



Molecular mapping of quantitative trait loci for drought tolerance in maize plants

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ABSTRACT. Drought tolerance is one of the most important but complex traits of crops. We looked for quantitative trait loci (QTLs) that affect drought tolerance in maize. Two maize inbreds and their advanced lines were evaluated for drought-related traits. A genetic linkage map developed using RFLP markers was used to identify QTLs associated with drought-related traits. Twenty-two QTLs were detected, with a minimum of one and a maximum of nine for drought-related traits. A single-QTL was detected for sugar concentration accounting for about 52.2% of the phenotypic variation on chromosome 6. A single-QTL was also identified for each of the traits root density, root dry weight, total biomass, relative water content, and leaf abscisic acid content, on chromosomes 1 and 7, contributing to 24, 0.2, 0.4, 7, and 19% of the phenotypic variance, respectively. Three QTLs were identified for grain yield on chromosomes

1, 5, and 9, explaining 75% of the observed phenotypic variability, whereas four QTLs were detected for osmotic potential on chromosomes 1, 3, and 9, together accounting for 50% of the phenotypic variance. Nine QTLs were detected for leaf surface area on chromosomes 3 and 9, with various degrees of phenotypic variance, ranging from 25.8 to 42.2%. Four major clusters of QTLs were identified on chromosomes 1, 3, 7, and 9. A QTL for yield on chromosome 1 was found co-locating with the QTLs for root traits, total biomass, and osmotic potential in a region of about 15 cM. A cluster of QTLs for leaf surface area were coincident with a QTL for osmotic potential on chromosome 3. The QTLs for leaf area also clustered on chromosome 9, whereas QTLs for leaf abscisic acid content and relative water content coincided on chromosome 7, 10 cM apart. Co-location of QTLs for different traits indicates potential pleiotropism or tight linkage, which may be useful for indirect selection in maize improvement for drought tolerance.

Key words: Drought tolerance; Genetic variation; Linkage maps; Molecular markers; Quantitative trait loci; *Zea mays*