PeanutBase: The Genomic Data Portal for Arachis

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PeanutBase ([http://peanutbase.org](http://peanutbase.org/%22%20%5Ct%20%22_blank)) was started in April 2013 at Iowa State University with funding from The Peanut Foundation and in kind contributions from the USDA-ARS. It provides a web portal for genomics, genetics and trait information for peanut. Compared to most crop species, resources for peanut breeders are in their infancy. PeanutBase will develop and deploy tools for harvesting both existing resources -- genetic maps, genetic and molecular markers, QTL data -- and new reources that are only now being developed for peanut: a reference genome, gene models, transcriptomes, proteome and functional gene model annotations. Data curation plays a prominent role in loading and presenting these data.

The genomes of the two wild progenitors of cultivated peanut, Arachis duranensis and Arachis ipaensis, have been sequenced and the data is now served from PeanutBase. Transcriptome data from peanut and these two wild species are being mapped to these two diploid genomes and are available via the Genome browser.

Genetic maps are being served as interactive CMap graphics in collaboration with the Legume Information System (LIS;[http://comparative-legumes.org](http://comparative-legumes.org/%22%20%5Ct%20%22_blank)). QTL data sets have also been collected and are available from PeanutBase.

PeanutBase is implemented with Tripal and Chado.