

International Coffee Genomics Network (ICGN)
Report Coffee Genomics

XXVII Plant and Animal Genome Meeting,
San Diego, California, January 11-15, 2020

Due to the proximity with the 28th Coffee Science ASIC meeting in Montpellier, France in June 2020, only one abstract was submitted to our ICGN Coffee Genomics Workshop at PAG in 2020 by Valérie Poncet (https://plan.core-apps.com/pag_2020/abstract/5adf47b7-6102-426e-8cfc-22f2093ecc1d) Rather than offering our Coffee Genomics Workshop that year, we moved the abstract with approval of the PAG organizers to the Genome Variation Workshop (https://plan.core-apps.com/pag_2020/event/680f532f0a26f8c2f8d1736dbb067973).

Unfortunately, the 28th ASIC meeting was later postponed due to the pandemic to June 28-July 1, 2021. See below text of abstract presentation.

Patterns of Adaptive Genetic Variation across *Coffea Canephora*

Valérie Poncet, IRD UMR DIADE, Montpellier cedex 5, France

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. 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.

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. 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.

Denoeud, F. *et al.* (2014) The coffee genome provides insight into convergent evolution of caffeine biosynthesis. *Science* **345**, 1181-1184.

Dereeper, A. *et al.* (2015) The coffee genome hub: a resource for coffee genomes. *Nucleic Acids Research* **43**, D1028-D1035.

Marraccini, P. *et al.* (2012) Differentially expressed genes and proteins upon drought acclimation in tolerant and sensitive genotypes of *Coffea canephora*. *Journal of Experimental Botany* **63**, 4191-4212.

- Merot-L'anthoene, V. *et al.* (2019) Development and evaluation of a genome-wide Coffee 8.5 K SNP array and its application for high-density genetic mapping and for investigating the origin of *Coffea arabica* L. *Plant Biotechnology Journal* **17**, 1418-1430.
- Gomez, C. *et al.* (2016) Shift in precipitation regime promotes interspecific hybridization of introduced *Coffea* species. *Ecology and Evolution* **6**, 3240-3255.

Note: 258 words