PATTERNS OF ADAPTIVE GENETIC VARIATION ACROSS *COFFEA CANEPHORA*

PONCET, Valérie[1]; TOURNEBIZE, Rémi[1]; AQUINO, Sinara[1,3]; MARRACCINI, Pierre[2]; MARIAC, Cédric[1]; BETHUNE kevin[1]; ANDRADE, Alan[4]; KIWUKA, Catherine[6]; CROUZILLAT, Dominique[5]; ANTEN, Niels[7]; MANEL, Stéphanie[8]; DE KOCHKO, Alexandre[1]

[1]IRD,UMR DIADE, Montpellier France;[2]CIRAD, UMR IPME, Montpellier, FRANCE; [3]Federal University of Lavras, MG, Lavras, BRAZIL; [4]EMBRAPA Coffee-INOVACAFÉ, Lavras, BRAZIL; [5]Nestlé R&D, Tours, France; [6]NARO, Kampala, Uganda; [7]Wageningen Univ. Wageningen, Netherlands; [8]EPHE, UMR CEFE, Montpellier, France.

RATIONALE

In the light of adaptation, understanding how organisms respond to their environment, by altering physiological processes, will increase our capacity to make predictions about adaptation to global climate change. Adaptive clines have been increasingly studied in plant species within temperate zones to understand adaptation of organism in natural populations. However, they are still poorly understood in tropical environments. *Coffea canephora,* cultivated as Robusta, is an interesting tropical tree model to investigate adaptation in the tropics as it is largely distributed within the range of the lowland tropical rain forests of Africa.

In particular, modifications occurring in genes related to abiotic stress tolerance make these genes candidate for enhanced resilience to future climate change

METHODS

We combined the use of both captured regions sequenced for a set of candidate genes related to drought tolerance and whole genome SNP markers.

Leveraging on a robust statistical approach combining multiple neutrality statistics, we provided a comprehensive map of selection signals in the genome of the *C. canephora* both at the species level and within its major genetic groups.

RESULTS

The genotype-environment association suggests regional adaptation to spatially varying environments of the recent past, with a special focus on the Eastern edge of the distribution, in Uganda. More specifically, we found signals of selection tightly linked to several genes involved in response to biotic and abiotic stress and in caffeine biosynthesis.

CONCLUSIONS & PERSPECTIVES

Our detection of selection signals support the hypothesis of present ecological gradient contributing to the structure of the genetic diversity. Moreover, assessing the genomic vulnerability of the present populations will help to predict their response to future environmental changes.

REFERENCES