

Minutes
Peanut Genome Consortium Meeting, Young Harris, GA
7/8/13

PARTICIPANTS

Victor Nwosu	Tom Stalker	George Birdsong
Peggy Ozias-Akins	Noelle Barkley	Darlene Cowart
Baozhu Guo	Guohao He	Tom Isleib
Corley Holbrook	Sean Tallury	Mark Kline
Mark Burow	Emory Murphy	Dan Swaggart
Richard F. Wilson	Nuveen Puppula	Jingping Wang
Charles Chen	Bill Branch	W. Pierce
Kim Moore	Barry Tillman	
Howard Valentine		

Ozias-Akins convened the meeting and welcomed those attending. The agenda was approved. Minutes from 6/17/13 were approved. These documents are posted on *peanutbioscience.com*.

AAGB-2013 Update: Stalker (Secretariat) reported the technical program is composed of 40 oral presentations and 72 posters. 186 (excluding special guests) have registered, representing the U.S. (23), Australia (2), India (5), Brazil (2), Niger/Mali (1), Israel (1) and China (152). Speakers received information on uploading presentations, and were asked to provide Wilson with copies of their ppt files for preparation of stakeholder reports. Speaker ppt will not be posted on the web or used in other ways without their expressed consent and the direction of the PGC. The U.S. delegation was reminded of the group picture after the opening ceremony with Chairman Luo. Guo gave details and information regarding various social events and research facility tours. Wilson described the purpose of Session VIII Breakout sessions, and accepted the gracious offer of volunteers to facilitate the discussion groups.

PROGRESS on GENOME SEQUENCING & ASSEMBLY. Group presented discussion on best ways to move forward on sequencing & assembly of the diploid and tetraploid genomes. BGI will explore a limited BAC approach. Other approaches will include MolecuLo™, PacBio™, LFR, and Spiril Genetics technologies.

GENOTYPING: Holbrook updated group on activities with 16 RIL populations. 8 populations are scheduled for seed increase in 2013, the remainder in 2014. Birdsong Inc has graciously stored all seed for genotyping in -18C freezers. A seed-inventory has been developed by Holbrook, and is posted on www.PeanutBioscience.com/. The first 8 populations are being phenotyped for CBR, LLS, TSWV, WM (Holbrook & Ozias-Akins); ELS (Islieb); pod & seed characteristics (Hovav); Sclerotinia (Tallury). The second 8 populations will be phenotyped in 2014. Discussions will be held with Sanders at APRES on screening for flavor traits. PAC resistance will be screened in 2014 on the T-population RILs developed by Guo. An X-ray machine may be available from USDA at Dawson for determining root architecture. Holbrook expressed concern that suitable plot combines are no longer commercially available, but will discuss issue with Graeme Wright in Australia. Noelle Barkley will serve as the nexus for permits & distribution of seed upon request, plus information on all available genotyping resources. This includes information from Varshney on ICRISAT lines and synthetic amphidiploids from Bertoli; MTAs from Waliyar; and weather data at each location. All phenotyping data per se will be sent to Cannon and Holbrook, who will establish and disseminate a standard protocol/format.

ULTRA-HIGH DENSITY DIPLOID MAPS. Colleagues at UC-Davis have received A- and B-genome specific sequence data from BGI for assembly. About 26 million SNPs from each genome were filtered to 2 million good homogeneous data. 40% of each diploid genome is positioned on a high density genetic map. Work continues to achieve 60%. A pipeline has been established for *A. duranensis* RILs from interspecific crosses provided by Bertoli, and the ICRISAT diversity panel.

GENE EXPRESSION: Ozias-Akins reported on the status of gene expression analyses of the Tifrunner transcriptome. Twenty-four libraries (triplicate libraries from 8 tissues) have been sequenced by Scheffler (2 x 100 bp reads) and are being assembled via CLCBio™ or Trinity™ software. Libraries are almost

complete, but there was limited sequencing on diploid transcriptomes from mixed tissues by Mi-Seq. Deeper sequencing will be conducted via Hi-Seq plus PacBio for annotation of diploid and tetraploid sequences. Froenicke and Ozias-Akins will coordinate their efforts. Burow has produced transcriptome reads from leaf and root tissues of 22 cultivated and wild accessions. Bertioli also has transcriptome data from synthetic amphidiploids. Colleagues in China (Xing Jun Wang) will share data on 60,000 unigenes from two Chinese libraries of widely grown cultivars. ICRISAT (Varshney) will contribute transcriptome data from diploids sequenced in India. All data sets or assemblies will be used to analyze diploid and tetraploid genomes. Andrew Farmer will help integrate data sets, to develop a gene expression atlas, and to develop a process for separating A and B-genomes. USDA-ARS (Cannon) agreed to establish a common ftp site and to receive all these data.

BIOINFORMATICS: Progress was reported on the development of **PeanutBase.org** for collecting published information on QTL, markers and maps to populate an informatics database (Peanut Breeders Toolbox). The Toolbox will be modeled after SoyBase and LIS. Cannon will convene a conference call on data set construction including: X.J. Wang, Varshney, Ozias-Akins, Burow, D. Bertioli, Scheffler, Froenicke, and Farmer.

EXPERIMENTAL SEQUENCING TECHNOLOGIES: Extremely good progress was reported with MolecuTM technology on diploid genomes. A-genome analysis at 4X coverage produced high quality long reads (mean, 3.7 kb, longest, 22 kb); and B-genome analysis at 6X coverage yielded reads with mean length of 4.1 kb (longest, 20 kb). These long reads can differentiate A- and B-genomes with very low error. However, the peanut genome is AT-rich which causes assembly bias and gaps. The gaps are reproducible; so very high coverage highly filtered Illumina mate-pair data could be used to scaffold between long-read contigs. It is possible to split the long-reads for assembly with short-read assemblers and then merge data onto existing scaffolds. MolecuTM was deemed the best protocol for Illumina mate-pairs. Illumina is developing a dedicated assembler for tetraploid assembly. Other companies with appropriate technology also will be consulted.

PUBLICATION: An ad hoc PGP Technical Committee (Jackson, Scheffler, Ozias-Akins, Froenicke, D. Bertioli, Cannon, Xin Liu, Xun Xu, Micheltmore, Varshney, Hovav, X. Zhang, Nwosu, Shapiro, Valentine, Wilson) convened on June 20 at AAGB-2013 to develop a plan on next-steps and to discuss publication of peanut A- and B-genome data. All agreed that it was appropriate to proceed with the paper as soon as possible. Micheltmore, Froenicke and Shapiro will lead the effort, with Froenicke serving as 'whip'. Froenicke presented a rough draft tentative outline for consideration of collaborating author assignments. Froenicke agreed to provide a revised outline and convene a teleconference among authors to establish timelines and format requirements. The group agreed on three additional actions to be completed within the next two months: 1) Provide Shapiro with a justification for development of a dedicated assembler for MolecuTM data (Jackson); 2) a full strength test of the BAC pool strategy (BGI); and 3) generating MolecuTM data from the tetraploid genome (Micheltmore/Froenicke).

OTHER BUSINESS:

- Wilson requested receipt of AAGB-2013 photos
- Valentine reported that David Hoisington will replace Tim Williams in USAID at UGA.
- Nwosu proposed future lab site-visits among PGP members to enhance coordination, cooperation.
- All agreed that AAGB-2014 should be held on a date between August and October 2014. A suitable venue in California was considered the most convenient for a majority of PGC members.
- Wilson polled the group on plans for meeting at PAG-2014 in San Diego

NEXT MEETING:

9 December 2013 (2:30 pm EST), prior to American Peanut Council Winter meeting in Washington DC.

ADJOURNED