

## **PeanutBase: Mining Genetic and Genomics Data Using the PeanutMine**

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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.

Tools are also being developed in parallel to visualize such data and aid in its utilization in crop improvement. In this presentation we will focus on using the PeanutMine for ease in mining genomic and genetic data.