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Funding Source: MU Monsanto Undergraduate Research Fellowship

QTL analysis for genes for brace root angle in zea mays l.
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Brace roots play a major role in determining amount of lodging, and are responsible for a significant portion of water and nutrient uptake. Using the randomly intermated B73 x Mo17 (IBM) RIL mapping population, we are identified chromosome regions which control brace root development. Previous work analyzed data from 94 mapping lines and identified numerous QTL. The number of potential candidates within these QTL intervals is too large to realistically test. For this reason, we are utilizing a larger number of mapping lines from this population in combination with additional markers, especially within known QTL regions, to refine the QTL intervals and reduce the number of candidate genes. The IBM mapping population was evaluated in the field in two replications in the summer of 2006. Pictures were taken and brace root angles were measured digitally using Image J. Analysis of variance was performed in SAS (SAS Institute, Raleigh, NC) with replicates and lines as main effects. Both replicates and lines had significant variation. Transgressive segregants were identified. A genetic map was generated using Mapmaker Experiment 1.16 with markers evenly spaced throughout the genome. Composite interval mapping was conducted using QTL cartographer 3.0 for Unix. Candidate genes are currently being identified through comparison of our mapping results with the Maize Bins, the IBM neighbors map (a computationally-derived composite map containing more than 14,000 genes and mutants mapped by the entire maize genetics community), and the 2005 Genetic Map.

This project was completed to fulfill a Capstone requirement.