The International Consortium in Advanced Biology presents:



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



BOOK OF ABSTRACTS

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Workshop on Biotic and Abiotic Stress Tolerance in Plants:

the Challenge for the 21st Century

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S04T07

Application of genomics tools for cacao disease resistance

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Biotic plant problems are caused by living organisms, such as fungi, bacteria, viruses, nematodes, insects, mites, and animals. Plant responses to different stresses are highly complex and involve changes at the transcriptome, cellular, and physiological levels. In Theobroma cacao the main biotic stresses are cause by fungi, causing the witches' broom (Moniliophthora perniciosa) disease of cacao, Black pod (Phytophthora spp.), frost pod (Moniliophthora roreri and, recently, Ceratocysts wilt (Ceratocystis cacaofunesta). Durable resistance is the key to hamper the advance of these diseases. The OMICS with the classical phytopatological and breeding approaches have allowed: to identify putative resistance genes; to deciphering the genomics of Thebroma cacao, to discover new microsatellite and SNP markers, and to find new QTLs linked to disease resistance. These informations are being integrating in the CEPLAC' breeding program to accelerate the search for new resistance material that carries different resistant genes. In parallel, we study these diseases at the histopatological level trying to characterizing the mechanisms of resistance underneath the hosts as well gene expression in situ. The adaptability of these plant pathogens has also been considered. Advances in the understanding of the breakdown of witches' broom resistance have been achieved. It was shown that the fungus has a high ability to evolve towards some genotypes. Partial results of these projects and the overall strategy will be presented.

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S04T08

Genomic selection on cacao for disease resistance

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Under favorable conditions, diseases can cause losses up to 100% in cacao. Breeding has been the most effective strategy in reducing these losses. However, breeding is limited by the: a) long generation time; b) large tree size (9 m²/tree); c) multiple measurements per year; d) low heritability; e) requirement of the presence of the pathogen; among others. Genomic selection (GS) overcomes some of these problems. In 2011, a project on genomic selection involving Ceplac and Cirad was started, aiming to implement GS on breeding for diseases resistance and yield. In 2013, a second project is being started involving Ceplac, Cirad and Catie, aiming preventive breeding for moniliasis (a disease still absent in Brazil) resistance through GS. In the first project, a training population of 380 progenies, out of 4000 trees of the third cycle of Cepec's breeding program, and 90 founder and pedigree clones were chosen. In the second project, a training population of 470 trees was chosen among 2500 trees established in progeny trials and evaluated for moniliasis at CATIE. Founder parents (resistant to moniliasis) of this population was also introduced in Brazil and involved in crosses for preventive breeding. Prediction equations developed in Costa Rica will be used in Brazil for selection in the absence of the pathogen. Aiming to have accurate "phenotype" measurements for the prediction equations, BLUP values from historical data have been used (around 800 thousand data points, of 15 thousand trees). The overall strategy and partial results of these projects will be presented.

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