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DOE-Joint Genome Institute EST and cDNA Program

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The purpose of the recently established EST program at DOE-JGI is to produce high quality EST data and full length cDNA sequence. This is used in support of gene-model training, genome annotation, identification of novel transcripts, and for clone resource generation. Since its inception in mid 2003, the program has grown from processing 4 species to 27 species resulting in a total of ~3 million EST sequences.

In order to handle this increase in throughput, an EST processing pipeline was developed. The pipeline serves two purposes, to optimize cDNA sequencing by providing the necessary information to determine the quality of the library and to provide a comprehensive content view across cDNA libraries. An overview of the analysis steps and summaries generated by the pipeline will be described. Results combined with publicly available data are used for intra and inter library comparisons. Many of the EST projects cover regions of the phylogenetic tree having few available EST sequences.

One organism of particular interest in the JGI collaboration with the Environmental Protection Agency (EPA), is the species *Pimephales promelas* commonly known as fathead minnow. The aim of the collaboration is to identify novel transcripts to assist in development of expression analysis tools, specifically microarrays. The ability to generate molecular data for *Pimephales promelas* in response to environmental exposure will aid in toxicity predictions and chemical risk assessments.

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