



Bayesian QTL analyses using pedigreed families of an outcrossing species, with application to fruit firmness in apple

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Key message Proof of concept of Bayesian integrated QTL analyses across pedigree-related families from breeding programs of an outbreeding species. Results include QTL confidence intervals, individuals' genotype probabilities and genomic breeding values. Abstract Bayesian QTL linkage mapping approaches offer the flexibility to study multiple full sib families with known pedigrees simultaneously. Such a joint analysis increases the probability of detecting these quantitative trait loci (QTL) and provide insight of the magnitude of QTL across different genetic backgrounds. Here, we present an improved Bayesian multi-QTL pedigree-based approach on an outcrossing species using progenies with different (complex) genetic relationships. Different modeling assumptions were studied in the QTL analyses, i.e., the a priori expected number of QTL varied and polygenic effects were considered. The inferences include number of QTL, additive QTL effect sizes and supporting credible intervals, posterior probabilities of QTL genotypes for all individuals in the dataset, and QTL-based as well as genome-wide breeding values. All these features have been implemented in the FlexQTL™ software. We analyzed fruit firmness in a large apple dataset that comprised 1,347 individuals forming 27 full sib families and their known ancestral pedigrees, with genotypes for 87 SSR markers on 17 chromosomes. We report strong or positive evidence for 14 QTL for fruit firmness on eight chromosomes, validating our approach as several of these QTL were reported previously, though dispersed over a series of studies based on single mapping populations. Interpretation of linked QTL was possible via individuals' QTL genotypes. The correlation between the genomic breeding values and phenotypes was on average 90 %, but varied with the number of detected QTL in a family. The detailed posterior knowledge on QTL of potential parents is critical for the efficiency of marker-assisted breeding.

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