

Report
Peanut Genome Consortium
Executive Committee, 3/29/12

PARTICIPANTS

Victor Nwosu	Richard F. Wilson	Pat Donahue	Tom Isleib
Lutz Froenicke	Richard Michelmore	Howard Valentine	Darlene Cowart
Peggy Ozias-Akins	Corley Holbrook	Tom Stalker	Manish Pandey
Baozhu Guo	Mark Burow	Noelle Barkley	Jiansin Ma

Ozias-Akins convened the meeting and teleconference. A quorum was established. The agenda was approved. Minutes from 1/16/12 were approved.

Discussion Items:

The BGI Proposal A final copy of the proposal was received by Wilson on 3/29/12. Mutual agreement was reached on all changes, suggestions and questions noted in the revision sent to Xun Xu on 3/19/12. The PGC EC accepted the proposal. The project will be conducted in two Phases as indicated below:

Phase	Activity	Delivery	Estimated Timeline
Phase 1 Whole genome sequencing and assembly	WGS sequencing (60 X depth sequencing for Tifrunner, 100X sequencing depth for <i>A. duranensis</i> and <i>A. ipaensis</i> ; 10X sequencing depth for SunOleic 97R, NC94022 and GT-C20;); RIL re-sequencing and genetic map construction	Genome assembly report I	2 months
	Whole Genome assembly		2 months
Phase 2 Chromosome-level assembly	BAC sequencing (6X genome coverage BACs for Tifrunner	Genome assembly report II	8 months
	BAC assembly		2 months
	Genome annotation	Final project report	1 month
	Comparative analysis		1 month
Total			16 months

Baozhu Guo indicated that DNA samples are ready for shipping to BGI. Xun indicated that BGI project managers Wenbin Chen (chenwenbin@genomics.cn) and Xin Liu (liuxin@genomics.cn) will follow up with logistics of sample delivery and related transactions.

Memorandum of Agreement (MOA) between the Peanut Foundation and Beijing Genomics Institute

A final copy of the MOA was received by Wilson on 3/29/12. Mutual agreement was reached on all changes, suggestions and questions noted in the revision sent to Xun on 3/19/12. The PGC EC accepted and presented the MOA to the Peanut Foundation Board for approval and ratification. Xun Xu signed on behalf of BGI. Patrick Archer, President of the American Peanut Council endorsed the MOA on behalf and with the approval of the Peanut Foundation Board. **Valentine will deliver the fully endorsed MOA to Xun Xu without delay.** The terms of the MOA provide the following payment schedule: 30% prepayment to initiate the project; 20% payment shall be paid within 30 days after the sequencing is finished; 20% payment shall be paid within 30 days after the assembly is finished; 30% payment (the balance) shall be paid after evaluation and the genome data and analysis is uploaded to a bioinformatic resource for public release. **Payments from the Foundation shall be made to BGI at One Broadway, 3rd Floor, Cambridge, MA 02142 USA.** Additional payments from Chinese PGC collaborators listed below will be applied toward the total amount of this grant. **BGI shall notify the Foundation when Chinese PGC collaborators make payment to the BGI account.** Chinese PGC collaborators at research institutions within the Peoples' Republic of China are listed below, but not limited to:

Henan Academy of Agricultural Sciences, Zhengzhou, China

Shandong Academy of Agricultural Sciences, Jinan, China

Chinese Academy of Agricultural Sciences Oil Crop Research Institute, Wuhan, China

Chinese PGP collaborators may make payments toward the total amount of grant TPF Project # 04-804-12 from the Foundation to BGI. Those payments will be made to the BGI at: BEIJING GENOMICS INSTITUTE AT SHENZHEN (Account NO.: 4000 0209 0920 0081 428; INDUSTRIAL AND COMMERCIAL BANK OF CHINA, SHENZHEN BRANCH; Bank address : NO.99 FINANCE RD. SHATOUJIAO TOWN, YANTIAN DIST., SHENZHEN; Swift code :ICBKCNBJSZN)

Nwosu and Baozhu Guo will travel to China within a few days to contact and help coordinate cooperative relations with Chinese PGC collaborators and other prospective members of the Peanut Genome Project.

PGP Updates

Component 2: Michelmore and Froenicke reported that algorithms and SNP mapping were progressing on schedule. Mate-pairs from the Tifrunner genome have been pooled and will be sent to the BGI facility at UC-Davis next week, along with DNA from 96 lines of the ICRISAT diversity panel and diploid parents and RILs from A-genome populations.

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. Assembly/validation of sequences is expected in 12 months.

Component 4: This component evaluates new sequencing technologies. Michelmore and Froenicke are testing an experimental approach for physical genome mapping that uses Oxford Nanopore technology. This system may be capable of generating high resolution 40 kb to 100 kb reads. The utility of nanopore technology would obviate the need for extensive BAC libraries, which account for about 60% of the budget presented in the BGI proposal. Oxford 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). 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 in 2012. 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. Phenotypic differences in F7 lines will be evaluated for: TSWV resistance, seed dormancy, flowering on the central axis, growth habit, pod and seed weight shelling percentage, pod density, seed oil/protein concentration, pod maturity at harvest. Genotypic associations will help annotate genetic maps of cultivated peanut.

Holbrook and Valentine will develop a plan for long-term storage and a protocol for distribution of seed from all germplasm materials generated or analyzed by the PGP. Current -20C freezers at Griffin GA do not have sufficient capacity for this material. Birdsong Peanuts Inc. will be asked for help.

Component 6: As authorized during the Executive Committee (EC) meeting on January 16, 2012, members of the Peanut Genome Consortium were asked to vote their approval or disapproval of the Steven Cannon, John Crow and Arvind Bharti for EC membership. Election protocol is documented in Section 2.02(6b) of the PGC Policies & Procedures v 5.7. Ballots have been distributed. **Fully executed ballots should be returned to Wilson by POST, FAX or PDF by April 15, 2012.**

Steven Cannon is USDA-ARS Research Geneticist, and an adjunct assistant professor in the Agronomy Department at Iowa State University. His research group focuses on bioinformatics for crop improvement, particularly in soybean and other crop legumes. Dr. Cannon develops software for analyzing and transferring information between crop and model species including: sequence, genetic, functional, and phenotype data. He investigates the evolution of disease resistance and nitrogen fixation, and the responses of genomes to polyploidy. Dr. Cannon

provides support for genome sequencing efforts in soybean and Medicago truncatula through the development of genetic markers, web-based tools for genomic data access and visualization.

John Crow received the Ph.D. in Mathematics from Oregon State University. He has served as a bioinformatics consultant at the University of Minnesota; Director, Center for Biomedical Research Informatics at the, University of Minnesota; and Associate Director at Center for Computational Genomics & Bioinformatics. As a bioinformatics consultant and senior software systems engineer at the University of Minnesota, his focus was the design and implementation of genomics research support information systems, and in the application of data mining methodologies to improve the research process. Currently, Dr. Crow is a Principal at Silicon Life Sciences, and a Principal Software Engineer at the National Center for Genome Resources.

Arvind K. Bharti received his PhD in Plant Molecular Biology from the University of Delhi, India and joined Rutgers University and University of Minnesota as a Research Associate. He received USDA's highest honor 'Group Honor Award for Excellence' given to the US Rice Genome Consortia by the Secretary of Agriculture. Currently as a Research Scientist at NCGR, Dr. Bharti is the NCGR PI of alfalfa genome-sequencing project funded by the Noble Foundation. He has applied his expertise in physical mapping and its integration with whole genome assembly to cacao, alfalfa and cotton genome projects. His skills in comparative genomics have contributed significantly to the Medicago truncatula and pigeonpea genome projects. He has been involved in the Medicago truncatula HapMap Project and also an active contributor to the LIS.

Pending results of the election, Michelmore and new members will form a taskforce to implement the PGP action plan for disposition, curation and analysis of bioinformatic resources

International Conference on Legume Genetics & Genomics:

Wilson presented a 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 with the help of Hari Upadhyaya and Vincent Vades. **Wilson, Noelle Barkley and Holbrook will develop a workshop Action Plan. Valentine will help organize the US delegation. Prospective international attendees are requested to send an RSVP to Wilson.**

Update on US-China MOST: Since February several items are relevant to the potential inclusion of the Peanut Genome Project in the US-MOST discussion: 1) Chairman Fuhe Luo had contact with Minister Wan Gang. An invitation was arranged for Dr. Xingyou Zhang (Henan Academy Agricultural Sciences); 2) Dr. Zhang met with Wang Yawu (Ministry of Science and Technology) who is involved in the discussion with USDA, and they had dinner with Vice Minister Zhang Laiwu who will lead the Chinese delegation; and 3) Wang Yawu now understands the importance of peanut and peanut genome sequencing and expressed his support. On the US side, Caird Rexroad and Kristofer Dodge have communicated with Howard Valentine. They believe the PGP fits nicely with what the Secretary is working to accomplish with MOST through a new MOU. They were pleased to know that that MOST is in support of the project. The next meeting will be hosted by MOST. MOST will draft the agenda. It will be up to the Chinese to include the PGP as a discussion item. Wilson provided Dodge with a briefing on the PGC with the names/affiliations of the US and Chinese cooperators.

Other Business:

- **Scott Jackson will lead a team to discuss funding opportunities with the Georgia Research Alliance.**
- Ozias-Akins reported tentative plans for a half-day PGP symposium on PGP and related activities during the 2012 APRES meeting in Raleigh NC.
- **Nwosu and Zhang will discuss the possibility of delaying AAGB-6, the next International Peanut Genome conference in Zhengzhou China, until June, 2013.**

Next Meeting:

American Peanut Research & Education Society annual meeting, July 10-12, 2012 in Raleigh NC

Adjourned