

*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-dichlorophenoxyacetic acid (2,4-D) are known to inhibit the growth of the primary root. Although 2,4-D is used as a 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.