**SoyCyc: A Metabolic Database and Exploratory Tool For Soybean**

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Metabolic functional analysis of soybean has been limited to transcriptomic analysis of the soybean gene complement captured in EST and cDNA libraries. With the publication of the soybean genomic sequence, we are now able to infer the total metabolic potential of soybean. A computational pipeline provided by the PlantCyc project was used to assign enzymatic activities to Glyma1.01 gene calls produced by the JGI soybean sequencing project. These enzymatic activities were assigned to plant metabolic pathways using Pathologic. We used these results to populate a PathwaysTools database of plant pathways with Glyma1.01 gene calls (SoyCyc; http://soybase.org/soycyc). Of the 75,778 gene calls analyzed, 4,212 were associated with 3,487 individual enzymatic functions by sequence similarity. These enzymatic functions were associated with 324 metabolic pathways, involving 1,736 separate enzymatic and 10 transport reactions. SoyCyc also includes data from the MedicCyc and PlantCyc databases to facilitate the comparison of soybean metabolic reactions to those of Medicago truncatula and the compilation of pathways from all sequenced plant genomes contained in PlantCyc. The underlying PathwayTools software also allows users to “paint” soybean metabolic pathways with data derived from transcriptomic analyses and observe the effect of treatments on metabolic fluxes through those pathways.

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