

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

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GENOMIC SESSION (S01)

S01T01

Population genomics : some lessons drawn from the ARCAD project

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The ARCAD programme aims at establishing in Montpellier a conservation and research center on crop agrobiodiversity. It is a pluri-institutional and multidisciplinary programme.

ARCAD's scientific agenda focus on the study of the history and patterns of crop domestication and adaptation as well as on the analysis of key parameters underpinning adaptation and diversity, at various time scales, through studies of evolutionary genomics, population genetics and social sciences.

The research aims at comparing diversity patterns between crops, and deals with crop diversity at the population, species and agroecosystem scales. The effect of domestication on genome evolution in 15 crop species is analysed through population genomics approach. Population genetics studies are conducted to detect genes submitted to selection and decipher crop adaptation to climate change. Social sciences and genetics are combined to study the diversity dynamics of major and underutilized cereals in Africa. The paper presents some results of the research and discuss the needs and means to reinforce synergies between studies across crops and across various biological scales.

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S01T02

Applied Coffee Genomics: Towards a GWS Program

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In recent years, significant advances have occurred in the development of genomic tools to help accelerating the genetic improvement of coffee, a perennial crop with high economic importance. The recent conclusion of the complete genome sequencing of *Coffea canephora* will serve as a reference sequence for use in advanced molecular genetics, applied directly to molecular breeding of this species, such as the establishment of genome-wide selection programs (GWS). In that direction, a population of 1300 *C. canephora* individuals maintained at the experimental field of Embrapa Cerrados is being currently phenotyped for different traits such as production, vigour, bean morphology and biochemical composition, as well as drought tolerance. A sample of 30 pools of genotypes, comprising the parentals of the population under study as well as representatives of the *C. canephora* diversity groups have been re-sequenced by Illumina Hi-seq for SNPs mining. A genotyping platform for coffee is being established and will provide the required tools for association studies. Results of this ongoing study will be presented and discussed.

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S01T03

Towards the understanding of grape response to abiotic stress: how to value at best the sequence data ?

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Since the publication of the grape genome, the tools for genetic and genomic analysis of complex traits increased dramatically. It is now possible to identify genes underlying the complex traits based on the sequence and to develop innovative strategies for the selection of these complex traits