SoyBase, The USDA-ARS Soybean Genetics and Genomics Database

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SoyBase, the USDA-ARS soybean database, is a central location for genetics, genomics and related data. The main SoyBase page (http://soybase.org) contains a News section, links to upcoming meetings, and acts as a portal to the Soybean Breeder’s Toolbox (SBT), the user interface to the data in SoyBase. SoyBase is organized around two related data types: the genetic and physical maps and the whole genome sequence. Genetic and physical maps allow side-by-side displays of multiple maps for comparing homoeologous regions of the genome. Along with the JGI genomic sequence users can choose to see sequenced genetic markers, soybean BACs, repetitive sequences, EST-based unigene sets, and the JGI automated gene calls. Features on the genetic, physical and sequence maps (eg. markers, QTL, BACs and FPC contigs) are linked to additional detailed textual data in SoyBase, and also provide connections between the genetic maps and the whole genome sequence. Controlled vocabularies for soybean growth, development and phenotypic traits are being developed and integrated with the Plant Ontology Consortium and Plant Trait Ontologies. Soybean ontologies are linked as appropriate to genes and QTL in SoyBase, thus allowing searching by trait or developmental stage as well as by gene or QTL name.

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