The Peanut Genome Consortium
'Creating a Better Future through Global Food Security'

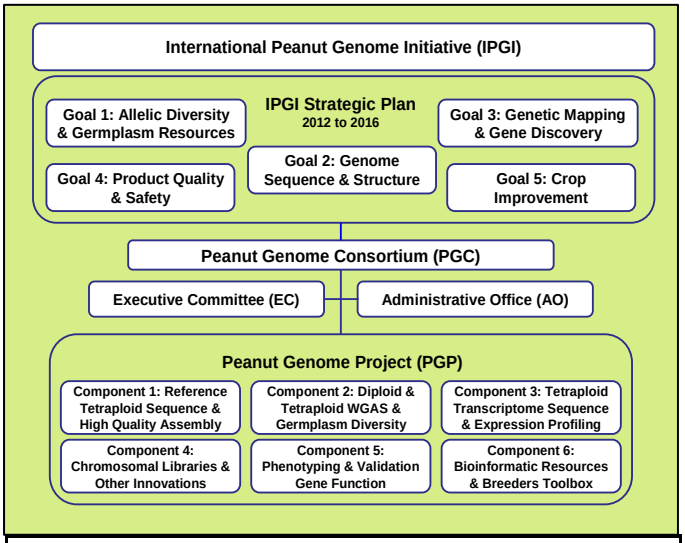
Background:
The Peanut Genome Consortium (PGC) is an extension of the International Peanut Genome Initiative (IPGI), and is embodied by a coalition of international scientists and stakeholders engaged in the Peanut Genome Project (PGP).

The IPGI was initiated by USDA-ARS-ONP in 2004 and currently has ca. 135 members at 79 institutions in 20 countries. The *International Strategic Plan of the Peanut Genome Initiative 2012-2016* documents IPGI research priorities. PGC governance is referenced in *Policies & Procedures*. See: http://www.peanutbioscience.com/.

The PGP is different from other genome projects in that it includes genome distinguishing gene expression studies, genotypic characterization of genetic diversity in U.S., Chinese & ICRISAT germplasm collections, a genome wide association study (GWAS) to identify DNA markers for targeted traits, a phenotyping component, high density consensus maps of the cultured variety & of wild peanut crosses, plus the generation of a reference sequence. The successfully achievement of PGP goals depends on research collaboration within and among each component.

Specific PGP goals include: 1) a high quality chromosome scale draft of a tetraploid (cultivated species) as the reference genome sequence, plus high density maps of both progenitor and synthetic amphidiploid genomes; 2) high throughput transcriptome characterization of the reference tetraploid cultivar; 3) characterization of gene space in amphidiploid and diploid (progenitor species) germplasm, 4) phenotypic association with mapped genetic markers, and 5) interactive bioinformatic resources for data curation and application in a breeder's toolbox to enable molecular breeding approaches for enhancing peanut yielding ability, optimizing resistance to diseases and insects, tolerance to environmental stresses, and improved quality traits. This technology will promote peanut crop competitiveness and enhance grower's profitability in an environmentally sustainable manner.

Issue: Whole genome sequence characterization of peanuts is needed to expedite elite variety selection & to help ensure global food security & safety.



PGC Executive Committee

Contributing Members

Howard Valentine	The Peanut Foundation (Administrator)
Howard Shapiro	MARS, Inc
Victor Nwosu	MARS, Inc
Richard Michelmore	University California-Davis (Co-Chairpersion)
Lutz Froenicke	University California-Davis
Scott Jackson	Univeristy Georgia (Chairperson)
Peggy Ozias-Akins	University Georgia (Co-Chairperson)
Baozhu Guo	USDA ARS
Corley Holbrook	USDA ARS
Brian Scheffler	USDA ARS
Greg May	National Center Genome Resources
David Bertioli	Univeristy Brasilia
Soraya Bertioli	EMBRAPA
Rajeev Varshney	ICRISAT
Xingyou Zhang	Henan Academy of Agricultural Sciences
Xun Xu	The Beijing Genome Institute
Xingjun Wang	Shandong Academy of Agricultural Sciences
Mark Burow	Texas A&M University
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Graeme Wright	Peanut Corporation of Australia
Sachiko Isobe	Kazusa DNA Research Institute, Japan
Ran Hovav	Agricultural Research Organization - the Volcani Center
Tom Stalker	North Carolina State University
Richard Wilson	Oilseeds & Biosciences Consulting

Ex Officio Members

Roy Scott	USDA, ARS, ONP
Pedro Arraes	President, EMBRAPA
Jean-Marcel Ribaut	Director, The GENERATION Challenge Grant Program
Chairman Luo Fuhe	Vice-Chairman CPPCC and, Executive Vice-Chairman CAPD Central Committee
David Hoisington	Deputy Director General for Research, ICRISAT

PGP Objectives & Deliverables (Abridged)
Component 1 Team: **BGI-Shenzhen & PGP Technical Steering Group**. Objective: *A high quality reference genome sequence of cultivated peanut that is anchored to chromosomal linkage groups*

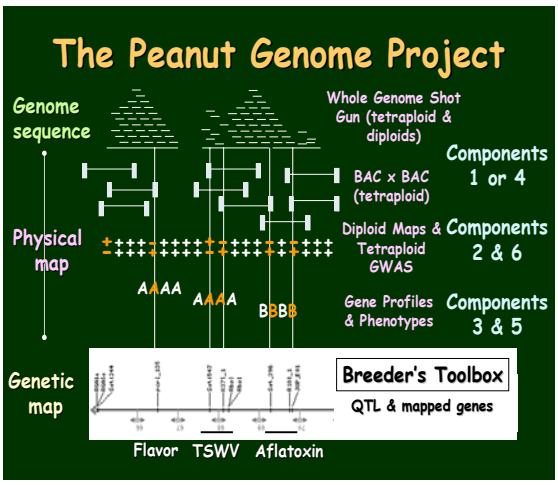
- BAC x BAC assembly of chromosomes of the cv Tifrunner
- A high-density genetic map based on whole genome shotgun sequencing and resequencing of the cv Tifrunner, GT-C20 & hybrid RILs
- Physical and genetic coordinates of the scaffolds and contigs in chromosomal linkage groups
- Data on genome assembly quality (euchromatic & gene region coverage with sequencing depth)
- Comparative genomics and evolution analysis of specific genome regions and gene families
- Validated genome assembly with a linear order of the contigs in chromosomal linkage groups

Component 2 Team: Richard Michelmore, David Bertioli, Rajeev Varshney, Lutz Froenicke, **Nicole Barkley, Boshou Liao**. Objective: *Genome mapping and allelic analysis through GWAS*

- High resolution genome maps of A and B genomes of the cultivated peanut ancestors; the amphidiploid synthetic hybrid of A x B genomes species; and RILs from each population.
- SNP maps of genetic variation diversity panels and germplasm collections from the U.S., India & China.
- GWAS studies of the agricultural traits phenotyped on the ICRISAT genetic diversity panel.

Component 3: Peggy Ozias-Akins, **Brian Scheffler**, Scott Jackson, **Baozhu Guo, Xingjun Wang, Weijian Zhuang**. Objective: *Catalog expressed genes and profile gene expression in cultivated peanut*

- Expression profiles of genes that mediate resistance to diseases and pests, such as: tomato spotted wilt virus (TSWV), leaf spot (early - *Cercospora arachidicola*; late - *Cercosporidium personatum*), rust (*Puccinia arachidis*), white mold (*Sclerotium rolfsii*), nematode (*Meloidogyne arenaria*), and pre-harvest aflatoxin contamination (*Aspergillus flavus*)
- Gene expression profiles for tolerance to abiotic stresses, such as: drought, temperature and nutrient deficiency
- Gene expression profiles for oil, fatty acid, protein, flavor, nutraceuticals and other quality traits
- A peanut gene atlas which includes the diploid genome origin of genes



Component 4 Team: Richard Michelmore, Lutz Froenicke, **Xun Xu**. Objective: *Evaluation of emerging technologies for genome sequencing & characterization*

- Direct sequencing of individual chromosomes using a Pac-Bio platform for single molecule real-time analysis
- Strobe sequencing for scaffolding contigs and assigning haplotypes in heterozygous and tetraploid genomes.

Component 5 Team: **Corley Holbrook**, Mark Burow, Soraya Bertioli, Ignacio Godoy, **Xuanqiang Liang, Xingjun Wang**. Objective: *Phenotypic validation of gene predictions*

- DNA markers that can be used in pre-breeding for disease and pest resistance including TSWV, Early & Late Leaf Spot, CBR, nematodes, PAC, drought.
- DNA markers that can be used in pre-breeding for quality traits including seed fatty acid composition, flavor quality, nutritional benefits, and other seed composition traits
- DNA markers for peanut yielding ability and other traits

Component 6 Team: Greg May, **Xun Xu, PGP Steering Group**. Objective: *Development of bioinformatic resources for peanut genome data & breeders toolbox*

- An International PGC Annotation Group to interface with BGI for peanut genome annotation and the establishment of a controlled vocabulary nomenclature.
- A peanut genomic database that facilitates navigation from maps to genes to traits
- An integrated database including available genetic stocks, mutants and germplasm collections
- A HapMap browser that connects the sequence to polymorphisms for traits of interest
- Ability to map RNA-seq and Sanger reads from expression data onto QTL data
- Integration of genome sequence with physical, genetics and transcriptome maps
- Molecular tools for the identification of candidate genes underlying QTLs.
- Integration of plant trait and phenotypic data with genetic maps and other genetic data.
- A plan for long-term curation of the peanut genome sequence and quality control

Summation:

Cultivated peanut poses the most difficult challenge that has been attempted in crop genome sequencing. Genome size is nearly equal to humans, and is distinguished by two sets of chromosomes from two different Arachis species.

Peanut varietal development worldwide is totally a function of the public research sector. DNA sequence assisted breeding methods are essential for timely increases in crop productivity & quality to ensure global food security.

The PGC is well positioned to deliver a reference peanut genome sequence within 2 to 3 years by virtue of multilateral multi-disciplinary cooperative research among world class scientists, organizations and institutions in the U.S., China, Brazil, India, and other countries that deploy advances in genomic technology