Genetic transformation of the main commercial citrus cultivars in Hunan
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A protocol for regeneration and genetic transformation using seedling and mature internode stem segments as explants were developed. ‘Kuxu’, ‘Dahong’, ‘Bingtang’ and ‘Succari’ sweet orange (Citrus sinensis (L.) Osbeck), ‘Xun’ ponkan (C. reticulata Blanco) and Shatianyou pumelo (C. grandis Osbeck) were transformed by using seedling explants, while a mature material transformation protocol was established for ‘Newhall’ navel orange, ‘Bingtang’ and ‘Succari’ low acid oranges and ponkan. By Agrobacterium infection, phyB, rolABC, chit42, terf1 (ethylene responsive factor 1), pthA-NLS (nuclear localization signals of the pathogenesis factor pthA of Anthomonas axonopodis pv. citri) and the ScFv gene of the monoclonal antibody against to PthA were transferred into the tested cultivars and about 900 transmants with various function genes were obtained. The transgenic sweet orange plants with terf1 were showed resistance to citrus canker and citrus anthracnose diseases. The transgenic ‘Succari’ sweet orange with pthA-NLS and ‘Dahong’ sweet orange plants with ScFv gene demonstrated high resistance to citrus canker disease in the in vitro assays. The plant transformed with phyB were improved their photosynthesis and those with rolABC characterizing.

Establishment of a high frequency plant regeneration system for Ponkan mandarin by using orthogonal experiment
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In this paper, 5 factors influencing the efficiency of adventitious buds inducing of Ponkan mandarin (Citrus reticulata Blanco), including the basic medium, α-naphthalene acetic acid (NAA), 6-benzyl adenine (6-BA), kinetin (KT), and zeatin (ZT), were evaluated by using the orthogonal experiment design. The explants from seedlings included young leaves, cotyledons, epicotyls and hypocotyls. The results showed that, (1) the optimum explant was epicotyl. (2) The frequency and quantity of shoot regeneration as high as 73.3% and 1.32 shoots/explant were obtained on MT medium supplemented with 0.1 mg·L-1 NAA, 2.5 mg·L-1 KT, and 2.0 mg·L-1 ZT, respectively. (3) Among 5 experimental factors, the order of influencing the efficiency of bud inducing was 6BA>NAA>KT>basic medium>ZT.

International Effort toward a SSR-based Linkage Map for C. clementina
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Following the difficulties encountered for assembling a 1.2 x sequencing of the highly heterozygous sweet orange genome, the International Citrus Genome Consortium (ICGC) decided to establish the first reference sequence of a whole nuclear citrus genome from a haploid Clementine. A saturated genetic linkage map of Clementine based on sequence-characterized markers was considered by the ICGC as an important tool for genome sequence assembly. In this framework, CIRAD proposed to use an interspecific population C. maxima x C. clementina to implement the reference Clementine genetic map. A population of 250 hybrids of Chandler pummelo x Clementine was established in Corsica and 190 hybrids were used in this first phase of mapping. Collaboration was established between two French organizations (CIRAD and INRA), two groups from United States (UF-CREC and UCR), one Spanish institute (IVIA), INRA Morocco and Çukurova University from Turkey. Forty markers were found heterozygous in Clementine among a previous set of 90 SSR markers developed by CIRAD from microsatellite-enriched genomic libraries. With the objective to integrate the physical and genetic maps of Clementine, CIRAD and IVIA have developed new SSR markers from microsatellite sequences identified in BAC End Sequences (BES) of diploid Clementine. On hundred and 10 of these new markers were found heterozygous for Clementine or Chandler pummelo and were used for genotyping. INRA France developed 500 SSR markers from ESTs databases and found 170 markers heterozygous for Clementine. INRA Morocco contributed to the genotyping of 112 SSR markers developed from EST databases and genomic libraries, while 50 ESTs SSR were analysed by Çukurova University. SSR markers mainly
Functional Study of Genes Potentially Involved in Juvenile-to-adult Transition in Citrus Plants Identified by Gene Expression Profiling

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In citrus the juvenile phase can be as large as 5-20 years depending on the variety, what is a very serious constraint for breeding of citrus varieties. With the aim of identifying regulatory genes involved in the process of juvenile-to-adult phase transition we have developed a citrus transcription factor (CTF) microarray, and used it to screen for transcription factors differentially expressed between juvenile and adult plants. The CTF microarray was generated with a specific oligonucleotide set for 1,152 citrus transcription factors. Meristems of juvenile and adult plants were harvested from sweet orange (C. sinensis (L.) Pineapple), Tangor Murcott (C. reticulata x C. sinensis), grapefruit (C. paradisi Macf. Duncan) and rough lemon (C. japonica (L.)), and samples were hybridized to the oligonucleotide microarray. Several transcription factors were identified as differentially expressed between adult and juvenile plants in all four species and this phase-specific regulation was validated by quantitative RT-PCR. To analyse the potential involvement of such TFs in the studied process, the putative function of one of them, CTF607, was further investigated by generating transgenic plants of the annual herbaceous plant Arabidopsis thaliana over-expressing and silencing the encoded TF. Over-expression of the TF caused shortening of the flowering time in transgenic plants while the CTF607 silencing plants showed a late flowering phenotype. Although developmental processes in annuals and woody perennial trees may share some genetic factors they differ in their life cycle. Arabidopsis has a short juvenile developmental phase followed by the production of flowers and seeds at the reproductive adult phase. Our results seem to indicate that transition to flowering may be interconnected with the juvenile to adult phase transition and therefore, these and future studies based on this approach could help us to decipher the molecular mechanisms involved in the juvenile-to-adult transition in citrus plants.