

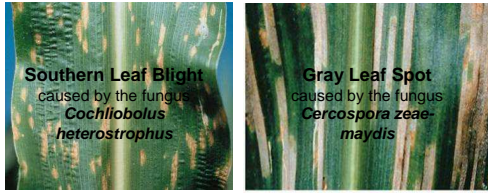
Analysis of Disease Resistance Loci in Maize

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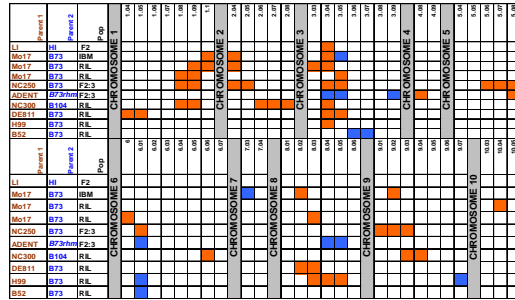
Introduction

The majority of disease resistance used in maize is **quantitative** in nature, i.e. incomplete but sufficient to protect yield. Quantitative resistance is generally extremely durable, but *very little is known about its molecular or physiological basis*.

We are characterizing genomic regions conferring quantitative resistance (also known as quantitative trait loci or **QTL**) to two maize diseases of significant importance in North Carolina – **gray leaf spot (GLS)** and **southern leaf blight (SLB)**.



Identification of SLB Resistance QTL

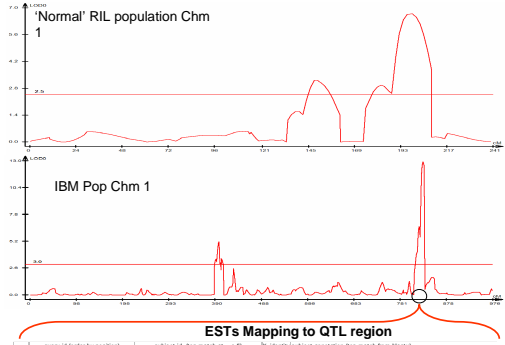


A summary of SLB QTL studies. With the exception of the LI/Hi study, all were performed in by the USDA-ARS in North Carolina. The maize genome is divided into 100 arbitrary sections known as bins. Bin 1.00 is at the top of chromosome 1, bin 1.01 is just below it etc. In the interests of space, not all maize bins are shown here. A colored cell indicates that an SLB QTL was identified in the corresponding bin in the corresponding population. The color of the cell corresponds to the parent from which the resistance allele was derived.

QTL for SLB resistance were identified on every chromosome. **Regions on chromosomes 1, 3 and 6 appear to be of particular interest.** Similar work is ongoing with GLS.

Fine Mapping of Resistance QTL

Using the IBM population we precisely defined SLB QTL on chms 1, 2 and 3. We also used a 'normal' B73/Mo17 RIL population to map the same QTL.

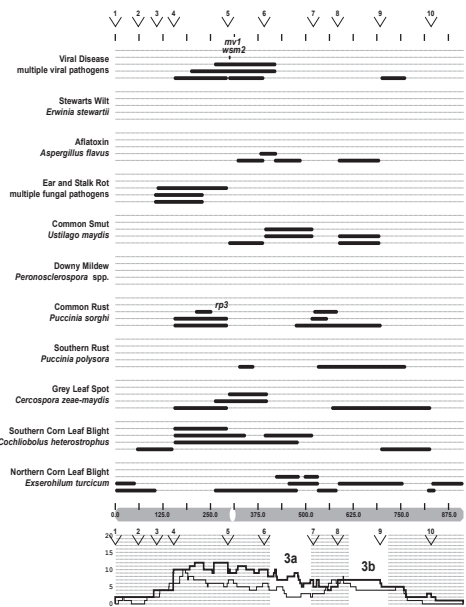


Query ID (order by position)	Subject ID (top match at ≤ 0.5)	% identity/subject annotation (top match from BLAST)
1	091	90.91 putative disease resistance protein
2	20thNov02-12-20-12417	g0212197(gMA1Y11207.1)
3	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
4	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
5	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
6	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
7	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
8	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
9	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
10	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
11	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
12	20thNov02-04-07-11505	g0594620(gMAM_462143.1)
13	20thNov02-04-07-11505	g0594620(gMAM_462143.1)

A resistance gene analog is also reported in this region Quilley et al. 2003

A Summary of Maize Disease Resistance Studies

Fifty publications reporting the locations of 437 QTL for disease resistance (or **dQTL**) in maize were summarized (Wisser et al. 2006 *Phytopath.* 96:120-129). Statistical tests indicated the **presence of clusters of dQTL for multiple diseases**. Evidence was also found for the **association of dQTL with maturity-related QTL**. It was evident from the distinct dQTL distributions for the different diseases that **certain breeding schemes may be more suitable for certain diseases**.



Consensus map of resistance loci in maize. Chromosome 3 is shown here for illustration purposes. At the bottom of the diagram is a histogram summarizing the QTL frequency per centiMorgan. The thicker line shows the frequency of dQTL and the thinner line maturity QTL. dQTL hotspots (taking into account gene density) are indicated as white areas in the histogram. On chromosome 3 there are two such hotspots, 3a and 3b.

Bins 3.04 and 6.01 are hotspots for both SLB and viral QTL. Bin 1.05 is a hotspot for GLS resistance QTL.

Analysis of Near-Isogenic Lines

We have identified several near-isogenic pairs of lines (NIPs) that which differ substantially for disease resistance. These are ideal candidates for further evaluation, as differences in phenotype can readily be ascribed to specific genomic regions.

NIP differing for SLB Resistance

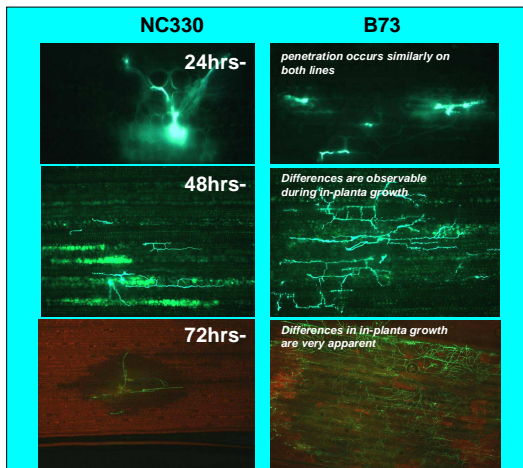


NIP differing for GLS Resistance



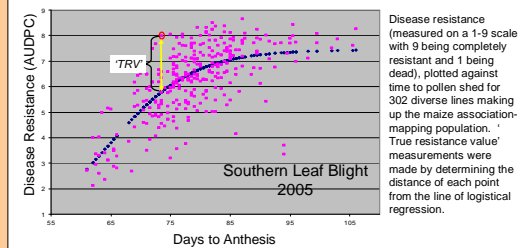
Analysis of pathogenesis on NIPs using a GFP-expressing pathogen

NC330 and B73 are a NIP differing for SLB resistance (NC330 is more resistant). Analysis using a GFP-expressing strain of *C. heterostrophus* (gift of C. Bronson), indicated that resistance in NC330 is expressed post-penetration, beginning around 24hrs after inoculation



Identifying Elite Germplasm

We screened the diverse 302-line association mapping population (Fint-Garcia et al 2005 *Plant J.* 44,1054-64) for SLB and GLS resistance over a number of years. Disease resistance is strongly correlated with maturity for both diseases. We corrected for maturity to get the 'True Resistance Value' (TRV) for each line.



Resistance Value Correlations

Significant correlations between the TRV values for SLB and GLS were found (see values highlighted below). This suggests that may be a **significant number of QTL with pleiotropic effects; conferring resistance to both diseases**.

	SLB 2005	GLS 2005	GLS 2004	SLB 2004	SLB 2003
SLB 2005	1.00	0.43 <0.001	0.39 <0.001	0.77 <0.001	0.73 <0.001
GLS 2005		1.00	0.61 <0.001	0.32 <0.001	0.34 <0.001
GLS2004			1.00	0.22 <0.003	0.20 <0.014
SLB_2004				1.00	0.73 <0.001
SLB_2003					1.00

Table showing the correlation between TRV scores for 3 different years of SLB ratings and two years of GLS ratings. Top number is the Pearson Correlation Coefficient, lower number is the p-value associated with the coefficient. Values highlighted indicate between disease correlation values.

Acknowledgements

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