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Poster Abstract - B.31

GENETIC MAPPING OF APPLE TRANSCRIPTION FACTORS

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Differential gene expression is controlled by a complex regulatory network in which specialized transcription factors (TF) relay the signals to specific target genes. Many of these transcription factors are DNA-binding proteins that bind to regulatory DNA elements located *cis* to the target genes.

The levels of the DNA-binding transcription factors, or rather their activities, are decisive as to whether their target genes are transcribed and to what extent.

The aim of this work was to map some transcription factors in the apple genome and to value if they are related to specific gene regulation.

We have founded 425 *Malus* ESTs sequences related to transcription factors in Gene Bank Database: 74 are DNA Binding Proteins, 27 Ethylene related proteins, 8 MADS Boxes and 316 are ungrouped proteins.

We have identified 21 sequences which contain microsatellite regions (SSRs) useful for mapping work.

After testing primers polymorphism we have mapped 15 TF on the "*Fiesta*"x"*Discovery*"population.