

The Peanut Genome Project

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The Peanut Foundation

The U.S. peanut industry is in the fourth year of a five year commitment to map the peanut genome. Financial commitments from grower organizations, sheller organizations, and manufacturers totaling \$6,000,000 are being used to fund research to not only map the genome, but to find beneficial genes and learn how to utilize them in peanut breeding programs. A portion of the research being funded is basic genomic research necessary to sequence and assemble the complex tetraploid peanut genome. Other funded projects involve gene and gene marker discovery, phenotyping of known genotypes and development of techniques to utilize desirable genes from wild peanut species. Projects have been funded at several USDA laboratories as well as numerous prestigious universities, including the University of Georgia, the University of Florida, North Carolina State University, Auburn University, Texas A&M University and others.

A significant recent accomplishment is publication of the genomes of the wild species progenitors to modern day cultivated peanut. This publication has been accepted by the prestigious journal *Nature Genetics*. The article is the first ever publication of progenitor genomes for any crop. The article concludes that the A and B genomes of cultivated peanut are very close to its wild species progenitors. Furthermore, it concludes that modern day cultivated peanut resulted from the natural hybridization of the two progenitors around 10,000 years ago in Argentina, where the relatively rare *Arachis ipaensis* existed. The resulting tetraploid peanut had desirable traits and has ever since been domesticated via human selection. Besides being a fascinating account of the history of domestication of a modern crop plant, it gives researchers insight into the genetic makeup of the tetraploid that we know as peanut.

There has also been considerable success in gene marker discovery. Markers have been found for several key pests affecting U.S. peanut production as well as peanut rust, which is not currently a major factor in the U.S. but has the potential to be. A device called a SNP (Single Nucleotide Polymorphism) Chip has been developed to detect up to 60,000 individual points of variation in the peanut genome, include those that mark genes important to the U.S. peanut industry and its consumers.

RIL (Recombinant Inbred Lines) have been developed that segregate many of the traits desirable to the peanut industry. Considerable progress has been made to genotype and phenotype the hundreds of lines resulting from these RILs. By doing so, researchers will be able to clearly define the trait that results from a specific gene marker. With this knowledge, we anticipate that breeders can more quickly make selections from crosses and begin the backcrossing necessary to produce uniform seed sources.