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## Reaping the rewards of RNAi

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Loss-of-function phenotype analysis in [nematode worms](#) has benefited tremendously from a well-annotated genome and the efficacy of [RNAi](#) gene-inactivation technology. In the January 16 [Nature](#) Kamath *et al.* report the results of the first genome-wide RNAi screen in *Caenorhabditis elegans* (*Nature* 2003, **421**:231-237). Worms were fed on bacteria expressing double-stranded RNA for each *C. elegans* target gene. A library of 16,757 bacterial strains, covering 87% of predicted genes, was screened for genes implicated in sterility, embryonic lethality, slow growth or post-embryonic defects. About 10% of strains gave clear mutant phenotypes. The most common RNAi phenotype is embryonic lethality. Worm genes that were orthologs in other species are more likely to have a detectable RNAi phenotype than other genes. And genes that exist as a single copy are 2-3 times more likely than others to have a phenotype. Some protein domains showed association with particular types of RNAi phenotypes. Also, genes with RNAi phenotypes are often found grouped together in [chromosomal clusters](#). In an accompanying paper, Ashrafi *et al.* describe how this RNAi library can be used as a powerful resource to identify genes that regulate body fat production (*Nature* 2003, **421**:268-272). In an accompanying 'News and Views' article Thomas Tuschl comments that these studies establish "a new standard for systematic, genome-wide genetic studies."

## References

1. WormBase, [<http://www.wormbase.org>]
2. Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans*.
3. *Nature*, [<http://www.nature.com>]
4. Transcriptional territories in the genome.