Report NCU grant

Report submission date: 1 April 2011

Main applicant: Tom Grotmol

Project title: A large population-based Swedish-Norwegian genetic association study of testicular cancer

NCU grant received (€): 70,000 (2009)

Project commencement and completion dates:

Please e-mail report to: ncu@kreftforeningen.no

---

1. Brief description of the project, written in a language understandable to non-scientists (Maximum length: 100 words)

The etiology of testicular cancer is still largely unknown, although genetic components and conditions during pregnancy are thought to play a role. The overall hypothesis is that hormonal disturbances during pregnancy are important in the development of this disease, and that polymorphisms in genes regulating the activity of enzymes metabolizing the sex hormones, play an etiologic role. These issues will be addressed in this Swedish-Norwegian study of testicular cancer patients and their parents (patient-parent triads). The aim is to investigate variation in selected genes relevant for testicular cancer risk in these patient-parent triads. The genetic material will be extracted from saliva sampled by the individual at home.

2. Summarize the major findings of the project (Maximum length: 400 words)

We have collected saliva samples and extracted DNA from 1000 patient-parent triads, 436 patient-parent dyads (patient and one parent) and 649 single patients (no parents), adding up to more than 4500 samples.

To identify genetic variation (in the form of single nucleotide polymorphisms, SNPs) in the genes of interest we will use tag-SNPs. Nearby SNPs are often inherited in blocks, the specific pattern of SNPs are called a haplotype. Only a few SNPs are required to uniquely identify the haplotypes in a block, these SNPs are called tag SNPs. Through a catalogue of common genetic variants generated from the International HapMap Project we will identify the tag SNPs needed to discover variation in the genes of interest. Initially we have selected 18 genes and more than 200 tag-SNPs for such analyses. Some of these genes have been selected based on previous studies (e.g., TERT, SPRY4, KITLG) and some because of their involvement in the sex-hormone pathway

(e.g., ER, SHBG). In addition, we will look for variation in especially interesting SNPs in about 20 other genes with previously shown association with testicular cancer or other relevant cancer types.

The samples have been sent to the Centre for Integrative Genetics (CIGENE), located at Ås outside Oslo, for genotyping using the Sequenom MassARRAY system, and results are expected in April 2011.

3. Describe how the project has increased our knowledge of the prevention, cause and/or cure for cancer (Maximum length: 150 words)

The results from our study are not ready, but we hope that our findings will contribute to a deeper understanding of the etiology of testicular cancer, and to the development of new strategies for detection, monitoring and treatment of this cancer form.

4. Outline how Nordic cooperation has added value to this project (Maximum length 100 words)

The project takes advantage of combining the populations of Sweden and Norway, which both have complete cancer registration. This enables us to conduct a study with a large study population and excellent power to detect risk alleles. Sweden has for several decades had about half the incidence rate of testicular cancer compared to Norway. The reason for this contrast is unknown, but it has remained in spite of a significant increase in both countries. In our study we are able to compare the results from the two countries, and hopefully shed light on this issue.

5. Publications resulting from this grant

No publications so far.