

Quantitative Trait Loci for Cell-Wall Traits in Corn

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Introduction

Improving forage quality by increasing cell-wall digestibility is a major goal of our research program. In this study we attempted to map and characterize quantitative trait loci (QTLs) associated with the polysaccharide and hydroxycinnamate components in corn cell walls. Advances in molecular marker technology have enabled the development of dense genetic linkage maps for major crops such as corn. These maps have been used to associate DNA markers with important physiological and morphological traits. Complex traits can be dissected into discrete factors, also referred to as QTLs. Identification of QTLs affecting traits of interest can be the first step in the map-based cloning of genes related to quantitative traits. Markers linked to QTLs can also be used in modern breeding programs to increase genetic progress. Objectives of our research were to (i) determine phenotypic correlations among corn cell-wall traits and (ii) ascertain the number and the chromosomal locations of QTLs and estimate the genetic effects of these QTLs involved in cell-wall trait expression.

Materials and Methods

A population of 48 recombinant inbred corn lines (RIL) was developed by Burr and co-workers by crossing the Cm37 and T232 inbreds. Plants were grown in two randomized blocks in St. Paul and Rosemount, MN in 1995. Mature leaves from the sixth and seventh internode of three or four plants per field replicate were collected at the pollen shedding stage of development, and oven dried at 50°C. The following cell-wall components were measured using standard procedures: arabinose, galactose, glucose, mannose, xylose, uronic acids, *p*-coumarate and ferulate esters and ethers, and Klason lignin and syringyl-to-guaiacyl (S/G) ratio of lignin composition. The linkage map was obtained from Brook Haven National Laboratory and a subset of 315 markers was selected to provide relatively even spacing (6-7 centimorgans) for QTL analysis. The composite

interval mapping method available in the Plabqtl program were used for estimating QTL positions and effects. The probability of the presence of a QTL at a particular location was expressed as a LOD score (\log_{10} of the likelihood odds ratio). The LOD threshold was estimated for each data set using the QTLcartographer program with permutations set at 1000. Because of the small population size of RILs used in this study, we adopted a stringent ($P < 0.01$) LOD score requirement to declare a QTL significant.

Results and Discussion

Significant phenotypic correlations were found among most cell-wall lignification traits in this RIL population. *p*-Coumaric (PCA) and ferulic (FA) acid esters were highly correlated to their corresponding ethers ($r = 0.90$ and 0.74 , respectively). In contrast, only half of cell-wall polysaccharide components had significant correlations with each other. Arabinose was highly correlated with galactose ($r = 0.82$) and glucose was moderately correlated ($r = 0.59$) with xylose. All hydroxycinnamate esters and ethers were positively associated with arabinose, galactose, and xylose, possibly indicating the coordinated deposition pattern of these components during cell-wall development. However, lignin lacked association with these three sugars. High correlations of S/G ratio with arabinose and galactose were also observed, but the physiological significance of these correlations is debatable. Genotypic variances among RILs were highly significant ($P < 0.01$) for all traits except Klason lignin. Location also exerted significant effects on concentrations of most sugars, FA ether, lignin and S/G ratio. Genotype x environment interactions were detected for glucose, xylose, and FA esters and ethers. A total of 44 QTLs were detected for five cell-wall polysaccharide components, ranging from five to 14 QTLs for each trait. These QTLs explained 59 to 91% of the phenotypic variance. Very few QTLs displayed QTL x environment interactions except for uronic acid where seven of nine QTL exhibited such interactions. Forty QTLs were detected for five lignification traits, accounting for 52 to 85% of the

phenotypic variance. Two markers associated with FA ether QTLs were located in the vicinity of two known brown midrib loci (bm3 and bm4). Some of the cell-wall polysaccharide and lignification traits shared the same molecular markers, an indication that genes associated with these overlapping QTLs may be responsible for the coordinated deposition of polysaccharide and lignin components in the cell wall.

Conclusions

Little previous work has been done on QTL analysis for forage quality traits in corn. Previous research has

used acid detergent fiber (ADF, a gravimetric measurement after extraction) as the cell-wall trait of interest. LOD scores and variance explained by the QTLs for ADF were relatively low. In contrast, our study of the molecular components of the cell wall found high LOD scores and coefficients of determination. However, population size may have contributed to the difference between the studies. The data suggest that these markers could be successfully used for breeding or map-based cloning of cell-wall traits.

Table 1. Quantitative trait loci (QTLs) associated with concentrations of cell-wall polysaccharide and lignification components of 48 recombinant inbred corn lines grown in two environments.

Trait	Number of QTLs	Chromosomes	Range of LOD Scores for QTLs	Variance Explained (r^2)
<u>Polysaccharide Components</u>				
Arabinose	5	5, 9, 10	5.83 - 16.41	0.61
Galactose	7	1, 4, 5, 6, 9, 10	6.03 - 17.97	0.79
Glucose	9	1, 3, 5, 7, 8, 9, 10	5.86 - 16.76	0.80
Xylose	14	1, 2, 4, 5, 6, 7, 9, 10	6.24 - 21.42	0.91
Uronic Acids	9	1, 2, 3, 4, 5, 9	8.10 - 13.67	0.59
<u>Lignification Components</u>				
Ferulate Esters	10	1, 3, 5, 6, 7, 8	8.31 - 18.15	0.85
<i>p</i> -Coumarate Esters	7	1, 2, 6, 7, 8, 9, 10	6.33 - 13.37	0.69
Ferulate Ethers	11	1, 2, 3, 4, 7, 9, 10	7.03 - 14.46	0.80
<i>p</i> -Coumarate Ethers	7	1, 2, 6, 7	7.02 - 16.47	0.74
S/G Ratio	5	2, 3, 4, 7	4.94 - 8.19	0.52