**Resources and tools for legume research at the Legume Information System**

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The Legume Information System (LIS, https://legumeinfo.org) has been under development for more than 20 years, but has seen especially rapid changes in the last five, corresponding with rapid improvements in sequencing technology. LIS now hosts genomic data for more than 25 legume genera and 60 species, including more than 150 assemblies and annotations. Collections reflect research community focus—for example, with 57 and 33 genomes for *Glycine* and *Medicago* respectively; but there is also good taxonomic coverage, with representatives from four of the six legume subfamilies. Data management and tool development is coordinated with sister projects SoyBase (https://soybase.org) and PeanutBase (https://peanutbase.org).

Pan-gene collections (sets of allelic genes across a set of annotations) are available for six genera (*Arachis, Cicer, Glycine, Medicago, Phaseolus, Vigna*), and rigorously constructed gene families are available that incorporate most of the genic data at LIS. Methods are provided for adding new annotations of interest to the families.

LIS provides many exploratory tools, including: InterMine instances for well-represented genera (InterMine is a data warehouse system that permits powerful queries); BLAST against all genome assemblies and gene sequences; the Genome Context Viewer for exploring synteny; search tools for genes by name or publication or description; JBrowse instances for viewing assemblies; ZZBrowse for exploring GWAS and QTL studies - and comparing marker-trait associations between two species of interest; a gene family viewer; comparative visualization tools for expression data; a tool for displaying germplasm origin in a geographic information system; and for annotating user-supplied sequences.