



Research

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GRANT SNAPSHOT

2009 Pancreatic Cancer Action Network – AACR Pilot Grant

Grantee:	Qingshen Gao, MD
Institution:	NorthShore University HealthSystem, Evanston, IL
Research Project:	Discovery of Novel Pancreatic Cancer Susceptibility Genes
Award Period:	July 1, 2009 – June 30, 2011
Amount:	\$200,000



Biographical Highlights

Dr. Gao is an Assistant Professor in the Department of Medicine at NorthShore University HealthSystem, Northwestern University. After receiving his MD in 1986 from Shandong Medical University in China, he completed a research fellowship in radiation oncology and taught at the New England Medical Center, Tufts University School of Medicine, Boston.

Dr. Gao's laboratory focuses on dissecting the BRCA2 tumor suppressor pathway, with the goal of identifying all the BRCA2 interacting proteins and the genes that are regulated by BRCA2. His lab has recently published three of the BRCA2 binding proteins they identified: centromin, MAGE-D1 and DSS1. Dr. Gao's laboratory became interested in pancreatic cancer research because of the important role of BRCA2 pathway in pancreatic cancer development.

Project Overview

Approximately 5-10% of individuals with pancreatic cancer report having one or more first or second-degree relatives with the disease. However, the responsible germline mutation is rarely identified. BRCA2 mutations likely account for the largest percentage of familial pancreatic cancers. BRCA2 helps to repair damaged DNA and is most often related to inherited breast and ovarian cancer. BRCA2 is an enormous protein. Likely it does not work alone but coordinates with many other proteins through interactions. Dr. Gao's laboratory has identified 13 BRCA2 binding proteins and has strong evidence that that these genes increase susceptibility to pancreatic cancer.

In the funded project, Dr. Gao plans to screen the 13 candidate genes that have been identified in his lab for germline mutations in familial pancreatic cancer patients. A control group will also be used for comparison purposes. Plans are to use the Pancreatic Cancer Family Registry, which now includes 137 participants with DNA samples suitable for analysis who have been diagnosed with pancreatic cancer and 139 that have a family history of pancreatic cancer.

A genetic scanning method called high resolution melt (HRM) plus sequencing will be used. HRM is novel, simple to use, and cost effective when analyzing a large number of candidate genes. If germline mutations of the candidate genes are discovered in the group of patients and are absent in the control group, it will indicate that these mutations likely predispose to hereditary pancreatic cancer. If it can be demonstrated that mutations of these genes predispose to hereditary pancreatic cancer, sequencing these genes for clinical purposes should have similar value to sequencing BRCA2. The results of this study are expected to have important clinical implications for pancreatic cancer risk assessment and ultimately pancreatic cancer management.