International Coffee Genomics Network (ICGN)

Report 9th Coffee Genomics Workshop held at the
XXIV Plant and Animal Genome (PAG) Meeting
San Diego, California
January 9-13, 2016

Coffee Genomics Workshop Speakers

1. **Marcela Yepes,** Alvaro Gaitán, and **Marco Cristancho**, Cornell University, School of Integrated Plant Sciences, Plant Pathology and Plant Microbiology Section, USA; Colombian National Coffee Research Center, CENICAFE, Colombia; and Colombian Center for Bioinformatics and Computational Biology, BIOS, Colombia. ***Building High Quality Reference Genome Assemblies using PACBio Long Reads for the allotetraploid Coffea arabica and its maternal diploid ancestor Coffea eugenioides.***
2. **Marcio Resende,** RAPID Genomics LLC. ***High Throughput Targeted Genotyping of Coffea arabica and Coffea canephora using next generation sequencing.***
3. **Luis Felipe Ventorin Ferrão.** Universidad of Sao Paulo (ESALQ/USP). ***Mixed Model to Multiple Harvest Location Trial Applied to Genomics Prediction in Coffea canephora.***
4. **Girma Adugna,** Jimma University, Ethiopia, ***Threats of Climate Change on Arabica Coffee (Coffea arabica L.) in its center of origin Ethiopia.***
5. **Kassahun Tesfaye,** Addis Ababa University, ***Molecular Markers reveal high variability among populations of Coffea arabica in its native range of the Afromontane forests of Ethiopia.***

See abstracts of all presentations included at the end of this report, and links to access pdfs of the last three presentations.

Coffee Genomics Workshop at PAG

The Plant and Animal Genome (PAG) meeting is the 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 meetings see http://www.intlpag.org. The XXV Plant & Animal Genome Conference will be held in San Diego, January 13-18, 2017.

A record 175 scientists participated in our 9th ICGN coffee genomics workshop held as part of the PAG Meeting in San Diego at the Pacific Salon, on January 10, 2016. 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. Abstracts of workshop presentations are included as an appendix at the end of this report, as well as links to access pdfs of the last three presentations. The 10th Coffee Genomics Workshop will be held January 15, 2016 as part of the XXV PAG meeting in San Diego, January 13-18, 2017. 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 survey and collaboration with the International Coffee Organization

Our ICGN coffee genomics workshops at PAG will celebrate 10 years in 2017. ICGN will conducted a survey in 2017 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 that are 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 2017 PAG meeting in San Diego.

As the first *de novo* coffee genome references and assemblies become available (see report on the status of on going projects included below), we would like to take advantage of the momentum to identify new priority projects of interest that ICGN can develop as a community to help mine the data generated and develop innovative tools and advanced resources in coffee genomics to address challenging issues for our community such as climate change adaptation and sustainability that could be accelerated with transforming genomic technologies and strategies. The African Coffee Research Network (ACRN) joined ICGN in 2011 as an institutional member, and its Director of Research and Development, Dr. Bayeta Bellachew helped us conduct the ICGN survey among ACNR members at several Coffee Research Institutions in Africa. We received through ACRN responses from scientists and scientific groups from the following countries: Ethiopia, Kenya, Rwanda, Uganda and Ghana with strong interest to work with ICGN on a global initiative to develop advanced genomic tools to speed up diversity characterization, enhanced utilization and conservation of *Coffea* germplasm in the context of climate change. In addition with support from the International Coffee Organization (ICO), ICO member countries have been contacted to discuss possible interest on 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 invitation by the ICO Executive Director Dr. Robeiro Oliveira Silva to participate as an observer in the ICO Council meetings in 2017, and we are looking forward to working closely with ICO officials on the preparation and submission of a first ICGN/ICO proposal, and to explore potential sources of finance for such joint initiative. Support from ICO and private sector will be key for ICGN to secure 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 different regions as well as for the coffee industry. Capacity building in developing

countries to participate in coffee genomic research can be supported through ICGN networking to help us secure international funding for those efforts.

ICGN is particularly grateful to Bioversity International and IRD/CIRAD for supporting our networking efforts by hosting at no cost to our community the ICGN website since its inception in 2005. Bioversity reiterated this year (2016), its interest to help us cover the cost of the ICGN www site hosting at no cost for an additional year.

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 17 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 on those 25 coffee producing countries, are involved in coffee growing. However, coffee production in Africa and around the globe continues to decline due to lack of basic agronomic techniques, lack of use of fertilizers, abiotic and biotic stresses due to excess of water or lack of water, increasing incidence of pests and diseases all exacerbated by climate change. ICGN targets a new approach to revitalize coffee production at a global scale and tackle the global challenges facing production for the coffee sector in the context of climate change. Attaining efficient production to ensure sustainability of the coffee sector is a major goal for the coffee community worldwide. ICGN's long term goal is to address key issues such as adaptation of the crop to climate change and help in the transformation of coffee production at a global scale with improved technologies to accelerate linkage of genotypic and phenotypic information in coffee.

Update status of the *Coffea canephora* genome sequencing

With funding from the Agence Nationale de la Recherche (ANR; Genoplante ANR-08-GENM-022-001), France, several Institutes (Genoscope-CEA, IRD and CIRAD) combined their scientific resources and expertise to sequence, assemble, and annotate the entire genome of *C. canephora*. Additional partners included several ICGN members (EMBRAPA/Brazil, ENEA/Italy, University of Trieste/Italy, University of Queensland/Australia, CCRI/India, University of Illinois, Urbana/USA, Hawaii Agriculture Research Center HARC/USA, SUNY Buffalo/USA, University of Ottawa/Canada). The *C. canephora* genome consists of 11 chromosomes, is about 710

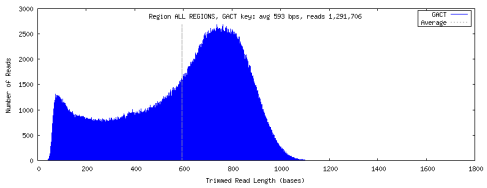
Mb in size, and was sequenced *de novo* with deep coverage using different sequencing platforms. Genoscope lead the sequencing and assembly of the *C. canephora* genome. Patrick Wincker, Head of Sequencing and Coordinator of Eukaryote Annotation and Analysis at Genoscope, presented the sequencing strategy and the status of the project during our 4th ICGN Coffee Genomics Workshop at PAG in San Diego in 2011. In 2013, France Denoeud from Genoscope presented at our 6th ICGN Coffee Genomics Workshop an update on the first genome assembly, and in 2014 Alexis Dereeper presented during our 7th ICGN Coffee Genomics Workshop the **Coffee Genome Hub**, an integrative genome information system accessible through the South Green Bioinformatics Platform, developed to provide centralized access to all the coffee scientific community of the full *C. canephora* genome sequence, as well as genomics, genetics, mapping, and breeding data and analysis tools to facilitate basic, translational and applied research in coffee (Dereeper, et al. 2014. Nucleic Acids Research. 43: D1028-D1035, access free manuscript at http://nar.oxfordjournals.org/content/43/D1/D1028.full.pdf+html) . **The manuscript for the sequencing of the *C. canephora* genome was published in 2014** (Denoed *et al.* 2014. Science 345: 1181-1184); access manuscript at http://www.sciencemag.org/content/345/6201/1181.full, and the genome assembly can be freely accessed at: http://coffee-genome.org.

Update status of the *Coffea eugenioides* genome sequencing

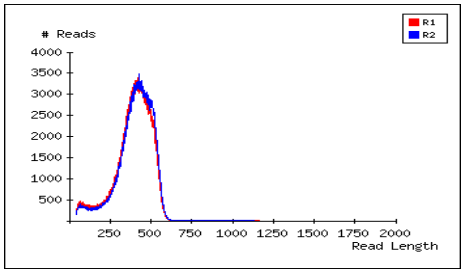
This project was funded by the Inter American Development Bank, (FONTAGRO/ SECCI), with co-funding from the Colombian National Coffee Growers Federation (FNC) and its National Coffee Research Center, CENICAFE. Additional funding for the project was recently secured from the US National Science Foundation (NSF). Genome sequencing for *Coffea eugenioides* was started towards the end of 2012. The project has been developed collaboratively by CENICAFE and Cornell University. Funding for this project was secured jointly through a proposal prepared and submitted by Cornell University and FNC/CENICAFE.

We mimicked the strategy used for the *C. canephora* sequencing to generate a high quality reference assembly for *C. eugenioides* using mixed next generation sequencing platforms: Roche 454 FLX+ and Illumina HiSeq 2500. We collaborated with Roche to construct and sequence a whole genome shotgun (WGS) library (fragment size >1,100 bases and <2,000 bases) using 454 FLX+ single end reads with mode length of 763 bases to generate a total of 6,082,341,937 bases for an estimated coverage of 9.2X for the *C. eugenioides* genome (~estimated genome size of 660 *Mb).* See below quality control results of a typical 454 FLX+run:

Region	Passed Filter	Total Bases	Reads ≥ 1000 bases (% Passed Filter)	Read Length (Bases)				
				Mean	Median	Mode	Min	Max
1	634,065	373,033,536	4,712 (0.74%)	588.3	653	763	40	1,735
2	657,641	392,830,440	3,723 (0.57%)	597.3	660	782	40	1,692
ALL REGIONS	1,291,706	765,863,976	8,435 (0.65%)	592.9	657	763	40	1,735



We collaborated with Roche to construct and sequence twelve 20 Kb long insert libraries (3.1X coverage) using paired end sequencing and Roche 454 FLX Titanium. Below is a graph of the paired end statistics profile for a run: Read length distribution of high quality reads. R1 = Coffee 20kb 1-1, R2 = Coffee 20kb 1-1. Linker positive displays statistics of reads with paired end linker sequence 71.47% and 73.62%. Linker Negative refers to reads with no paired end linker sequence 28.53% and 26.38%.



The overall data generated for the twelve 20 Kb-insert libraries paired end-sequenced using Roche 454 FLX Titanium includes:

Paired end reads 57% 5,876,463 reads x 170 bases x 2= 1,997,997,420 bases/660,000,000 = **3.03 X Coverage**
Non paired end reads 43% 4,225,283 reads x 298 bases = 1,259,134,334 bases/660,000,000 = **1.91 X Coverage**

The first genome assembly for *C. eugenioides* using the 454 data described above and Newbler v.3.0 was completed in collaboration with Roche in 2014, and was presented by Marco Cristancho from CENICAFE at our 8th ICGN Coffee Genomics Workshop and at the Roche Workshop during the PAG meeting in San Diego in January, 2015. Below is a summary table comparing the initial raw assembly for *C. eugenioides* with the initial raw assembly for *C. canephora* (statistics from Table S2 of manuscript Denoeud *et al.* 2014, and from data presented by Genoscope at PAG 2013):

Initial Raw Assembly Summary	***C. eugenioides***	***C. canephora***
	Heterozygous	Homozygous Double haploid
No. of contigs (>100 bp)	364,530	211,157
No. of contigs (>500 bp) raw assembly	146,520	96,182
No. of scaffolds	30,263	13,345
Average scaffold size	**15,897 bp**	**42,606 bp**
Genome size assembled	508 Mb	569 Mb
Estimated genome size	630-660 Mb	710 Mb
% genome assembled	77-80.6%	80.14%
N50	**209,891 bp (502 scaffolds)**	**1,260,636 bp (108 scaffolds)**
Largest scafold	4.0 Mb	9.0 Mb
Assembler Newbler	v.3	v.2.3
Q40	97.85%	
Inferred read error	1.41%	
Percent repeats	7%	

In addition, we have constructed and sequenced a *C. eugenioides* library using PACBio P6/C4 chemistry (read N50 16 Kb) to 59X genome coverage, and generated also Illumina Moleculo (synthetic 10 Kb fragments) to help us connect and reduce the overall number of contigs and scaffolds in the *C. eugenioides* assembly, as well as to increase the overall percent of genome assembled. Curation of the *C. eugenioides* genome assembly, anchoring of the contigs to chromosomes, and annotation are on going. The reference genomes of the diploid species *C. canephora* and *C. eugenioides* (parental diploid ancestors of the allotetraploid species *Coffea arabica)* will serve as frames for assembly of *C. arabica*, the major cultivated coffee species worldwide.

Update *Coffea arabica* sequencing

With funding from the Inter American Development Bank (IDB/FONTAGRO) and the US National Science Foundation (NSF), Cornell University and CENICAFE have sequenced also the allotetraploid *Coffea arabica* genome generating a high quality deep coverage PACBio only assembly of *C. arabica* (69-73X genome coverage); N50 read length 12-15 Kb (Average 12 Kb; longest read 65 Kb). The allotetraploid assembly is been validated using the genome assemblies of its two diploid ancestral species. We have also generated Illumina Moleculo (synthetic 10 Kb fragments) data for *C. arabica* that has been used to validate the PACBio only assembly. Transcriptome assemblies and the recently published *Coffea arabica* high density molecular genetic map, developed by CENICAFE in collaboration with Cornell University (Moncada et al. 2016 Tree Genetics and Genomes 12: 5 DOI 10.1007/s11295-015-0927-1), as a well as a physical map developed by CENICAFE in collaboration with Rod Wing at University of Arizona, are being used to validate genome assemblies and anchor contigs to chromosomes. This high quality reference genome is being annotated and should dramatically improve our current understanding of coffee genetics and genomics providing direct applications to breeders for climate change adaptation. Integration of genomic studies of equivalent quality among the allotetraploid *C. arabica* and it diploid progenitors will maximize scientific insights into the complex biology of polyploids.

Updates on the status of the *C. arabica* sequencing projects funded by private companies, Nestlé and IllyCaffé/Lavazza, were presented in our 8th ICGN Coffee Genomics Workshop at PAG in 2015 (see report in our ICGN www site) and for a more recent update see abstracts that will be presented at the upcoming ASIC meeting in Yunnan, China in 2016 at http://www.asic2016china.org/.

Perspectives High quality coffee genome and transcriptome assemblies for *C. arabica* and its diploid ancestral species will provide an invaluable resource for future coffee improvement strategies. They will speed up the identification of genes involved in important agricultural traits, and help build crucial information on the structural variation between *Coffea* wild species and cultivated accessions. They will be a precious template for positional cloning of agriculturally important genes, for re-sequencing and deep diversity analysis in the *Coffea* gene pool, and an important support to develop genomic

tools for whole-genome expression analysis. They will also provide a solid foundation to study the evolution of euasterids and accompanying genomic changes.

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 of Oral Presentations
9th ICGN Coffee Genomics Workshop at PAG
co-organizers

Marcela Yepes, Cornell University (my11@cornell.edu)
Philippe Lashermes, L'Institut de Recherche pour le Développement
(IRD), France (philippe.lashermes@ ird.fr)
(Program and abstracts and pdfs of some of the presentation are also posted at:
https://pag.confex.com/pag/xxiv/webprogram/Session3070.html)

Building High Quality Reference Genome Assemblies using PACBio Long Reads for the allotetraploid *Coffea arabica* and its maternal diploid ancestor *Coffea eugenioides*.

Marcela Yepes[1], Alvaro Gaitán[2], **Marco Aurelio Cristancho**[3], Carlos Ernesto Maldonado[2], Luis Fernando Rivera[3], Juan Carlos Correa[3], Carmenza Góngora[2], Ricardo Acuña[2], Andres Mauricio Villegas[2], Huver Posada[4], Aleksey Zimin[5], Keithanne Mockaitis[6], James Yorke[5], and Herb Aldwinckle[1]

[1]*Cornell University, School of Integrated Plant Sciences, Plant Pathology and Plant Microbe Biology Section, Geneva, New York, USA*
[2]*Colombian National Coffee Research Center, CENICAFE, Chinchiná, Caldas, Colombia*
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[5]*University of Maryland, College Park, Maryland, USA*
[6]*Indiana University, Bloomington-Indianapolis, Indiana, USA*

Allopolyploids originate from hybridization between divergent genomes associated with chromosome set doubling. As a consequence, the genomes may undergo a wide range of structural, epigenetic, and functional changes. The world's most widely cultivated coffee species, representing 70% of the coffee market, is the allotetraploid, *Coffea arabica* (2n=4x=44; genome size 1.3 Gb). *C. arabica* evolved through the interspecific hybridization of the ancestors of two diploid *Coffea* species: *Coffea eugenioides* (2n=22, maternal donor, genome size 0.66 Gb) and *C. canephora* (2n=22, paternal donor, genome size 0.73 Gb). Sequencing and assembly of the *C. canephora* genome was published recently (Denoed *et al.* 2014. Science 345: 1181-1184; genome assembly can be accessed at: http://coffee-genome.org). We report here progress to produce a high quality

reference assembly for *C. eugenioides* and *C. arabica* using Pacific BioSciences (PACBio) long reads to enable coffee genetics and genomics of coffee and speed up adaptation of the crop to climate change. Climate change is probably the most severe threat currently facing the coffee industry on the global scale. In recent years, extreme weather events in Central America, Colombia, and Brazil have led to coffee production losses of more than US $2 bn. Of major concern is the very narrow genetic base of cultivated coffee varieties, and therefore the urgent need to develop advanced genomic tools to speed up characterization of *Coffea* diversity in its Center of Origin, Ethiopia, which accounts for 98% of the genetic pool, to help broaden the genetic base of cultivated *C. arabica* and speed up adaptation of the crop to climate change.

This project is co-funded by the US National Science Foundation, the InterAmerican Development Bank, and the Federación Nacional de Cafeteros de Colombia through its National Coffee Research Center, CENICAFE.

This abstract had an extended time and was presented by co-authors Marcela Yepes and Marco Cristancho.

High-throughput targeted genotyping of *Coffea arabica* and *Coffea canephora* using next generation sequencing.

Resende Jr. MFR[1], Caixeta ET[2,3], Alkimin ER[2], Sousa TV[2], Resende MDV[2,3], Chamala S[1], Neves LG[1]

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[2] *Federal University of Vicosa, Brazil*
[3] *Empresa Brasileira de Pesquisa Agropecuária (Embrapa), Brazil*

Coffee is an important tropical crop in the world. Among the different species, *C. canephora* and *C. arabica* are the most widely planted. One of the challenges for the breeding and genomic characterization of Coffee, specially *C. arabica,* is the low genetic diversity and complex polyploid nature of its genome. Here, we present the development of a multi-species, genome-wide, high-throughput genotyping platform for Coffee. The strategy is based on the targeted genome capture of 40,000 regions in the Coffee genome followed by next-generation sequencing. These regions were bioinformatically identified to avoid repetitive elements and screen a large number of annotated genes. To capture these regions, we designed probes using a combination of genomic resources, including the *C. canephora* reference genome and assembled unigenes specific to each of the two species. We evaluated the method on 72 samples from *C. canephora* and 72 from *C. arabica*. This population resulted in the discovery of 162,026 SNPs in 27,651 polymorphic probes, with a median of 5 SNPs per probe. From this total, 33,239 SNPs were specific to *C. arabica* and 87,271 SNPs were specific to *C. canephora.* The assay resulted in 3% median missing data, out of which 967 and 40 SNPs were missing in all the individuals of *C. arabica* and *C. canephora*, respectively, indicating the discovery of inter-specific presence and absence (PAV) variants. This assay represents a new tool for the Coffee community that can help future genome assemblies, accelerate breeding, unravel the genetic basis of traits of interest and manage genetic diversity in the species.

Mixed model to multiple harvest location trial applied to genomic prediction in *Coffea canephora*

Luis Felipe V. Ferrão[1], Romario G. Ferrão[2], María A. G. Ferrão[3], Aymbire Fonseca[3], Antonio Augusto Franco Garcia[1]

[1]*University of São Paulo (ESALQ/USP), PIRACICABA, Brazil*
[2] *Instituto Capixaba de Pesquisa,Assistencia Tecnica e Extensio Rural*
[3]*Instituto Capixaba de Pesquisa e Assistencia Tecnica e Extensio Rural / Embrapa Cafe*

Genomic Selection (GS) has been studied in several crops and has shown potential to increase the rate of genetic gain and reduce the length of the breeding cycle. Despite the relevance, there is a modest number of reports applied to the genus *Coffea*. Nevertheless, the effective implementation depends on the ability to consider genomic models that represent with adequate reliability the breeding scenario in which the species are inserted. Coffee experimentation, in general, is represented for evaluations in multiple locations and harvests (MET), in order to understand the interaction magnitude and predicting the performance of untested genotypes. Therefore, the main objective of this study was to investigate GS models that accommodate MET modeling. For this, an expansion of the traditional GBLUP was proposed in order to accommodate the interactions in the GS model. Different scenarios that mimic coffee breeding were proposed to assess the predictive ability. In terms of goodness of fit, this approach showed the lowest AIC and BIC values and, consequently, the best goodness of fit. The predictive capacity was measured by cross-validation and, in contrast with the GBLUP, the incorporation of MET modeling showed higher predictive accuracy (on average 1017% higher) and lower prediction errors. All the genomic analyses were performed using the Genotyping by Sequencing (GBS) approach, which showed a good potential to be used in coffee breeding programs. Thus, in conclusion, the results achieved may be used as a basis for additional studies into the Genus *Coffea* and expanded for other perennial crops that have a similar experimentation design.

(PDF available at https://pag.confex.com/pag/xxiv/webprogram/Session3070.html)

Threats of Climate Change on Arabica Coffee (*Coffea arabica* L.) in its Center of Origin Ethiopia

Girma Adugna[1], Gezahegn Berecha Yadessa[1], and Fikre Lemessa[1]

[1]Associate Professors, Department of Horticulture and Plant Sciences, College of Agriculture and Veterinary Medicine, Jimma University, PO Box 307 Jimma Ethiopia

Arabica coffee (*Coffea arabica* L.) contributes 70% of the world's coffee bean production and consumption. Because *C. arabica* evolved in the moist evergreen afromontane rain forests of Ethiopia, it is a remarkably climate-sensitive species. Over the past decade, documented evidence indicates that climate variables, mainly scarce rainfall, increased drought, and increasing temperatures cause major detrimental effects

to Arabica coffee production/yield and quality, and ultimately threaten existence of the crop in its center of origin, Ethiopia, the major reservoir of genetic diversity for the species. The direct impact of climate change includes stressed growth of the coffee tree, limited flowering and berry development leading to poor yield and unacceptable quality. Emergence and/or resurgence of severe outbreaks of diseases (leaf rust, coffee berry disease, wilt, and leaf blight), insects (coffee berry borer, antestia bug, leaf miners, scales and aphids) and nematodes are inevitable. The current global areas of coffee production are projected to shrink by 9.5, 17, and 33% in 2020, 2050 and 2070, respectively. Moreover, the future distribution of indigenous Arabica coffee in Ethiopia is forecast to decline by about 65% in a number of bioclimatically suitable locations, and in the worst scenarios 100% reduction by 2080. Climate change is inevitably threatening the world coffee industry and unique Arabica coffee genetic resources in Ethiopia, unless adaptation and mitigation strategies are collectively implemented soon. Development of advanced genomic tools to accelerate diversity characterization and their enhanced utilization for genetic improvement to generate drought/stress-tolerant, disease- and insect- resistant coffee varieties are major priorities.

(PDF available at https://pag.confex.com/pag/xxiv/webprogram/Session3070.html)

Molecular markers reveal high variability among populations of *Coffea arabica* in its native range of the Afromontane forests of Ethiopia

Kassahun Tesfaye[1], L. A. H. Muller[2], Kim Govers[3], Endashaw Bekele[1], and Thomas Borch[3]

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Coffea arabica L. is the only tetraploid species (2x = 44) of the genus *Coffea*, and is the most widely cultivated and traded. The southwestern forests of Ethiopia are its native habitat, where domestication began. Forest (wild), semi-forest (semi-wild), garden, and plantation coffee are the major conventional production systems in Ethiopia, whereby subsequent selection of coffee from wild populations has led to the formation of numerous landraces (farmer's varieties) and cultivars. Exploring the genetic diversity of Arabica coffee populations in its natural range is an important parameter for conservation and sustainable use. A total of 10 ISSR and 14 different AFLP primer combinations were used to analyze 9 wild populations and several cultivated genotypes; these markers selectively amplified 84 and 565 fragments, respectively. The NJ and UPGMA clustering analysis of 125 *C. arabica* individuals using 84 polymorphic ISSR markers clearly separated wild genotypes from landrace/cultivars and underscored the existence of wild coffee distinct from the semi-domesticated genotypes. Diversity measure using Shannon's index showed various levels of variability within wild populations in Ethiopia. Those in Yayu (0.47), Bonga (0.46), and Berhane Kontir (0.41) showed the highest diversity. Furthermore, AFLP markers detected moderate to high polymorphism (68 -

92%) with overall values of 73.5% (415 loci) among 130 *C. arabica* accessions. Overall our molecular markers clearly revealed the presence of vast genetic diversity within wild and cultivated coffee landraces and this warrants the need for a multi-site *in situ* conservation approach. Development of advanced genomic tools for diversity characterization should accelerate future conservation efforts.

(PDF available at https://pag.confex.com/pag/xxiv/webprogram/Session3070.html)

Pictures of our ICGN 9th Coffee Genomics Workshop Speakers and Participants at XXIV PAG 2016

Left, Marcela Yepes and Stephanie Fuchs (Cornell University, USA), Keithanne Mockaitis (Indiana University, USA); Center, Kassahun Tesfaye (Addis Ababa University, Ethiopia), Girma Adugna (Jimma University, Ethiopia); Right, Herb Aldwinckle (Cornell University) and Aleksey Zimin (University of Maryland/ Johns Hopkins University, USA).

Left, Luis Felipe Ventorin Ferrão (Universidad of Sao Paulo (ESALQ/USP), Brazil), Right, Girma Adugna (Jimma University, Ethiopia)

Marcio Resende, RAPID Genomics LLC.

Back (from left to right) Kassahun Tesfaye (Addis Ababa University, Ethiopia), Marcela Yepes and Stephanie Fuchs (Cornell University, USA), Keithanne Mockaitis (Indiana University, USA), Marco Cristancho (Colombian Center for Bioinformatics and Computational Biology, BIOS, Colombia); Front (from left to right) Girma Adugna (Jimma University, Ethiopia), Herb Aldwinckle (Cornell University), and Aleksey Zimin (University of Maryland/ Johns Hopkins University, USA).

From left to right: Marcela Yepes, Herb Aldwinckle, and Stephanie Fuchs, Cornell University, with Chifumi Nagai, Hawaii Agriculture Research Center.

From left to right, Stephanie Fuchs and Marcela Yepes (Cornell University), Girma Adugna (Jimma University, Ethiopia), Tessahun Tesfaye (Addis Ababa University, Ethiopia), Herb Aldwinckle (Cornell University).

Marcela Yepes, Cornell University; Juan Fernando Medrano, University of California, Davis; Chifumi Nagai, Hawaii Agriculture Research Center

ICGN thanks Michael Schatz from Cold Spring Harbor Laboratory, for inviting us to his workshop at PAG on Resurgence of Reference Quality Genomes to present our abstract entitled "Using PacBio Long Reads to Generate a High Quality Reference for the Allotetraploid *Coffea arabica* and its Maternal Diploid Ancestor *Coffea eugenioides.*" Abstract of this presentation can be accessed at: https://pag.confex.com/pag/xxiv/webprogram/Session3180.html

Upcoming Meetings of interest to the ICGN community

- 14th Solanaceae Genomics Network SOL Meeting, Valencia, Spain, 2017, September 3-6, 2017, solcuc2017.org / Abstracts of 2016 13th Sol meeting are available at http://solgenomics2016.ucdavis.edu/
- 10th ICGN Coffee Genomics Workshop at XXIV Plant and Animal Genome (PAG) Meeting, San Diego, California, January 13-18, 2017, http://www.intlpag.org/
- 26th ASIC International Conference on Coffee Science, Yunnan, China, November 13-19, 2016 http://www.asic2016china.org/