

## **Stephen Scherer, PhD, DSc, FRSC**

M.I.N.D. Institute Distinguished Lecturer Series – June 12, 2013

### ***Biographical Information***

**Stephen Scherer**, PhD, DSc, FRSC, holds the GlaxoSmithKline-Canadian Institutes of Health Research Endowed Chair in Genome Sciences at The Hospital for Sick Children and University of Toronto. Dr. Scherer is director of the University of Toronto's McLaughlin Centre and The Centre for Applied Genomics. He has made numerous contributions to medical genetics including mapping, sequencing and disease gene studies of human chromosome 7. In 2004, his team co-discovered global gene copy number variation (CNV) and has since shown that CNV is the most abundant type of genetic variation of human DNA. His group then identified CNV that contribute to the etiology of autism and many other disorders. The *Database of Genomic Variants* that he founded facilitates hundreds of thousands of clinical diagnoses each year. His work is documented in over 300 publications and patents and cited more than 20,000 times, ranking him as one of the top cited scientists over the past decade worldwide. Dr. Scherer has won numerous honors such as the 2004 Steacie Prize, an International Howard Hughes Medical Institute Scholarship, and the Premiers Summit Award for Medical Research. He is a distinguished Fellow of the Canadian Institute for Advanced Research, the American Association for the Advancement of Science, and the Royal Society of Canada.

### ***Presentation Abstract (4:30 pm)***

#### ***Detection of Clinically Relevant Genetic Variants in Autism Spectrum Disorder***

Autism Spectrum Disorder (ASD) demonstrates high heritability, familial clustering and ~4:1 male to female bias, yet the causes are only partially understood, due to extensive clinical and genetic heterogeneity. Whole genome sequencing (WGS) promises added value to identify novel ASD risk genes, as well as new mutations in known loci, but an assessment of its full utility in an ASD group has not been performed. In a pilot study, we used WGS to examine 32 families with ASD to detect de novo or rare inherited genetic variants predicted to be deleterious (loss-of-function and damaging missense mutations). Among ASD probands, we identified deleterious de novo mutations in 6 of 32 (19%) and X-linked or autosomal inherited alterations in 10 of 32 (31%) families (some had combinations of mutations). The proportion of families identified with such mutations was larger than has been previously reported, a yield that is in part due to the more comprehensive coverage afforded by WGS. Deleterious mutations were found in four novel, 9 known, and 8 candidate ASD risk genes. Examples include CAPRIN1 and AFF2 (both linked to the FMR1 gene that is involved in fragile X syndrome), VIP (involved in social-cognitive deficits), and other genes such as SCN2A and KCNQ2 (also linked to epilepsy), NRXN1, and CHD7, which causes ASD-associated CHARGE syndrome. Taken together, these results suggest that WGS and thorough informatic analyses may improve the detection of genetic variants likely associated with ASD or its associated clinical symptoms.