

GENETIC TRANSFORMATION OF CHERRY ROOTSTOCK GISELA 6 (*PRUNUS CERASUS* X *PRUNUS CANESCENS*) USED AS MODEL TO STUDY GENE FUNCTION IN *PRUNUS* SPECIES

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In the post genomic era, the assessment of plant gene function is a mandatory step and gene overexpression and silencing by stable genetic transformation are widely used approaches. One major drawback in gene transfer to peach fruit tree (*Prunus persica*) is due to its tedious recalcitrance to regeneration. Protocols for peach transformations have been reported, though they are still few, cultivar specific and based on immature embryo manipulation. Our group has been focussing on class 1 *KNOTTED*-like genes from peach, which encode homeodomain transcription factors and regulate meristem identity and cell fate. These genes are tightly conserved in *Prunus* species, hence we approached overexpression of peach *KNOPE1* into Gisela 6, a cherry rootstock, which is a genotype suitable to transformation starting from leaf discs. Co-cultivation was performed with *A. tumefaciens* strain EHA105 containing the cassettes *CaMV35S:KNOPE1:NOS* and *CaMV35S:mGFP:CaMV35Ster*. Both transgenes behave as visual non destructive markers: the former causes leaf margin fringing, while the latter is detected by fluorescence microscopy, allowing an easy discrimination between transgenic and escape shoots. Shoot regeneration frequency and transformation efficiency were estimated 11% and 4%, respectively. We will present results on one line overexpressing *KNOPE1*, which showed leaf margin lobing and vascular system alteration, and on three independent lines which expressed GFP protein.