Geneticists Receive $2 Million Grant to Study Parasites That Infect 2 Billion

St. Louis, May 25, 2004 — Scientists at the Genome Sequencing Center (GSC) at Washington University School of Medicine in St. Louis have received a four-year, $2 million National Institutes of Health (NIH) grant to study the genetics of two groups of parasitic roundworms, ascaris and hookworm.

These roundworms, also known as nematodes, infect an estimated 2 billion humans in tropical and developing countries, inflicting symptoms ranging from intestinal discomfort to mental retardation to life-threatening blockages of key digestive structures.

The principal investigator of the new grant is Richard K. Wilson, Ph.D., director of the GSC and professor of genetics. Sandra Clifton, Ph.D., assistant director of the GSC and research assistant professor of genetics, is co-principal investigator.

“We plan to produce the data scientists need to develop new treatments that interfere with the activities of key genes in ascaris and hookworm,” says Clifton. “We’re also going to investigate unusual aspects of their biology, hoping to identify unique proteins that will make it possible to develop vaccines.”

A recent study of mostly urban Peruvian women found 65 percent had ascaris and 48 percent had hookworm. In the Philippines, a sample of 333 school-age children revealed 75 percent had ascaris and 45 percent had hookworm.

“One major effect of hookworm is anemia — the worms sit in the intestine and drink the host’s blood,” explains investigator James McCarter, M.D., Ph.D., an adjunct GSC faculty member. “In children, this can lead to stunted growth and detrimental effects on cognitive development.”

Mc CARTER is also president of Divergence, a private biotechnology company devoted to developing new techniques for fighting parasitic roundworms.

Ascaris lives in the small intestine and can grow to 12 inches in length, causing diarrhea and, in rare cases, a potentially life-threatening impairment of the bile duct.

There are two ascaris species and five hookworm species, and GSC scientists plan to identify at least half of their genes. The information they produce will be made publicly available through Nematode.net, an online database of roundworm genetics created by GSC researchers during earlier nematode research.

In that previous research, funded by the NIH and the National Science Foundation, geneticists focused on a broader range of roundworms that infect humans, animals and plants. The Washington University effort identified and made publicly available about 10 to 20 percent of the roundworms’ genes.

Under the new NIH grant, GSC researchers are already comparing the genomes of individual species of ascaris and hookworm.

“We’re determining how the various species are similar and different. We hope that will help other researchers find some way of fighting them that is universal or would at least work on several different species,” Clifton says.

Makedonka Mitreva, Ph.D., a postdoctoral fellow who came to the GSC from Wageningen University in the Netherlands, which is world-renowned for its expertise in roundworms, has already been able to perform several innovative comparisons among both parasitic and non-parasitic...
Scientists at the GSC have also begun integrating Nematode.net and two other nematode genetics databases, Nembase of the United Kingdom and Wormbase, a genetics database dedicated to the nematode C. elegans, which was the first multicellular organism to have its entire genome sequenced. Researchers at the GSC and the Sanger Center in the United Kingdom completed assembly of the C. elegans genome in 1998.

“We’re going to compile these three databases to form a new database that will help us more quickly determine what role newly identified genes may have in nematode biology, or whether the gene is nematode-specific and produces a protein whose precise structure and function we haven’t encountered before,” Clifton says.

Such genes might provide potent new avenues of attack for pharmaceutical researchers, Clifton notes. GSC scientists hope to identify 250 such genes in ascaris and hookworm.

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