Minutes v2

Peanut Genome Initiative (PGI) at Charleston, SC, 13 July 2015

PARTICIPANTS

George Birdsong	Baozhu Guo	Kim Moore	Dan Ward
Steve Brown	Guohao He	Linda Moore	Ruoyu Wen
Mark Burow	Keith Hendrix	Joe Morrissey	Demarquine Wilson
Kelly Chamberlin	David Hoisington	Victor Nwosu	Richard F. Wilson
Charles Chen	Corley Holbrook	Dan O'Connor	Graeme Wright
Josh Clevenger	Ran Hovav	Peggy Ozias-Akins	David Bertioli
Darlene Cowart	Scott Jackson	Bob Parker	Soraya Bertioli
Jamison Cruce	David Jordan	William Pearce	Brian Scheffler
Albert Culbreath	Mark Kline	Ze Peng	Steven Cannon
Phat Dang	David Langston	Tom Stalker	Lutz Froenicke
Jack Davis	Chris Liebold	Shyam Tallury	Rich Michelmore
Anne DeLorenzo	Greg MacDonald	Yu-Chen Tseng	Rajeev Varshney+
Jim Elder	Dave MacKill	Howard Valentine	Haile Desmae+
Stanley Fletcher	James Maku	Jianping Wang	

Jackson convened the meeting and welcomed tele-conferees. A quorum was established. Agenda and Minutes-v3 (from 20 May 2015) were approved with amendments.

PGC Membership

Wilson requested outstanding ballots for the 2015 membership election; receiving none officially closed the voting. All candidates received enough votes for election. New members are: Ray Schnell-MARS, Xin Liu-BGI, Haile Desmae-ICRISAT, WCA). New Ex Officio members are: Howard Shapiro, Xun Xu, Steve Brown, Jeff Ehlers, and T. Radhakrishnan. Wilson will notify the winners. In accordance with these election results, Section 2.02(b1) PGC Polices & Procedures (July 2015) was amended to read 'The EC will consist of twenty-six (26) members plus 10 Ex Officio members as indicated in the table below."

Update on USDA Peanut Germplasm Collection

Gary Pedersen reported that the USDA-ARS curator (vice-Barkley) position at Griffin GA will be filled. Three candidates will be interviewed by the end of August 2015. In addition, considerable discussion was given to the status of about 300+ lines received from ICRISAT. Karen Williams reported that at least two-thirds of the material still is under quarantine at Griffin. The material should be processed for inclusion in the USDA collection when 1) permit authority is transferred to the next curator with backup authority, and 2) when USDA completes repairs to ensure improved website security. Holbrook offered to field test lines that clear quarantine to expedite evaluation and increase seed supply. Greg MacDonald reported that other accession increases (about 1000 lines per year) will continue at Citra FL.

Update on Diploid Sequence Publication

D. Bertioli reported the final draft of the paper entitled, 'The genomes of the ancestral species of peanut-a remarkable case of living archaeology', has been sent to authors for endorsement. Page limitations by the journal prevented inclusion of some data, which will be saved for subsequent publications. **Lutz Froenicke agreed to provide raw data from diploid RIL sequencing and haplotype data with RIL assignments (as extra information that should not delay submission of the paper).** The goal is to submit the manuscript to NATURE GENETICS within two weeks. All authors should realize that immediate action is imperative because an EMBARGO is in effect on other papers that utilize peanut genomic data developed by the PGP. This is causing unintended delays in documentation of annual professional performance of colleagues. To expedite this matter, **Jackson, D. Bertioli, Scheffler and Cannon will ensure that necessary reference materials (sequence, mapping, GBS, Moleculo data; paired end libraries from BGI; etc) required for review of the manuscript will be submitted to GenBank or posted on ftp sites).**

A resolution passed unanimously that commends D. Bertioli for coordinating the development of the manuscript, and extends the option of first authorship of the paper to D. Bertioli.

Plans for Tetraploid Genome Assembly

***Progress on Dovetail Genomics project*:** The Peanut Foundation entered an agreement with Dovetail Genomes to provide a 10X better assembly of the *A. ipaensis* genome. Pending satisfactory results, the *A. duranensis* genome would be assembled. Froenicke reported that very high quality DNA was required by the cHiCago protocol. However, Dovetail has not yet demonstrated acceptable DNA extraction from lettuce, which should be easier than DNA extraction from peanut. Dovetail Genomics must demonstrate ability to prepare peanut DNA with sufficient quality to move forward or the agreement will terminate.

***Progress on Hudson-Alpha project*:** No new report was received from Hudson Alpha since the 20 May 2015 meeting in Huntsville AL. However, Ozias-Akins indicated that additional sequencing was needed on 10 to 20kb insert pairs. DNA extraction would be outsourced to Clemson University Genomics Institute (CUGI) or University of Arizona. Data will be sent to Jeremy Schmutz.

Scheffler raised discussion concerning who and how the anticipated tetraploid data sets would be assembled. Hudson Alpha will use programs from ALLPATHS-LG (for kmer assembly) and MERACULOUS (a whole genome assembler developed by JGI that uses Illumina sequence to assemble large-sized genomes on commodity clusters). Froenicke reported that ANYTAG assembler crashes frequently. Michelmore and Cannon will determine feasibility, utility & cost of other short-read DNA assemblers such as ARACHNE: All information on assemblers will be coordinated with Jeremy Schmutz.

Scheffler reported that USDA ARS would expand capabilities in high performance computing in conjunction with the federal BIGDATA Initiative. Cannon and Scheffler will evaluate CPU statistics and requirements. Jackson will follow up with Jeremy Schmutz and Jerry Jenkins (Alpha Hudson).

ICRISAT SNP-chip Genotyping Resource

Ozias-Akins reported that a 60K ICRISAT SNP chip service should soon be available from Affymetrix for beta-tests & validation. After the first 5000 samples, the cost may be $55/sample. Qzias-Akins suggested that the 60K chip might be used to genotype RIL populations. Higher definition analyses such as KASP then could be used to discover QTL, trait markers and eventually candidate genes in selected lines.

2014-2015 Research Accomplishment Report to Stakeholders:

George Birdsong, Darlene Cowart, Dan Ward, Steve Brown have edited the draft report prepared by Valentine and Wilson. The following is reprinted from the Executive Summary of the final draft:

How Key Research Accomplishments in 2014-2015 Tie Together & Help Define the Future Direction of Peanut Breeding. The six Components of the Peanut Genome Project generate research findings that enable three avenues of investigation: 1) *Generating Detailed Maps* of the peanut genome, 2) development of *Tools for Marker Assisted Selection,* and 3) *Application of Markers and Maps in Breeding* programs. The following shows how the outstanding 2014/15 research accomplishments summarized in this Executive Summary and presented in more detail in the full report fit in the overall performance of the Peanut Genome Project.

Generating Detailed Genome Maps. Because cultivated peanut is a very young crop, the two wild parent genomes present in cultivated peanut are very similar to each other since there has not been enough evolutionary time to accumulate genetic differences that help distinguish the two genomes. Maps of the cultivated peanut genome are needed to show the location of all genes and to discover useful DNA markers for those genes. However, assembling a more detailed map of the cultivated peanut genome depends on ability to distinguish the pieces of DNA that came from each of the two wild parent genomes.

- About 70% of the DNA in each wild parent genome is very similar. A new method was used to sort a mixed pool of DNA pieces to their original genome with 98% accuracy. This approach in conjunction with specialized software that determine the order, length and orientation of fragments helps ensure accurate assembly of high definition maps of the genomes of the two wild parents and cultivated peanut (**See Component 1**).
- As parts of the genome map are assembled, the connected sequences may be visualized as a series of small 'Gene Islands'. A new technology called 'Moleculo' was used to bridge between the small islands, thus creating larger islands which finally will be joined into a continent, a complete cultivated peanut genome map (**See Component 4**).

Tools for Marker Assisted Selection. As more DNA markers are discovered in peanut, a better way is needed to screen hundreds of lines in a breeding population simultaneously with thousands of markers.

- A device called a 'chip' was created that holds 60,000 DNA fragments each in individual wells. DNA fragments from a breeding line that stick in each well can be traced to a point on the cultivated peanut genome map. Phenotyping shows positions on that map are important in achieving the breeding objectives. (**See Component 2**).
- For the first time in plant genomics history, our scientists demonstrated an accurate and innovative way to track the part of a gene sequence that helps locate the best markers for the gene. (**See Component 3**).

Application of Markers & Maps in Breeding. Marker Assisted Selection has been shown to reduce the time needed to add a new trait to a current cultivated variety. Good markers have been found for resistance to late leaf spot (LLS), early leaf spot (ELS), tomato spotted wilt virus (TSWV), root knot nematode (RKN), and high oleic acid. More useful markers are being developed through genome mapping for traits such as cylindrocladium black rot (CBR), white mold (WM), peanut rust and drought tolerance. 'Chip' technology facilitates new breeding strategies for stacking all these traits in improved varieties for each market type and geographic production area. Many breeders are beginning to use these markers in their breeding programs. Their work will create new varieties that help reduce the cost of production, enhance peanut quality and ensure an adequate/safe supply of peanut products. Continued work on markers and maps will help expand breeding objectives to address critical needs of producers, shellers, manufacturers and consumers as presented during APRES-2015 and as will be documented in the next Strategic Plan for Peanut Genome Research during 2016 to 2020.

- Markers identified the location of three different major genes each for resistance to TSWV, ELS, and LLS resistance in the cultivated peanut genome. In addition, it was found that genes for LLS resistance may be linked to peanut rust resistance (**See Component 5**).
- The training exercises and genomic resources in the 'Breeders Toolbox' in the website 'PeanutBase' were accessed by 5,797 users since July 2014 (**See Component 6**).

When accepted by the APC membership, the full final report will be posted on PeanutBioscience.com/.

Development of the IPGI Strategic Plan 2016-2020:
Wilson provided updated worksheets representing an abridged draft of the IPGI Strategic Plan (2016-2020). Holbrook and David Jordan volunteered to coordinate completion of priorities for the CROP IMPROVEMENT Section (which will be listed as the first section of the new plan). Darlene Cowart and Victor Nwosu will coordinate documentation of priorities for the PRODUCT QUALITY & SAFETY section of the plan. This input will be compiled for discussion of all IPGI research priorities during AAGB-2015 in Brisbane, Australia.

Update on AAGB-2015 (November 5-7, 2015):
O'Connor reported AAGB-2015 will be held at the Rydges Hotel, Brisbane, Queensland, Australia. The 2nd announcement posted on the Peanut Bioscience and Peanut Foundation websites contains links for registration and hotel reservations. Deadlines for Abstract submission, reduced hotel rate and late registration fees also are posted with an outline of the Technical Program & Social events.

Next Meeting: AAGB-2015 at Brisbane, Australia on November 5-7, 2015.

ADJOURNED