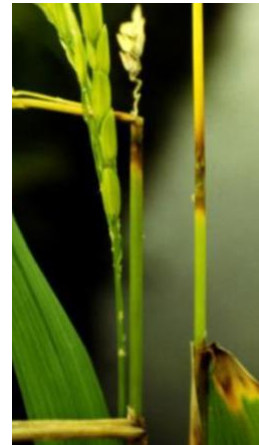


LSU AgCenter Rice Variety Pedigrees: Variety Releases and Founding Germplasm

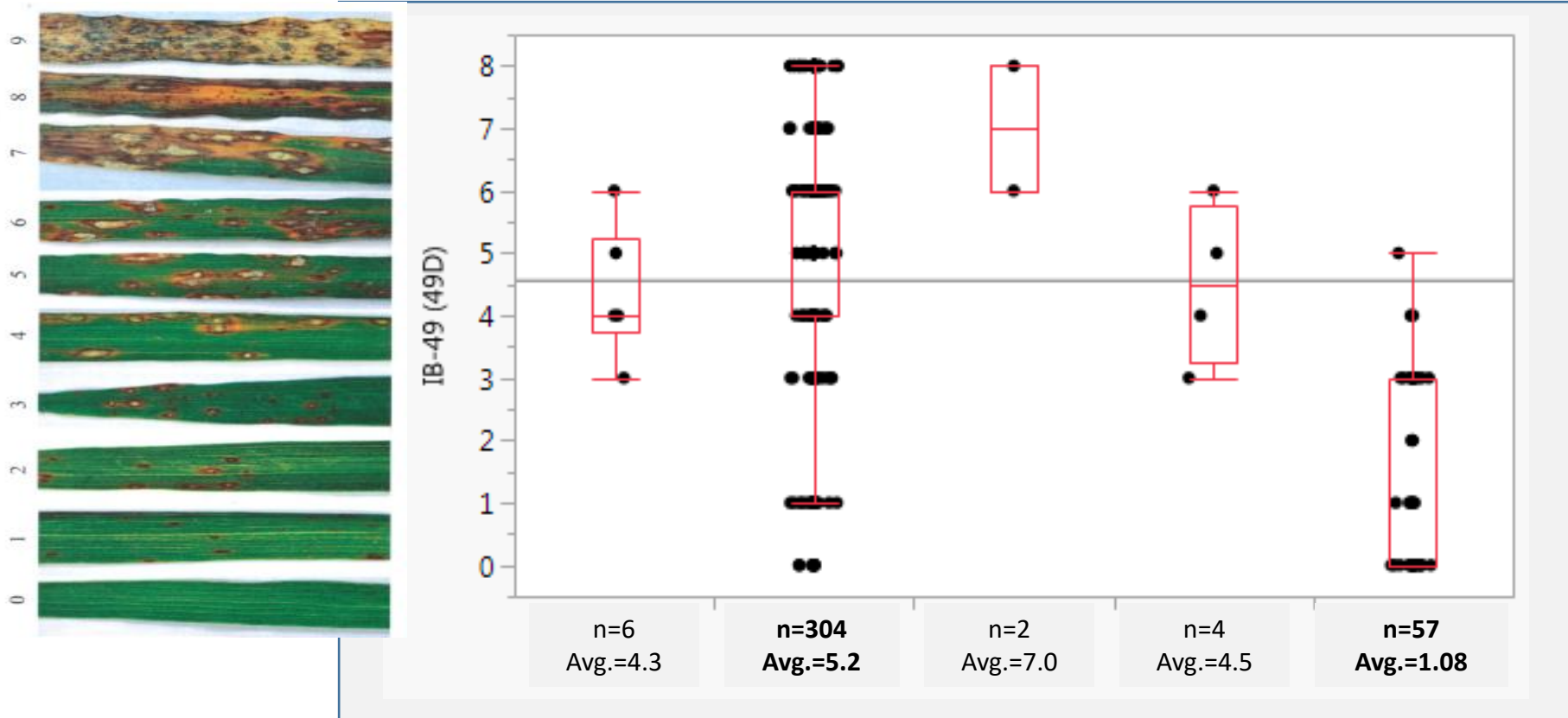


Blast Resistance: Pita gene

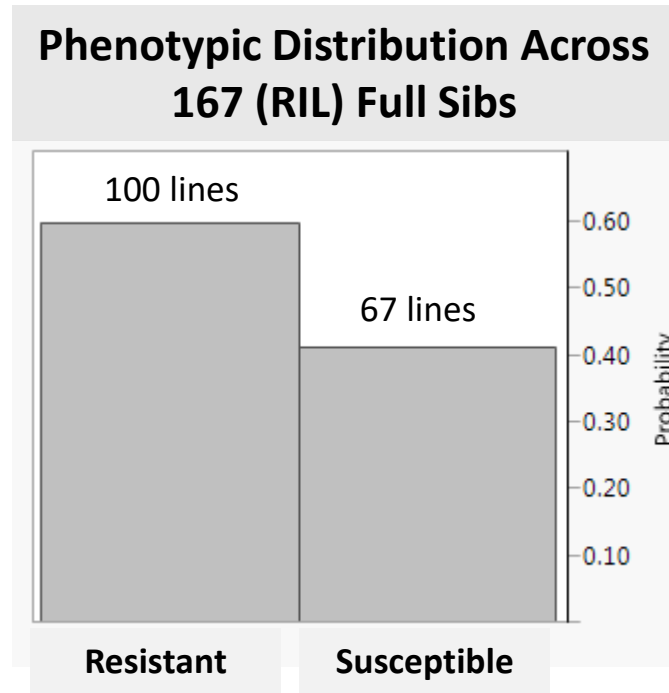
- *Pita* blast resistance gene is broad spectrum
- Best source of blast resistance in US germplasm
- Only found in long grain germplasm



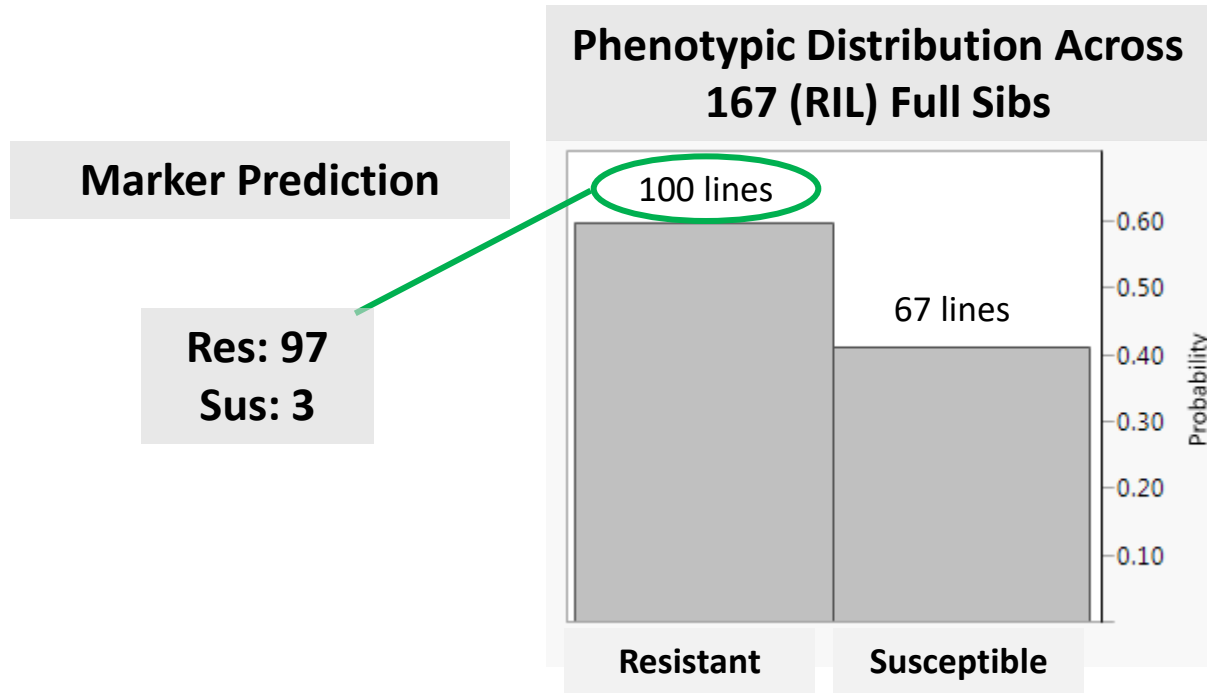
Phenotypic Characterization of Blast Resistance Among Haplotype Classes Present in US Breeding Germplasm



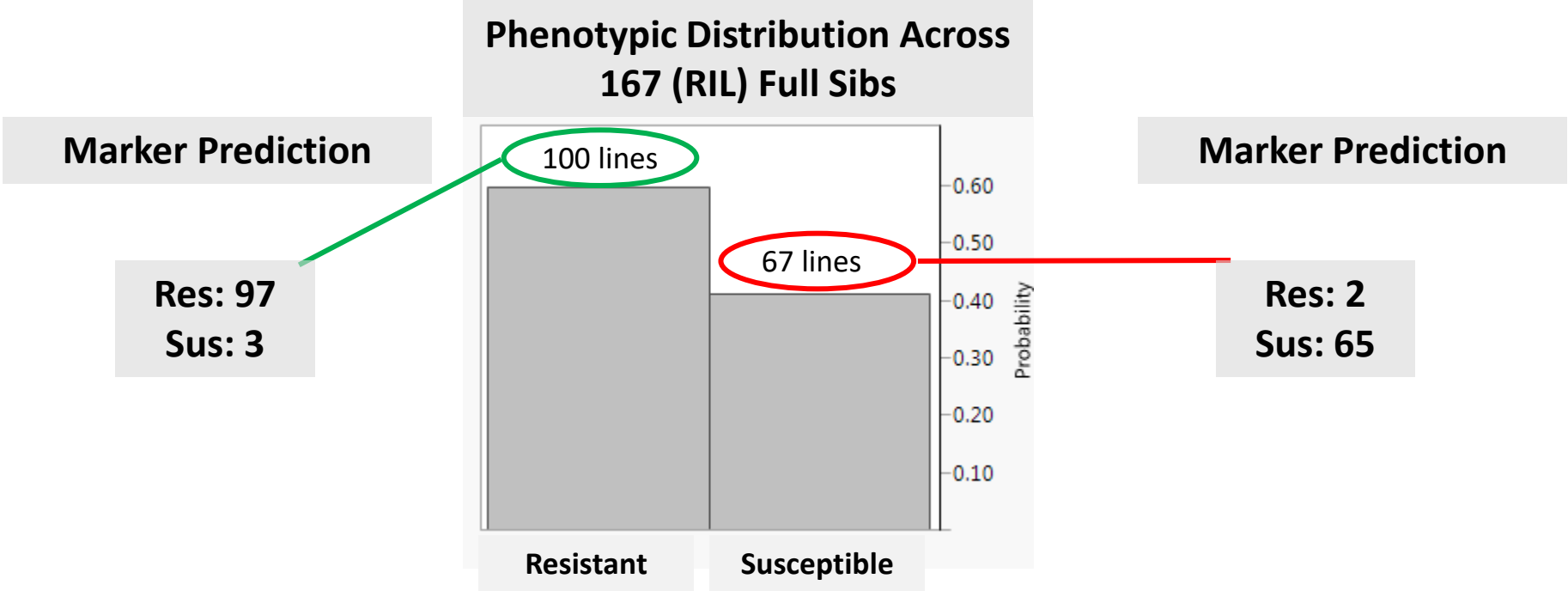
Phenotypic Prediction within Bi-Parental Breeding Population



Phenotypic Prediction within Bi-Parental Breeding Population



Phenotypic Prediction within Bi-Parental Breeding Population



Identification and Characterization of a Novel Resistance Gene to Narrow Brown Leaf Spot

- Research of Ph.D Student Christopher Addison
- *Cercospora janseana*
- Late season disease
- Prevalence and severity increased in the early 2000s
- Now a primary breeding target



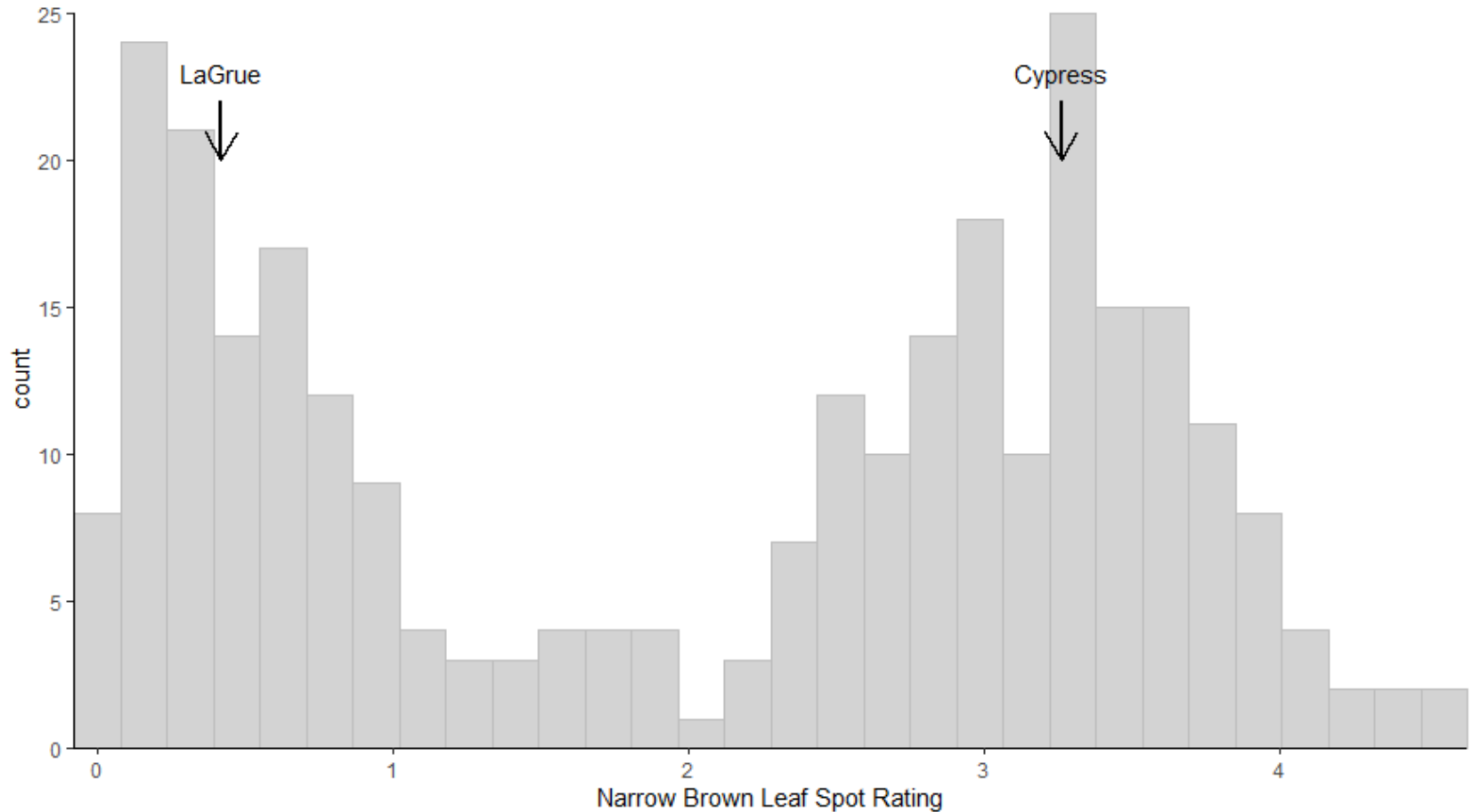
<https://www.lsuagcenter.com/topics/crops/rice/diseases/photos/cercospora/cercospora->
<https://www.ricefarming.com/departments/feature/producer-meetings-offer-crawfish-raising-tips/>

MY2 RIL Population

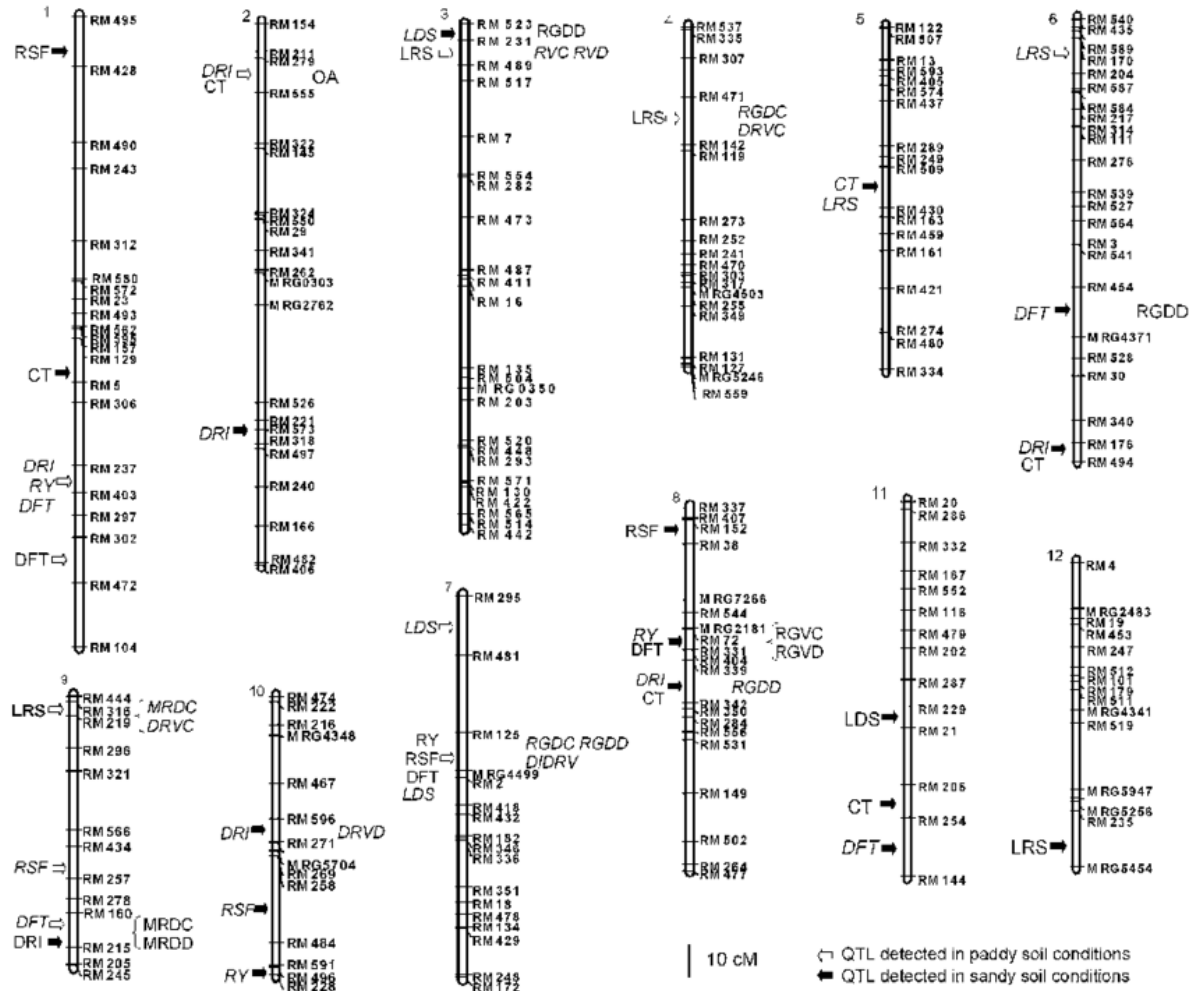
- 286 F10-derived RILs
- Cypress x LaGrue
- Evaluated for NBLS under natural field conditions from 2016-2018
 - Rated on a 1-9 scale
- Heading data collected as days to 50% heading (DTH)



Distribution of Narrow Brown Leaf Spot in the MY2 RIL Population



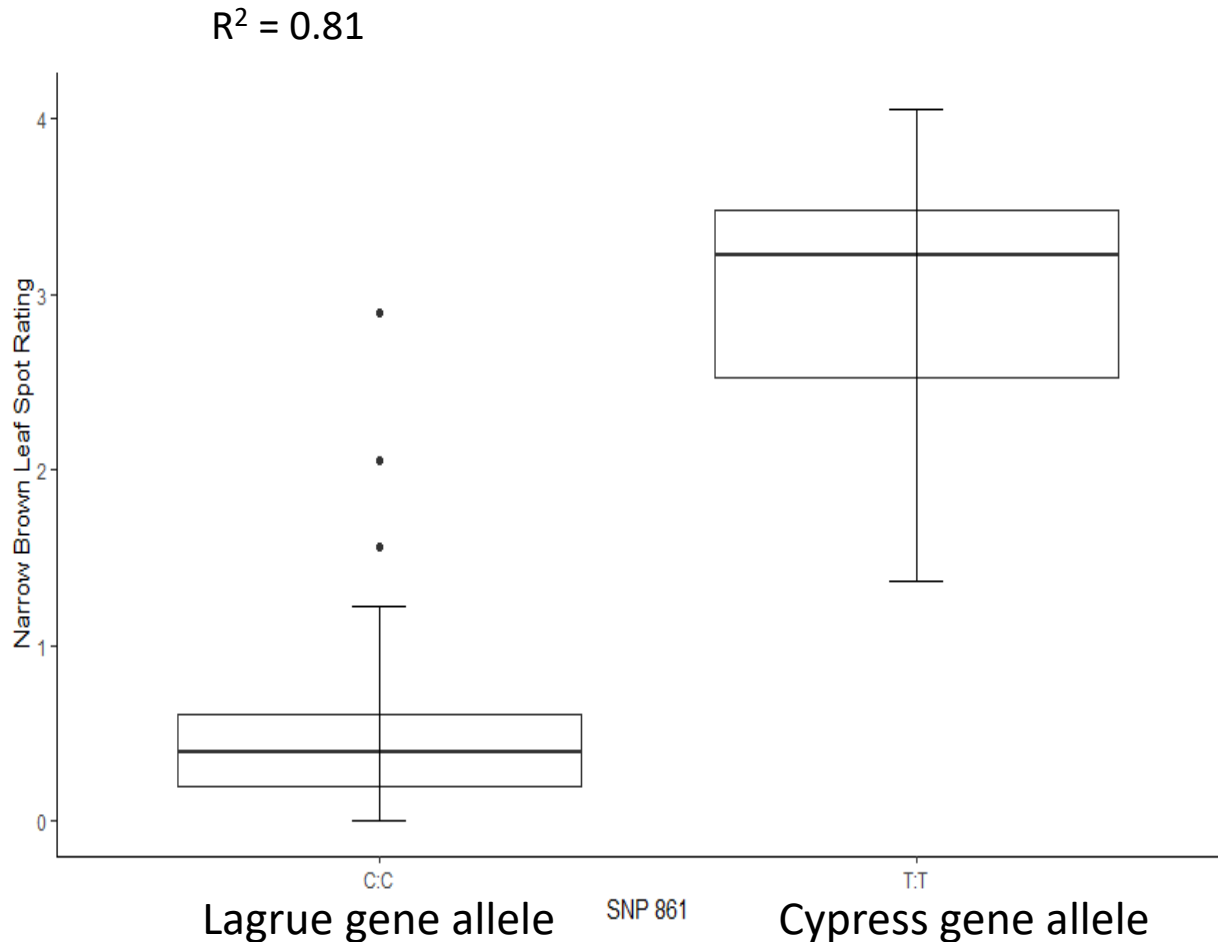
QTL Mapping: DNA marker association to NBLS



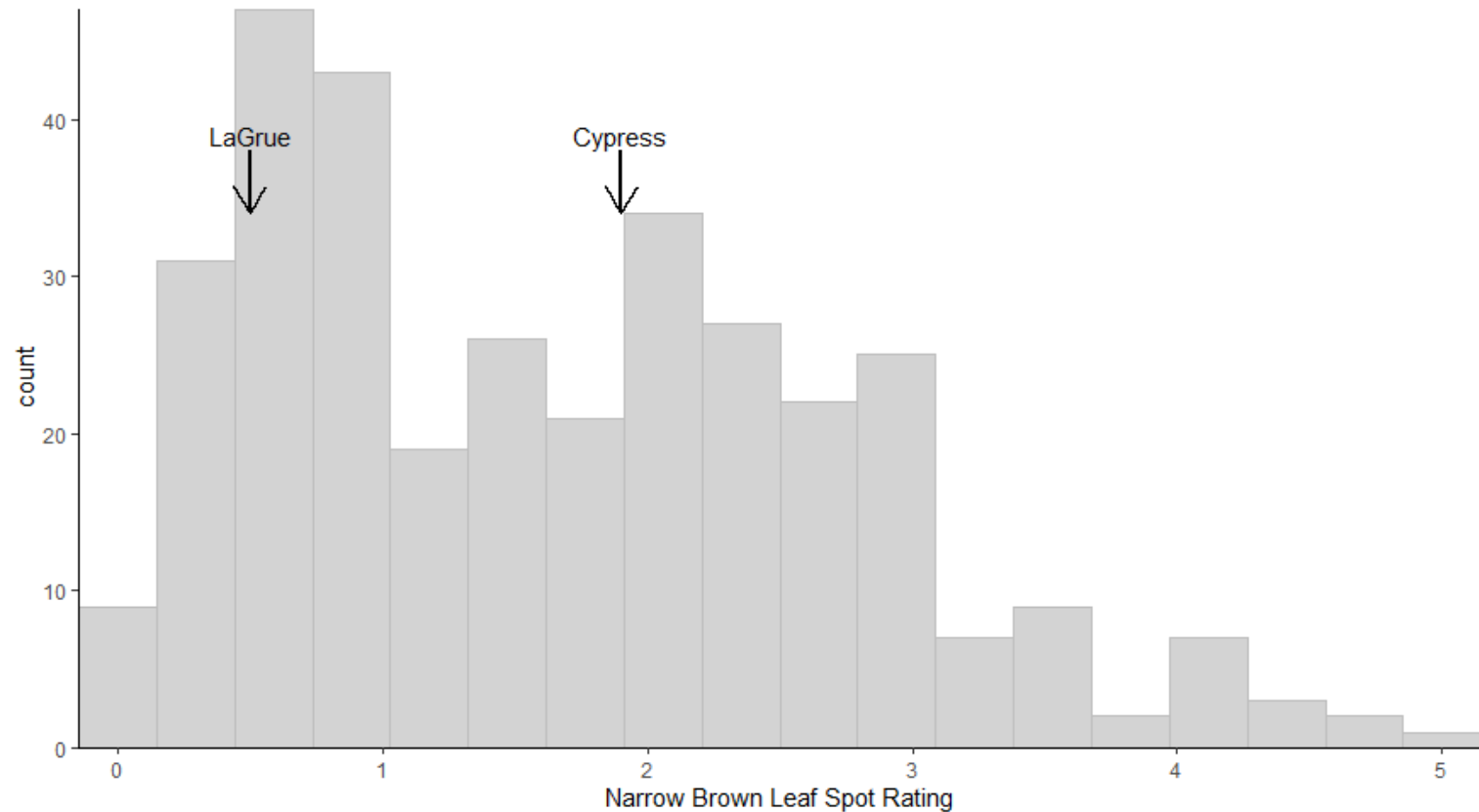
Genotyping and QTL Analysis

QTL Name	Trait	Chr.	Left Marker				Right Marker			LOD	PVE	Add	Donor	Year Detected
			Position	Marker	Position	IRGSP V.1	Marker	Position	IRGSP V.1					
			(cM)	Name	(cM)	Position	Name	(cM)	Position					
CRSP-2.1	NBLS	2	138.00	SNP790	137.64	24,477,977	SNP792	139.74	24,693,023	116.9	81.4	1.29	LaGrue	All Years
MY2dth-1.2	DTH	1	203	SNP522	148.31	38,413,377	SNP303	211.36	38,413,377	3.9	5.2	0.97	LaGrue	
MY2dth-2.1	DTH	2	48	SNP11	46.55	7,284,870	SNP258	57.17	10,595,313	4.5	3.2	-0.72	Cypress	2018
MY2dth-2.2	DTH	2	140	SNP792	139.74	24,693,023	SNP793	140.66	24,791,557	12.5	8.4	-1.19	Cypress	2016, 2017
MY2dth-2.5	DTH	2	180	SNP803	178.91	30,829,996	SNP812	186.49	31,672,631	4.8	3.2	-0.72	Cypress	2018
MY2dth-3.1	DTH	3	0	SNP478	5.62	1,505,315	SNP249	10.82	2,526,047	8.1	5.6	0.96	LaGrue	2016, 2018
MY2dth-7.1	DTH	7	69	SNP194	65.70	7,435,646	SNP467	70.42	11,618,172	5.1	3.5	-0.75	Cypress	2017, 2018
MY2dth-7.3	DTH	7	126	SNP359	123.07	27,961,782	SNP195	126.55	28,374,660	3.9	2.5	0.65	LaGrue	2018
MY2dth-8.1	DTH	8	169	SNP422	160.34	24,800,446	SNP173	173.34	25,899,361	12.9	10.8	1.35	LaGrue	All Years
MY2dth-10.1	DTH	10	71	SNP200	53.76	19,306,698	SNP212	71.83	21,817,967	18.1	13.5	-1.49	Cypress	All Years

NBLS DNA Marker Effect in MY2 Population



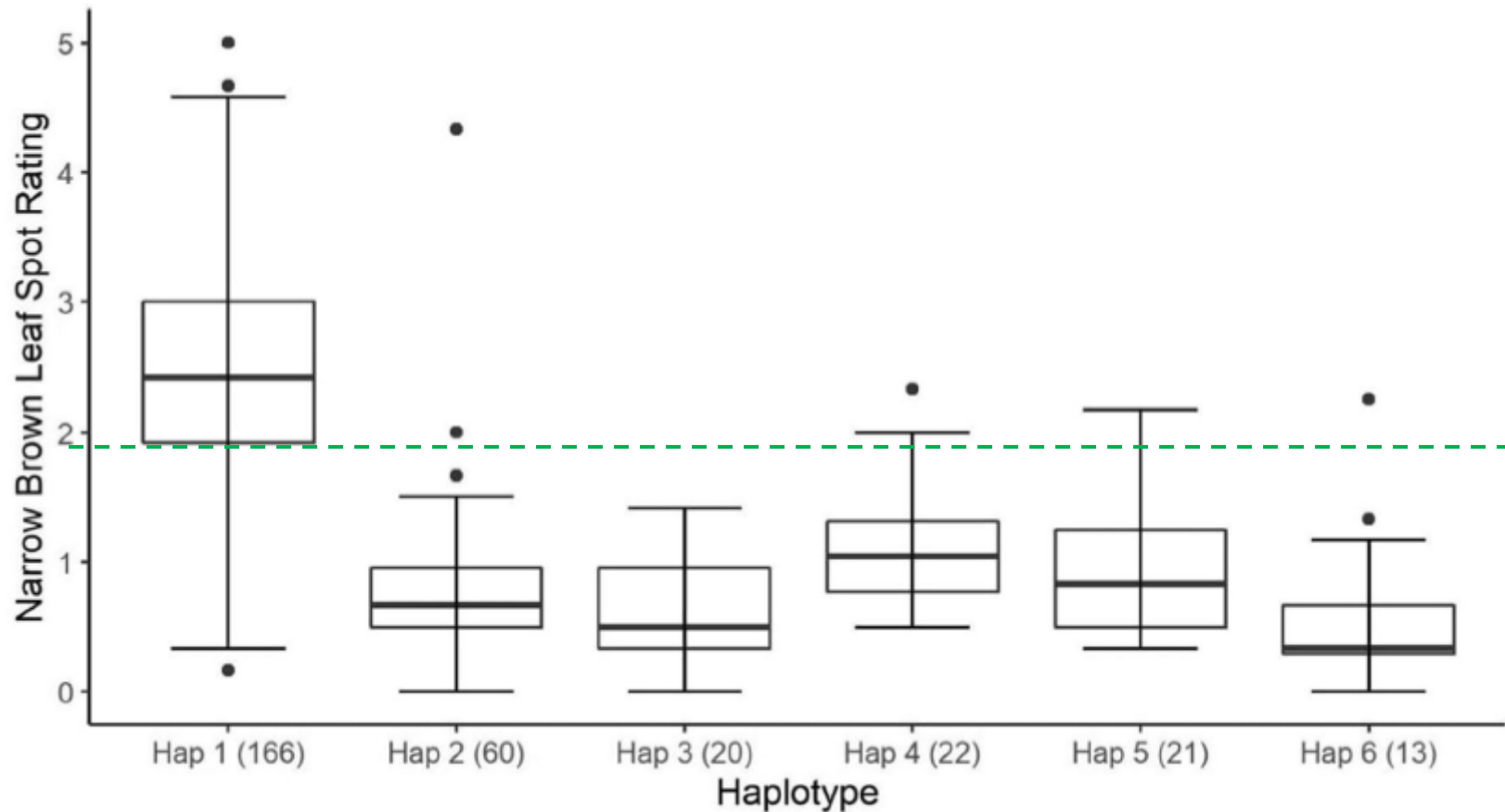
NBLS Distribution Across 387 U.S. Rice Germplasm Lines



Characterization of *CRSP2.1* Across U.S. Germplasm

IRGSP V.1			24,128,810	24,176,693	24,198,717	24,226,125	24,260,038	24,272,048	24,288,919	24,386,096	24,478,053	24,478,341	24,478,452	24,502,704	24,661,686
HAP ID	# of Lines	NBLS Rating (se)	858	1356	787	1357	1359	1358	859	861	878	881	882	862	868
Hap 1 (Cypress)	170 (166)	2.46 (0.07) <i>M. Sus</i>	T	C	C	G	A	A	T	T	C	T	C	T	C
Hap 2	93 (60)	0.83 (0.08) <i>Res</i>	G	T	T	A	A	C	A	C	C	T	C	T	C
Hap 3 (LaGrue)	27 (20)	0.65 (0.08) <i>Res</i>	G	T	T	A	G	C	A	C	T	C	T	C	A
Hap 4	28 (22)	1.15 (0.10) <i>Res</i>	G	T	T	A	A	C	T	C	C	T	C	T	A
Hap 5	31 (21)	0.96 (0.12) <i>Res</i>	G	T	T	A	A	A	A	C	T	C	T	T	C
Hap 6	16 (13)	0.61 (0.15) <i>Res</i>	G	T	T	A	A	C	A	C	T	C	T	C	A

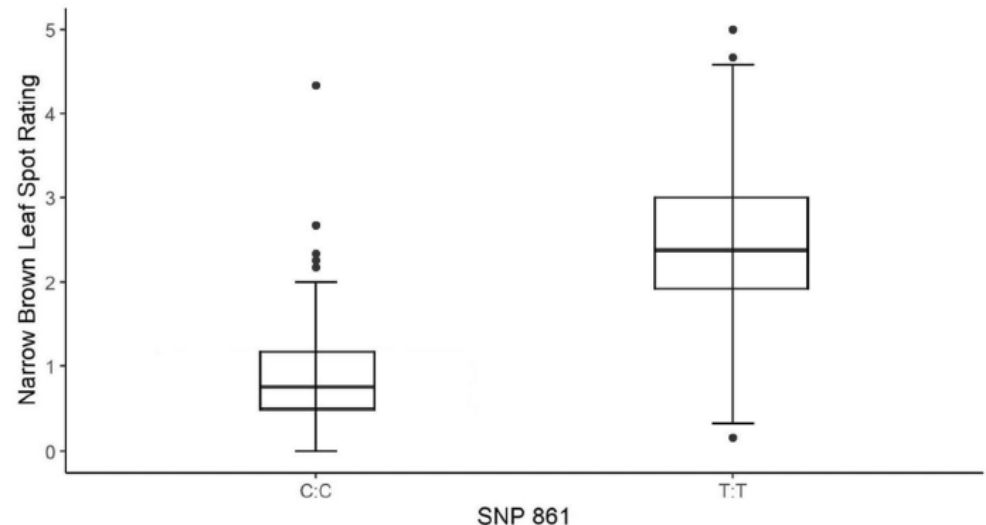
Characterization of *CRSP2.1* Across U.S. Germplasm



Identification of Trait Marker for *CRSP2.1*

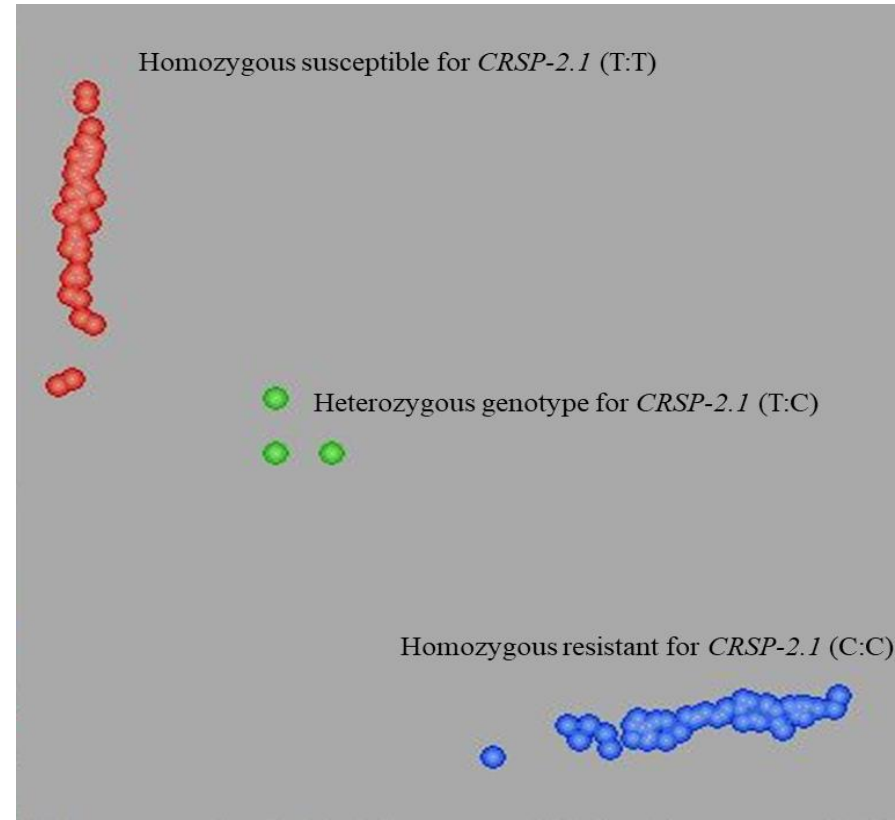
			IRGSP V.1													
			24,128,810	24,176,693	24,198,717	24,226,125	24,260,038	24,272,048	24,288,919	24,386,096	24,478,053	24,478,341	24,478,452	24,502,704	24,661,686	
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- SNP861 differentiates the susceptible Hap1 from all other resistant haplotypes
- SNP861 explains 53% of phenotypic variation across years
- Is positioned in the middle of the QTL region



KASP Assay SNP861 for *CRSP2.1*

- Clear, distinct clusters
- Reproducible across jobs and tissue sources
- Reliable results with quick and dirty extractions

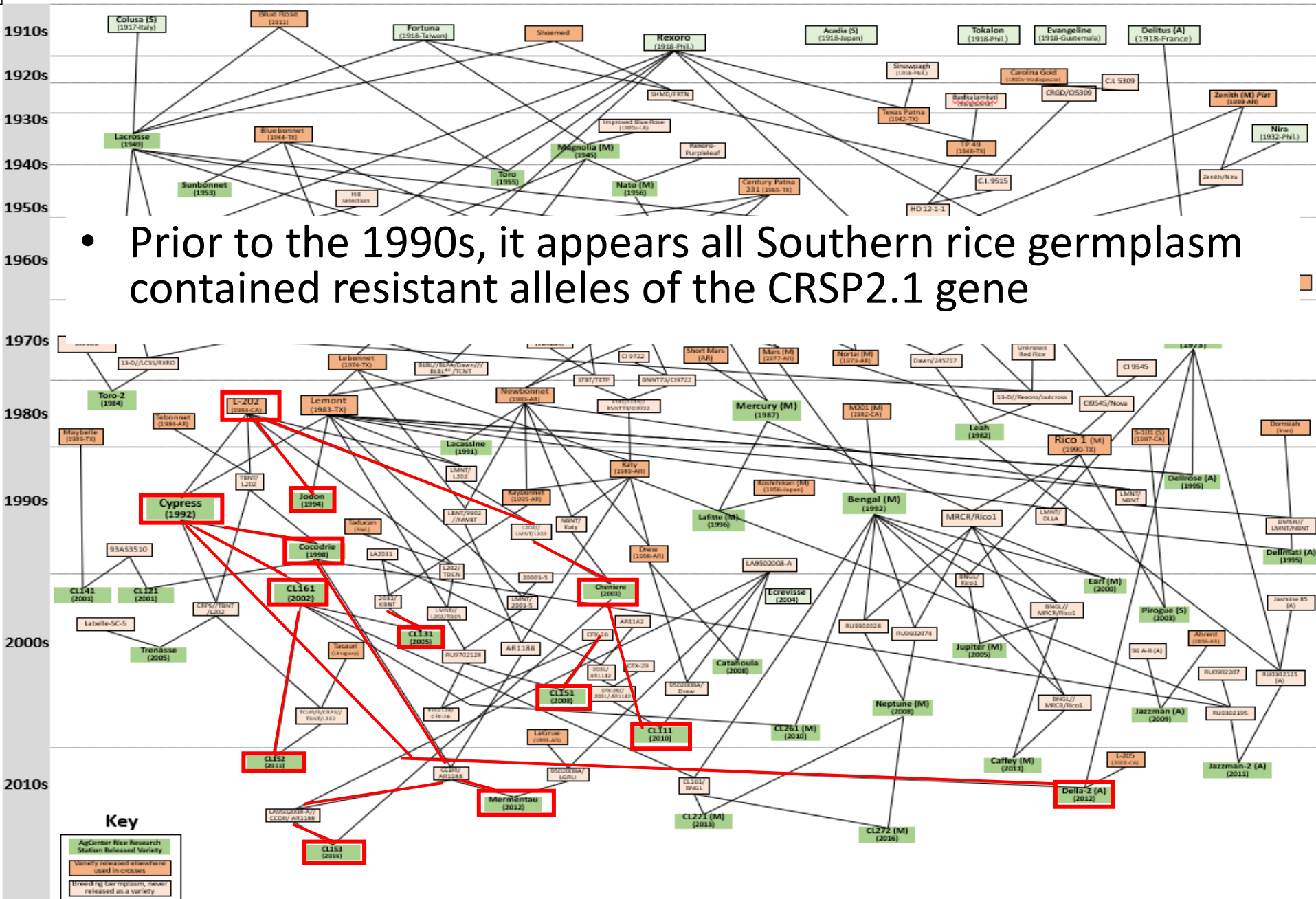


Where did the Susceptible Allele Come From?

IRGSP V.1			24,128,810	24,176,693	24,198,717	24,226,125	24,260,038	24,272,048	24,288,919	24,386,096	24,478,053	24,478,341	24,478,452	24,502,704	24,661,686
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Hap 6	16 (13)	0.61 (0.15) Res	G	T	T	A	A	C	A	C	T	C	T	C	A

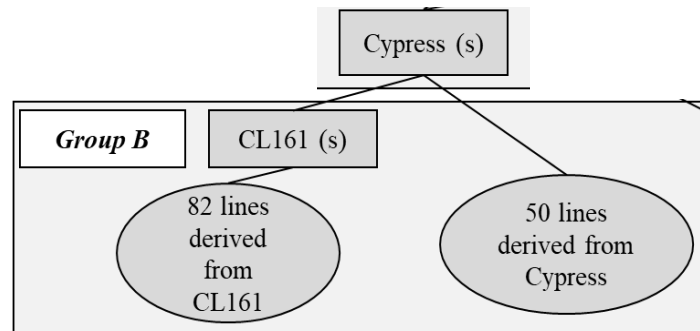
- Appears to be one susceptible allele and that all other alleles confer resistance

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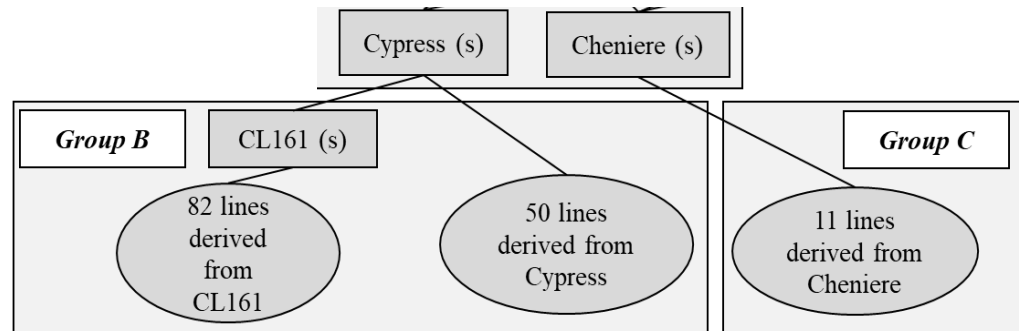
Where did the Susceptible Allele Come From?

- Pedigree analysis of 170 genotypes containing the Susceptible HAP1 allele
- 132 lines with Cypress pedigree



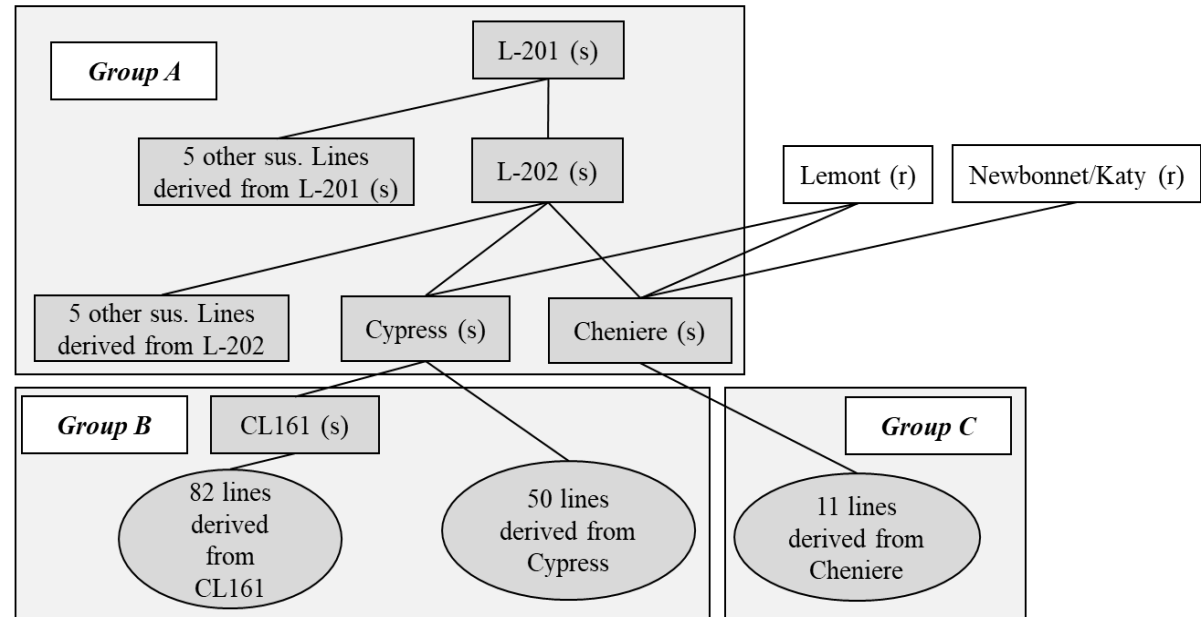
Where did the Susceptible Allele Come From?

- Pedigree analysis of 170 genotypes containing the Susceptible HAP1 allele
- 132 lines with Cypress pedigree
- 11 lines with Hap 1 Sus Cheniere pedigree
- Cypress and Cheniere share common pedigrees



Where did the Susceptible Allele Come From?

- Pedigree analysis of 170 genotypes containing the Susceptible HAP1 allele



- 132 lines with Cypress pedigree
- 11 lines with Hap 1 Sus Cheniere pedigree
- Cypress and Cheniere share common pedigrees
- Both trace back to the CA lines L-201 and L-202
- 157/170 lines with the SUS HAP 1 allele trace back to L-201

Where did the Susceptible Allele Come From?

- Prior to the 1990s, it appears all Southern rice germplasm contained resistant alleles/versions of the *CRSP2.1* gene
- *CRSP2.1* gene happens to be on the same chromosome as the CL gene, which may be causing an increased frequency of susceptibility in CL germplasm
 - 63% of modern CL germplasm contains the susceptible version of *CRSP2.1*
 - 41% of modern Conventional germplasm contains the susceptible version of *CRSP2.1*

2006 NBLS Outbreak

- A major outbreak of NBLS occurred in 2006, causing significant damage to the rice crop
- Prior to this, NBLS was said to be considered of limited concern
- Although this outbreak and subsequent presence of NBLS is likely due in part to the environment and disease evolution, its interesting to note the acreage
- In 2006, five varieties accounted for 90% of the acreage:
 - Cocodrie (25%)
 - Cheniere (25%)
 - CL131 (24%)
 - CL161 (11%)
 - Cypress (5%)
- Each of these varieties contains the susceptible version of *CRSP2.1*
- *Had NBLS not been prevalent in previous decades because all varieties had been resistant?*

Thank You

- Questions or Comments?
- Acknowledgements
 - Breeding Project
 - Adam Famoso and Brijesh Angira
 - Valerie Dartez, Blaise Frey, Joseph John, Brady Williams, Colby LeJeune
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 - Brijesh Angira, Jennifer Dartez, Madeline LeJeune
 - Student Workers: Kristin Theunissen