

Abstract

Hitherto, most quantitative trait loci of maize growth and biomass yield have been identified for a single time point, usually the final harvest stage. Through this approach cumulative effects are detected, without considering genetic factors causing phase-specific differences in growth rates. To assess the genetics of growth dynamics, we employed automated non-invasive phenotyping to monitor the plant sizes of 252 diverse maize inbred lines at 11 different developmental time points; 50 k SNP array genotype data were used for genome-wide association mapping and genomic selection. The heritability of biomass was estimated to be over 71%, and the average prediction accuracy amounted to 0.39. Using the individual time point data, 12 main effect marker-trait associations (MTAs) and six pairs of epistatic interactions were detected that displayed different patterns of expression at various developmental time points. A subset of them also showed significant effects on relative growth rates in different intervals. The detected MTAs jointly explained up to 12% of the total phenotypic variation, decreasing with developmental progression. Using non-parametric functional mapping and multivariate mapping approaches, four additional marker loci affecting growth dynamics were detected. Our results demonstrate that plant biomass accumulation is a complex trait governed by many small effect loci, most of which act at certain restricted developmental phases. This highlights the need for investigation of stage-specific growth affecting genes to elucidate important processes operating at different developmental phases.