BCCGN
British Columbia Clinical Genomics Network

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BCCGN Newsletter

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BCCGN News and Updates

Genomics Workshops for Physicians

BCCGN has developed a practical hands-on genomics workshop specifically designed for physicians. The workshop will be held at the Child & Family Research Institute, BC Children's Hospital in Vancouver in January, 2011. This 1-day workshop is for those clinicians with no prior knowledge of genomics and/or their related technologies. The workshop caters to small groups and is highly interactive with an emphasis on clinical applications. Topics to be covered include DNA extraction, SNP genotyping, high-throughput copy number variation, an introduction to study design and analysis, and interactive lab tours. CME credits pending approval.

New Patient Registry List

There are numerous research databases in BC that are accumulating large amounts of information, but there is no central point to list them all. BCCGN hopes to facilitate further collaboration and networking within the community of clinical researchers by providing that central resource. We are able to give assistance for new collaborations that use the datasets via study design, data analysis, technology access and networking services. If you wish to have your patient datasets included, please return this form with your study details by fax or email

Research in Focus

Role of Bacteria in COPD

An exciting new field of genomic research called Metagenomics now offers powerful insight into the world of microbes. Metagenomics is used to determine the presence of bacterial, fungal and/or viral species within environmental samples as well as human and animal tissues.

With the assistance of the BC Clinical Genomics Network, Dr. James Hogg of the iCAPTURE Centre for Cardiovascular and Pulmonary Research, St. Paul's Hospital, Vancouver has investigated the role of bacteria in the pathogenesis of Chronic Obstructive Pulmonary Disease (COPD) using metagenomics. Based on a recent observation of the presence of commensal microbial communities within the lower respiratory tract of healthy subjects, Dr. Hogg tested the hypothesis that airway obstruction and emphysematous lung destruction are associated with replacement of the normal flora of commensal organisms by an overgrowth of one or more pathogens in the diseased tissue of COPD patients.

In this pilot study Dr. Hogg obtained 2 regional lung biopsies from a healthy non-smoker and 5 regional lung biopsies from the lesions in the lung of a COPD patient. DNA isolated from these samples underwent unbiased massively parallel metagenomic sequencing as well as qPCR to quantify the microbiome in the samples. This was followed by computational analysis or bioinformatics. During this analysis sequences that aligned with human and commensal *E.Coli* DNA were eliminated. The remaining sequences were then compared to known bacterial reference samples that are stored within several databases.

Preliminary results demonstrate a large microbial diversity of both number and type of bacterial species in control and COPD samples. The presence of large microbial communities in healthy controls confirms the earlier observation. COPD samples also displayed a marked change in several species examined compared to the control samples. Dr. Hogg's study challenges the medical teaching that lower airways are sterile, provides further evidence that many species of bacteria are present and suggests differences between normal and COPD tissue. Dr. Hogg and his collaborators will now investigate more on the exact role that pathogenic bacteria play in the progression of COPD.

Technology in Focus

Metagenomics is a relatively new approach, to identify huge numbers of unculturable, unpurified microbes found in environmental, human or animal samples by brute-force sequencing. Prior to this, no more than ~1% of all microbial species were identified or characterized as laboratory techniques were unable to grow or purify them in culture. Metagenomics overcomes this problem by using next-generation sequencing technologies combined with powerful computational tools to identify & compare the DNA sequences of individual microorganisms such as bacteria, viruses, fungi and protozoa in a single experiment. This approach also allows investigators to determine the relative amounts of each species present in a given sample, all in a single experiment.

All genomic DNA in the sample is isolated then fragmented creating a pool of mixed DNA fragments. These millions of short fragments are attached to a single microchip and the sequencing phase begins. Here, the fragments read in parallel and imaging data is generated through many iterative cycles. This method provides a cost savings and results in large volumes of data. The challenge in metagenomics is determining the species of origin for the DNA fragments. This requires the short sequenced fragments to be reassembled computationally into longer sequences which provide sufficient information for identification. Different computer programs and web-services are used for this process. Scientists use these genomic and computational tools to compare sample sequences with known reference sequences stored in various databases. As more metagenomics sequencing data is generated and more species are identified and characterized, the more accurate and larger these databases will become. These, in turn, will serve to provide better reference information for those looking to identify different species within complex samples.

BCCGN Activities

BCCGN News and Updates (Continued)

Gene Screen BC – Film Competition Results
Gene Screen BC was a huge success and the films are now being used as educational tools. 1st prize went to "Sequence Me" by Suraaj Aulakh and team; 2nd prize to "Superbug, Be Gone" by Aliya Sadeque & Daniel Vasquez; 3rd prize, "Epigenetic Landscapes" by Ben Paylor & Lauren Elliot.

Heal or Harm? Prescription Drugs, the Truth
Oct 2010 *Today's Parent* magazine featured the work of Dr Bruce Carlton, Dr Michael Hayden and Dr Rod Rassekh of BC Children's Hospital and how their research is improving drug safety for children.

Announcements:
► The next Rare Disease Foundation Microgrant deadline for submission is November 30, 2010.

Events:
► BCCGN sponsored Mini Med School XI - Clinical Genomics, Oct 13 – Nov 24, 2010.
► Am. College of Medical Genetics 20th Annual Conference, March 16-20, 2011, Vancouver, BC.

Member Awards:
► Dr. Marco Marra, Dept. Med. Gen. UBC and Director of the BC Cancer Agencies Genome Sciences Centre was awarded the Order of BC

Publications
► Ldlr-/- mice display decreased susceptibility to western-type diet-induced obesity due to increased thermogenesis. Ngai YF *et al*. Endocrin. 2010 Sep 29
► Fetal alcohol syndrome: a phenocopy of spondylocarpotarsal synostosis syndrome? Vassel J *et al*. Clin Dysmorphol. 2010 Oct 19(4):175-80.
► The principles of teratology: Are they still true? Friedman JM. Birth Defects Res A Clin Mol Teratol. 2010 Aug 12
► Family history screening: use of the three generation pedigree in clinical practice. Brock JA et al. J Obstet Gynaecol Can. 2010 Jul 32(7):663-72.
► Treatment of intractable epilepsy in a female with SLC6A8 deficiency. Mercimek-Mahmutoglu S. et al. Mol Genet Metab. 2010 Aug 26
► Spinocerebellar ataxia with axonal neuropathy. Walton C. et al. 2010 Adv Exp Med Biol. 685:75-83.
► Genome-wide identification of human micro-RNAs located in leukemia-associated genomic alterations. Starczynowski DT et al. 2010 Blood Oct 20