**PeanutBase.org**

The Genomic Data Portal for Arachis

Ethalinda K.S. Cannon1, Sudhansu Dash2, Scott R. Kalberer3, Wei Huang5, Nathan T. Weeks3, Deepak Bitragunta3, Andrew D. Farmer7, Julie A. Dickerson1,6, Steven B. Cannon3,5

1 Genetics, Development and Cell Biology, ISU; 2 Virtual Reality Application Center, ISU; 3 USDA-Agricultural Research Service; 4 Agronomy, ISU; 5 Electrical and Computer Engineering, ISU; 6 National Center for Genomic Research

---

**PeanutBase** provides peanut researchers and breeders with trait, genetic and genomic data for *Arachis* and provides means for connecting peanut data to closely related plants with more developed datasets, for example, soybean and common bean.

**PeanutBase** is being developed in collaboration with the Legume Information System (LIS: http://legumeinfo.org)

---

**Marker Assisted Selection (MAS)**

MAS pages are being created with help from experts in the community on particular traits of interest. Each page combines information and data pertaining to a particular trait.

---

**Traits and QTL maps – TSWV example**

Both genome assemblies can be explored by genome browser and are available as FASTA downloads.

**Gene models** have been created for both *A. duranensis* and *A. ipaensis* using two methods, MAKER-P and GLEAN and are available as genome browser tracks.

*Arachis* gene models can be compared to *Glycine max* (soybean) and *Phaseolus vulgaris* (common bean) gene models to find likely gene function.

---

**Sequence Search**

BLAST and BLAT are available for searching and aligning sequence against the reference assemblies and gene models. Both show the alignments on the reference sequence browsers.

---

**A reference genome assembly for *Arachis hypogaea***

Because of the complexity of the tetraploid *A. hypogaea*, its likely diploid progenitor species, *A. duranensis* and *A. ipaensis* were sequenced and assembled first. Although the two species diverged ~ 3 mya, they still maintain significant synteny, although some large rearrangements have occurred... but there have been some significant rearrangements as well.

The two progenitor diploid genomes are remarkably similar...

---