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***C. elegans*: The Nematode as a Model Organism**

Status	Past
Competition	I
Sector	Health
Genome Centre	Genome British Columbia
Project Leader	Donald Moerman

Project Description

C. elegans, a tiny roundworm that has been extensively studied to provide insight into the workings of other organisms, has about 7,000 genes in common with the human genome. When dysfunctional in humans, these genes can lead to inherited diseases, susceptibility to cancers and other health problems. Understanding the basic biological function of *C. elegans* will likely have direct consequences for medical diagnosis and treatment in humans.

Over the past four years, our international team has identified deletion mutations in over 2,000 genes. Prior to this project, only 700 genes had been identified through mutation by the entire research community in the last 25 years. A number of the genes targeted for knockouts are homologous to human disease genes.

To obtain the knockouts, the team established a world-class facility – part of an international consortium of laboratories that includes the Oklahoma Medical Research Foundation and the Tokyo Women's medical University School of Medicine – and developed innovative new procedures. Our 'poison primer protocol' is now a standard in many laboratories around the world, and our more recent innovation, array Comparative Genome Hybridization (aCGH), could revolutionize how knockouts are obtained and prove crucial for studies in evolutionary and population biology.

As the biology of these genes is unraveled, this should lead to better diagnostic tools and eventually therapeutic products. One worthwhile downstream effect of this work would be improved health and quality of life in countries ravaged by nematode diseases (e.g., river blindness). The research will also prove useful to companies using *C. elegans* for drug discovery and to understand the effects of drugs, as an inexpensive first level bioassay and screen for chemicals, and for developing 'nematicides' to combat agricultural pests.

Fast Facts

Highlighted outcome: identified mutations in approximately 2,000 genes, several of which are homologous to human disease genes

Number of research personnel employed by the project: 13

Number of peer reviewed publications published: 2 papers, 7 abstracts, and 14 invited presentations; more than 160 peer-reviewed papers have been published by other scientists using the mutations

Resources generated: all knockouts and related data and information have been made publicly available via the project website, the WormBase depository for all data pertaining to *C. elegans*, and the Caenorhabditis Genetics Center (CGC) all knockouts and related data and information have been made publicly available via the project website, the WormBase depository for all data pertaining to *C. elegans*, and the Caenorhabditis Genetics Center (CGC)