## OP09: COFFEE

**P0363 TARGETED CAPTURE OF DREB SUBFAMILY GENES AS CANDIDATES GENES FOR DROUGHT TOLERANCE POLYMORPHISM IN NATURAL POPULATION OF COFFEA CANEPHORA**

*Sinara AQUINO[1], Pierre MARRACCINI[2], Cédric MARIAC[3], Kevin BETHUNE[3], Alan ANDRADE[4], Olivier DARRACQ[5], Maud LEPELLEY[6], Dominique CROUZILLAT[5], Catherine KIWUKA[6], Niels ANTEN[7], Alexandre de KOCHOKO, Valérie PONCET[2]*

[1]*Federal University of Lavras, MG, Lavras, BRAZIL; IRD,UMR DIADE, Montpellier France;*
[2]*CIRAD, UMR AGAP, Montpellier, FRANCE*
[3]*IRD,UMR DIADE, Montpellier France;*
[4]*EMBRAPA Coffee-INOVACAF?, Lavras, BRAZIL;*
[5]*Nestlé R&D, Tours, France;*
[6]*NARO, Kampala, Uganda;*
[7]*Wageningen Univ. Wageningen, Netherlands.*

### 1 Full text

*Coffea canephora*, (Robusta), provides 33% of worldwide coffee production, 80% and 22% of Ugandan and Brazilian coffee production, respectively. Abiotic stress such as temperature variations or drought periods, aggravated by climate changes, are factors that affect this production. This sensitivity threatens both the steady supply of quality coffees and the livelihood of millions of people producing coffee.

The natural genetic diversity of *C. canephora* offer a potential for detecting new genetic variants related to drought adaptation. In particular, modifications occurring in genes related to abiotic stress tolerance make these genes candidate for breeding programs in order to enhance the resilience to climate change.

*C. canephora* transcription factors from the *DREB* subfamily (Dehydration Responsive Element Binding Protein) have been recently identified as candidate genes. Indeed, in the *C. canephora* Conilon group, the *CcDREB1D* gene showed an increased expression in response to drought in the leaves of a drought tolerant clone[1].

The objectives of this study are to identify and characterize the allelic diversity (Single Nucleotide Polymorphism, SNPs) within drought-tolerant candidate genes with a special focus on the DREB subfamily genes. These genes will be annotated on the reference genome sequence of *C. canephora*[2,3] and on anew assembly. A targeted capture array will be designed for these entire genes, and their flanking regions. These captured regions will be sequenced in a set of wild Ugandan populations. Subsequent detection of SNPs for the whole set will be used to test correlation of these SNPs with traits related to drought tolerance.

We expect to understand the adaptive strategies developed by crops in the wild in order to respond to climate change and use the genetic resources within wild populations, as a basis for transferring drought- and heat-tolerance traits.