

S02P06**Preliminary research on genes and proteins related to a spontaneous mutant of *Citrus reticulata***Zeng J.W.¹, Yi G.J.², Jiang B.¹, Zhong Y.¹, and Zhong G.Y.¹¹Institute of Fruit Tree Research, Guangdong Academy of Agricultural Science, China; and ²Guangdong Academy of Agricultural Science, China. zhongyun99cn@163.com

Bud mutations of citrus happen frequently and are the main natural resource for new cultivars. 'Mingliutianju' (*Citrus reticulata* 'Mingliutianju', MP) is a novel late ripening, very productive mandarin cultivar selected from 'Chuntianju' (*C. reticulata* 'Chuntianju', CP) through spontaneous bud mutation. In addition, the cultivar is morphologically contrast to the smooth fruit of its parent 'Chuntianju' by having prominent vertical narrow strips on its fruit surface. Large-scale analysis of gene expression differences between peels of MP and CP was performed at the 12th week and the 23rd week post flowering using Affymetrix GeneChip® citrus genome array. Altogether, 395 differentially expressed genes, including 132 up-regulated and 263 down-regulated genes, were identified in the mutant. Singular Enrichment Analysis (SEA) and Parametric Analysis of Gene Set Enrichment (PAGE) were performed and 7 statistically significantly differential-expressed genes were selected for further studies. Results from semiquantitative RT-PCR performed on these 7 genes were generally correlated with those observed with the microarray. These seven genes include three UDP-glucosyltransferase genes, two disease resistance-responsive protein-related genes, one chitinase gene and one protein kinase gene. Thirty three differentially expressed proteins were identified by two-dimensional gel electrophoresis using the same material. The differential proteins included 17 up-regulated and 16 down-regulated in the mutant. Pathway identification was conducted on these 33 differential expressed proteins through the web-based platform KOBAS. When these KEGG pathways were arranged according to their P values, flavonol biosynthetic process pathway ranked first.

S02P07**Allelic diversity of *Ferritin III* and *PMT IV* genes related to iron chlorosis in some citrus rootstocks**Aka Kacar Y.¹, Simsek O.¹, Donmez D.¹, Boncuk M.¹, Yesiloglu T.¹, and Ollitrault P.²¹Cukurova University (Cu), Horticulture Department, Turkey; and ²Instituto Valenciano de Investigaciones Agrarias (IVIA), Centro de Protección Vegetal y Biotecnología, Spain. ykacar@cu.edu.tr

Iron (Fe) is one of the most important elements in plant mineral nutrition. Fe deficiency is critical abiotic stress factor for Mediterranean citriculture and the development of marker assisted selection (MAS) for this trait would be a great aid for rootstock breeding. In this study DNA sequencing and SSCP (Single Stranded Conformation Polymorphism) analysis were performed to discover allelic diversity of genes related to iron chlorosis tolerance in citrus. Two iron chlorosis tolerance candidate genes were selected from existing Citrus ESTs databases and *Arabidopsis thaliana* genome databases. *Ferritin-3* chloroplast precursor and putative membrane transporter candidate gene sequences were used to define primers in conserved regions. Six citrus genotypes from the basic taxon of *Citrus* where used to identify polymorphic areas in the genes. Direct sequencing of amplified DNA fragments of candidate genes was performed and SNPs (single-nucleotide polymorphisms) and InDels (Insertions/Deletions) where searched after sequence alignment. A total of 6840 bp DNA fragments were sequenced and 263 SNPs and 15 InDels were determined. New primers were defined, in conserved areas flanking polymorphic ones, for Single Strand Conformation Polymorphism (SSCP) analysis. SSCP-PCR analysis was performed with twenty-five *Citrus* genotypes. The neighbor joining method was used for cluster analysis. Phylogenetic origin of the alleles and genetic relationships of genotypes were discussed.

S02P08**Genetic mapping of QTLs associated with drought tolerance in citrus**Dutra-Souza J.¹, Cristofani-Yaly M.², Machado M.A.², and Oliveira A.C.¹¹Universidade Estadual do Sudoeste da Bahia (UESB), Brazil; and ²Centro de Citricultura Sylvio Moreira, Instituto Agrônômico (IAC), Laboratório de Biotecnologia, Brazil. mariangela@centrodecitricultura.br

A population of 73 hybrids of 'Rangpur' lime (*Citrus limonia*) and 'Swingle' citrumelo (*Citrus paradisi* x *Poncirus trifoliata*), kept in plastic bags of 3.8 liters in a greenhouse, had water removed for 15 days. The gradient