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 (NILs). 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

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

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 regions have been produced.

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.

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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