Profiling **O**f **P**ancreatic Cancer **S**urvivors **(POPS)**

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I am pleased to provide the following update about my clinical and research activities over the past year. I had a productive year gaining additional experience working with internationally renowned physicians and researchers at The Princess Margaret.

Having chosen a career in medicine I quickly realized medical oncology was the area I wished to specialize in, being a research driven speciality with opportunities for an academic career. After completing my medical oncology training and PhD at the University of Cambridge, I applied for a fellowship outside of the UK. I was extremely interested in spending time working in a different health care system. I believe this gives me a unique advantage to ascertain the benefits and disadvantages of how differing methods of health care in cancer are utilized on a different continent.

There were many reasons I chose to work at The Princess Margaret specifically for my fellowship. **The Princess Margaret has achieved an international reputation as a leader in the fight against cancer. Clinical and research staff at Princess Margaret represent many of the world's leading experts in oncology.**

Working with Dr. Moore in the fields of pancreatic cancer and drug development is an ideal opportunity to study the areas I am particularly captivated by. I have been involved in the planning, coordination, and implementation of selected innovative early stage clinical trials and research, including pancreas specific trials. The opportunity to conduct timely and high quality clinical and translational studies would be difficult to gain in any other program.

The following POPS study is one of the two projects I have designed for my fellowship and is currently being funded in addition to my fellowship in partnership with Pancreatic Cancer Canada:

Profiling of Pancreatic Cancer Survivors (POPS):

Approximately 20% of patients with pancreatic cancer are operable at presentation; however, unfortunately less than 20% of these patients live to 5 years, despite aggressive surgery and, for most patients, adjuvant chemotherapy. There are currently no accurate methods to identify the few long-term survivors from the outset other than simple clinic-pathologic staging variables. The aim of this project is to identify genetic signatures of long-term survival following curative surgery for pancreatic ductal adenocarcinoma (PDAC). Such biological classifiers would be clinically useful to identify patients with a good long-term prognosis and stratify treatment options for those at higher risk of relapse following surgery.

Aim and Objectives

The overall aim of this project is to identify genetic signatures of long term survival following curative surgery for pancreatic ductal adenocarcinoma (PDAC), and compare this to genetic signatures from patients that succumb to disease early after operative resection, and patients that present with metastatic disease at the outset. Such biological classifiers would be clinically useful to identify patients with a good long term prognosis and stratify treatment options for those at higher risk of relapse following surgery. The study will be restricted by the number of long term survivors from PDAC with surgical samples available. **We have currently identified 100 long-term survivors of pancreatic cancer within Ontario.** We are now investigating the quality of the stored tissue and blood we have for these patients for DNA and RNA extractions. We will then sequence the samples with the hope of identifying a unique genetic signature.

Methods

Once the correct patients are identified and their cancer histology has been confirmed, we will be extracting DNA from formalin fixed paraffin embedded (FFPE) tissue from previous pancreatic surgical specimens or tumor biopsies. Next generation sequencing will be utilized to sequence the genome to identify the genetic signature for each patient. We plan to use three groups of patients; survivors (over 5 years post-surgery for PDAC), early relapses (relapsed within a year of surgery for PDAC) and patients who present with metastatic disease. These will be analyzed separately and then compared for differences in genomic signatures. We have collaborations with groups in the UK and Germany for validation datasets.

Outcomes

The anticipated outcomes include:

- Identification of candidate biomarkers of prognosis with clinical utility that may facilitate clinical decision-making, particularly with regard to patient selection for operative resection
- Identification of genes and/or molecular mechanisms associated with particularly aggressive or metastatic disease