Identification and Analysis of Maize QTL for Southern Leaf Blight and Gray Leaf Spot resistance

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Introduction: Quantitative resistance is the major form of resistance used in cultivated maize. Very little is known about the molecular genetic basis or mechanism of action of quantitative resistance in maize or any other crop. Working with the foliar diseases Gray Leaf Spot (GLS) and Southern Leaf Blight (SLB), we are developing materials and methods for the detailed characterization and fine-mapping of selected QTLs, including sets of Near Isogenic Lines. We are also working to identify and map new sources of resistance from diverse germplasm.

Questions being addressed:

- Are there disease resistance QTL hotspots in the genome?
- Does the same QTL provide resistance to more than one disease?
- What are the mechanisms of action of disease resistance QTLs?
- What genes underlie these traits?

Which QTL to examine?

We are selecting loci based on several criteria:

1. Large Effect QTL
   - Easier to study
   - Of more importance
2. QTL that are effective throughout the life of the plant
   - Can be studied in the field with adult plants and in the greenhouse with seedlings
3. QTL found in a range of studies
   More likely to be of general utility

Comparison of SLB QTL studies

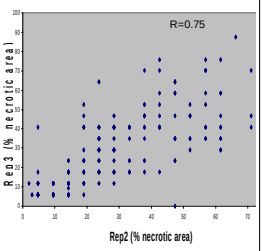
	Population/Environment					
BIN	HI/LI F2 FIELD	B73/Mo17 RIL FIELD	B73/Mo17 RIL Seedlings in Greenhouse	NC250A/B73 F2:3 FIELD	Adent/B73 F2:3 FIELD	B104/NC300 RIL FIELD
1.02						
1.07-10						
2.04						
2.09						
3.03-05						
3.09						
4.08-09						
5.04						
5.05-06						
5.08						
6.00-6.02						
6.07						
7.01-03						
8.03-05						
9.01-04						
10.04						

Bin 3.03-05 was identified as a QTL for SLB resistance in all of the studies we are aware of, constituting 5 different populations, including mature plant and seedling studies.
- A good candidate for further analysis

To analyze QTLs in detail we need

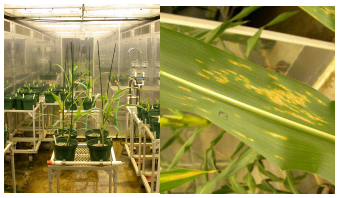
1. Standardized environmental conditions using controlled environment assay
2. Standardized genetic background using Near Isogenic Lines (NILs)

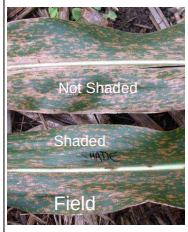
Controlled Environment assays

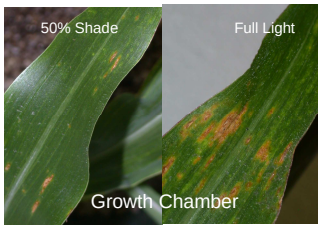


Spray assay is scored subjectively but gives reproducible results

GLS: Controlled environment assays for GLS are slower and less reproducible







The growth chamber assay is being used to examine the effect of light intensity on GLS symptom development

Near Isogenic Lines

We have identified recombinant inbred lines with residual heterozygosity in regions of interest. NIL pairs differing in these region have been produced.

A pair of Near Isogenic Lines, derived from a RIL heterozygous for a marker in bin 3.04, infected with SLB in a greenhouse assay

Tx303/B73 NILs

We screened a NIL population consisting of 90 lines with different segments of Tx303 genome introgressed into a B73 background for GLS. In 2 reps we identified 6 lines with much increased susceptibility compared to B73 and 3 lines with moderately increased susceptibility

Susceptible line TBBC3-03

Resistant line TBBC3-03

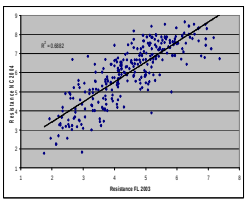
All 90 lines had been scored for SSR markers spanning the genome. The most susceptible lines all shared a Tx303 marker (umc1071) on chromosome 1s. These 5 lines were the only lines in the population to have the Tx303 marker at this position

Line	Marker						
	u1071	b1429	b1953	UMC076	p001	u1917	b2295
TBBC3-03	T	H	.	B	B	B	T
TBBC3-35	T	B	.	T	T	H	T
TBBC3-36	T	B	.	T	H	H	T
TBBC3-41							
TBBC3-42	T	T	.	B	B	B	B
TBBC3-60	B	B	.	B	B	B	B
TBBC3-65	B	B	.	B	B	B	B
TBBC3-74							
TBBC3-77	T	T	T	T	B	B	B

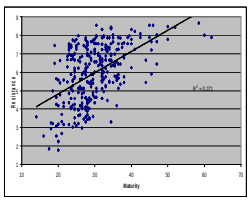
Table showing selected markers on the short arm of chm1. T= Tx303 allele, B= B73 allele, H= heterozygous, shaded= no data available. The nine lines shown are the most GLS susceptible lines identified. The lines highlighted in yellow were the most susceptible amongst these lines

Screening Diverse Lines

With a view to eventual association mapping, we are screening 300 diverse maize inbred lines for resistance to GLS and SLB. We have 2 years data for SLB and one for GLS. Maturity is significantly correlated with disease resistance for both these diseases.



SLB resistance of 300 diverse inbred lines scored in Florida 2003/04 and in North Carolina 2004.



SLB resistance of 300 diverse inbred lines plotted against maturity in Florida 2003/04

Conclusions/Next Steps:

- We have identified regions of interest for detailed analysis.
- NIL pairs have been developed/identified and are being analysed.
- Further mapping and NIL development is underway.
- Detailed analysis of NIL pairs is progressing

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