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Linkage disequilibrium analysis to enable more efficient gene and QTL mapping in apple

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The estimation of marker-trait association based on linkage disequilibrium (LD) analysis across germplasm collections can provide an efficient alternative for gene/QTL mapping and cloning. This is particularly true for species with a long generation time such as apple (*Malus X domestica*) where mapping based on experimental crosses is very time-consuming. In order to better implement this mapping strategy, the average nucleotide diversity, the LD level across the genome and the existence of hidden population subdivisions should be investigated. For these aims, we assembled a collection of 185 apple accessions, including a comprehensive set of wild apple species as well as cultivars representative of the elite apple germplasm. The collection was genotyped using publicly available SSRs and several hundreds SNPs originally discovered within the IASMA Golden Delicious genome sequencing project. Markers were selected for being distributed evenly across the genome. A preliminary survey of our results will be presented. Faster discovery of useful alleles using LD-based approaches should lead to a more efficient marker-assisted breeding.

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