

PeanutBase: Making Genetic and Genomic Data Accessible and Relevant for Peanut Improvement

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PeanutBase was started in 2013 to serve as the primary repository for peanut genetic and genomic data generated by the International Peanut Genomics Initiative. The website and database, which has been supported by The Peanut Research Foundation over this period, has matured in concert with the Genomics Initiative, and now provides tools that allow researchers to explore the diploid ancestral genomes (*A. duranensis* and *A. ipaensis*) and the cultivated peanut (Tifrunner) genome.

The website integrates most major data types involved in peanut genetics and genomics, including: genetic markers from numerous genetic maps and from the main genotyping chip (Affy 48k SNP set); images of accessions/varieties in the U.S. peanut collection; an interactive map of the geographic origins of all *Arachis* material in the U.S. collection; mapped traits; and gene expression data for all genes and for a wide range of tissues and developmental stages. The current efforts are directed to keep PeanutBase current with rapidly-progressing research in peanut.

This has required integrating large amounts of new data, including: genome assemblies for several new wild *Arachis* species, the densely genotyped U.S. core collection and phenotypic descriptions of the core, and genetic markers for high-value traits, for direct use in crop breeding programs. Tools are also being developed in parallel to visualize such data and aid in its utilization in crop improvement. They include: the PeanutMine for ease in mining genomic and genetic data, the Genotype Chromosome Visualization Tool (GCViT) that provides side-by-side visualization and comparison of genotype data to quickly identify large-scale differences (haplotypes) in different accessions, the Genomic Context Viewer (GCV) enabling researchers to explore similarity between regions on the peanut and related genomes, and a tool for viewing of GWAS results.