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Becoming a worm

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Sequencing of the [worm genome](#) has allowed Hill *et al.* to design oligonucleotide arrays representing 18,791 (98%) of the predicted worm open reading frames (ORFs). In the 27 October [Science](#), they report the use of these arrays to analyze transcripts from six developmentally staged worm populations from eggs to adults (*Science* 2000, **290**:809-812). Only 56% of the ORFs are detected at least once, suggesting that others are missed because they are expressed at very low levels in specific tissues or under specific conditions. Aging worms show transcriptional correlates of impaired muscle function, reduced metabolic activity and extracellular matrix defects. During development, expression of genes specific to worms becomes more predominant, at the expense of expression of genes that are evolutionarily conserved.

References

1. Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.
2. *Science*, [<http://www.sciencemag.org/>]