

Minutes v3

Peanut Genome Consortium Meeting, Savannah GA, 14 November 2014

PARTICIPANTS

Scott Jackson	Steven Cannon	Corley Holbrook	Tom Stalker
Peggy Ozias-Akins	Brian Scheffler	Boshou Liao	Liu Xin
Richard F. Wilson	Baozhu Guo	Rajeev Varshney	David Hoisington
Lutz Froenicke	Howard Valentine	Spurthi Nayak	Deb Valentine
Soraya Bertoli	Victor Nwosu	Xingyou Zhang	Steve Brown
David Bertoli	Rich Michelmore	Mark Burow	

Jackson convened the meeting and welcomed those attending and tele conferees. Spurthi Nayak represented Varshney (who called in). Steven Brown was introduced as the incoming Executive Director, The Peanut Foundation, replacing Valentine on January 1, 2015. Lutz Froenicke was introduced as the new manager of the DNA Technologies and Expression Analysis Cores Genome Center, University of California, Davis. Froenicke also will supervise the new scientist on the peanut project (Charlotte Acharya cacharya@ucdavis.edu) in the Michelmore lab.

A quorum was established. An agenda was approved. Valentine was honored for service to the IPGI and PGC. Stalker noted three pending Executive committee vacancies (Shapiro, Waliyar, Valentine). Incumbents of vice-positions may be considered for Ex Officio status. Guillermo Seijo, Steven Brown and Ray Schnell were suggested for membership. Formal nominations are expected during the PGC meeting in Washington DC on December 9.

Discussion Items

Public Release

Cannon reported that prior to AAGB-2014, the *A. duranensis* and *A. ipaensis* genome data sets were opened to public access on PeanutBase.

BAC Sequencing Strategy

Xin Liu reported BGI continues to improve their pipeline for BAC sequencing. Recent results of BAC pooling experiments showed higher quality compared to prior studies, and although assembly protocol has been optimized it is still difficult to assemble BACs from peanut DNA. The single BAC pool strategy was still preferred over multiple BAC pools. Froenicke confirmed that a 2 BAC pool was not promising compared to single-BAC sequencing. It was agreed that scaffolds needed longer reads for tetraploid peanut genome assembly. A decision on approval of a BAC x BAC sequencing strategy for Tifrunner using one pool of two BAC libraries (250 bp, 500 bp) with an average sequencing depth of 50X for each BAC was postponed again, pending evaluation of results from the generation of long-reads using Hi-Seq by Hudson-Alpha on tetraploid (DNA provided by Ozias Akins) and both diploid (DNA in preparation from D. Bertoli) genomes.

Xin Liu agreed to summarize BGI work completed & sent to Froenicke and others. BGI data sets include assembly and raw data from: 1) Tifrunner and both diploid genomes (diploid data does not include long mate pairs); and 2) the four tetraploid parents and 100 RIL from the S & T populations developed by Guo.

Other Approaches Evaluated by Froenicke

- BioNano technology. Beta-tests gave spotty results. 70% of data did not align with the reference genome. Error rates ranged from 20 to 30%. Will continue to evaluate.
- PacBio technology. New chemistry is being tested on 3 soybean genomes (by Froenicke). Error rates at about 7% on 15-20 kb reads. Throughput range is 500 to 600 Mbases with good quality DNA; but new chemistry protocol has not been optimized for peanut.
- Moleculo. Illumina has developed data sets (0.5X coverage) of A-T rich regions in the tetraploid peanut genome. Still under evaluation.
- NimbleGen. SeqCap EZ Library technology will be evaluated for capture of the whole peanut exome in a single extract. Exome capture should enhance discovery of coding variants. No exome data has been generated for peanut. Michelmore suggested a mapping experiment based on in silico analysis with exome capture probes. Xin Liu agreed to send Froenicke BGI resequencing data from the S & T population parents & RILs to help determine if exome capture is cost effective.

A & B-Genome Ancestral Accessions:

Bertioli reported two observations of keen interest from analysis of the diploid genomes.

- Each diploid genome evolved independently based on intrinsic structural features. The *A. ipaensis* (B-genome) contains more gene mutations, local gene duplications and transposons than the *A. duranensis* (A-genome) which is distinguished by more inversions and reciprocal translocations.
- The *A. ipaensis* genome appears to be the first example of a sequence of an exact ancestral accession of a cultivate crop species. The *A. duranensis* accession is not an exact ancestral genome, but Seijo is collecting new accessions and 60 accessions exist in germplasm collections. Michelmore proposed use of exome capture to evaluate haplotypes among *A. duranensis* accessions. The cost estimate for all 60 accessions was ca. \$20K. It was agreed that exome capture could be a useful means to assess variation across entire A-genomes of the diploid accessions.

ACTION ITEMS

JACKSON will appoint a committee led by **STALKER** to develop a list of RIL resources which have both genotyping & phenotyping data. **CANNON** will post this information on PeanutBase. These resources will be used to evaluate and compare efficacy of exome capture & GBS technology.

D. BERTIOLI will assume the role of editor for the journal publication of the diploid genome sequences. The outline developed by Froenicke will be followed. Much of the writing assignments have been completed. Authors of outstanding components of the paper to complete & submit sections to Bertioli in 2-weeks. Target date for first draft is January 1, 2015.

MICHELMORE, FRONICKE, D. BERTIOLI, STALKER, SEIJO will evaluate the efficacy of exome capture for discovery of the exact ancestral accession of the A-genome among *A. duranensis* resources.

JACKSON agreed to chair a site selection committee consisting of IPGI officers and International Liaisons for the next AAGB meeting. Committee members are: Michelmore, Ozias-Akins, Varshney, Guo, D. Bertioli, F. Waliyar, Graeme Wright, Sachiko Isobe, Ran Hovav. Invitations to host the meeting were received from: Varshney (Hyderabad), Ruey-Shyang Chen (Taipei), and O'Connor (Brisbane). Hoisington also suggested a joint meeting in Zambia. Subsequently, the site selection committee, as directed by the IPGI, formally accepted the proposal from Australia to host AAGB-2015 in Brisbane in November 2015.

WILSON confirmed the deadline for submission of 2015 research proposals to TPF was extended until November 20, 2014. Only 3 proposals have been submitted to date. All were encouraged to consider this opportunity.

NEXT MEETINGS:

- No formal PGC meeting will be held during the APC Winter conference in Washington, DC (December 8-9, 2014). Accomplishment reports on TPF funded grants for 2014 will be presented on Dec. 9. Holbrook and Isleib will present PGC accomplishments to stakeholders. Wilson will report peer review panel results for TPG proposals for 2015 to the Foundation Board.
- No formal PGC meeting will be held during PAG XXIII in San Diego, CA (January 10-14, 2015). Jackson will organize informal discussions with PGC members in attendance. No teleconference option is being considered at this time.
- Varshney will organize the 5th International Conference on Next Generation Genomics and Integrated Breeding for Crop Improvement in Hyderabad, India (February 18-20, 2015)
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ADJOURNED