

ANALYSIS OF LINKAGE DISEQUILIBRIUM AT A QTL FOR FLOWERING TIME IN MAIZE

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It has been proposed that a collection of germplasm accessions can be exploited to identify an association between specific alleles or combination of alleles (haplotypes) and a trait of interest. The rationale is based on the existence of some level of linkage disequilibrium (LD) between molecular marker loci and the locus controlling the target phenotype within the population under analysis. Preliminary analyses in maize have already shown a rather low, albeit variable, level of LD, making unrealistically high the number of markers to be screened for a whole-genome screen. Conversely, the low LD level would provide high resolution power thus making association mapping a strategy to verify the role of candidate genes (Rafalski, 2002). In a positional cloning effort, we developed molecular markers genetically and physically linked to *Vgt1*, a QTL controlling flowering time in maize (Salvi et al., 2003). Aim of this research was to verify the possibility to detect an association between *Vgt1* haplotypes and flowering time by using an LD-based approach.

A collection of ca. 100 maize inbred lines kindly provided by Ed Buckler and already characterized with molecular markers was grown in replicated trials in Cadriano (Bologna) over two years. The phenotypic traits analyzed were flowering time (as days to pollen shed), node number and plant height. Based on the DNA sequence spanning ca. 80 kb and encompassing the *Vgt1* locus, several gel-based molecular markers were developed and utilized to screen the collection of inbred lines. Data will be reported on the level of LD across the region and on the association of alleles/haplotypes with phenotypic traits.