Model Organisms for Developmental Biology Studies

GeneChip® *C. elegans* Genome Array

GeneChip® Drosophila Genome Array

Image of *Caenorhabditis elegans*, Sinclair Stammers/Science Photo Library.

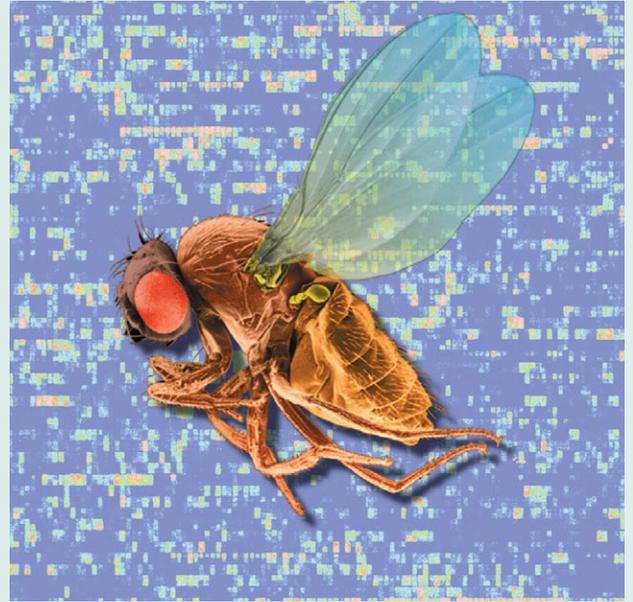
Image of *Drosophila melanogaster* (SEM x60), provided by Dennis Kunkel, Ph.D., University of Hawaii.

C. elegans Gene Expression Analysis

Whole genome analysis of *Caenorhabditis elegans*, a non-parasitic soil nematode, is possible on the GeneChip® *C. elegans* Genome Array. The array contains oligonucleotide probes synthesized *in situ* and designed to measure gene expression in over 22,500 transcripts. Utilize the power of GeneChip technology to accelerate your *C. elegans* research program.

Drosophila Gene Expression Analysis

The GeneChip® Drosophila Genome Array is the most comprehensive gene expression analysis tool for *Drosophila melanogaster*. With this array, you can measure gene expression in greater than 13,500 transcripts. Employ the versatility and power of GeneChip technology to move your Drosophila research program forward.

Applications

The expressed genome of each of these model organisms is represented on a single array and can be used to investigate applications in the following areas:

Study Genes Involved in Development

Short generation time and well defined genetics make *C. elegans* and *Drosophila melanogaster* integral model organisms for the study of developmental biology.

Using the GeneChip technology, you can analyze global gene expression of either model organism in a single hybridization experiment.

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Apply *C. elegans* or Drosophila to Functional Genomics Programs

Many homologs to human disease genes have been identified in these model organisms. With this information, complex biological processes can be identified and applied back to human biology. Therefore, model systems are an attractive option for expanding your functional genomics program.

Analyze the Global Effect of Mutations

Understanding the effect that a gene mutation or knockout may have on the entire organism is critical to understanding the role of that gene. Combining that technology with whole genome expression profiling will dramatically expand your research program.

Use in Agricultural Research

C. elegans and Drosophila are model systems for crop safety and pesticide research. These arrays can be used to measure gene expression changes in samples that have been exposed to pesticides and other crop treatments.

Build Quantitative Databases

GeneChip expression arrays allow for highly parallel, reproducible quantification of gene expression levels. The arrays for these model organisms are ideal tools for developing robust expression databases.
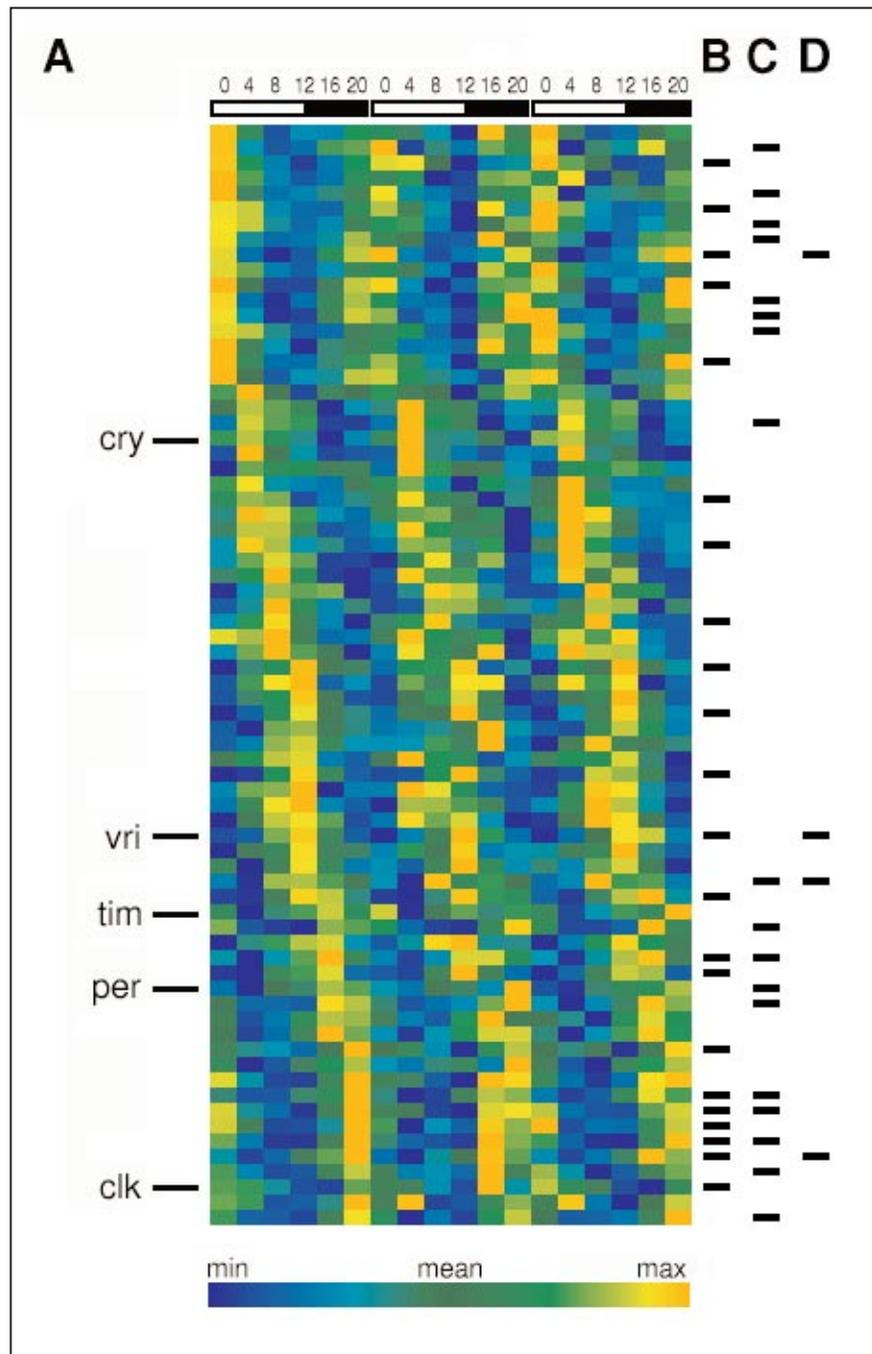
Analysis of Rhythmic Gene Expression in Control and Period Mutant Flies Using GeneChip® Drosophila Genome Arrays.

In this figure, **A** illustrates the phase-ordered expression patterns of the 72 genes identified as diurnally expressed in control flies. The positions of five known rhythmic genes of the circadian systems are denoted on the left. Tick marks show the positions of those diurnally expressed genes also found to be rhythmic in control flies kept in the following conditions: Wild type flies kept in total darkness have tick marks in column **B**, Flies mutant for per and kept in 12 hours light / 12 hours dark have tick marks in column **C**, and Flies mutant for per and kept in total darkness have tick marks in column **D**. Lin, *et al,* "Influence of the period-dependent circadian clock on diurnal, circadian, and aperiodic gene expression in Drosophila melanogaster." *PNAS* **99** (2002). Copyright 2002. National Academy of Sciences, U.S.A.

C. elegans Genome Array

Array Profile

The *C. elegans* genome array was designed using the December 2000 genome sequence, predicted transcripts, and EST sequences from the Sanger Center. Messenger RNA sequences from GenBank (release 121) were used as well. EST and mRNA sequences were aligned to the *C. elegans* genome and then merged with the Sanger transcript annotations to create a non-redundant set of total transcripts. EST and mRNA sequences which did not align to the genome were aligned and subclustered against each other. Probe sets were then selected against the 3' ends to generate greater than 22,500 probe sets against 22,150 unique transcripts. Over 18,800 Sanger Center transcript annotations are represented on the array. Approximately 2,300 3' EST clusters assembled on the genome and 300 GenBank mRNAs aligned to the genome are also represented and distinct from the Sanger Center predicted transcripts.

Ordering Information:

Part No.	900383
Name	*C. elegans* Genome Array
Description	Contains 5 *C. elegans* Genome Arrays
Part No.	900384
Name	*C. elegans* Genome Array
Description	Contains 30 *C. elegans* Genome Arrays

Drosophila Genome Array

Array Profile

The sequences used to develop this array are accessible through FlyBase. Greater than 13,500 predicted transcripts from the annotation of the Drosophila genome (version 1) are represented on the array. This includes genes for which confirming EST or full-length cDNA evidence is available (over 8,000 genes have at least 1 EST / cDNA match). Approximately 3,000 genes were identified using prediction algorithms and the remaining (_2,500) had not only a gene predicted algorithmically, but also showed some homology to genes from other organisms. For approximately 4,000 genes, recent expressed sequence alignment information from the Drosophila Gene Collection was used to modify the boundaries of the predicted transcript. In these cases, the GeneChip probe sets correspond to the modified exon boundaries. In addition, several hundred ESTs close to predicted gene sequences — but lying outside predetermined gene inclusion boundaries — are also included on the array.

Ordering Information:

Part No.	900335
Name	Drosophila Genome Array
Description	Contains 5 Drosophila Genome Arrays
Part No.	900336
Name	Drosophila Genome Array
Description	Contains 30 Drosophila Genome Arrays

Specifications for GeneChip *C. elegans* Genome Array

Number of Arrays	1
Number of Sequences Represented	>22,500
Feature Size	18 micron
Oligo Length	25-mer
Probe Pairs/Gene	_11
Control Sequences	Hybridization controls: *bioB*, *bioC*, *bioD* from *E. coli* and *cre* from P1 bacteriophage
	Poly-A controls: *dap, lys, phe, thr, trp* from *B. subtilis*
	C. elegans maintenance genes: actin, catalase, GAPDH, gly14, ubiquitin
Detection Sensitivity	1:100,000*

Specifications for GeneChip Drosophila Genome Array

Number of Arrays	1
Number of Sequences Represented	>13,500
Feature Size	20 micron
Oligo Length	25-mer
Probe Pairs/Gene	14
Control Sequences	Hybridization controls: *bioB*, *bioC*, *bioD* from *E. coli* and *cre* from P1 bacteriophage
	Poly-A controls: *dap, lys, phe, thr, trp* from *B. subtilis*
	Drosophila maintenance genes: Actin (Actin 42A), GAPDH (Glyceraldehyde 3 phosphate dehydrogenase 2), Eif-4a (Eukaryotic initiation factor 4a)
Detection Sensitivity	1:100,000*

*As measured by detection in a comparative analysis between a complex target containing spiked control transcriptions and a complex target with no spikes.

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