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USING SOYBEAN GENE EXPRESS FOR GENE EXPRESSION PROFILING IN SOYBEAN

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The latest advances in understanding the composition and organization of the soybean genome have culminated in its publication. This, in conjunction with the development of next-generation sequencing or high-throughput sequencing technologies, is opening new doors into the field of molecular biology studies in soybean. Among the major applications of next generation sequencing is RNA-Seq applied to gene expression profiling with several advantages over hybridization-based methods like microarrays. The background error rate is extremely low; the capacity for data collection is greater; the results are digital and use a discrete distribution; the dynamic range of expression levels is greater; and transcripts can be detected without the prerequisite of pre-existing probes.

Here we present a case study on using Soybean Gene Express, a database system for managing, analyzing, visualizing, and extracting useful information from RNA-Seq data. The system supports Brazilian Soybean Genome Consortium (GENOSOJA, http://bioinfo.cnpso.embrapa.br/ genosoja/) researchers, going from raw data to visual reports comparing the levels of gene expression between pairs of samples or multiple samples following different biological samples/conditions. Also, it allows exploring the power of link-based integration with other sources of biological meaning information and databases such as ontologies, KEGG pathways, Pfam, Smart, Panther and others, to uncover the biological meaning of these data. Several criteria are available in the system to explore what the data are telling us about the biological conditions being investigated. For example, using filtering thresholds we can identify groups of genes that are differentially expressed among several conditions. The ultimate goal is to facilitate the discovery of new biological insights into fundamental molecular processes as responses to biotic and abiotic stresses in soybean.