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W255 : Fruit and Nut Crops

LD Estimation And Analysis Of Diversity In Apple

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For species with a long generation time, such as apple (*Malus x domestica* Borkh), gene and/or QTL mapping based on experimental crosses can be very demanding in terms of time and costs. Marker-trait association based on linkage disequilibrium (LD) analysis across germplasm collections can provide an efficient alternative. To implement this mapping strategy, the LD level, the existence of hidden population subdivisions, the transferability of the marker systems, and the average nucleotide diversity level should be investigated. For these aims, we assembled a collection of about 200 apple accessions, including more than 100 cultivars representative of the elite apple germplasm and several wild apple accessions. The collection was genotyped using several hundreds SNPs originally discovered within the FEM-IASMA Golden Delicious genome sequencing project, 35 publicly available SSRs and the direct re-sequencing of several pairs of genes within a distance of 60-200 Kb between them. Markers and gene-pairs were selected evenly distributed across the genome. The average transferability of the Golden Delicious SNPs was 41% within the cultivated apple accessions whereas a much lower rate was observed for most of the wild species. LD level was investigated between SNP pairs at various genetic distances on apple chromosomes and was shown to decay at distances longer than 1 cM, while occasional significant level of r^2 was observed at closer distances. Knowing such parameters will be necessary in order to properly design strategies and tools for genome-wide association mapping.

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