SoyBase, the USDA-ARS soybean genetics and genomics database

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SoyBase, the USDA-ARS soybean genetics and genomics database, provides a comprehensive collection of data, analysis tools, and links to many external resources of interest to soybean researchers. SoyBase is an actively curated database, with new data regularly being incorporated, including additions to the controlled vocabularies (ontologies) for soybean growth, development and phenotypic traits, soybean genes, QTL, and genome sequences and annotations. The data in SoyBase are provided through intuitive interfaces, and are linked together wherever possible to allow easy identification and browsing of related subjects.

The SoyBase home page (https://soybase.org) contains the SoyBase Toolbox, which provides quick access to a search of SoyBase, the SoyCyc metabolic pathways, the data download page, a genome sequence BLAST tool, and direct links to the genetic and sequence maps. An extensive navigation menu and site description provides facile access to all sections of SoyBase. Numerous data types are available including genetic and QTL maps, the reference genome sequence with annotation tracks covering, among others, genetic markers, genome organization, and gene annotation and expression. Pedigrees for the entries in the Soybean Uniform Trials and recent cultivar registrations in J. Pl. Reg. are available. SoyBase includes an extensive RNA-Seq gene atlas and >100 gene expression and genome methylation studies. Innovative tools for identifying fast neutron-induced mutants affecting genes or traits of interest and several -omics tools, for example a GO Term Enrichment tool, enable sophisticated queries on lists of genes.

Please join us on Tuesday or Thursday from 5-6 for the SoyBase workshop, which will include an overview of the data and tools available at SoyBase. The templates used for submitting research results to SoyBase will be described along with examples of their use. Ample time will be available for questions and use cases from the audience.