Dear Delegates,

On the behalf of the all the members of the Organising Committee, it is our pleasure to welcome scientists from all over the world to the Current Opinion Conference on Plant Genome Evolution.

With more than 30 plant genomes available for analysis and comparison, and many more on the way, these are exciting days for plant biologists. Furthermore, besides complete genome information, also more and more functional genomics data are being generated for a wide variety of plants. All this makes this an extremely fascinating era for plant science and allows studying plants and their evolution at many different levels. It is therefore my great pleasure to chair this Current Opinions Conference on Plant Genome Evolution, where you will be able to meet the leading experts in the field and to hear about their latest discoveries. It is also a great venue to share your latest findings on topics as diverse as plant genomes, gene and genome duplications, genetic variation, plant systems biology, and plant bioinformatics.

We have received one hundred and sixty abstracts for oral and poster presentations. The reviewing process involved five recognised scientists from all over the world, members of the Executive, Organising and Scientific Committees. The organisers are grateful to the authors for their enthusiasm and to all the reviewers for their work and time given to evaluate the volunteered submissions in detail.

The Organising Committee were pleasantly surprised by the large number of high quality proposals submitted. We are grateful to workshop organizers for their considerable efforts in contributing to the success of the conference.

Poster presentations have been organised in two sessions dedicated to specific themes. In total eighty posters will be presented. Posters will be easily available for viewing also during coffee breaks and lunches as well as during the dedicated poster sessions.

The associated exhibition will provide you with up to date information on commercially available support for your line of work. These will be available during the sessions, lunches, and breaks.

We thank Elsevier, especially the staff members Gilles Jonker,Marie-Claire Morley, Ying Wang, Bill Rutledge and Caroline van der Zanden for their support in the management and organization of this conference.

We specially thank all members of the committee for their contribution to the organization of this conference.

Kind Regards
Yves Van de Peer

[P2.21]

Multilocus snps analysis allows phylogenetic assignation of DNA fragments to decipher the interspecific mosaic genome structure of cultivated *Citrus*

F. Curk*[1,2], G. Ancillo[2], A. Garcia-Lor[2], F. Luro[1], P. Ollitrault[3,2], L. Navarro[2]
[1]*INRA, France,* [2]*IVIA, Spain,* [3]*CIRAD, France*

All current studies seem to support the theory that four basic taxa (*C. medica*, *C. maxima*, *C. reticulata* and *C. micrantha*) have generated all cultivated *Citrus* species. It is supposed that the genomes of most of the modern *Citrus* cultivars, vegetatively propagated, are interspecific mosaic of large DNA fragments issued from a limited number of inter-specific meiosis. In the present work we analyse how multilocus study of closely linked SNPs allows a phylogenetic assignation of DNA fragments of the main cultivated species.

Genomic fragments of 25 genes dispersed in the different chromosomes covering more than 12,5 Kb were amplified by PCR and sequenced (Sanger) for 24 accessions representative of 10 species. Moreover we checked the potential of parallel pyrosequencing (454 Roche) for direct multilocus haplotyping of heterozygous genotypes. Amplified fragments from 7 genes in 8 genotypes were obtained by using an original new method based on universal primers. C. clementina (Clementine) was used as model for secondary species.

Citrus reticulata was the most polymorph basic taxa with an average of 4.2 SNPs/kb. The average differentiation between the basic taxa was about 20 SNPs/kb. For each amplified gene fragment, this polymorphism was enough for unambiguous multilocus differentiation of the basic species and assignation of a phylogenetic origin for the secondary species. A preliminary reconstitution of phylogenetic structure of chromosome 3 is proposed for sweet orange, sour orange, grapefruit, lemon and lime. Consensus haplotype sequences were successfully obtained from 454 sequencing with genotype sequence in total agreement with Sanger control. Each haplotype sequence of Clementine was univocally assigned to one of the haplotype clusters of the basic taxa.

Phylogenetic origin of specific DNA fragments can be assigned from multilocus analysis of closely linked SNPs. Multilocus haplotyping by parallel sequencing of individual DNA molecule will be a very powerful tool to decipher the interspecific mosaic genome structure of cultivated citrus.

Keywords: snp, mosaic sturcutre genome, phylogeny, Citrus

[P2.23]

Nuclear and maternal phylogeny within Citrus and four related genera based on nuclear genes sequence SNPs and mitochondrial InDels

A. Garcia-Lor*[1], F. Curk[1,2], F. Luro[2], L. Navarro[1], P. Ollitrault[1,3]
[1]IVIA, Spain, [2]INRA, France, [3]CIRAD, France

Despite considerable morphological differentiation *Citrus*, *Fortunella*, *Poncirus*, *Microcitrus* and *Eremocitrus* genera are sexually compatible. Species of these genera are mainly diploid (2n=18). If the origin of cultivated *Citrus* from four basic taxa (*C. maxima, C. medica, C. reticulata* and *C. micrantha*) is now well documented, their phylogenetic relationships with *Citrus* wild species and related genera is still unclear. In the present work we analyse their nuclear and maternal phylogeny by using respectively SNPs on gene sequences and mitochondrial InDels.

A total of 7.15 kb were amplified by PCR from 11 genes (Table1) and sequenced (Sanger) for 33 genotypes. The varietal sample was composed of 7 *C. reticulata*, 5 *C. maxima*, 5 *C. medica*, 4 papeda, 5 *Fortunella*, 3 *Poncirus*, 2 *Microcitrus*, 1 *Eremocitrus. Severinia buxifolia* was used as outgroup. SNPs were mined using BioEdit and SeqMan softwares and phylogenetic analysis done in http://phylemon.bioinfo.cipf.es with different approaches (Phylip (v. 3.68), Phyml Best AIC Tree (v. 1.02b), PhyML (v. 3.00). For maternal phylogeny, 4 InDel markers developed by (Froelicher et al. 2011) have been used.

The average frequency per Kb of SNPs and InDels were respectively 59.88 and 1.33 in coding region and 110.99 and 16.31 in non-coding ones. A total of 506 SNP and 23 InDels were identified (Table1). Within *Citrus*, the papeda group was the most polymorphic species, with 185 polymorphisms, followed by *C. reticulata* (125), *C. maxima* (48), *and C. medica* (27).

A newmitotype was observed for *Microcitrus australasica* while two different mitotypes were identified for *Fortunella*.

Nuclear and mitochondrial phylogenetic analysis reveal that *C. reticulata* and *Fortunella* form a consistent clade clearly differentiated from the clade including the other basic taxa of cultivated citrus (*C. maxima, C. medica and C. micrantha).*.

Inclusion of more genes sequences is undergoing and will improve the resolution of the phylogenetic analysis.

Table 1. Statistics in the population studied.

Gene	CS	CDS	NCS	SCF	SNCF	ICF	INCF

Chalcone isomerase	652	206	446	53.40	170.40	0	17.94
Chalcone synthase	565	565	0	35.40	-	0	-
Flavonol Synthase	473	419	54	90.69	111.11	0	55.56
Flavonoid 3'-hydroxylase	613	569	44	70.30	45.45	0	0
Enzyme malique	428	128	300	54.69	86.67	7.81	13.33
Vacuolar citrate/H+ symporter	795	657	138	60.88	115.94	0	7.25
Malate dehydrogenase	712	712	0	39.33	-	0	-
Acid invertase	673	409	264	85.57	136.36	0	3.79
Lycopene β-cyclase	738	738	0	88.08	-	6.78	-
Lycopene β-cyclase	941	941	0	39.32	-	0	-
9-cis-epoxy hydroxy carotenoid dyoxygenase	560	560	0	41.07	-	0	-

(CS) Cleaned sequence (bp); (CDS) Coding sequence (bp); (NCS) Non-coding sequence (bp); (SCF) SNP frequency in coding region, x/Kb; (SNCF) SNP frequency in non-coding region; (ICF) InDel frequency in coding region, x/kb; (INCF) InDel frequency in non-coding region

Keywords: Citrus, Phylogeny, Diversity, SNP