Complex Traits Group and the McGill University and Genome Quebec Innovation Centre
SPECIAL SEMINAR

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Title: "Search for causative genes in inflammatory bowel disease"

Monday, May 11, 2015

Room 1034, 4:00 PM

McIntyre Medical Sciences Building

"GWAS has identified 163 risk loci for inflammatory bowel disease (IBD). However, most causative genes among positional candidates remain unknown. We previously reported enrichment of protective rare variants in IL23R as one of evidence for causality by target sequencing of 63 positional candidate genes in several hundred individuals. On the other hand, we also realized this method had limited statistical power. We need to preselect candidate genes among positional candidates and to increase the number of individuals for target sequencing. We decided to use eQTL information to pinpoint likely causative genes in known risk loci as follows. It is becoming increasingly apparent that a substantial proportion of inherited risk is due to regulatory variants that alter the expression profile of the causative genes. In that case, disease association profile (the combination of p-values exhibited by all variants in a risk locus) and eQTL association profile should be highly correlated in the disease-relevant tissue. Therefore, we collected nine cell types considered relevant to IBD in 350 individuals to develop eQTL information in Liege. Combined analysis of GWAS data and eQTL information pinpointed 72 genes with strong correlation of both profile. We developed a high throughput target sequencing method based on multiplex PCR. This method enables us to perform target sequencing for translated regions of the 72 genes in ~6,000 cases and ~6,000 controls in Riken. Latest results will be presented".

LOCATION: **McIntyre Medical Sciences Building, Room 1034, 4:00 PM**

HOSTED BY: DR. MAYA SALEH