

Peanut Genomics Research Update

Soraya Leal-Bertioli (on behalf of the Peanut Genome Initiative)

The Peanut Genome Initiative (PGI) grew out of the International Advances in Arachis Genomics and Biotechnology meeting in 2012, as an attempt to add new strategies to work out industry wide problems that have been difficult to solve. Research partnerships were formed by scientists from the U.S., China, Japan, Brazil, Argentina, Australia, India, Israel, and several countries in Africa. The U.S. is represented by scientists at University of California-Davis; UGA; Texas A&M; USDA-ARS at Tifton, GA, Griffin, GA, Stillwater, OK, Ames IA and Stoneville MS; NC State University; Auburn University; University of Florida at Marianna; and NCGR at Santa Fe, NM.

When the PGI began there were relatively few molecular markers available to associate with useful genes and knowledge about the peanut genome was rudimentary. The Peanut Genome Initiative was thus organized to establish a path to create the genetic resources needed to enhance cultivar development for more productive, disease resistant, and higher quality peanuts.

The strategy of The Peanut Genome Project was organized into six components that would merge together to create a highly useful resource.

Research Component 1: Sequencing and assembly of the peanut genomes

- The first objective in the project was to create a high-quality assembly of peanut chromosome structure in the diploid wild species that gave rise to cultivated peanut. This served as a backbone assembly used to sequence and annotate the genome of cultivated peanut.
- Subsequently, by evaluating new sequencing and assembly technologies (Research Component 4) and applying them to peanut, has resulted in the genomic sequence of *A. hypogaea* now being more than 99.996% completed.

Research Component 2: Developing maps and markers for finding QTL

- Molecular markers have been developed from the sequencing data, which has led to two generations of thousands of single nucleotide polymorphism (SNP) chip that is currently being utilized by breeders to evaluate breeding populations.

Research Component 3: Developing markers for specific genes in QTL

- Molecular markers for genes conveying resistance have been associated with late leaf spot, early leaf spot, white mold, TSWV, root knot nematode, and rust. Markers for high oleic oil chemistry have also been identified. Some of these are already being used in active breeding programs.
- Many genes have been identified that express traits at different developmental stages of growing peanut.

Research Component 4: Evaluating new sequencing & assembly technologies

Research Component 5: Identifying breeding lines with QTLs for key traits

- Populations, for breeders use, have been developed with high levels of leaf spot resistance from wild species.
- Hybrid populations have been generated that contain an array of highly desirable characters for use by breeders to associate molecular markers with specific traits.
- Interspecific hybrid populations have been generated that are being used to introgress desirable genes from diploid peanut species into the cultivated genome.
- Thousands of different lines of peanut are being phenotyped for dozens of different traits. These phenotypes are being matched with genotypes which will help identify markers for even more desirable traits.

6: Creating on-line tools for genomic assisted breeding

- PeanutBase, the on-line Breeders Toolbox, was developed and is widely used as a resource for genomic information and tools — as well as information about germplasm and the peanut community in general.

Researchers are now working to help translate these tools into results for breeders. A genotyping platform, and workshops are being discussed.