Abstract

QTL mapping with segregating populations results in poor map resolution which limits the applicability of mapped QTL in further research such as gene cloning. The current research project aimed mainly at developing STepped Aligned Recombinant Inbred Strains (STAIRS) covering the top region of chromosome 3 and demonstrating the feasibility of using STAIRS in high resolution mapping of QTL in *Arabidopsis*. The top region of chromosome 3 of *Arabidopsis* had been reported to house QTL related to flowering time. This region was first saturated with 24 polymorphic microsatellite markers and 23 narrow STAIRS were produced within the region via a marker-assisted backcross breeding programme using whole chromosome substitution lines. The analysis of QTL with the narrow STAIRS revealed a major pleiotropic QTL within 2-3 cM affecting flowering time, leaf number at day 20 and rosette and cauline leaf numbers at flowering. A second QTL with less but opposite effect on the same traits were located within 15-20 cM. The search for candidate genes within 2-3 cM of chromosome 3, to locate possible candidate genes revealed COL-2, CONSTANS-Like gene which affects flowering time. Microarray gene expression profiling was performed using the two genotypically closest lines which differ for flowering time to compare the two lines at the same chronological and physiological ages in two experiments respectively. The lists of differentially expressed genes were obtained from the two experiments. Differential expression was observed for the possible candidate gene in the latter experiment. The results emphasized the power of STAIRS in fine mapping of QTL and the possibility of using them in transcriptional profiling to study the expression of genes.