Mapping loci responsible for auxin-mediated development of the primary root in maize

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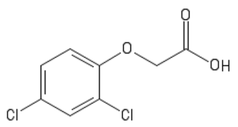
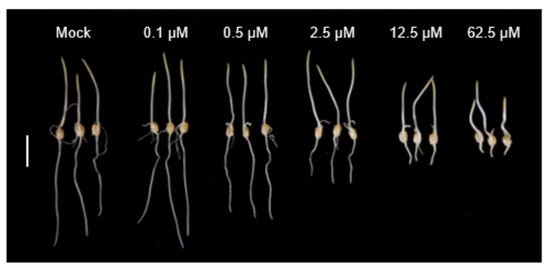
Abstract

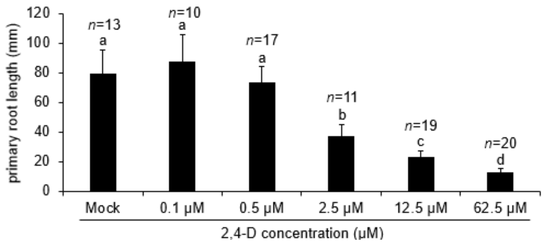
Zea mays (maize) has been thoroughly studied in order to improve the structure of the plant, nutritional value, and resistance to drought, rain, and insects. However, because maize was normally bred to produce better ears and stronger stalks, root architecture has not been heavily selected for in modern commercial hybrids. Thanks to previous research in establishing the Nested-Association Mapping (NAM) population, recombinant inbred lines (RILs) between the reference line B73, and the 25 NAM founders, we are now able to do high sensitivity QTL mapping in maize. Through our research in testing standing genetic variation in the NAM founders, we found that there were many differences in primary root length, as well as their sensitivity to the phytohormone auxin. Naturally occurring auxins and the synthetic auxin 2,4-dichlorphenoxyacetic acid (2,4-D) are known to inhibit the growth of the primary root. Although 2,4-D is used as an herbicide for dicot plants and maize is a monocot, the roots are still affected. The B73 reference line is very sensitive to auxin, but the NAM founder line Mo18W is hyposensitive. Thus, utilizing RILs between B73 and Mo18W will allow us to conduct QTL analysis to determine the locus or loci responsible for sensitivity to auxin. Using this data, the root architecture could then be modified to improve root growth by modulating auxin mediated growth.

2,4-D inhibits root growth in maize



2,4-dichlorophenoxyacetic acid

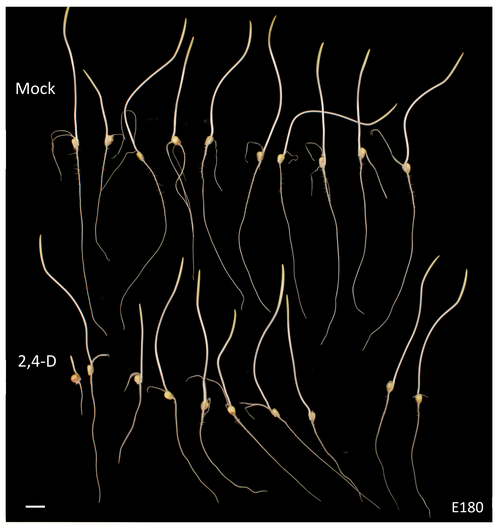




Paper rolls of recombinant inbred lines in a 2,4-D solution (left) and a mock solution (right)

Results

- 2,4-D was used because it had the greatest inhibitory effect on B73 compared to other forms of auxin and because Mo18W is very insensitive to 2,4-D
- Each RIL was grown for five (5) days in a paper roll. Half of the seeds from each RIL were grown in a mock solution of dimethyl sulfoxide (DMSO) and deionized water. The other half were grown in a solution of DMSO, deionized water, and 2,4-D



We saw extensive genetic diversity throughout the recombinant inbred lines, shown by RILs E180 and E036 above

Acknowledgments

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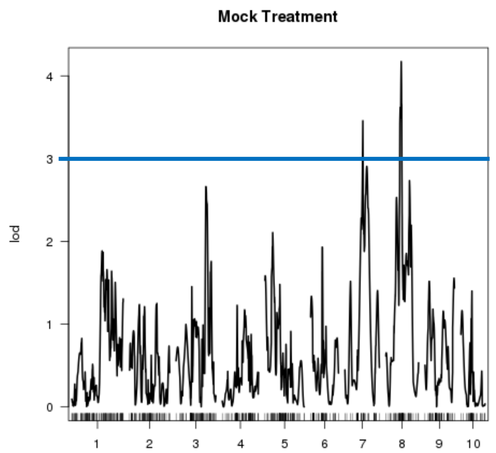
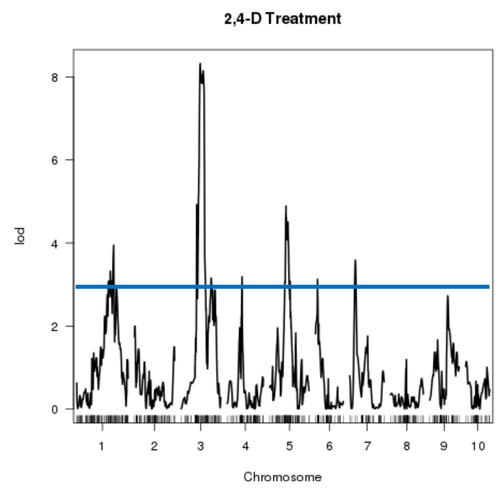
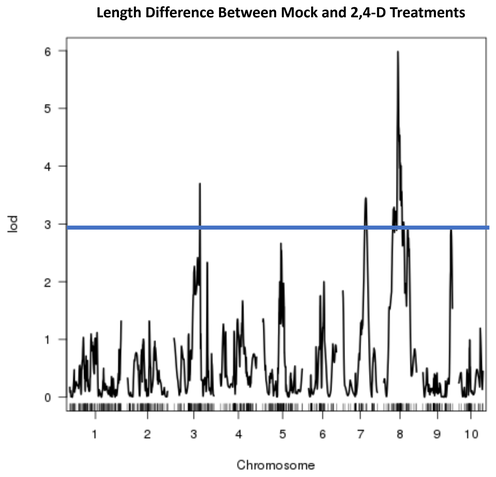
QTL Analysis







The peak on chromosome 3 and 5 in the second graph indicates that the traits associated with auxin inhibited development are located here and that there are multiple traits associated with auxin mediated development

Future Work

- Determine which traits are responsible for auxin sensitivity
- Analyzing the primary root tips of both B73 and Mo18W treated with and without 2,4-D to determine differences in the elongation zones

Created by Paige Spencer