

# International Peanut Genome Initiative

## Research Progress & Accomplishment Chart

| Initial | 2012 | 2013 | 2014 | 2015 | 2016 |
|---------|------|------|------|------|------|
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### Allelic Diversity & Germplasm Resources

#### **Conservation of *A. hypogaea* and wild peanut species collections**

An updated catalog of wild species accessions with origins of collection and nursery site for each germplasm line

Identification of *A. hypogaea* accessions in international germplasm collections that must be replaced

Freedom to exchange germplasm in a systematic manner among institutions & nations.

International adoption of comprehensive uniform standards for herbarium and photo-documented peanut phenotypic descriptors.

Sound, long-term infrastructure for preserving peanut genetic resources.

#### **Evaluation of *A. hypogaea* accessions for important agronomic traits**

Standard procedures for screening accessions of section *Arachis* for new sources of disease resistances and molecular variation.

Discovery of new sources of resistance for leaf spot resistance and other crop protection traits

A diversity panel of accessions representing the genetic and phenotypic diversity in international peanut germplasm collections

Customized core and mini core-collections that facilitate genotypic and phenotypic characterization

#### **Access to genetic diversity thru germplasm that facilitate transfer of useful traits to cultivated peanut**

Diploid RIL mapping populations for both genomes of the progenitor species

Synthetic amphidiploid RIL mapping populations that exhibit substantial allelic variation from progenitor diploid species

A tetraploid mapping population from *A. hypogaea* x a synthetic amphidiploid that is a polymorphism-rich model for allelic variation

Generation of backcross progeny that demonstrate the utility of amphidiploids in the introgression of agronomic traits into peanut

### Genome Sequencing & Structural Characterization

#### **Production of a reference genome sequence for cultivated tetraploid peanut.**

BAC x BAC assembly of chromosomes of the cv Tifrunner, GT-C20 & 100 RIL from respective hybrid population

A high-density genetic map based on whole genome shotgun sequencing and resequencing of the cv Tifrunner, GT-C20 & 100 RIL

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.

#### **Comparative structural analysis of A and B diploid genomes**

BAC libraries for wild species representing the component genomes of *A. hypogaea*

A set of characterized probes for cytogenetic analysis of *Arachis* species

Assembly simulations using homologous A and B-genome BAC sequences

WGS sequences of wild species representing the component genomes of *A. hypogaea*

Markers linked to genes/QTL based on diploid and amphidiploid mapping populations

Assignment of gene expression profile origin among A and B genomes

Validated A and B genome assembly with a linear order of the contigs in chromosomal linkage groups.

#### **Annotation of the genome sequence**

An International Annotation Group to standardize peanut genome annotation and controlled vocabulary nomenclature.

Conversion of linkage groups to numbered chromosomes & standards for expression, protein and metabolite profiling

Confirmation of predicted expressed genes in A, B and tetraploid transcriptomes

Integration of transcriptome, genetic and physical maps from A, B, amphidiploid & tetraploid genome sequences

Integration of phenotypic descriptors with genetic maps and other genetic data derived from accessions of germplasm collections.

Annotation resources for transposons, repeats, sRNAs, and conserved non-coding elements

Integration of annotation data with orthologous genes, expressed genes and regulatory networks in a comparative context

Correlation of expression profiles with QTL to measure both copy number and allelic variation.

#### **A 'breeder-friendly' database to house and curate the primary and annotated genome sequences**

A PGP Technical Steering Committee to address current and future informatics needs.

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

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 and quality control of the peanut genome sequence

#### **Evaluation of emerging technologies for genome sequencing and characterization**

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Exploratory investigation of new techniques such as microfluidic methods and direct sequencing of chromosomes

### Genetic Trait Mapping & Gene Discovery

#### **Useful molecular marker resources in peanut**

Centralized accessible database for molecular genetic marker information

Identification of a core set of informative markers for deployment in genotyping systems for breeding programs

DNA markers that contribute to the assembly and annotation of the peanut genome

Allele specific DNA markers that can be used in pre-breeding for disease and pest resistance

Allele specific DNA markers that can be used in pre-breeding for quality traits

Allele specific DNA markers for peanut yielding ability and other agronomic traits

#### **Genetic and consensus maps for diploid and tetraploid peanut**

Compilation of marker genotyping data for different mapping populations

Improved understanding of the genome affinities of wild species within the section *Arachis*.

Improved gene rich reference maps for the component AA and BB, diploid genomes

Identification of candidate genes for induced and constitutive traits and their placement on the genetic map of *Arachis*.

Integration of diploid and tetraploid maps

A consensus genetic map for cultivated tetraploid

Placement of candidate genes for disease resistance on the genetic map of *Arachis*.

Analyses of genome synteny of *Arachis* with other legumes, especially the model plant *L. japonicus*

#### **Phenotypic validation of gene predictions**

Compilation of QTL data and development of a consensus QTL map

Core sets of DNA markers for QTL discovery for disease and pest resistance

Core sets of DNA markers for QTL discovery for quality traits

Core sets of DNA markers for QTL discovery for peanut yielding ability and other agronomic traits

#### **Genome mapping and allelic analysis through Genome-Wide-Association-Studies**

High resolution genome maps of progenitor A and B genomes and the amphidiploid synthetic hybrid of A x B genome species.

SNP maps correlated with the variation captured in the diversity panels and germplasm collections.

GWAS studies on accessions of international peanut germplasm collections and genetic diversity panels

#### **Catalog expressed genes and profile gene expression in cultivated peanut**

A standardized methodology for submitting data towards annotation of the whole peanut genome.

Expression profiles of genes that mediate resistance to diseases and pests

Expression profiles of genes that mediate tolerance to stresses such as: drought, temperature and nutrient deficiency

A peanut gene atlas which includes a comprehensive list of alternative splice products, co-regulated genes and gene networks.

### Product Quality & Safety

#### **Improved food safety by minimizing aflatoxin level in finished food products**

Improved cost reliability and competitiveness of biocontrol strategies for *Aspergillus* contamination

Elite, short season varieties with inherent resistance to *Aspergillus* infection

Molecular markers for QTL associated with substantial reduction of pre-harvest aflatoxin contamination

Changes in plant architecture that minimize peanut colonization by *Aspergillus*

Improved peanut harvesting and handling practices that reduce foreign material in farmer stock

#### **Improved consistency and quality of raw peanuts**

Find genetic factors that control flavor & develop useful molecular markers for specific traits

Define chemical reactions and metabolic intermediates that control the expression of flavor components in roasted peanuts

Raise "roasted peanut" flavor scores to a 7 as measured by trained panels

Improve levels of folate and/or essential nutrients above the thresholds that are required to make health claims

Genomic and biotech tools to manipulate metabolic and proteomic factors that govern the activity of biosynthetic pathways

Elite high oleic acid varieties that exhibit high or low oil content for specific markets

Commercial production of early maturing high-oleic peanut varieties

Industry adoption of practices that minimize admixtures that reduce the O/L ratio below 20:1 in marketed peanuts

Improved protein digestibility and completeness of protein.

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### Crop Improvement

#### **Characterization of genetic diversity for phenotypic traits in reference germplasm populations**

Libraries of documented descriptors of phenotypic variation among accessions of peanut germplasm collections

Publication of an internationally accepted CODEX for phenotypic descriptors in Section Arachis

Phenotypic characterization of reference sets of germplasm that represent genetic diversity for productivity, protection & quality traits .

#### **Support policies & initiatives for unrestricted international exchange of peanut germplasm**

A catalog of genotypic/phenotypic traits of germplasm and breeding populations for exchange among cooperative research efforts

Suggest protocol and procedures to help facilitate exchange of germplasm with as few IP restrictions as possible

#### **Develop and provide user-friendly, affordable genomic services and tools to all peanut breeders**

Establishment of regional or local laboratories to provide marker data.

Provision of bioinformatics tools to breeders to use for marker analysis.

Internet-accessible database with comprehensive lists of populations, pedigrees, available markers, and DNA sequences.

Marker technology that allows freedom-to-operate without IP restrictions

#### **Improved methods for phenotyping**

Guidelines and protocol for standardizing phenotypic description of mapping populations

Develop or modify existing phenotyping methods for greater efficiency, throughput and accuracy

#### **Provide multipurpose breeder training in employment of phenotyping methods**

Compilation of a list of venues for training.

Training in phenotyping at next AAGB meeting.

Further development of training materials.

#### **Develop Recombinant Inbred (RIL) & Near-Isogenic (NIL) lines for discovery of useful markers and genes**

Initial phenotyping on "T" populations, and other populations in appropriate environments

Phenotypic characterization of appropriate mapping populations for genetic variation in protection and/or quality traits

#### **Generating new populations for varietal development via modern breeding technology**

Develop highly sustainable peanut varieties with improved water use efficiency

Develop early maturing varieties to help improve flavor characteristics of roasted peanuts.

Develop elite cultivars with genetic resistance to major weed problems.