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# Biotic and Abiotic Stress Tolerance in Plants: the Challenge for the 21st Century

## BOOK OF ABSTRACTS

### 6 to 8 • NOVEMBER • 2013

### Cana Brava Resort • Ilhéus - Bahia - Brazil

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# Workshop on Biotic and Abiotic Stress Tolerance in Plants: the Challenge for the 21st Century

Cana Brava Resort • Ilhéus-Bahia, Brazil • 6th-8th November 2013

## GENETICS / BREEDING SESSION (S04)

### S04T01

#### **Citrus breeding for biotic and abiotic stress tolerances; new tools and strategies for biodiversity mobilization**

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Citrus industry is affected worldwide by several fungal, bacterial and viral diseases. Some production areas also suffer of strong abiotic constraints such as water deficit, salt stress and iron chlorosis. Resistance or tolerance traits for most of these constraints are present in the citrus germplasm but their mobilization by conventional breeding is hampered by the complex interspecific genome structures of the modern citrus, the partial apomixis of most genotypes and the long juvenile phase. Beside these constraint the vegetative propagation of grafted plants is an important advantage. Indeed it allow dividing breeding objective between scions and rootstocks and to select any complex elite genotype that will be then asexually propagated. A fundamental progress of the last years, to improve citrus breeding efficiency, was the elaboration and public release, by the International Citrus Genome Consortium, of the first citrus reference genome anchored with a medium density genetic map and the increasing availability of resequencing data. A first application was to study the interspecific genomic structures of the main cultivated species. The origins of sweet oranges (*C. sinensis*), sour oranges (*C. aurantium*), grapefruits (*C. paradisi*), limes (*C. aurantifolia*) and lemons (*C. limon*) and their interspecific genome structure along the genome are already deciphered. A huge number of DNA polymorphism have been identified from resequencing data and genome wide association studies are going on using GBS approaches. When useful SNP polymorphisms are encountered they are easily converted in genetic markers with tools adapted to (i) highthroughputs studies by using arrays systems or (ii) more targeted studies using competitive allele PCR methods such Kaspar methodology allowing for allele dosis evaluation in polyploid genotypes. Molecular markers studies have also provided useful information on segregation and recombination at diploid and polyploid levels. It will allow improving the progenitor choice and the inheritance of the parental value to their progenies particularly for project aiming to create seedless triploid varieties or tetraploid rootstock cumulating tolerances to abiotic and biotic constraints. Joining genetic and genomic approaches, a cluster of resistance genes, genetically associated with resistance to *Alternaria alternata*, was located in chromosome 3. *Alternaria* resistance is actually one of the rare traits for witch SAM is routinely applied in citrus. New breeding approaches are also developed or possible, including (i) tetraploid rootstock breeding to improve abiotic stress adaptation, (ii) the reconstruction of modern species ideotypes from germplasm or (iii) the introgression of useful traits from citrus relatives combining MAS and GMO with early flowering genes. By the whole, the new genetic and genomic insights and tools will change greatly the potential for biodiversity mobilization in future breeding projects for biotic and abiotic stress tolerances.

Most of the presented data results from CIRAD/INRA/IVIA collaboration

### S04T02

#### **The EucHIP60K.br to boost genome-wide prediction of complex phenotypes in *Eucalyptus***

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Despite important advances in QTL mapping, association genetics (AG) and gene identification for complex traits such as growth, productivity, quality, disease and stress tolerance traits in plants, a growing body of evidence is showing that ascertaining the effects of such individual genetic elements is proving much more elusive than originally thought. QTL effects are classically overestimated, candidate-gene or genome-wide AG captures negligible fractions of trait heritability to be useful to breeding while single gene transfer technologies have not yet become a reality for improving complex traits. In molecular breeding we are now moving from the dissection approach of discovering genes and their individual effects, back to dealing with the aggregate of the genome, after recognizing that complex