



# Near-Isogenic Lines for the Genetic Dissection of Quantitative Resistance to Southern Leaf Blight and Grey Leaf Spot in Maize

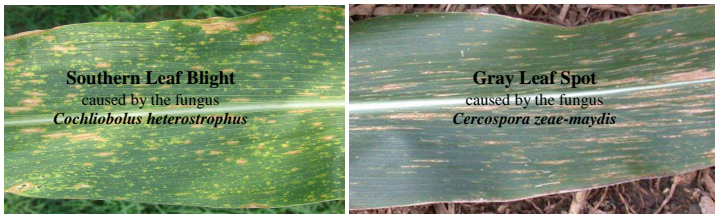
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## Introduction

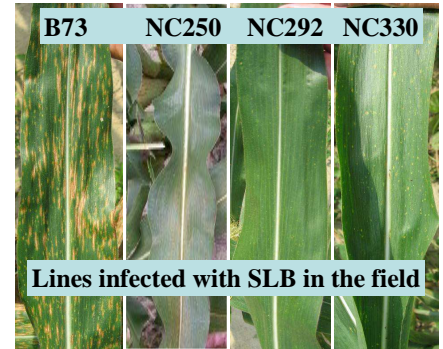
Most disease resistance used in maize is *quantitative* in nature, i.e. incomplete but sufficient to protect yield. Quantitative resistance is generally extremely durable, but *very little is known about its molecular or physiological basis*.

We are characterizing genomic regions conferring quantitative resistance (also known as quantitative trait loci or **QTL**) to **gray leaf spot (GLS)** and **southern leaf blight (SLB)**. In order to standardize the genetic backgrounds in which these QTL are evaluated, we are developing sets of near-isogenic lines (NILs), that differ only for specific disease resistance QTL. In most cases these NILs are in a B73 inbred background.



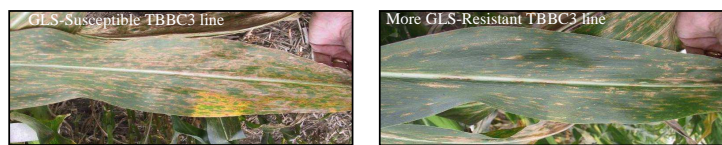
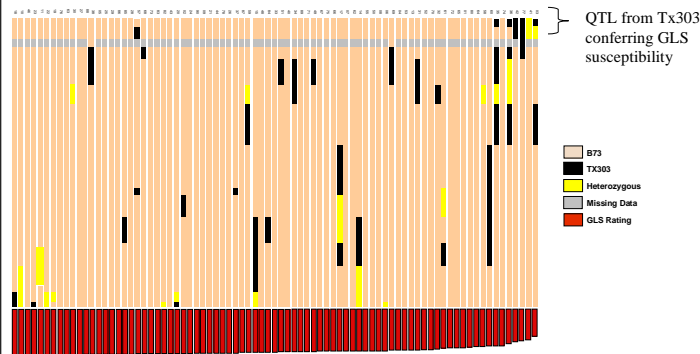
## Analysis of lines from the NCSU Breeding Program

The lines NC292 and NC330 were developed as B73-NILs (~95% B73 background) with contributions from the line NC250 which conferred greatly enhanced SLB resistance compared to B73. We characterized these line to identify the introgressions derived from NC250 in NC292 and NC330.

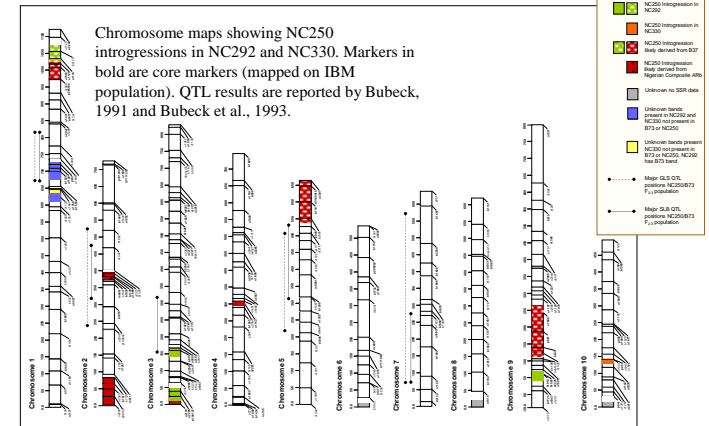
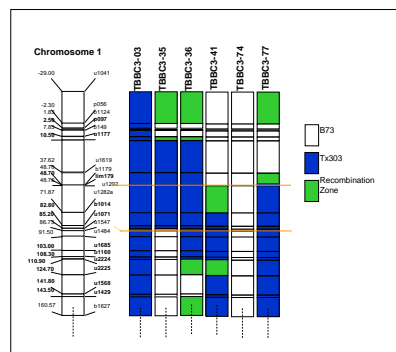


## Screening a Introgression Library

We screened a population made up of 90 lines all with ~95% B73 background with different introgressions from Tx303 in each line (the TBBC3 population - Szalma et al 2007). The figure below shows the makeup of chromosome 1 of all 90 lines. The lines are arranged in order of resistance to GLS based on three replicated field trials over 2 years (the shorter the red bar the more susceptible the line). A region at the tip of chromosome 1 appears to be associated with resistance.



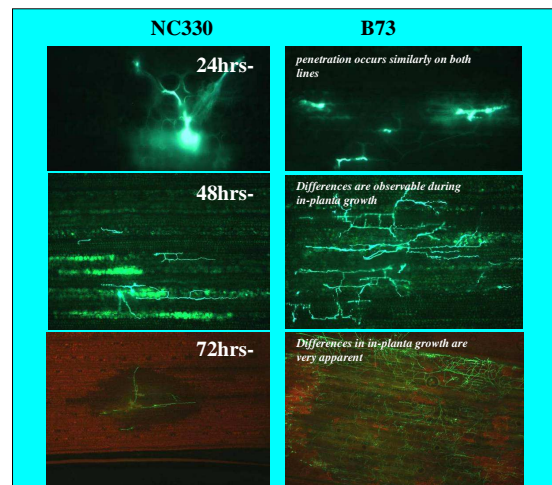
By detailed characterization of some of the GLS susceptible lines (see figure on the right) we have delimited the putative GLS QTL region. Studies are now under way to confirm the effect of the region and to further delimit it.



We have now developed lines carrying each of these individual introgressions in a B73 background and will be field trialing them in summer 2007

## Analysis of pathogenesis on NILs using a GFP-expressing pathogen

Pathogenesis on NC330 and B73 was compared using a GFP-expressing strain of *C. heterostrophus* (causal agent of SLB, gift of C. Bronson). Initial analysis indicated that resistance in NC330 is expressed post-penetration, beginning around 24hrs after inoculation



**Conclusions:** We are developing several sets of NILs differing for disease resistance QTL. In addition to those described above we have developed and are testing several lines carrying SLB resistance loci derived from Mo17 in a B73 background and have derived several sub-lines from inbred lines that appear to differ in disease resistance. We have identified NILs differing for SLB resistance in a Va35 inbred background (collaboration with Peg Redinbaugh, USDA-ARS, Wooster Ohio). We are also collaborating with Rebecca Nelson (Cornell University) to develop NILs differing for resistance to Northern Leaf Blight. We are now starting to use these NILs for detailed characterization of the phenotypes conferred by specific disease resistance QTL, and for fine mapping of the underlying genes.

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## REFERENCES

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Bubeck, D.M., Goodman, M.M., Beavis, W.D., and Grant, D. 1993. Quantitative Trait Loci Controlling Resistance to Gray Leaf Spot in Maize. *Crop Sci.* 33: 838-847.  
Szalma, S. J., B. M. Hostert, J. R. Ledeaux, C. W. Stuber and J. B. Holland. 2007 QTL mapping with near-isogenic lines in maize. *Theor appl genet*, In Press