

## **ANALYSIS OF LINKAGE DISEQUILIBRIUM IN APPLE**

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*association mapping, core-collection, linkage disequilibrium, Malus domestica, SNP*

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 implement this mapping strategy, the transferability of the marker systems, the average nucleotide diversity, the existence of hidden population subdivisions and the LD level should be investigated. For these aims, we assembled a collection of 184 apple accessions, including many wild apple species as well as more than 100 cultivars representative of the elite apple germplasm. The collection was genotyped using 35 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. The average transferability of the Golden Delicious SNPs within the cultivated apple accessions was 41% whereas a lower rate was observed for wild species accordingly with the phylogenetic distances. Preliminary results about LD levels showed a rapid decay of  $r^2$  values for distances longer than 1 cM, implying the need of a large number of markers in order to carry out genome-wide association mapping. Final aim is to enable a faster discovery of agronomically useful alleles in order to implement efficient marker-assisted breeding programmes.