Poster Abstract – G.06

CLASS I *KNOTTED1*-LIKE GENES IN PEACH (*P. PERSICA* L. BATSCH): GENOMIC FEATURES OF THREE NEW MEMBERS AND EXPRESSION PATTERNS DURING STEM DEVELOPMENT

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Prunus persica, stem development, class I knotted1-like genes

Members of the class 1 *Knotted1*-like homeobox (*KNOX*) gene family regulate the processes of organ morphology and function, and subsequently of plant architecture. They are differentially required for meristem development and function to inhibit cell expansion and differentiation associated with organogenesis. The architecture of aerial organs and vegetative habit of fruit trees are important traits for productivity and quality. In the model species *A. thaliana*, *KNAT1* (or *BP*) was demonstrated to play a role in internode patterning and lignin deposition, however *KNOX* function in trees has been poorly investigated so far, though there is evidence that they play a role in wood formation and bud dormancy. The determinism and variability of these traits is alleged to be under the control of *KNOX* genes and their mapping and use as markers may have a potential for assisted breeding.

We have cloned three new cDNAs from herbaceous stems using RT-PCR based on conserved functional domains and they were named *KNOPE2*, *KNOPE4* and *KNOPE5*. The deduced product of the first was 75% identical to *A. thaliana* KNAT6, whereas the latter two were 80% and 87% identical to STM, respectively. The genomic features of class I *KNOPE* genes indicated that intron position was conserved throughout plant species. Patterns of transcript abundance and localisation (by in situ analysis) were also monitored during stem development and putative roles are discussed.