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Identification of QTL associated with root architecture under well-watered, and water-stressed conditions in *Zea mays*

Drought alone contributes 17% to the average annual yield loss in maize (Zea mays). It is the single most significant environmental obstacle to improving grain yield. Many physiological traits have been linked to drought resistance including osmotic adjustment, anthesis-silking interval, leaf surface area and root architecture. QTL associated with root architecture play an integral role in drought resistance by facilitating the uptake of water from sources deep below the soil line. Our goal was to identify the QTL involved in root architecture in Zea may under well-watered, and water-stress conditions. Two QTL experiments were performed one well-watered and one water-stressed. In the well-watered experiment, a subset of 94 mapping lines from the intermated B73 x Mo17 (IBM) population was planted in five reps in a randomized complete block design. The seed was sown in a peat based growth medium and the plants were grown in a greenhouse under well-watered conditions for two weeks. After the two-week period, shoot mass, root branching, primary root length, seminal root number and root mass were measure for each plant. The water-stressed experiment was conducted in the same manner. To prevent immediate desiccation of the plants a polyacrylamide water retainer was added to the growth media. After the initial two week, well-watered period the plants were allowed to grow without water for ten days. At the end of the 10 days the same traits were measured along with the relative water content of the 4th leaf. Genotypic data for 251 markers, evenly distributed throughout the maize genome, were used to construct a genetic map with Mapmaker Exp version 3.0 for Unix. QTL analysis was performed by using QTL Cartographer version 1.16. 32 total QTL were identified, 20 for the well-watered traits, and 12 for the water-stressed traits. The 20 QTL identified in the well-watered experiment accounted for 74%, 38%, 77% and 81% of the phenotypic variance in primary root length, root branching, seminal root number and shoot mass respectively. The 12 QTL identified in the water-stressed experiment accounted for 25%, 13.5%, 41.2%, 17.2%, of the phenotypic variance in primary root length, root branching, seminal root number and root mass. QTL identified were compared to previous QTL experiments. Many of the well-watered QTL correspond to QTL regions previously identified in other root architecture studies. Novel QTL for root growth under water-stressed were identified in bins 3.05, 8.01, 10.01 and 10.05. Candidate genes were selected for the QTL using the maize bin map.