

Minutes
Peanut Genome Consortium Meeting, Executive Committee
Raleigh, NC 7/9/12

PARTICIPANTS

Victor Nwosu	Zhanji Liu	Jim Elder	Steven Cannon
Lutz Froenicke	Lixian Qiao	Shyam Tallury	Brian Scheffler
Peggy Ozias-Akins	Rodney Coe	Sukhvindu Kandhola	Arvind Bharti
Baozhu Guo	James Hall	Hongyun Li	Andrew Farmer
Richard F. Wilson	Naveen Puppala	Sunum Joyloy	Jessica Wang
Richard Michelmore	Noel Chen	Nimitr Vorasoot	Mouhuan Wang
Corley Holbrook	Elizabeth Grabau	Rat Koolachart	Li Xin
Mark Burow	Tim Williams	Kim Moore	Yue Cai
Howard Valentine	Rebecca Bennett	William Pearce	
Tom Stalker	Kelly Chamberlin	Scott Jackson	

Scott Jackson convened the meeting. A quorum was established. The agenda was approved. Minutes from 3/29/12 were approved. Steven Cannon, Arvind Bharti and John Crow were welcomed as new members.

Discussion Items:

The US Peanut Industry White Paper

The subject document dated June 17, 2012 was prepared by George Birdsong, Darlene Coward, Victor Nwosu, Howard Valentine and Rich Wilson. The paper presented a non-technical description of the IPGI, significant research accomplishments 2008-2012, the Peanut Genome Project, Milestones and targeted budget 2012-2016, and benefits to be gained from DNA-marker assisted selection. The paper was presented to and endorsed by The Peanut Foundation, American Peanut Council, and National Peanut Board. Plans are underway to secure remaining funds needed for the \$6 million project. The paper targeted US interests, but represents an example that international collaborators may find useful in attracting funding within their own countries. **Wilson was asked to draft examples of the briefing papers that focus on international interests. Jackson also requested a one-page summary of the US paper for distribution to potential investors at the University of Georgia in two weeks.**

PGP Updates

Component 1: Zhe (Jessica) Wang introduced the BGI team. WGS paired-end libraries of Tifrunner have been completed and large insert (mate pair) library construction will begin within the week. WGS of GT-C20, SunOleic, NC 94022 is finished and proceeding toward bioinformatic analysis. Sequencing of 176 samples of the T and S RIL populations is finished. Sequencing of the remaining 24 samples will be completed in mid-August. The 2kb-10kb library construction of Tifrunner is finished; sequencing will be finished in mid-August. BGI has not received DNA from the diploid progenitors. **Ozias-Akins, D. Bertioli, and Scott Jackson will provide the diploid DNA soon, ensuring the same species as used to make amphidiploids for genome mapping by Michelmore. It would be good to ensure that different genotypes are sequenced from those being sequenced by Michelmore.** Bertioli reported via email that diploid DNA extractions should be completed in Brazil in the next few weeks. Wang reported BGI will initiate bioinformatic pipelines, BAC clones for Tifrunner. Seed has been received by BGI. **Ozias Akins will send BGI a germination protocol.** Xin Liu reported having sufficient DNA for all short insert libraries, but will wait for QC report to decide about longer insert libraries. Steven Cannon asked if BGI QC steps would be able to break scaffolds that overlap different linkage groups. Xin Liu responded in the affirmative. Cannon also cautioned that it would be prudent to spend time to manually fix problem areas to ameliorate assembly difficulties that may be encountered; and not to expect a perfect sequence alignment in the beginning. Michelmore concurred. Liz Grabau offered Illumina assemblies from the characterization of transgenic versions of the cv. Perry; which was welcomed by all.

Component 2: Michelmore and Froenicke reported progress of the B genome map, and that libraries have been made for the A genome. Sequencing by BGI-Davis has been slowed by logistical delays but the facility in Sacramento is now operational. 170-500 bp inserts are currently being sequenced. Mate pair library construction is in progress; however, large mate-pair libraries are more challenging than paired-end libraries. Scheffler inquired about WGS or double strand approach on germplasm collections. Michelmore reported a library for the ICRISAT collection, and 99 samples from the Chinese collection. However, he and Lutz will complete high-density maps of A & B genomes first in accord with available

funding. The US mini core collection has been pure lined by Charles Chen. Sequencing coverage is yet to be determined. An alternative GBS map approach has been successfully used with pigeon pea by Doug Cook. GBS is a less comprehensive approach, but less expensive than WGS and therefore suitable for studying large numbers of samples while still providing high resolution maps. **Froenicke will consult with Cook.** If GBS is appropriate, it will be applied to the germplasm collections and the segregating populations from ICRISAT. WGS of germplasm would then be restricted to a smaller number of accessions selected based on their GBS profiles. Holbrook has phenotypic data on the US minicore. Ozias-Akins and Isleib also have data from studies of three market types. Burow has RNA-seq data on tissues from 14 southwestern US peanut germplasms.

Component 3: Ozias-Akins reported on gene expression profiling of tissues from Tifrunner. The transcriptome from leaf, node, root, nodule, flower, gynophore tip, pod, pericarp, and seed tissues will be sampled at several stages of plant organ development to identify tissue specific expression patterns. High quality total RNA extracted from the designated tissues will be used to construct RNA-seq libraries which will be sequenced using an Illumina Hi-Seq platform. Data will be compiled in a gene atlas for validation of genes predicted from genome sequence. Work at Tifton GA has been delayed due to available funding, but a NIFA grant has been received relative to profiles for genes association with aflatoxin contamination, and Hovav has a BARD grant for studies of podwort gene expression in Israel. The Michelmore lab is testing several protocols for strand-specific, high complexity RNA-seq libraries from plant samples.. Due to the potential variation in the quality of RNA-seq data a standardized protocol for RNA-seq would be beneficial. **Jackson, Ozias-Akins, Scheffler agreed to discuss aspects of an acceptable RNA-Seq protocol.**

Component 4: This component evaluates new sequencing technologies. Michelmore and Froenicke are testing an experimental approach for physical genome mapping to order scaffolds. In addition, the Oxford Nanopore technology has been reported recently. This system may be capable of generating high resolution 40 kb to 100 kb reads. IF this technology performs as reported, it could obviate the need for extensive BAC libraries, which account for about 60% of the budget presented in the BGI proposal. Oxford Nanopore may launch commercial sales of this product in 2013.

Component 5: Holbrook presented a timeline for development of 16 structured RIL populations (referred to as CAP populations) is on schedule. Set-A populations grown at Tifton GA , Puerto Rico and Raleigh NC include: Tifrunner x Bailey high O/L, Tifrunner x C76-16, Tifrunner x NC3033, Florida07 x Bailey High O/L, Florida07 x SPT06-6, Florida07 x C76-16 and Florida07 x NC3033. These populations will be advanced to the F7 generation this summer. A second set of populations (Set-B) will be grown at Tifton GA, Marianna GA and Puerto Rico. These populations include: Tifrunner x SSD6, Tifrunner x Olin, Tifrunner x New Mexico Valencia-A, Tifrunner x Florunner, Florida07 x SSD6, Florida07 x Olin, Florida07 x New Mexico Valencia-A, and Florida07 x Florunner. These lines will in the F7 generation in 2014. This material constitutes the largest planting ever attempted at Tifton, which stirred concern for the time and labor that will be required at harvest. Evaluation of phenotypic differences in F7 lines has been delayed due to funding, but Valentine agreed to forward funds as soon as possible. **Holbrook is developing an electronic library for phenotyping methods from international collaborators.**

In response to a request from Holbrook and Valentine, Birdsong Inc. will provide long-term storage for seed from all germplasm materials generated or analyzed by the PGP. A plan for long-term seed distribution is still needed. .

Component 6: Steven Cannon reported on USDA funding for LIS. USDA base-funding plans could involve a clade-wide dbase. Andrew Farmer will assume PGP responsibilities of John Crow at NCGR. Cannon requested QTL data for inclusion in the peanut dbase (similar to SoyBase). The principal format will feature the navigation path: Trait-Germplasm-populations-markers-QTL-genetic maps-expression profiles-candidate genes-alleles-advanced markers. Guo reported publication of two reference maps with 900 markers over 20 linkage groups in 11 populations by ICRISAT. Varshney provided a reprint of that publication via subsequent email. Isobe also will soon publish a map with 4000 markers. **Nwosu renewed a call for a plan for disposition, curation and analysis of bioinformatic resources.** It was agreed that BGI will move data to NCGR. Nong Chen also suggested that BGI will construct (possibly with IBM) a high-throughput (Cloud-based) data center to facilitate large data set transfers. This resource could be quite useful for handling resequencing data sets. **Jackson, Cannon, N. Chen, and Farmer will develop**

procedure for timing of data transfers and release of data to the public. Farmer reported that LIS has installed a new feature (Trait-QTL-Phenotype); which facilitates data submission from breeders. Cannon reported that browser development will depend on analysis of scaffolds provided by BGI, and stated that one FTE with bioinformatic experience and biological knowledge of peanut would be required to develop and manage the peanut-dbase. **Barkley, Bharti, Froenicke, Cannon (Vilas Vilancar) will propose standard protocol for marker trait association for the browser (dbase).**

International Conference on Legume Genetics & Genomics:

Wilson, Jackson, Ozias-Akins, Froenicke, Stalker, Holbrook edited the tentative agenda for a PGP workshop on October 2, 2012 at ICLGG-VI in Hyderabad India. The program would convene with an opening address, progress reports on PGP progress, and a planning session to seek international consensus on phenotyping protocol for germplasm resources. A tour of ICRISAT facilities may be arranged separately with the help of Hari Upadhyaya and Vincent Vades.

The US delegates will include: Valentine, Nwosu, Wilson, Jackson, Ozias-Akins, Froenicke, Barkley, Guo, Bharti, D & S Bertioli, Cannon, Holbrook, Scheffler, Cook, and members from the BGI team to be determined. Two scientists at large have sent RSVP to attend. **Wilson will contact Varshney to organize workshop logistics.**

Advances in Arachis through Genomics & Biotechnology (AAGB-2013)

Zhang (HAAS) chairperson of AAGB-2013 has issued the first announcement of the subject conference on June 17-21, 2013 in Zhengzhou, PRC. Valentine, Stalker, Guo, Wilson assisted Zhang, and developed a tentative program for consideration. The announcement and relevant information will be posted on peanutbioscience.com. Guo will visit Zhang in China soon to discuss organizational plans.

Update on US-China MOST: Next meeting is scheduled in October 2012 between USDA and MOST.

Wilson will develop a briefing on US-China Cooperative Research to Improve Peanut. If acceptable, the document will be made available as a briefing document.

Other Business:

Ozias-Akins convened a half-day PGP symposium during the 2012 APRES meeting in Raleigh NC.

Varshney nominated Professor Swapan Datta, Deputy Director General-Crops Research, Indian Council Agricultural Research (ICAR) for Ex Officio membership in the PGC Executive Committee. Professor Datta is distinguished by several prestigious honors recognizing his expertise in plant biotechnology, molecular breeding and food safety. A quorum was established, and the PGC EC voted unanimously to accept Professor Datta as a new member. **Wilson or Valentine will send formal congratulations and invite Datta to the PGC workshop at ICLGG-VI in Hyderabad.**

Next Meetings:

- 1st International Conference on Genomics (sponsored by BGI), September 27-28, 2012, Philadelphia PA
- International Conference on Legume Genetics & Genomics-VI, October 2-7, 2012, Hyderabad, INDIA
- Plant & Animal Genome-XXI, January 2013, San Diego, CA
- PGC-Executive Committee, March 2013, Atlanta GA

Adjourned