International Coffee Genomics Network (ICGN)
Report 11th Coffee Genomics Workshop held at the
XXVI Plant and Animal Genome Meeting,
San Diego, California, January 13-17, 2018

Coffee Workshop Speakers

1. **Aleksey Zimin**[1, 2], **Carlos Maldonado**[3], and **Marcela Yepes**[4], [1]Johns Hopkins University, [2]University of Maryland, [3]Colombian National Coffee Research Center, CENICAFE, Colombia, [4]Cornell University, School of Integrated Plant Sciences, Plant Pathology and Plant-Microbe Biology Section, USA. ***Chromosome Scale Scaffolding of the High-Quality Genome Assemblies of the Allotetraploid Coffea arabica and its Maternal Ancestor C. eugenioides and Validation using Genetic and Physical Mapping Data.***
2. **Carlos Maldonado**, Colombian National Coffee Research Center, CENICAFE, Colombia. ***Targeted Sequencing in Allopolyploids: Comparison of BAC-by-BAC and Whole Genome Approaches using Third Generation Sequencing.***
3. **Carmenza Góngora**, **Claudia Flórez**, **Carlos Maldonado**, Colombian National Coffee Research Center, CENICAFE, Colombia. ***Resistant, Resilient, Highly Productive, High Cup-Quality Coffea arabica Varieties for the Colombian Coffee Farmers on the 80th Anniversary of the Colombian National Coffee Research Center (CENICAFE).***
4. **Guyot Romain**, Institut de la Recherche pour le Developpement, France. ***Coffea Centromeric Retrotransposons Play the Central Role in Centromere Organization and Function.***
5. **Bing Cheng**, QAAFI, the University of Queensland. ***Better Coffee Quality from the Lower Canopy?***
6. **Dominique Crouzillat**, Centre R&D Nestlé Tours. ***Using the Coffea arabica Genome to Expedite Coffee Breeding.***

See abstracts of all presentations included at the end of this report.

Coffee Genomics Workshop at PAG

The Plant and Animal Genome (PAG) meeting is the world largest international scientific conference reporting on animal and plant genomics advances, with >3,000 participants from >65 countries around the world. For those interested in participating in future PAG meetings see http://www.intlpag.org. The XXVII Plant & Animal Genome Conference will be held in San Diego, January 12-16, 2019.

Our 11th ICGN Coffee Genomics workshop was held as part of the PAG Meeting in San Diego at the Pacific Salon 3, on January 14, 2018. The co-organizers of the workshop, Marcela Yepes (Cornell University, my11@cornell.edu), and Philippe Lashermes (IRD-CIRAD, France, philippe.lashermes@ird.fr), thank the speakers and workshop participants for their contributions. Over the past 13 years our coffee genomics community has focused efforts on bringing coffee to

the forefront of plant genomics research. Abstracts of our 11th coffee genomics workshop presentations are included at the end of this report, with links to download pdf files of all presentations. Please mark your calendars for our 12th ICGN Coffee Genomics Workshop that will be held Sunday January 13, 2019 during the XXVII PAG meeting in San Diego, January 12-16, 2019. Please contact one of the organizers if interested in presenting a talk or poster, or with suggestions for new topics for workshop presentations or for round table discussion at the ICGN meeting. The coffee genomics workshop is an excellent opportunity to present advances in coffee genomics research to the International Plant and Animal Genomics Community and is helping our community explore new collaborations as well as funding opportunities.

ICGN collaboration with the International Coffee Organization (ICO) and participation in the First World Coffee Producers Forum organized by the Colombian National Coffee Growers Federation

ICGN supports ICO's efforts to promote global coffee sustainability with emphasis in economic, social and environmental sustainability. We participated in the first World Coffee Producers Forum in Medellín, Colombia, from July 10-12, 2017. The forum brought together 1,300 participants from 44 countries to analyze major challenges to the coffee value chain including: coffee farmers' economic sustainability, productivity, price volatility, the next generation of coffee growers, the consequences of climate change, how to increase quality and traceability for consumers and the increasing demand of 50 million bags in the next 10 to 15 years. The forum addressed principles of global co-responsibility and cooperation needed for future sustainability of the coffee chain.

ICGN shares the priorities that were discussed at the first Coffee Producers Forum and will continue to network the world coffee genomics scientific community to help prioritize and advance topics of major relevance for future competitiveness and sustainability of the coffee chain. The 2nd Global Coffee Sustainability Conference will be in Belo Horizonte, Brazil, November 8-10, 2018. https://www.globalcoffeeplatform.org/latest/2018/gcsc-2018-save-the-date

The first Coffee Producers Forum aimed at building, with the help of representatives of the different links (coffee producers, exporters, importers, roasters, traders, etc.), an accurate diagnosis of the main challenges of the coffee value chain to achieve future sustainability for the benefit of everybody, starting with producers and involving consumers. The forum addressed the main challenges and problems of coffee farming to identify strategies for a better distribution of value and responsibility among all players, in search of sustainability of the global chain from seed to cup. Because of its significance, the forum was without doubt one of the most important events of the global coffee industry in recent years, and was attended by US former President Bill Clinton, Colombian President Juan Manuel Santos, Honduras President Juan Orlando Hernández, Costa Rican President Luis Guillermo Solís, and ICO's Executive Director José Dauster Sette, all pictured below. The Forum was organized and hosted by the Colombian National Coffee Growers Federation (FNC) in celebration of its 90 years (see FNC's CEO Roberto Vélez pictured next to the iconic Juan Valdez who has represented the Colombian coffee farmers since 1958).

ICGN survey and networking efforts

ICGN is conducting a survey to help us update our mailing list, identify future priority projects for the community as well as new leadership to help secure funding for new proposals. ICGN members interested on collaborating in these efforts are asked to help us contribute by completing and submitting the survey available at our www site (http://www.coffeegenome.org). Survey results will be discussed at the next ICGN meeting held in conjunction with the 2019 PAG meeting in San Diego.

Background Coffee importance

Coffee is the world's most valuable agricultural export commodity, second only to oil in international trade (International Coffee Organization, http://www.ico.org), with an estimated 21 billion pounds of green coffee produced around the world each year on over 25 million acres. Global coffee consumption continues to increase at an annual rate of 3%. About 125 million people in more than 60 developing countries depend on coffee for their food security and livelihoods. In some countries rural employment in coffee production accounts for 80% of foreign trade earnings, and nearly 75% of global coffee production comes from small farms of less than 5 acres. The retail value of the coffee industry is estimated to be 90 billion US dollars per year and yet, remarkably, coffee remains an understudied crop, receiving very little funding for genetics and genomics research.

For most coffee growing countries, coffee production is a powerful job creator and a major economic driver. In Africa, eight out of 25 coffee producing countries are among the ten poorest countries in the world, and 53% of the rural population in those 25 coffee producing countries, are involved in coffee growing. However, coffee production in Africa, Latin America, and around the globe continues to decline due to biotic and abiotic stresses exacerbated by climate change. ICGN targets an innovative approach to revitalize coffee production on a global scale and tackle the global challenges facing production for the coffee sector in the context of climate change. **It is**

predicted that large areas of land currently used for coffee production will be rendered unsuitable (almost 50% by 2050), migration of production into new areas will be limited due to nature conservation and other physical and economic constraints. In contrast, coffee consumption is predicted to double by 2050 as rising incomes and living standards are positively correlated with coffee consumption. Yet, meeting the future demand for coffee will require to double production by 2050. Attaining efficient production to ensure sustainability of the coffee sector is a major goal for the coffee community worldwide. ICGN efforts to address critical issues such as adaptation of the crop to climate change and help in the transformation of coffee production on a global scale are focused currently on the development of advanced genomic tools to accelerate linkage of genotypic and phenotypic diversity in coffee.

Our report describes progress on the generation of the first high quality *Coffea arabica* genome references and assemblies (see abstracts below). ICGN is also interested in the development of state-of-the-art advanced genomic tools to speed up diversity characterization, enhanced utilization and conservation of *Coffe*a germplasm in the context of climate change. With support from the International Coffee Organization (ICO), ICO member countries were contacted to discuss possible interest in developing a global initiative in collaboration with ICGN/ICO aiming at improving conservation and characterization of the world coffee gene pool for varietal development in a world of changing farming systems and climate. Other ICO member countries that have expressed strong interest in working on an ICGN/ICO collaborative proposal include, for Europe: France (IRD-CIRAD); for Latin America: Brazil, Colombia, Guatemala, Costa Rica, Mexico; for Africa: Cote D'Ivoire, Ethiopia, Kenya, Malawi, as well as the Inter-African Coffee Organization; and for Asia: India and Vietnam.

ICGN is grateful for the continuous support by previous ICO Executive Directors Dr. Nestor Osorio and Dr. Robério Oliveira Silva who invited ICGN to participate as an observer in the ICO Council meetings. We look forward to working closely with ICO officials under the leadership of Executive Director José Dauster Sette on the preparation and submission of a first ICGN/ICO proposal, and to explore potential sources of finance for such joint initiatives. Support from ICO and the private sector will be key for ICGN securing future funding for diversity conservation efforts in *Coffea* with a broader funding base, and to promote coffee genomics research for coffee improvement targeting priority traits for the coffee industry. Capacity building in developing countries to participate in coffee genomic research is being supported through ICGN networking efforts and our yearly workshops at PAG.

ICGN is particularly grateful to Bioversity International and IRD/CIRAD for continuously supporting our networking efforts by hosting at no cost to our coffee genomics community the ICGN website since its inception in 2005. Bioversity reiterated recently interest to help us cover the cost of the ICGN www site hosting at no cost for our community for an additional year.

To ensure full benefit from the generated coffee genomic sequences and resources by the coffee sector, ICGN continues to explore additional funding from international funding agencies to support our community efforts.

Abstracts ICGN 11th Coffee Genomics Workshop

XXVI Plant and Animal Genome Meeting,
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https://pag.confex.com/pag/xxvi/meetingapp.cgi/Session/4760

Chromosome Scale Scaffolding of the High-Quality Genome Assemblies of the Allotetraploid *Coffea arabica* and its Maternal Ancestor *C. eugenioides* and Validation using Genetic and Physical Mapping Data

A. Zimin[1, 2], **C. E. Maldonado**[3], **M. Yepes**[4], K. M. Mockaitis[5], P. Moncada[3], C. Guanote[5], S. A. Sanders[5], C. Góngora[3], C. Florez[3], J. A. Yorke[2], A. Gaitan[3], H. Aldwinckle[4]

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https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/31774

Cost effective strategies for sequencing and assembly of complex polyploid and highly heterozygous diploid genomes are a major need for plants, in particular because polyploidy frequently occurs in flowering plants (~70%) providing an important pathway for plant evolution and specialization. *De novo* assembly of such genomes remains a critical unsolved technical problem resulting in incomplete and fragmented assemblies. In this project, we produced high quality assemblies of the allopolyploid *C. arabica* genome and one of its ancestors, the diploid *C. eugenioides* genome. The genome of the other ancestor, *C. canephora* was published previously (Denoeud *et al.* 2014) and is publicly available. Our success in the assembly project stemmed from using ~80X coverage long PacBio reads, error corrected with ~120X coverage of PCR-free Illumina 2x250bp paired end reads for the initial genome assembly using the MaSuRCA assembler (Zimin *et al*. 2017), combined with assembly of just PacBio reads with Falcon-unzip assembler (Chin *et al*. 2016), followed by mid- and long-range scaffolding using 10X Genomics (Gemcode and Chromium), and Dovetail Hi-C data. The availability of both ancestral genomes for *C. arabica* combined with genetic (Moncada *et al.* 2016) and physical mapping data allowed us for the first time to gain a panoramic view of all the homologous chromosomes of *C. arabica* corresponding to each sub-genome. For *C. arabica*, we were able to achieve a contig N50 of 3.91 Mb, and were able to construct the 22 pseudo-chromosomes split by sub-species. Our assembly is the most contiguous and complete so far generated for this species with 91% of the genome anchored to chromosomes. An accurate chromosome scaffolded high quality genome reference assembly is crucial for advancing coffee genomics and climate change adaptation studies. The assemblies *of C. arabica* and *C. eugenioides* are being used to improve downstream analyses, including gene annotation, synteny, comparative genomics and population genetics using natural and breeding populations being phenotyped for climate change adaptation.

This research is co-funded by the US National Science Foundation (Award 1444893), the Inter-American Development Bank, and the Colombian National Coffee Growers Federation (FNC). This abstract was presented by coauthors A. Zimin (genome assembly and chromosome scaffolding); C. Maldonado (physical mapping) and M. Yepes (project introduction and outreach).

Presentation pdf available at https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/31774

Targeted Sequencing in Allopolyploids: Comparison of BAC-by-BAC and Whole Genome Approaches using Third Generation Sequencing

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https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/31900

A targeted sequencing approach was implemented to characterize genomic regions containig QTLs associated with important agronomic traits in the allotetraploid *Coffea arabica*. The physical map of *C. arabica* var. Caturra was integrated with the *C. canephora* genome using the programs FPC and SyMap, and the Minimum Tilling Path (MTP) that covers the target region was selected, sequenced by single molecule real time sequencing (SMRT-Seq) and assembled by HGAP and postHGAP software from PACBio and the Arizona Genomics Institute respectively. A second dataset included the whole genome obtained by PACBio long read sequencing of 20 Kb libraries (WGS-SMRT ~80X coverage) and assembled using Falcon/Falcon Unzip (Chin *et al*. 2016) and MaSuRCA (Zimin *et al*. 2017) and the transcriptome from pooled and MID labeled tissues (meristem, leaves and flowers), whole length transcrips were obtained by cDNA sequencing (Iso-Seq PacBio) of *C. arabica* var. Caturra. For both approaches a region covering 30 cM upstream and downstream from the markers (SNV, DArT and SSR) associated with the QTL was determined by the integration of genetic and physical maps of *C. arabica* and the *C. canephora* genome, used as a reference, by alignment of the specific marker or BAC end sequence (BES) using BLAT or e-PCR as mapping tools. The *C. arabica* WGS was aligned to *C. canephora* using SyMap and the contigs covering the target region were selected. As was expected for an allotetraploid species several WGS contigs mapped over the same reference region; contigs with higher identity to *C. canephora* were assigned to that subgenome and those with lower identity to the *C. eugenioides* subgenome. Contigs of non-overlapping regions were assigned to both subgenomes in the scaffolding process. In the case of the BAC-by-BAC sequencing the assembly was performed using Minimus. Gene prediction was done using the program MAKER and functional annotation was done uysing Blast2GO-pro, and repeats annotation using REPET.

An assembled sequence of 7.38 Mb with 1,188 predicted genes was obtained from the BAC-by-BAC approach. WGS derived scaffolds of 10.2 Mb with 1,675 predicted genes for the *C. canephora* subgenome and 10.7 Mb with 1,991 for *C. eugenioides* subgenome. Dot-Plot analysis showed evidence of chimeric assembly between subgenomes in the BAC-by-BAC approach. By functional annotation the enzyme category with greater representation was transferases. The results of Interproscan showed 11 NBS domains of disease resistance genes in the *C. eugenioides* subgenome, and 9 in the *C. canephora* subgenome. These results coupled with annotation of P-loop domains and leucine-rich regions domains suggest that this region could be associated with disease resistance that could be contributing to coffee yield. Overall, the best sequencing strategy to obtain high quality data from the tetraploid genome was WGS sequencing, demonstrated by no apparent presence of chimeric regions and a clear differentiation of subregions between subgenomes.

This research is co-funded by the US National Science Foundation (Award 1444893), the Inter-American Development Bank, and the Colombian National Coffee Growers Federation (FNC).

Presentation pdf available at https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/31900

Resistant, Resilient, Highly Productive, High Cup-Quality *Coffea arabica* Varieties for the Colombian Coffee Farmers on the 80th Anniversary of the Colombian National Coffee Research Center (CENICAFE)

C. Góngora[1], **C. Flórez**[1], **C. E. Maldonado**[1], M. Yepes[2], A. Zimin[3, 4], K. Mockaitis[5], J. A. Yorke[4], H. Aldwinckle[2], and A. Gaitán[1]

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https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/32071

CENICAFE was founded by the Colombian National Coffee Growers Federation in 1938 with the mission to generate scientific knowledge and technologies for sustainable coffee production for the Colombian coffee growers. Research covers a wide agronomical spectrum, from breeding of coffee varieties to improved planting and harvesting/post-harvesting practices.

Coffee genomics and transcriptomics research is on-going in collaboration with Cornell University, University of Maryland/ Johns Hopkins University, and Indiana University to identify the location of genes of interest (resistance to diseases and pests, physiological traits and yield) on the chromosomes, their sequences (structural genomics) and function (functional genomics). Sequencing of the coffee genome has been one of our major milestones to develop advanced genomics tools to accelerate the development of varieties resilient to climate change with enhanced use of the diversity present in non-cultivated *Coffea* germplasm. The project also targets the genome of the coffee berry borer, *Hypothenemus hampei* the major insect pest of coffee. Genomic and transcriptomic studies are on-going on the biological mechanisms involved on insect/coffee interactions using host genotypes with differential response for analysis of pathways and novel candidate genes that could enhance pest management strategies.

In addition, CENICAFE maintains one of the largest *ex situ* collections of *Coffea arabica* outside its center of origin Ethiopia, that includes >1,000 accessions. The collection is maintained in the field and is being genotyped and phenotyped for traits of interest including resilience to climate change (biotic and abiotic stresses), plant architecture, high yield and high quality. Microsatellites were used to select 190 accessions of *C. arabica* that were characterized by genotype by sequencing (GBS). Genomic variants were mapped on our recently generated *C. arabica* reference genome assembly to identify 1.15 million di-allelic SNPs. This analysis allowed determination of population structure with seven ancestral populations (K) with diversity coefficients (Fst) between populations varying from 0.179 to 0.487.

A mini core collection was selected based on this study and planted under contrasting environmental conditions throughout Colombia, and is being phenotyped for agronomically important traits. Integration of genotypic and phenotypic information has been crucial to reshaping the current composition of the rust resistant Castillo variety and for the release of the Cenicafe1 variety and Regional Castillo variants, as well as to accelerate the development of new varieties that are highly productive, durably resistant and resilient, in addition to yielding excellent cup quality.

This abstract was co-presented by co-authors C. Góngora (CENICAFE sustainable coffee production, coffee berry borer/coffee plant interaction), C. Flórez (phenotyping, abiotic stress and climate change), and C. Maldonado (Population Structure and Diversity studies in non-cultivated *Coffea* germplasm). This multi-component presentation will have an extended time (30 min).

This research is co-funded by the US National Science Foundation (Award 1444893), the Inter-American Development Bank, and the Colombian National Coffee Growers Federation (FNC).

Presentation pdf available at https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/32071

Coffea Centromeric Retrotransposons Play the Central Role in Centromere Organization and Function

Guyot Romain

Institut de Recherche pour le Developpement
https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/28534

Centromeric regions of plants are generally composed of large array of satellites organized with a specific lineage of *Gypsy* LTR-retrotransposons, called Centromeric Retrotransposons (CR). Repeated sequences interact with a specific H3 histone, playing a crucial function in the kinetochore formation. To study the structure and composition of centromeric regions in *Coffea*, we annotated and classified into ten distinct families Centromeric Retrotransposons sequences (called hereafter CRC) from *C. arabica* genome and its two diploid ancestors: *Coffea canephora* and *C. eugenioides*. The sequence mapping and FISH experiments of CRC Reverse Transcriptase domains in *C. canephora*, *C. eugenioides* and *C. arabica* clearly indicate a strong and specific targeting mainly onto centromeric regions, which can be associated also with heterochromatin. Sequence analysis of putative centromeric regions on *C. arabica* and *C. canephora* chromosomes showed an exceptional density of one family of CRC elements, and the complete absence of satellite arrays, contrasting with usual structure of plant centromeres. Altogether, our data demonstrated a specific centromere organization in *Coffea*, suggesting that one CRC family alone might play the central role for the continuation of the centromere function.

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Better Coffee Quality from the Lower Canopy?

Bing Cheng

QAAFI, The University of Queensland
https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/27682

From an evolutionary viewpoint, seeds have developed to store nutrients to support plant reproduction. They also have a defence system to survive environmental treats to survival of the seed. With the threat of climate change, a comprehensive understanding of how the growth environment influences seed maturation and composition is required. The Arabica coffee bean, a tropical dicotyledonous albuminous seed, was used in this research to study how seed ripening was influenced by the micro-environment as determined by canopy position. The transcriptome of the developing coffee beans (covered by green, yellow and red pericarp) was analysed for both the upper and the lower canopy (above and below 170 cm). A long read coffee transcriptome obtained from the same samples was used as a reference. Comparative transcriptome analysed was used to investigate the influence of canopy position at different developmental stages. Phenotypic variations of the bean were analysed, including the key physical and chemical attributes influencing coffee quality. Additional sensory testing was also conducted to investigate the aromatic differences in the beans. This comprehensive study will facilitate an improved understanding of the molecular basis coffee quality and provide insights to the variation of seed ripening in different canopy position that produce different phenotypic traits.

Presentation pdf available at: https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/27682

Using the *Coffea arabica* Genome to Expedite Coffee Breeding

Dominique Crouzillat

Centre R&D Nestlé Tours
https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/27975

The Arabica Coffee Genome Consortium (ACGC) undertook the sequencing of the *Coffea arabica* genome and that of its two parents: *C. eugenioides* and *C. canephora*. The resulting genomic resources were used to better assess the *C. arabica* genetic diversity and characterize the neo-diversification induced by man through selection and/or introgression. For this purpose, the consortium re-sequenced 21 wild accessions and 14 varieties of *C. arabica*. The *C. arabica* lectotype conserved at the Natural History Museum in London was also re-sequenced using ancient DNA sequencing techniques. This re-sequencing confirmed the drastic genetic bottleneck that occurred with the cultivation of *C. arabica* varieties and the genetic reservoir still available in the wild pool. It also allowed the development of modern genomic tools such as DNA chip. Furthermore, it brings a large amount of genetic markers covering the entire genome allowing new breeding approaches (GWAS) for this economically important crop species.

In parallel, ultra high-density genetic maps were obtained for *C. arabica* and *C. canephora* by sequencing segregating populations, and thus allowing to anchor genomic to genetic data. This will allow a more fine definition of QTLs for a large number of agronomic and sensory traits and precise their relation to candidate genes. All the obtained data will be made available through a public database giving access to performing tools allowing breeders and agronomists to answer present and future challenges such as higher tolerance to pests, quality of the coffee beverage and resilience to climate change

Presentation pdf available at: https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/27975

Abstracts of oral presentations in other PAG workshops of interest to our ICGN community:

Deciphering the Allotetraploid Genome of *Coffea arabica* L.

Alexandre de Kochko

IRD UMR DIADE
https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/30630

Coffea arabica, one of the two coffee cultivated species, is the sole tetraploid species of the *Coffea* genus, which contains to date 125 accepted species. *C. arabica* resulted from a recent and spontaneous cross between *C. eugenioides*, a wild species growing in East Africa and *C. canephora*, the other cultivated species. The two parental genomes are highly homeologous, up to 98% in their conserved regions, which constitutes a difficult challenge for reconstructing the two parental genomes anchored on 22 pseudomolecules. The international Arabica Coffee Genome Consortium (ACGC) has undertaken the sequencing of this genome as well as that of the two parental species.

The most advanced technologies were used to reach this goal: long and short read sequencing (genomic and transcriptomic), optical mapping and chromosomal conformation capture (Hi-C). Finally the results were anchored to genetic maps. Genome assemblies indicate that, as expected, no important chromosomal rearrangements intervene between the two subgenomes, which present a high colinearity. A peculiar situation characterizes the *Coffea* genomes, indeed, while centromeric retrotransposons are present on all chromosome pairs but one, no centromeric repeats (satellite sequences) have been identified.

A comparative analysis, based on the gene annotation of the three genomes, indicates minor differences between them, at the opposite, a fast and efficient mechanism of transposable elements control and elimination took place in *C. arabica*. The uniqueness of the event leading to the *C. arabica* species formation will be also discussed.

Presentation pdf available at: https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/30630

Abstracts of poster presentations at PAG of interest to our ICGN community:

Targeted Capture of Dreb Subfamily Genes as Candidates Genes for Drought Tolerance Polymorphism in Natural Population of *Coffea canephora*

S. Aquino[1], P. Marraccini[2], C. Mariac[1], M. Couderec[1], K. Bethune[1], A. Andrade[3],

D. Oliver[4], M. Lepelley[5], Y. R. Vigouroux[1], C. Kiwuka[6], N. Anten[7],
A. De Kochko[8], and V. Poncet[a]

[1]IRD, [2]CIRAD UMR AGAP, [3]Embrapa Café/INOVACAFÉ – UFLA, [4]Nestlé R&D,
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https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/27965

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.

1. *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 a new assembly. A targeted capture array[4] 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.

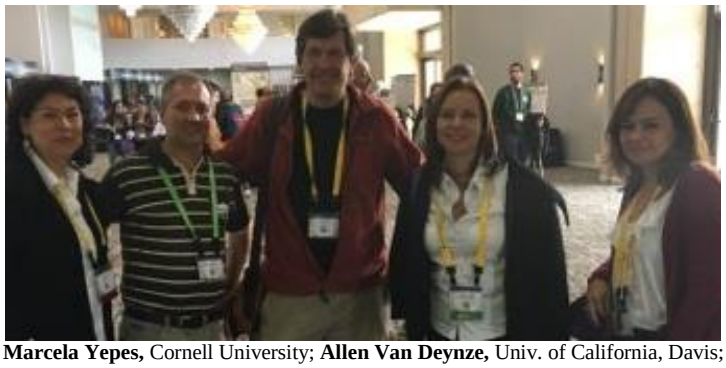
[1]Marraccini, P. et al. (2012) Differentially expressed genes and proteins upon drought acclimation in tolerant and sensitive genotypes of *Coffea canephora*. *Journal of experimental botany*, **63**, 4191-212.
[2]Denoeud F. et al. (2014) The coffee genome provides insight into convergent evolution of caffeine biosynthesis. Science 345(6201): 1181
[3]Dereeper, A. et al. (2015) The coffee genome hub: a resource for coffee genomes. *Nucleic Acids Res*, **43**, D1028-35.
[4]Mariac C. et al. (2014). Cost-effective enrichment hybridization capture of chloroplast genomes at deep multiplexing levels for population genetics and phylogeography studies. Mol Ecol Resour 14: 1103-1113

Pictures of our ICGN 11th Coffee Genomics Workshop Speakers and Participants at XXVI PAG 2018

Claudia Flórez, CENICAFE; **Aleksey Zimin**, Johns Hopkins University/University of Maryland; **Herb Aldwinckle**, Cornell University; **Carmenza Góngora** and **Carlos Maldonado**, CENICAFE; **Marcela Yepes**, Cornell University.

From left to right, **Claudia Flórez**, CENICAFE; **Aleksey Zimin**, Johns Hopkins University/University of Maryland; **Dominique Crouzillat**, Nestle Tours; **Alexander de Kochko**, IRD UMR DIADE; **Carmenza Góngora** and **Carlos Maldonado**, CENICAFE; **Marcela Yepes**, Cornell University.

Claudia Flórez and **Carmenza Góngora,** CENICAFE; **Marcela Yepes**, **Herb Aldwinckle**, and **Matthieu Fuchs**, Cornell University (back row); **Carlos Maldonado**, CENICAFE; and **Jerson Domínguez**, CENICAÑA



Marcela Yepes, Cornell University; **Allen Van Deynze,** Univ. of California, Davis; **Lukas Mueller**, Boyce Thompson Institute; **Carmenza Góngora** and **Claudia Flórez**, CENICAFE.

Marcela Yepes and **Matthieu Fuchs**, Cornell University
Fernando Medrano, University of Davis (center)

Keithanne Mockaitis, NCGAS, Indiana University

Sheri Sanders, Carrie Guanote (sitting center), and **Keithanne Mockaitis,** NCGAS, Indiana University

Upcoming Meetings of interest to our ICGN community

- 27th International Coffee Science Meeting (ASIC- Association for Science and Information on Coffee) Portland, Oregon September 16-20, 2018, hosted by the US Specialty Coffee Association (SCA). https://www.asicportland.org/

- 15th Solanaceae Conference, Applied Genomics, Accelerated Breeding, Gene Targeting, Chiang Mai, Thailand, September 30-October 4, 2018
  https://www.solanaceae2018.com/front

- 2nd Global Coffee Sustainability Conference, Belo Horizonte, Brazil, November 8-10, 2018. https://www.globalcoffeeplatform.org/latest/2018/gcsc-2018-save-the-date

- 12th ICGN Coffee Genomics Workshop as part of the XXVII Plant and Animal Genome (PAG) meeting, San Diego, California, January 12-16, 2019 http://www.intlpag.org/2019/

- World Coffee Conference in April 2020 in Bengaluru, India
  http://www.ico.org/documents/cy2016-17/Presentations/icc-wcc-2020-india-march.pdf