S05P14

Assessment of pollen-mediated transgene flow in citrus under experimental field conditions

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Despite potential benefits granted by genetically modified (GM) citrus trees, their release and commercialization raises concerns about their potential environmental impact. The transfer via pollen of transgenes to cross-compatible cultivars is deemed to be the greatest source for environmental exposure. In this work, three different citrus genotypes carrying the *uidA* (GUS) tracer marker gene (pollen donors) and a non-GM self-incompatible contiguous citrus genotype (recipient) were used in conditions allowing natural entomophilous pollination to occur. The examination of 603 to 2990 seeds per year showed unexpectedly low frequencies (0.17-2.86%) of transgene flow. Paternity analyses of the progeny of subsets of recipient plants using 10 microsatellite (SSR) loci demonstrated a higher mating competence of trees from another non-GM pollen source population that greatly limited the mating chance of the contiguous cross-compatible and flowering-synchronized transgenic pollen source. This mating superiority could be explained by a much higher pollen competition capacity of the non-GM genotypes, as was confirmed through mixed-hand pollinations, indicating that pollen competition strongly contributed to transgene confinement. This is the first study on transgene flow in citrus. It provide crucial information on the safety and field performance of GM citrus that can serve as a basis for further field trials and as a guide for (case-by-case) regulatory policies.

S05P15

Functional analysis of a citrus transcription factor with mature fruit-specific expression using transgenic tomato

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Citrus fruit changes color drastically at maturation with reduction of chlorophyll and accumulation of carotenoids in peel. This color change is known to be suppressed with exogenous gibberellin and, in contrast, promoted with ethylene treatment. In order to identify genes regulating metabolisms involving citrus fruit color change, we have screened transcription factor genes with the profile as their expression is induced by ethylene and reduced by gibberellin treatment in mature fruit peel using a microarray. Among them, a *bHLH* gene, *TF-BFC*, with mature fruit-specific expression has been selected, introduced and overexpressed in tomato 'Micro Tom'. Three independent transgenic lines with high transgene expression were selected and analyzed. Transgenic plants were dwarf, had deep-green and curled leaves and orange-colored fruit. The chlorophyll content in transgenic leaves was about two times higher than in controls. Microarray analysis of transgenic plants showed that over 3,000 genes had significant expression changes (>2-fold) in red fruit, but in green fruit, the number of genes with significant expression changes was only about half. Gene homologs probably encoding enzymes of carotenoid biosynthesis, such as phytoene synthase, phytoene desaturase, z-carotene desaturase and b-ring hydroxylase were shown to be highly expressed in transgenic red fruit, in accordance with the results from RT-PCR analysis. These results suggest that *TF-BFC* induced gene expression of carotenoid biosynthesis and suppressed genes involving photosynthesis in transgenic tomato mature fruit, showing important roles in carotenoid biosynthesis.

S05P16

Effect of the citrus *lycopene* β*-cyclase* transgene on carotenoid metabolism in transgenic tomato fruits

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Lycopene β-cyclase (*LYCB*) is the key enzyme for the synthesis of β-carotene, a valuable component of the human diet. In order to evaluate the effect of constitutively expressing a citrus *Lycb-1* gene on carotenoid synthesis,