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Mapping of dwarf growth habit trait in apple (Malus pumila Mill.)

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Introduction

Apple (*Malus pumila* Mill.) is one of the most widespread and commercially important fruit crops worldwide. There is increasing interest in the genetics of tree architecture. Various dwarf genes have been described in the literature but few if any have been mapped and characterised. At the Agricultural Research Council (Infruitec-Nietvoorbij) Bien Donné Experimental Farm, there are young progenies, derived from 'McIntosh', segregating for a novel dwarf trait. These progenies are being scored with microsatellite markers to map the trait and to identify potential candidate genes. A transcriptomic approach will also be pursued in parallel to identify candidate genes. Thus, this study aims at identifying candidate genes controlling the underlying molecular genetics of dwarf growth habit trait in apple.

Materials and Methods

 McIntosh mapping populations segregating for dwarf growth habit, McIntosh x MM106 (Fig. 2) and McIntosh x M9 (Fig. 1 and Fig. 3) with 101 and 150 seedlings, respectively



Fig. 1. Young McIntosh x M9 progeny segregating for dwarf trait

Phenotyping

Genotyping

- Parental and seedlings genomic DNA extracted using CTAB extraction method modified with the addition of PVP
- Trueness-to-parentages confirmed with fluorescently labelled SSRs
- Progenies will be genotyped further with well spaced set of SSRs selected from published apple maps

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Fig. 2. One-year-old McIntosh x MM106 progeny segregating for dwarf trait ~ 3:1

Fig. 3. Two-year-old McIntosh x M9 progeny segregating for dwarf trait ~ 1:1

DNA extraction

Allele scoring (GeneMapper)

Transcriptomic Analysis

- Subset of seedlings of normal versus dwarf growth habit will be subjected to the next generation sequencing technology, RNA-seq
- Transcriptomes will be compared in identifying differentially expressed candidate genes

Mapping traits

- Co-segregation analysis of phenotypic and genotypic loci will be undertaken with JoinMap[®]4
- Relevant sections of apple genome will be examined for potential candidate genes

RNA-Sequencer

 Comparison of candidate genes from both mapping and transcriptomic analyses to unravel the underlying molecular genetics of this dwarf phenotype in apple

Expected Outcomes

- Clarification of the molecular genetics and the mechanisms behind this dwarf growth habit trait in apple
- Development of functional molecular markers allowing markerassisted selection
- Tracing the genes in relevant pedigrees to help avoid raising progenies segregating for this trait in future

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