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## Probing the worm germline

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## Abstract

Genes expressed during *C. elegans* germline development have been identified using DNA microarrays.

## Significance and context

DNA microarray technology is revolutionizing scientific research by allowing the simultaneous analysis of transcription levels of thousands of genes. Reinke *et al.* describe the first application of microarrays to understanding the development of the nematode *Caenorhabditis elegans*, an important model organism. Microarrays can detect differences in individual transcript levels in RNA populations from two different samples. In this case, the authors focused on genes whose regulation is specific to the development of the worm germline.

## Key results

The authors constructed DNA microarrays containing almost 12,000 genes (63% of all those predicted to be present in the *C. elegans* genome). By hybridizing labeled RNA from a mutant in which all germ cells are absent to these arrays, and comparing the profiles obtained to similar hybridizations of wild-type RNA, they could determine which genes had significantly enriched transcript levels in the germline. Likewise, they compared RNA expression levels between two other mutants, one that produces only sperm and one that produces only oocytes (the worm is usually a hermaphrodite). In all, almost 12% (1,416) of the genes on the microarray were enriched in the germline. Among these were 650 genes enriched in sperm, 258 enriched in oocytes, and 508 genes expressed at similar levels in both mutant lines, suggesting that they are general factors required in the germ line. These experiments were repeated over a time span encompassing the last three larval stages and the adult animal. Sperm-enriched transcripts are present mostly in the final larval stage, whereas most oocyte and general germline genes are activated in the adult.

## Links

The complete dataset from these microarray experiments can be found at the Kim lab website on the appropriate page - [A global profile of germline gene expression in \*C. elegans\*](#).

## Conclusions

The sperm-enriched gene set included a large number of cytoplasmic protein kinases and phosphatases, reflecting the fact that most of sperm development involves post-translational events. Enzymes required for fatty acid metabolism, to provide energy for mobility were also well-represented in the sperm-enriched gene set. The oocyte set included a large number of genes involved in DNA replication, early cell division, and embryonic patterning. Genes involved generally in the germline included those required for stem-cell maintenance, RNA metabolism, and RNA processing.

## Reporter's comments

Transcripts of almost all genes previously known to be involved in the worm germline were enriched in the germline according to the microarray experiment. Furthermore, screening a sperm cDNA library identified several genes indicated as sperm-enriched by the microarray data. These results help validate the experimental approach taken by Reinke *et al.* Unfortunately, the microarrays developed by the authors only encompass about two thirds of *C. elegans* genes. As the worm's genome is completely sequenced, including all the potential genes on the array would have made for a more complete analysis. Lastly, like most microarray-based expression studies, the information gained by the analysis is functionally limited. This data reveals many genes that are expressed in the germ line, and even some specific for either sperm or oocytes, but we are no closer to knowing how they function. So this study is a great starting point for many interesting experiments to come.

## Table of links

[Molecular Cell](#)

[A global profile of germline gene expression in \*C. elegans\*](#)

## References

1. Reinke V, Smith HE, Nance J, Wang J, Doren CV, Begley R, Jones SJM, Davis EB, Scherer S, Ward S, Kim SK: A global profile of germline gene expression in *C. elegans*. *Mol Cell*. 2000, 6: 605-616. 1097-4164