Grants support use of state-of-the-art technology to determine cancer risk

Baylor College of Medicine
HOUSTON -- (August 18, 2010) -- Recent grants to a Baylor College of Medicine [1] geneticist will help fund studies that seek to understand why some children are more at risk for cancer.
Dr. Sharon Plon, professor of pediatrics – hematology/oncology, received a $2.1 million grant from the Cancer Prevention and Research Institute of Texas (CPRIT) and a $1.6 million grant from the National Cancer Institute for two different studies that both use DNA sequencing to find gene mutations that make families susceptible to pediatric cancer.

"We'll be using the newest technology to understand why some families are more at risk," Plon said. "People want to understand why this happens to their family, and we want to be able to provide those answers."

Cancer history

The CPRIT-funded study will examine people who have had more than one cancer – for example, a childhood cancer and a second malignancy later in life – and those who have cancer history in their extended family.

CPRIT was established through a state constitutional amendment to expedite innovations in cancer research and lower the incidence of cancer in Texas. A total of $3 billion over 10 years has been committed to fund cancer prevention research in Texas.

The NCI study will include families where siblings have both been diagnosed with cancer as well as children diagnosed with cancer who also have other birth defects and learning disabilities to identify gene mutations that contribute to these susceptibilities.

Participants for this research have been enrolled from Texas Children's Cancer Center, MD Anderson Cancer Center, the University of Texas Health Science Center at San Antonio and the Children's Hospital of Philadelphia.

Both studies will use state-of-the-art, large-scale DNA sequencing available at BCM's Human Genome Sequencing Center (HGSC) to study all the genes of the participants genes.

Cancer risks

"Dr Plon's pioneering work recognizes the incredible importance of inherited

disposition to cancer – and can potentially transform our view of this disease," said Dr. Richard Gibbs, director of the HGSC and professor of molecular and human genetics at BCM. "We are collaborating to show how new methodologies developed in the Human Genome Sequencing Center can be applied to a major health issue."

Analysis will be conducted by BCM and Rice University researchers to determine which gene sequence changes impact cancer risk.

"Our overall goal is to identify novel genes that, when altered, increase the risk of childhood cancer," said Plon, who is also a professor in the department of molecular and human genetics and director of the Baylor Cancer Genetics Clinic. "Knowledge of genes that predispose to cancer also teaches us about how cancer develops in the general population and will provide new ideas about improved treatment of cancer."

New wave of research

The research got started through an innovation grant from Alex's Lemonade Stand Foundation, a nonprofit committed to finding a cure for childhood cancer. In that initial study, 50 known cancer genes were sequenced in 48 families. In six of the families, a cancer-causing mutation was found, Plon said. The impetus for the new studies was to find the causative mutation in the remaining 42 families.

"Both of these studies are part of a new wave of research examining how effective sequencing the whole genome will be in finding the genes where there is a change or mutation that causes cancer," Plon said.

Collaborators on both studies include Dr. Richard A. Gibbs and Dr. David Wheeler, both of the Human Genome Sequencing Center at BCM; Dr. Louise C. Strong, department of cancer genetics, MD Anderson Cancer Center; Dr. Gail Tomlinson, UT Health Science Center San Antonio; Dr. Marek Kimmel, Rice University (CPRIT project); and Dr. John Maris, Children's Hospital of Philadelphia (NCI project).

SOURCE [2]

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