

Peanut Genome Initiative - Executive Summary

THE INDUSTRY CHALLENGE: *“One of the biggest challenges for the U.S. peanut industry is the ability to compete with other crops for production. Most growers today are focused naturally on yield and production costs. As an industry, peanut varieties with improved yielding ability and enhanced disease resistance give producers a competitive edge. **Maximizing yield while minimizing inputs can best be done through marker-assisted breeding without using GMO technology.** The industry is committed to peanut consumption growth. As consumption grows, we must grow peanut yield potential to sustain our industry. The Peanut Genome Project is the key to a sustainable future for peanuts”-Dr. Darlene Cowart.*

This report is the 4th edition of annual research accomplishments from the 5-year The Peanut Genome Project (PGP). Achievements in 2015-2016 are documented in technical detail within the main body of the full report. Highlights are summarized here. Compared to other crop genome projects PGP rises to the top based on: 1) degree of difficulty in comparison to other legumes such as soybean; 2) the extraordinary quality of genome maps and gene markers; and 3) the sophistication of on-line databases that make genomics useful in peanut breeding programs. However, **tangible deliverables that range from scientific publications to new varieties developed by marker-assisted-selection (MAS)** distinguish PGP from other crop genomic programs.

- This year the paper on genome sequences in the ancestral parents of cultivated peanut was chosen as a classic feature article in *Nature Genetics*
- Since 2012, PGP scientists have published at least 193 papers
- Since 2014 PGP breeders have released at least 8 registered commercial varieties such as: Ole, Georgia 14N and TifNV-HiO/L; and
- Over 117 accessions have been added to the USDA Peanut Germplasm Collection for breeders use

Breeding programs have always been the heart of the PGP. Genome sequence driven MAS technology enables breeders to ‘maximize yield while minimizing inputs’ in a timely manner. This feature makes the PGP special, and inspires a great sense of pride among the PGP workforce. The progression from crude (general vicinity) markers to high-definition markers that pinpoint the exact location of a gene by its exclusive fingerprint. **High-definition markers are being used to make it easier to move genes from wild to cultivated peanuts.**

Drs. Corley Holbrook, Tom Isleib, Mark Burow, Barry Tillman, Peggy Ozias-Akins and many others have created **a massive pipeline for development of more high-definition markers for disease resistance and other traits in cultivated peanuts.** Their work is based on the response of the markers in resistant and susceptible lines from at least 20 highly inbred populations. This year the team reported 25 new high-definition markers for: ELS, LLS, TSWV, RKN, yield and maturity. It is just the tip of the iceberg.

One more highlight suggests that the PGP has established **a launch pad for many future deliverables for breeders, and ultimately the entire peanut industry.** High-definition markers are being developed for specific networks of genes. The first example showed when genes governing pod and seed traits were active during seed development in Tifrunner and NC3033. A network of genes was tagged for traits that define the period of seed filling and maturation. Dr. Peggy Ozias-Akins, University of Georgia, says, *“There are not many methods that help producers determine when a crop is mature. Monitoring the genes that are active at the start of kernel maturation could lead to development of DNA markers that can help improve the selection of early maturing varieties”.*

Sequencing the reference cultivated peanut genome is 95% complete, and final assembly of a working cultivated peanut genome will be finished within the next year.