Saskatoon NGS Symposium: Improving Genomics through Collaboration and Innovation

2016

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February 25

Saskatoon NGS Symposium: Improving Genomics through Collaboration and Innovation

Thursday February 25, 2016
9 am – 4pm Symposium, 4-6pm Poster Competition and Social
Marquis Hall Exeter Room, University of Saskatchewan

Genomics holds great promise for advancing our understanding of all living organisms. Technological advancements in Genomics continue to come at alarming rate; there are numerous complexities to consider. For the uninitiated this can create confusion and make planning for an initial experiment difficult. In order to help demystify applications in NGS (Next Generation Sequencing), we have assembled leading experts, both academic and industry, to share their work and experiences in Genomics. The objective of this symposium is to provide a forum for sharing, learning, and networking. The symposium is open to anyone who is interested in or already using NGS in their research or diagnostic programs. A poster competition and social will be held from 4-6 PM, there are cash prizes to be won!

Breakfast, lunch, and coffee breaks are provided at no cost to attendees thanks to our gracious sponsors.

Overview

Next generation sequencing holds great promise for advancing the understanding the genetics of all organisms. Advances in this area continue to come at an increasing rate, and there are now several platforms to choose from. For the uninitiated this can create confusion and make planning for an initial experiment difficult. In order to help demystify NGS as an application, we have assembled a panel of academic and industry speakers experienced in the field. The objective of this symposium is to provide an overview of NGS, move on to a more detailed look at instrumentation and methods, and then hear directly from academics putting local NGS platforms to work. The symposium is open to anyone who is interested in or is already using NGS in their research or diagnostic programs. Each talk will last 20-30 minutes, and ample time will be made available for discussion.

Poster Competition

A poster session will be held from **4-6 PM** following the symposiums, featuring NGS research from industry and academia. Refreshments will be provided, and **prizes** will be awarded for the best 3 posters. Judges will be selected from the main workshop speakers.

For more information on the Canada NGS Symposia series, please contact:

Jeffrey Seitz, Vice President, D-MARK Biosciences (jeffrey.seitz@d-markbio.com)

Invited Speakers:

Andrew Sharpe, Ph.D.
Global Institute for Food Security (GIFS) and NRC Canada, Research Scientist

Dr. Andrew Sharpe received his BSc (Hons) in Biological Sciences from the U. of Leicester, UK in 1988 and his PhD in Plant Genetics from the U. of East Anglia, Norwich, UK in 1997 while working at the John Innes Centre. He has significant experience in plant genetics and genomics throughout his career both at the NRC (since 2008) and previously at AAFC in Saskatoon. He is currently working at the Global Institute for Food Security (GIFS) at the U. of Saskatchewan to establish integrated crop genomics, informatics and phenomics capacity.

"Genome Sequencing in Polyploid Crops"

Rapid advances in sequencing technologies and informatics tools have yielded new resources in terms of high quality sequenced genomes for multiple crops, including the recent delivery of the very large and complex hexaploid bread wheat genome. The presentation will outline the technical approaches to achieve these milestones as well as describe the establishment of new approaches for high throughput field phenotyping that together with the available genomics tools and resources, promise to expedite variety development of important Canadian crops.

Aaron P. White, Ph.D.
Research Scientist, Vaccine and Infectious Disease Organization
Adjunct Professor, Department of Microbiology and Immunology, University of Saskatchewan
Jarislowsky Chair in Biotechnology

I started my research life as a Biochemist (B.Sc. at University of Alberta, Ph.D. at University of Victoria), working on bacterial cell surface structures. My post-doctoral fellowship with Dr. Michael Surette at the University of Calgary focused on bacterial genetics and modern approaches to studying infectious disease. I began my research at VIDO and the U of S in 2009. I am particularly interested in understanding the lifecycle of human bacterial pathogens - the connections between environmental survival, persistence, transmission and virulence.

"NGS approaches to understand transmission of pathogenic Salmonella isolates"

For bacterial pathogens, survival is dependent upon transmission to new hosts. In the case of Salmonella Typhimurium, a common cause of human gastroenteritis, there are numerous examples of extreme persistence in food products and environmental reservoirs, but it is not well understood how this relates to virulence. We recently discovered that S. Typhimurium cells exposed to environmental stress are able to differentiate into two specialized cell types: single cells and multicellular aggregates. Transcriptome analysis revealed that 35% of genes in the genome were differentially expressed between the two populations. The single cells had many key Salmonella virulence genes up-regulated whereas the aggregates had many resistance genes highly expressed. Subsequent in vivo and in vitro testing proved that each cell type was adapted for either virulence or persistence. This research has helped us to understand potential transmission strategies for gastroenteritis-causing Salmonella isolates. We hypothesize that the single cells are best suited for direct host-to-host transmission and the aggregates can survive long-term in the environment and transmit at later time points. We are now mining the transcriptome data to identify new virulence and persistence genes.

Markus Hecker, Ph.D.
Associate Professor & Canada Research Chair in Predictive Aquatic Ecotoxicology
School of Environment and Sustainability, University of Saskatchewan

I served as an expert to the OECD and US-EPA, and am frequently invited to give presentations to national and international organizations and governments. For example, I was invited as the introductory speaker on the topic of endocrine disruption at the 17th Annual German-American Kavli Frontiers of Science Symposium of the National Academy of Science of the US. I hold a patent for Steroidogenesis Modified H295R Cells and Methods for Screening for Endocrine Disrupting Chemicals (Patent #s US 08501401 and US 08299238), and have developed, validated, and implemented several toxicity test methods, some are components of mandatory chemical screening programs such as the Endocrine Disruptor Screening Program of the US Environmental Protection Agency.

Areas of Interest - aquatic ecology/fish biology, development and application of bioanalytical techniques to assess environmental pollution, ecotoxicology, effect directed analysis, endocrine disruption, environmental risk assessment, investigation of biological effects of environmental stressors

"Toxicogenomics in Support of 21st Century Chemical Risk Assessment"

Chemical contamination of our natural ecosystems and water resources is regarded as one of the planet's greatest threats. Regulatory agencies and industry are tasked with assessing the risks of the tens of thousands of chemicals used by society, and which are ultimately released into the environment. However, current testing strategies for these chemicals rely on whole animal studies, which, in addition to ethical concerns, are associated with prohibitive time and monetary costs (e.g. to meet European Union registration goals there is a need for 54 million vertebrate animals and $13.6B USD). Thus, there is an urgent need for faster, focused, ethical, and economic testing tools. With the recent advent and advances in 'omics, bioinformatics, systems biology, and computational toxicology, scientists seem poised to make critical breakthroughs that will revolutionize predictive toxicology and elicit a paradigm shift in regulatory toxicity testing and risk assessment. This presentation reviews current developments and concepts that focus on applying 21st Century 'omics' technologies to chemical risk assessment and ecotoxicity testing.

Janet E. Hill, Ph.D.
Professor, Head & Graduate Chair
Department of Veterinary Microbiology, University of Saskatchewan

Originally from Toronto, Ontario, Janet has a background in Biology and Microbiology. Her Ph.D. research at Queen's University was in baculovirus (insect virus) pathogenesis. She did postdoctoral work in plant virology (geminivirus movement) and molecular parasitology (Trypanosoma cruzi pathogenesis) at the University of Illinois at Urbana-Champaign. Her next step was to work as a research scientist at the National Research Council of Canada Plant Biotechnology Institute, developing cpnDB and cpn60 sequence-based methods for microbial ecology and diagnostics. Janet is currently Professor and Head of Veterinary Microbiology at the University of Saskatchewan.

"Exploiting the cpn60 universal target for microbiome profiling and investigating genomic diversity in microbial communities"

Next-generation sequencing technologies present unprecedented opportunities to exploit the diagnostic potential of microbiome profiling for improving human and animal health. The ability to relate microbial community composition to clinical outcomes can be greatly affected by the resolving power of the sequence data generated. Although approaches based on sequencing of selected variable regions of the 16S rRNA gene have utility in resolving microbial community structure at the phylum, family or genus level, resolution beyond this level is limited. The universal target (UT) region of the gene encoding the 60 kDa chaperonin protein, cpn60, has been demonstrated to be a preferred sequence barcode for Bacteria, consistently providing resolution to the species or subspecies level. cpn60-based microbiome profiling has been used successfully on multiple sequencing platforms to provide high resolution profiles of animal, human, plant, soil and industry-associated microbiomes. It has also been demonstrated that the cpn60 UT sequence can be used to predict whole genome sequence relationships between bacterial taxa. This presentation will review our experience with cpn60-based microbiome profiling and demonstrate how its application has led to the discovery of previously unrecognized diversity in the human vaginal microbiome.

Leon Kochain, Ph.D.
Center Director & Research Leader
Robert Holley Center for Agriculture and Health, USDA-ARS, Cornell University

Leon V. Kochian is Director of the USDA Agricultural Research Service (ARS) Robert W. Holley Center for Agriculture and Health on the Cornell University campus. He also is Professor in the Plant Biology Section and also the Soil and Crop Science Section at Cornell University, as well as an Adjunct Scientist at Boyce Thompson Institute He received his Bachelor's degree in Botany at the University of California at Berkeley in 1978, and his Ph.D. in Plant Physiology at the University of California at Davis in 1984. In 1985 he took a position as a Plant Physiologist with USDA-ARS at the U. S. Plant, Soil and Nutrition Laboratory on the Cornell campus. Dr. Kochian became Director of the U.S. Plant, Soil and Nutrition Laboratory in 1997, and Director of the newly established USDA-ARS Robert Holley Center on the Cornell campus in 2007. Dr. Kochian's research deals with the molecular biology, physiology and genetics of mineral ion transport processes as they relate to mineral nutrient acquisition, plant responses to abiotic environmental stresses, and the role of root architecture in nutrient acquisition efficiency. This involves the interdisciplinary application of research approaches from molecular biology, genetics, physiology, membrane biophysics and computer science to understand fundamental mechanisms and genes underlying mineral nutrient acquisition, tolerance to both mineral deficiencies and mineral excess (toxic metals) in the soil, and the role of root system architecture in efficient acquisition of water and mineral nutrients. Dr. Kochian is a Fellow of the American Association for the Advancement of Science (AAAS) as well as an American Society of Plant Biologists Fellow, and is a member of the ARS Hall of Fame. Dr. Kochian was also recently named to Thomson Reuter's list of 2015's "Most Influential Scientific Minds", a citation analysis identifying the scientists who have made the most significant global impact within their respective field of study over the past 11 years.

"Investigating the Genetic Control of Root System Architecture and its Role in Mineral and Water Uptake on Marginal Soils"

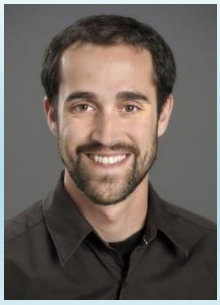
In recent years, considerable attention has been focused on root system architecture (RSA), as it has been shown that plants exert a significant degree of genetic control over this complex trait. Furthermore, there is an increasing awareness that RSA plays an important role in crop nutrient acquisition efficiency. Differences in RSA can lead to root archetypes that are more efficient and effective at acquiring nutrients such as phosphorous that have relatively low mobility in the soil, as well as root architectures better designed to acquire mobile soil nutrients such as nitrate and water. In an effort to address the major bottleneck in research on the molecular genetics of root architecture – phenotyping of RSA with high enough throughput and resolution to genetically analyze RSA traits, a number of new root imaging/analysis platforms have been developed. In this presentation, a root system architecture phenotyping and analysis platform is described that was designed to improve the flexibility and throughput for root system phenotyping. The platform employs digital imaging and software analysis tools to quantify root system architecture (RSA) in 3-dimensions (3D). Our initial work on rice employed plants whose roots were grown in transparent gellan gum containing all essential mineral nutrients. Subsequently, a specially constructed plastic mesh system was developed that maintains 3D RSA but does not impede root growth, and this system is being used to phenotype root systems in hydroponics and soil-like media. Research findings will be presented using the 3D phenotyping platform to quantify RSA traits for roots of rice and sorghum plants from linkage and association populations, and then genome wide and candidate gene association mapping studies were performed in order to investigate the genetic components of root development leading to different root system architectures.

Chris Yost, Ph.D.
Professor, Canada Research Chair in Microbes, the Environment and Food Safety
Department of Biology, University of Regina

Dr. Yost is a Professor in the Biology Department at the University of Regina. He received his PhD. in the Biological Sciences Department at the University of Calgary in 1998. He has professional research experience as a scientist with Agriculture and Agri-food Canada (Lacombe Research Centre, Lacombe, Alberta), where he studied meat microbiology and food safety. He also has international research experience as a research associate at the University of Aarhus (Aarhus, Denmark), where he studied root nodulation in *Lotus japonicus* following infection with *Mesorhizobium loti*. Dr. Yost is currently a Tier II Canada Research Chair in Microbes, The Environment and Food Safety. His expertise is on bacterial genetics of the plant symbiont *Rhizobium* where he developed INSeq technology for use in *Rhizobium.* He also has expertise in using genetic tools in applied and environmental microbiology and in particular tracking enteric pathogens and antibiotic resistance gene mobility in agricultural environments.

"Using functional genomics to study gene networks in bacteria-plant interactions"

Insertion sequencing (INSeq) is a technique for high throughput forward genetic screening that has recently (ca. 2009) become a favorable approach to studying gene function at the genome scale. INSeq relies on the use of high throughput DNA sequencing to audit the presence of hundreds of thousands of unique transposon insertions present in a pool of mutants that collectively saturate that organism's genome with transposition events. The approach can be applied under several biologically relevant conditions to identify gene function including genes involved in colonization of hosts, resistance to antibiotics, genes essential for metabolic pathways, and deducing core essential genomes . The Yost lab developed an INSeq vector for use within the Rhizobiaceae to identify genes essential for rhizobial-legume interactions. The Yost lab also uses RNA-seq methods to investigate regulatory networks in Rhizobium leguminosarum that are important in rhizosphere colonization and adaptation to environmental stressors. The talk will demonstrate how combining INSeq and RNA-seq data sets creates a powerful functional genomics approach for discovery based research in the field of plant-microbe interactions.



Andrew Cameron, Ph.D.
Associate Professor, Bacteriology
Department of Biology, University of Regina

Bacteria may be invisible but they possess vast genetic and metabolic diversity, they are found in almost every environment, and they compose the bulk of biomass on Earth. Thus, bacterial processes determine the health of our planet and our bodies.

The Cameron lab uses molecular genetics to understand the invisible niches and interactions that link the members of microbial communities. For example, what metabolites are passed between bacterial species in petroleum-contaminated soils, or how does an invasive pathogen sense that it has entered the small intestine? These questions can be answered by studying how bacteria use their genes to adapt to their surroundings. Our lab uses genomic approaches (RNA sequencing, chromatin immunoprecipitation) to gain broad insight into bacterial lifestyles by studying all genes simultaneously. Then we zoom in to the molecular level and use diverse genetic and biochemical techniques to study protein-DNA and protein-protein interactions at gene promoters.

"Whole genome sequencing for epidemiology and antibiotic resistant gene discovery"

The severe health burden of bacterial infections will continue to increase with the loss of effective antibiotics, growing and aging human populations, and eroding environmental quality. We are using next-generation DNA sequencing for: i) functional genomic studies of antibiotic resistance gene expression in model organisms and emerging pathogens, and ii) epidemiology with whole-genome sequencing to identify sources and routes of transmission of infectious disease, and to discover genes that contribute to pathogenesis and environmental persistence. I will describe our work to identify genes for environmental persistence in *Salmonella* Typhimurium and *Salmonella* Enteritidis, antibiotic resistance mechanisms and their regulation in the emerging pathogen *Acinetobacter baumannii*, and epidemiological studies of *Salmonella* and *Mycobacterium avium*.

Isobel Parkin, Ph.D.
Agriculture Canada, Research Scientist
Adjunct Professor, Department of Plant Sciences, University of Saskatchewan

Dr Parkin is an established researcher at Agriculture and Agri-Food Canada in Saskatoon. Her research focuses on the application of genomics technologies to study various important traits in Brassica species. Her group co-led the genome sequencing of a number of Brassica (and related) species important to Canadian agriculture. Dr Parkin's research exploits the now developed genome sequences to study plant evolution and control of homologous pairing in polyploid species.

"The developmental transcriptome atlas of the biofuel crop Camelina sativa"

About the organizers:

D-MARK Biosciences
www.d-markbio.com

D-MARK Biosciences specializes in providing solutions to molecular biology laboratories, genome research institutes, and diagnostic laboratories across Canada and the globe. The company was founded in 2008 by the former Canadian General Manager of a top 15 Multinational Life Sciences supply company, focusing on solutions for sequencing and PCR/qPCR. D-MARK works with the most innovative manufacturers of advanced solutions for molecular biology, allowing cutting edge research to be performed faster, more accurately, and at a lower cost. Our technologies include advanced solutions for sample collection and bio-banking, nucleic acid extraction, engineered polymerases, nucleic acid shearing and size selection, quality control instrumentation and reagents, automation, library preparation… all prior to sequencing, and then data analysis and finally data storage and security.

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For more info, please contact Jeffrey Seitz: jeffrey.seitz@d-markbio.com

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