DRIVE

Discovery, Research, Innovation and Education

Friday, April 21
&
Saturday, April 22, 2017

Bernard Snell Hall
Classroom A – 2F1.01
Classroom D – 2F1.04
Classroom F – 2J4.02
Walter MacKenzie Centre
University of Alberta Hospital
8440-112 Street
Edmonton, AB
<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Position</th>
<th>Title</th>
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</thead>
<tbody>
<tr>
<td>8:00-8:15</td>
<td>Welcome - Dr. Michael Mengel</td>
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</tr>
<tr>
<td>8:15-8:30</td>
<td>Albert Zuehlke</td>
<td>MSc</td>
<td>A Protein-Initiated DNAzyme Nanomachine</td>
</tr>
<tr>
<td>8:30-8:45</td>
<td>Colin Lloyd</td>
<td>MSc</td>
<td>Molecular epidemiology of <em>C. difficile</em> in colonized children compared to cases of <em>C. difficile</em> infection</td>
</tr>
<tr>
<td>8:45-9:00</td>
<td>Bill Chan</td>
<td>MLS Student</td>
<td>Optimizing Phenotyped Blood Inventory in Alberta Rural Hospitals</td>
</tr>
<tr>
<td>9:00-9:15</td>
<td>Carrie Malin</td>
<td>MLS Student</td>
<td>Optimization and Validation of a Robust Multiplex PCR Assay to Detect BCR-ABL1 Translocations</td>
</tr>
<tr>
<td>9:15-9:30</td>
<td>Janet Zhou</td>
<td>MLS Student</td>
<td>Proof of Concept: Evaluation of a Luminex-Based Assay for the Detection of ABO Antibodies</td>
</tr>
<tr>
<td>9:30-9:45</td>
<td>Hanyong Peng</td>
<td>Post-Doctoral Research Fellow</td>
<td>A microRNA-initiated DNAzyme motor operating in living cells</td>
</tr>
<tr>
<td>9:45-10:00</td>
<td>Ran Zhuo</td>
<td>Post-Doctoral Research Fellow</td>
<td>Luminex xTAG® Gastrointestinal Pathogen Panel Failed to Detect the Majority of Genogroup II Genotype 2 (GII.2) Noroviruses Associated with Acute Gastroenteritis in Children</td>
</tr>
<tr>
<td>10:00-10:15</td>
<td>Break</td>
<td></td>
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<tr>
<td>10:15-10:30</td>
<td>Joseph Andrews</td>
<td>Resident</td>
<td>Alberta Physician Assistance in Dying, a Review of Deaths during the First Year</td>
</tr>
<tr>
<td>10:30-10:45</td>
<td>Peter Dromparis</td>
<td>Resident</td>
<td>Molecular Injury and Repair Assessment of Ex Vivo Perfused Swine Lung Transplants</td>
</tr>
<tr>
<td>10:45-11:00</td>
<td>Lindsay Blackstock</td>
<td>PhD- Pre Candidacy</td>
<td>Sweetened Swimming Pools and a Taste of Global Media Attention</td>
</tr>
<tr>
<td>11:00-11:15</td>
<td>Yiren Cao</td>
<td>PhD- Pre Candidacy</td>
<td>Simple and Sensitive Detection of Biomarkers via Binding-induced Formation of DNA Enzyme</td>
</tr>
<tr>
<td>11:15-11:30</td>
<td>Jinhua Li</td>
<td>PhD- Post Candidacy</td>
<td>Effects of isomeric structures on cytotoxicity, formation of reactive oxygen species, and genotoxicity of halobenzoquinones, an emerging class of disinfection byproducts</td>
</tr>
<tr>
<td>11:30-11:45</td>
<td>Lin Xu</td>
<td>PhD- Post Candidacy</td>
<td>An Universal Fluorescence Assay for Homogeneous Detection of Aflatoxin B₁</td>
</tr>
<tr>
<td>11:45-12:00</td>
<td>Mahalakshmi Kumaran</td>
<td>PhD- Post Candidacy</td>
<td>Germline Copy Number Variations harboring small non-coding RNA genes and their role in conferring Breast cancer risk</td>
</tr>
<tr>
<td>12:00-1:00</td>
<td>Lunch (Bernard Snell Lower Foyer)</td>
<td></td>
<td>IMMUCOR Presentation in Bernard Snell Theatre - Next Generation Sequencing: Advancing Transplant Healthcare</td>
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</tbody>
</table>
### Innovation Sessions
**Bernard Snell Theatre**

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Position(s)</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:00-1:30</td>
<td>Dorothy Ward</td>
<td>MHRH Laboratory Manager, AHS</td>
<td>Transition (journey, success, lessons learned, tools and tips, etc.)</td>
</tr>
<tr>
<td>1:30-2:00</td>
<td>Dr. Mathew Estey</td>
<td>Clinical Chemist and Co-Director of Chemistry, DynaLIFE dx &amp; Associate Clinical Professor, Dept. of Lab Medicine and Pathology</td>
<td>In search of an improved screening test for Cystic Fibrosis-Related Diabetes: the utility of fructosamine</td>
</tr>
<tr>
<td>2:00-2:15</td>
<td>Dr. Steven Drews</td>
<td>Associate Professor, Dept. of Lab Medicine and Pathology &amp; Clinical Microbiologist, Provincial Laboratory for Public Health</td>
<td>Current clinical lab respiratory data to help inform public health decision making</td>
</tr>
<tr>
<td>2:30-3:00</td>
<td>Sharon Redel, Dr. Anna Fuezery</td>
<td>Point of Care Supervisor, AHS Clinical Biochemist, AHS &amp; Assistant Clinical Professor, Dept. of Lab Medicine and Pathology</td>
<td>&quot;A success story – Total quality management of an Epoc program in a mobile setting&quot;</td>
</tr>
</tbody>
</table>

**3:00-4:00**  
*Poster viewing & judging (Bernard Snell Upper Foyer)*

**4:00-4:15**  
*Presentation Awards / Teacher Awards / Macgregor Lecture Introduction*

**4:15-5:15**  
*Dr. John W. Macgregor Memorial Lecture  
Dr. Awadalla*

**5:30-8:00**  
*Dinner (Bernard Snell Lower Foyer)*
<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
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<tbody>
<tr>
<td>8:00-8:15</td>
<td>Anne Halpin and Deanna Manna</td>
<td>Welcome and round table introductions</td>
</tr>
<tr>
<td>8:15-8:45</td>
<td>Dr. Luis Hidalgo &amp; Anne Halpin, Alberta Health Services</td>
<td>HLA Epitopes in HLA Antibody Analysis</td>
</tr>
<tr>
<td>8:45-9:15</td>
<td>Deanna Manna &amp; Rebecca Middleton, Alberta Health Services</td>
<td>Case Study Presentation</td>
</tr>
<tr>
<td>9:15-9:45</td>
<td>Dr. Justine Turner, Pediatric Gastroenterologist</td>
<td>Celiac Disease and the HLA Laboratory: Allies in Diagnosis</td>
</tr>
<tr>
<td>9:45-10:15</td>
<td>Coffee Break</td>
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<tr>
<td>10:15-10:45</td>
<td>Kathy Tachynski</td>
<td>Transplant from the patient perspective</td>
</tr>
<tr>
<td>10:45-11:15</td>
<td>Blake Murdoch, Health Law Institute</td>
<td>Selected Topics in Organ Donation and Transplantation Ethics</td>
</tr>
<tr>
<td>11:15-11:45</td>
<td>Iwona Galaszkiewicz, Calgary Laboratory Services</td>
<td>Case Study Presentation in Hematopoietic Stem Cell Transplantation</td>
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<tr>
<td>11:45-12:15</td>
<td>Transition to joining DRIvE Days in Bernard Snell for lunch</td>
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<tr>
<td>12:45-1:15</td>
<td>Transition back to HLA Workshop in 4B1.38</td>
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<tr>
<td>1:15-1:45</td>
<td>Paul Sikorski, One Lambda Thermofisher</td>
<td>Update on current methodologies</td>
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<tr>
<td>1:45-2:00</td>
<td>Aaron Hirshfeld, BD</td>
<td>Current and new technologies from BD</td>
</tr>
<tr>
<td>2:00-2:30</td>
<td>Janet Zhou</td>
<td>Medical Laboratory Science Student Research Presentations</td>
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<tr>
<td></td>
<td>Sally Abou-Zeki</td>
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<td>Wing Kwan-Tsoi</td>
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<tr>
<td>2:30-3:00</td>
<td>Round Table Discussions</td>
<td>Discussion of Histotrac Issues and CTR Updates</td>
</tr>
<tr>
<td>3:00-3:15</td>
<td>Anne Halpin</td>
<td>Overview of HLA Learning Resources</td>
</tr>
<tr>
<td>3:15-4:15</td>
<td>Join ongoing DRIvE Days Poster Viewing in Bernard Snell Upper Foyer</td>
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<tr>
<td>4:15-4:30</td>
<td>Presentation Awards/ Teacher Awards/ MacGregor Lecture Introduction</td>
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<tr>
<td>4:30-5:30</td>
<td>Dr. John W. Macgregor Memorial Lecture Dr. Awadalla</td>
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<tr>
<td>5:30-8:30</td>
<td>Dinner (Bernard Snell Lower Foyer)</td>
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<tr>
<td>7:45-8:00</td>
<td>Registration &amp; Continental Breakfast</td>
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<tr>
<td></td>
<td><strong>Session 1 - 8:00-8:50</strong></td>
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<td><strong>Bernard Snell Theatre</strong></td>
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<tr>
<td></td>
<td><strong>Classroom A</strong></td>
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<tr>
<td></td>
<td>Marie-France Provost – Dept. of National Defence Techs: “Experience in Afghanistan”</td>
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<tr>
<td></td>
<td>Dr. Josh Raizman &amp; Dr. Kareena Schnabl: “Advances in prenatal testing using non-invasive prenatal testing: perspectives from the lab and patient”</td>
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<td><strong>Classroom D</strong></td>
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<td></td>
<td>Tsega Workineh, Terry Meunier, Barb Romansky: “Reducing the number of standing orders for inpatients”</td>
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<td><strong>Classroom F</strong></td>
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<tr>
<td></td>
<td>AP – Year in Review – Dr. Terence Colgan: “Benefits and challenges of sub-specialization in Anatomic Pathology an Ontario and College of American Pathologist’s perspective”</td>
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<td><strong>Session 2 - 9:00-9:50</strong></td>
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<td><strong>Bernard Snell Theatre</strong></td>
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<td><strong>Classroom D</strong></td>
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<tr>
<td>Simon Charlebois: “Developing the Laboratory Tech training for the Afghan National Security Forces”</td>
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<td>Dr. Patrick Nation: “Zoonoses in Alberta pets”</td>
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<td><strong>Classroom F</strong></td>
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<td></td>
<td><strong>Extra Session - 10:00-10:50</strong></td>
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<td><strong>Bernard Snell Upper Foyer</strong></td>
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<td><strong>Classroom F</strong></td>
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<td>Poster Judging</td>
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<td></td>
<td><strong>AP – Year in Review</strong></td>
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<tr>
<td>10:00-10:25 a.m.</td>
<td>Dr. Consolato Sergi: “Diagnosing Gluten-Sensitive Enteropathy-An Update”</td>
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<tr>
<td>10:30-10:55 a.m.</td>
<td>Drs. Farshid Siadat &amp; Rob West: “Scientific Rationale and Practical Implications of the recent changes in the Prostate Synoptic Reports”</td>
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<td><strong>11:00-11:15</strong></td>
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<td></td>
<td>Poster Awards &amp; Dr. RE Bell Lecture Introduction (Bernard Snell Theatre)</td>
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<td><strong>11:15-12:15</strong></td>
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<td>Dr. RE Bell Memorial Lecture (Bernard Snell Theatre) Dr. Cervinski</td>
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<td><strong>12:15-1:00</strong></td>
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<td>Lunch (Bernard Snell Lower Foyer)</td>
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<td><strong>Session 3 - 1:00-1:50</strong></td>
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<td><strong>Bernard Snell Theatre</strong></td>
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<td><strong>Classroom A</strong></td>
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<tr>
<td>Newson Ly: “Blood Bank &amp; HLA”</td>
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<td><strong>Classroom F</strong></td>
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<tr>
<td>Dr. Kinga Kowalewska-Grochowska: “Lady bouncers, X-files, and tingling throats: parasite eccentricities”</td>
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<td><strong>Session 4 - 2:00-2:50</strong></td>
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<td><strong>Bernard Snell Theatre</strong></td>
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<tr>
<td>Denise Forwick-Whalley: “The Good, the Bad, and the Ugly of the Funeral Industry”</td>
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<td><strong>Classroom A</strong></td>
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<tr>
<td>Resident Career Workshop</td>
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<td><strong>Classroom F</strong></td>
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<tr>
<td>Prenilla Naidu: “STI Testing: We Catch “Em All!””</td>
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<td><strong>3:00-3:30</strong></td>
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<td>Closing Remarks (Bernard Snell Theatre)</td>
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<tr>
<td>Presenter</td>
<td>Affiliation</td>
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<tr>
<td>Andrea Whyte</td>
<td>MLS Student</td>
<td>Evaluating the Pilot of Electronic Performance Tracking Forms for Medical Laboratory Science Students in Clinical Rotations</td>
</tr>
<tr>
<td>Christine Granley</td>
<td>MLS Student</td>
<td>Standardizing the Medical Laboratory Staff Training Curriculum Using Competency Based Assessments within the Edmonton Zone</td>
</tr>
<tr>
<td>Cindy Mah</td>
<td>MLS Student</td>
<td>Comparing the alloimmunization rates using phenotype matched units in the chronically transfused population</td>
</tr>
<tr>
<td>Jenna Smith</td>
<td>MLS Student</td>
<td>An Assessment of Discovery Learning in Medical Laboratory Science</td>
</tr>
<tr>
<td>Jessica Kilgour</td>
<td>MLS Student</td>
<td>Assessment of Bacterial Growth on Clothing Fabrics</td>
</tr>
<tr>
<td>Jing Yang (Peter) Xu</td>
<td>MLS Student</td>
<td>Development of hypersensitive tandem amplification assay for protein detection</td>
</tr>
<tr>
<td>Kelsey Dacosta</td>
<td>MLS Student</td>
<td>Quality Improvement Assessment of the Utilization of Fibrinogen Concentrate in the Edmonton Zone (EZ)</td>
</tr>
<tr>
<td>Sally Abou-Zeki</td>
<td>MLS Student</td>
<td>Frequency of AT1R-Autoantibodies in Pediatric Heart Transplant Patients: Investigating Positive Reactions</td>
</tr>
<tr>
<td>Sarah Sy</td>
<td>MLS Student</td>
<td>Predefined Criteria for Cancellation of Low Clinical Utility Peripheral Smear Requests</td>
</tr>
<tr>
<td>Wing Kwan Tsoi</td>
<td>MLS Student</td>
<td>Assessment of HLA Expression on Organ Donor Lymphocytes: Impact to Pre-Transplant Compatibility Assessment</td>
</tr>
<tr>
<td>XinNeng (Lily) Han</td>
<td>MLS Student</td>
<td>Quality Assurance in Red Cell Components – Does Number and Total Time of Transportation Event Affect Level of Hemolysis?</td>
</tr>
<tr>
<td>Younghoo Kim</td>
<td>MLS Student</td>
<td>Are we using the right red cell units and plasma components for transfusion?</td>
</tr>
<tr>
<td>Carol Chan</td>
<td>MLS Student</td>
<td>Transfusion reactions to red cells – are there donor issues at play?</td>
</tr>
<tr>
<td>Ursal Williams</td>
<td>MLS Student</td>
<td>Reducing the length of stay in the Rural Emergency Department with Point Of Care Testing</td>
</tr>
<tr>
<td>Ryan Wilson</td>
<td>MLS Student</td>
<td>Simulated Urgent Release of Fibrinogen, Platelets and other Blood Products for Bleeding Patients in Hospital Setting</td>
</tr>
<tr>
<td>Fiona Ko</td>
<td>Summer Student</td>
<td>The identification of variables for measuring the impact of near-patient respiratory virus testing in an emergency department: A literature review</td>
</tr>
<tr>
<td>Oanh Nguyen &amp; Homun Yee</td>
<td>Summer Student</td>
<td>Fluorescent in situ hybridization detection of viable Helicobacter pylori from spiked untreated river water samples</td>
</tr>
<tr>
<td>Brittney Loney</td>
<td>MSc</td>
<td>Estrogen induces G1 phase cell cycle arrest in “luminal-A-like” breast cancer cells while promoting growth in luminal B breast cancer cells.</td>
</tr>
<tr>
<td>Betty Kipkeu</td>
<td>MSc</td>
<td>Evaluation of the functional properties of cryopreserved buffy-coat derived monocytes for monocyte monolayer assay</td>
</tr>
<tr>
<td>Name</td>
<td>Degree/Candidacy</td>
<td>Project</td>
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<tr>
<td>Faisal Hirji</td>
<td>MSc</td>
<td>The detection of surface phosphoglycerate kinase (PGK) on distinct Group A Streptococcus (GAS) strains</td>
</tr>
<tr>
<td>Ian Gault</td>
<td>MSc</td>
<td>Process-Affected Water in the Oil Sands Industry of Alberta: Toxicity Attribution and Evaluating Aging as a Remediation Strategy</td>
</tr>
<tr>
<td>Ian Vander Meulen</td>
<td>MSc</td>
<td>Assessing ionic liquids as novel precursors of N-nitrosamines during water disinfection</td>
</tr>
<tr>
<td>Jeffrey Tao</td>
<td>MSc</td>
<td>A DNAzyme-motor for Detection of Intracellular ATP</td>
</tr>
<tr>
<td>Nikhita Arora</td>
<td>MSc</td>
<td>The University of Alberta Hospital Anatomical Pathology (UAH AP) Turnaround Time (TAT) Improvement Initiative</td>
</tr>
<tr>
<td>Angela Ma</td>
<td>PhD- Pre Candidacy</td>
<td>Identification and characterization of heat resistant Escherichia coli clinical isolates possessing the locus of heat resistance</td>
</tr>
<tr>
<td>Ao Ma</td>
<td>PhD- Pre Candidacy</td>
<td>CIP-1, a calcium sensor protein, encodes an important component of the p53-mediated stress response pathway</td>
</tr>
<tr>
<td>Ashley M. Newbigging</td>
<td>PhD- Pre Candidacy</td>
<td>Development of a Novel DNA-Based Bioanalytical Assay for the Detection of a Mitochondrial Disease</td>
</tr>
<tr>
<td>Bhumi Bhatt</td>
<td>PhD- Pre Candidacy</td>
<td>Diverse roles of Small RNAs: Piwi-interacting RNAs (piRNAs) and their role in cancer cachexia</td>
</tr>
<tr>
<td>Yasser Abuetabh</td>
<td>PhD- Pre Candidacy</td>
<td>Regulation of p53 and its E3/E4 ubiquitin ligases by Wip1</td>
</tr>
<tr>
<td>Yung-Hsing (Winston) Huang</td>
<td>PhD- Pre Candidacy</td>
<td>Myeloma cells acquire STAT3 activity and dependence in established three-dimensional reconstructed bone matrix (3D/rBM) model</td>
</tr>
<tr>
<td>Chengsen Chai</td>
<td>PhD- Post Candidacy</td>
<td>Regulation of tumor suppressor PTEN and its E3 ligase NEDD4-1 by selected microRNAs</td>
</tr>
<tr>
<td>Gurnit Kaur</td>
<td>PhD- Post Candidacy</td>
<td>Differences in the Biliary Excretion of Arsenic by Rat and Human Sandwich-Cultured Hepatocytes</td>
</tr>
<tr>
<td>Lacey Haddon</td>
<td>PhD- Post Candidacy</td>
<td>Using Chromatin Loops to Unravel the Paradox of Diagnosing ER+ Breast Cancers</td>
</tr>
<tr>
<td>Maram Hulbah</td>
<td>PhD- Post Candidacy</td>
<td>Group B Streptococcal virulence is enhanced in the presence of erythritol, a polyol (sugar alcohol)</td>
</tr>
<tr>
<td>Ruqayyah J. Almizraq</td>
<td>PhD- Post Candidacy</td>
<td>Characterization of Extracellular Vesicles Is Influenced by Method of Detection, Blood Manufacturing Processes and Storage Duration</td>
</tr>
<tr>
<td>Sudha Bhavanam</td>
<td>PhD- Post Candidacy</td>
<td>A history of Bacillus Calmette–Guerin (BCG) vaccine is associated with sustained reduced mycobacterial load and transiently increased interferon-γ production in an eight day in vitro model of Mycobacterium tuberculosis H37Ra infection</td>
</tr>
<tr>
<td>Yanwen Lin</td>
<td>PhD- Post Candidacy</td>
<td>Detection of proteins using a DNA three-way junction and gold nanoparticle amplification by ICP-MS</td>
</tr>
<tr>
<td>Eloisa Hasing</td>
<td>Post-Doctoral Research Fellow</td>
<td>Molecular epidemiology of Norovirus Outbreaks in Alberta, Canada: 2012-2016</td>
</tr>
<tr>
<td>Name</td>
<td>Role</td>
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<tr>
<td>Fan Shen</td>
<td>Post-Doctoral Research Fellow</td>
<td>Nuclear acids modifications in type 2 diabetes mellitus (t2dm): a human and a t2dm animal model</td>
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<tr>
<td>Guang Huang</td>
<td>Post-Doctoral Research Fellow</td>
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**Title:** A Protein-Initiated DNAzyme Nanomachine

**Authors:** Albert Zuehlke and Hongquan Zhang

**Background and Aim:**
Onsite analysis relies on portable and convenient assays that retain high sensitivity. Current methods for protein biomarker detection have difficulty adapting to point-of-care testing due to labour intensive procedures, non-portable instrumentation, and operator training. Herein, we aim to develop a rapid, sensitive and specific protein biomarker detection assay that is adaptable to different protein targets, while retaining a simple mix-and-read format.

**Material and Methods:**
This assay features gold nanoparticles (AuNPs) functionalized with two types of DNA strands (Figure 1). The AuNPs serve two functions: i) a scaffold for DNA attachment and ii) a highly efficient fluorescence quencher. The first type of DNA strand contains a fluorophore for signal generation. The second type of DNA strand contains a DNAzyme inactivated by a hybridized blocker strand. Removal of the blocker strand is dependent on binding-induced DNA assembly (BINDA). BINDA is initiated by the presence of a target protein bound by two target-specific probes. The probes partially hybridize to each other, initiating toehold-mediated displacement of the blocker strand. The unblocked DNAzyme then cleaves hundreds of nearby fluorophore labelled strands, generating an amplified signal.

**Results:**
Proof of concept using biotin probes and streptavidin target yields a detection limit approaching 1pM. Dynamic range is between 0-200pM of target.

**Conclusions:**
Combining the specificity of BINDA with the amplifiable signal from the DNAzyme Nanomachine allows for development of a sensitive, specific, homogeneous, isothermal, and adaptable assay for onsite analysis with health and environmental application potential.

**Figure 1:** Protein-Initiated DNAzyme Nanomachine a) AuNPs are labelled with tens of a biotin short-arm DNA strand and hundreds of a fluorescein labelled DNA strand. Fluorescence is quenched due to close proximity of fluorophore to the AuNP surface. Using streptavidin as an adaptor, biotinylated DNAzymes hybridized with a blocker strand are linked to the AuNP. Probes L1 and R1 are free in solution and bind to the specific protein target. This BINDA event results in stable, partial hybridization between L1 and R1. b) The partial non-hybridized sequences of L1-R1 then mediate a toe-hold displacement of the blocker strand. The unblocked DNAzyme is then able to recognize its target DNA sequence through complementary regions. c) Cleavage of the fluorescein substrate strand removes the...
fluorophore from the quenching proximity of the AuNP, generating a fluorescent signal. d) The activated DNAzyme moves along the AuNP surface cleaving all available substrate strands, leading to amplified fluorescent signal.

**Title:** Molecular epidemiology of *C. difficile* in colonized children compared to cases of *C. difficile* infection.

**Authors:** Lloyd, C., Parsons, B., Chui, L. and The APPETITE Team.

**Background and Aim:** Community-acquired *C. difficile* infections (CDI) are an area of increasing concern in *C. difficile* epidemiology. Previous studies have identified that infant contact could be a risk factor for CDI and that *C. difficile* strains in colonized children are similar to those in CDI cases by molecular typing. Infants are typically asymptptomatically colonized which confounds CDI diagnoses. Our study aims to identify the *C. difficile* strains detected in a community pediatric cohort compared to strains implicated in cases of CDI in Alberta.

**Material and Methods:**
*C. difficile* was isolated from the stool of asymptomatic children and those with diarrhea and/or vomiting from the community for comparison to adult and pediatric CDI cases. Molecular fingerprinting of *C. difficile* isolates was performed using PCR-ribotyping and Pulsed-Field Gel Electrophoresis (PFGE). Toxin production was determined using the C. DIFF QUIK CHEK COMPLETE®.

**Results:**
Production of *C. difficile* toxin was comparable in colonized children regardless of symptoms (42.9% asymptomatic vs 62.2% symptomatic). Ribotype 106 was predominant in colonized children and pediatric CDI (27.6% and 27.8% respectively) while adult CDI cases were predominated by the epidemic ribotype 027 (44.3%). Overall, 18 ribotypes were shared between colonized infants and CDI cases, and subtyping identified highly related isolates that were shared between cohorts.

**Conclusions:**
Given similar toxin positivity between symptomatic and asymptomatic children, it is unlikely *C. difficile* colonization contributed to diarrhea or vomiting even though these strains share some common ribotypes with pediatric and adult CDI cases. This observation is further supported by previous published studies.
Title: Optimizing Phenotyped Blood Inventory in Alberta Rural Hospitals

Authors: Chan B, Stepien J, Maguire A, To L, Nahiriak S, Hannon J, Lagrange C, Richardson T, Clarke G

Background and Aim:
Blood is a perishable, scarce resource that requires proper inventory management to ensure appropriate supply while minimizing waste. Remote locations of rural hospitals can limit quick access to phenotypically matched blood for patients who have clinically significant antibody(ies). To circumvent long transport times, antigen negative units may be stocked proactively.

Material and Methods:
Utilization data from 16 rural hospitals were collected. Total red blood cell (RBC) transfusions, redistribution outdates and clinically significant antibodies were reviewed for all sites from previous 2 years. Current blood inventory was assessed and compared to determine the need for adjustment. Estimates for antigen negative unit numbers and ABO types were developed using a published inventory calculator, and based on the medical services each hospital provided; recommendations for phenotyped inventory were developed.

Results:
Analysis of RBC utilization data demonstrated the need for a phenotyped inventory. Inventory was individually adjusted based on the site-specific antibody history. Antigen negative unit numbers reflects the site demand and the antigen frequency in the donor population. E-,K- units are the highest in demand.

Conclusions:
Clinically significant antibodies can cause delays in transfusion availability. Increased turnaround times are a problem in remote hospitals because of their delayed access to blood suppliers secondary to distance. Creating an optimized blood inventory that has antigen negative units may allow for efficient clinical support. This process may eliminate long wait times while maintaining high quality and safety. Follow-up assessment of delay between blood orders and transfusions will allow us to assess efficacy of this strategy.

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Figure 1: Yearly Comparison of Total Red Blood Cell Transfusion in North Zone Hospitals
Title: Optimization and Validation of a Robust Multiplex PCR Assay to Detect BCR-ABL1 Translocations

Authors: Malin C, Coffin J, Hart T, and Izevbaye I

Background and Aim:
The product of a t(9;22) reciprocal translocation is the BCR-ABL fusion gene, expressed in approximately 95% and 15-25% of CML and ALL patients, respectively. Depending where the genes break and fuse, 14 transcripts are theoretically possible. To date, 9 breakpoints have been published: b3a2 (e14a2), b2a2 (e13a2), e1a2, e6a2, e8a2, e19a2, b3a2, b3a3, and e1a3. The b3a2 and b2a2 transcripts comprise 95% of CML patients whereas 70% of B-ALL patients express the e1a2 transcript. The remaining 6 breakpoints are rare. This project aimed to increase robustness of BCR-ABL transcript detection, reliably detect all published transcripts, and determine their limit of detection.

Material and Methods:
Design of the assay was based on the work of Burmeister and Reinhardt. This assay utilized previously tested patient cDNA amplified using fluorescently labeled primers in a single-round, highly sensitive PCR. Capillary electrophoresis using the ABI 3500XL instrument was then performed to identify the resultant PCR products.

Results:
This assay is rapid and robust and can detect 8 of 9 published transcripts. Transcripts from b3a2, b2a2, and e1a2 fusions can be detected at a 10-4 dilution from 100% whereas the rare transcripts can be detected at 100 copies/μL.

Conclusions:
Implementation of this assay in the Molecular Pathology lab at the University of Alberta will increase sample throughput, which will help technologists meet established turnaround time to ensure optimal patient care.
Title: Proof of Concept: Evaluation of a Luminex-Based Assay for the Detection of ABO Antibodies

Authors: Janet Zhou¹, Anne Halpin¹,²,³,⁴, Jean Pearcey²,⁴, Todd L Lowary⁵,⁶, Christopher W Cairo⁵,⁶, Gour Daskhan⁵,⁶, Bruce Motyka²,³,⁴, Lori J West²,³,⁴,⁶,  
1. Laboratory Medicine and Pathology, University of Alberta  
2. Department of Pediatrics, University of Alberta  
3. Canadian National Transplant Research Program  
4. Alberta Transplant Institute  
5. Department of Chemistry and Alberta Glyomics Centre, University of Alberta  
6. Canadian Glycomics Network

Background and Aim:  
ABO antibody levels are traditionally assessed by hemagglutination. However, hemagglutination cannot accurately differentiate antibody isotypes, nor distinguish between ABO-subtype antigens, which are expressed differently on tissues and organs vs erythrocytes. Our goal was to develop a Luminex-based assay for the detection of IgG and IgM ABO subtype antibodies.

Material and Methods:  
Synthetically made human blood group antigen subtypes A-II, -III and -IV were conjugated to bovine serum albumin (BSA), and then coupled to Luminex beads by a carbodiimide reaction. Antigens were detected with IgG and IgM anti-A monoclonal antibodies either directly labeled with phycoerythrin (PE) or indirectly, with PE-labeled secondary antibodies. Different amounts of antigen were coupled to optimize mean fluorescence intensity (MFI) output on a Luminex-200. Finally, a checkerboard titration was performed to determine the optimal dilutions of human plasma containing anti-A and IgG PE-labeled antibody.

Results:  
The subtype antigens were successfully coupled to Luminex beads, as demonstrated by linear increases in MFI as concentrations of primary antibodies doubled. Saturated bead MFIs were achieved, demonstrating sufficient upper limit sensitivity. Similar results were also seen with human plasma. A(II-IV)-specific antibody was detected in a multiplex assay, demonstrating the assay’s specificity.

Conclusions:  
A novel Luminex-based assay for the detection of ABO-subtype antibodies was developed with the potential to be adapted for clinical assessment of IgG/IgM ABO subtype-specific antibodies in ABO-incompatible transplant patients. Future studies will optimize this assay using plasma with known levels of ABO antibody. Additional antigen-subtypes will be tested similarly.

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**Figure 1:** Representative graphs chosen from many trials demonstrating the success of antigen coupling as well as the ability to detect subtype antigens using IgG and IgM monoclonal anti-A antibodies.
**Title:** A microRNA-initiated DNAzyme motor operating in living cells

**Authors:** Hanyong Peng, Hongquan Zhang, Xing-fang Li, and X. Chris Le

**Background and Aim:**
Synthetic DNA motors have great potential to mimic natural protein motors in cells; but the operation of synthetic DNA motors in living cells remains challenging and has not been demonstrated. Here, we aim to construct a DNAzyme motor that operates in living cells in response to a specific intracellular target.

**Material and Methods:**
The non-cancerous (MCF-10A), primary cancerous (MCF-7), and metastatic breast cancer (MDA-MB-231) cells are used in this project. Specifically designed oligonucleotides were conjugated to gold nanoparticles to build a nanomotor for miRNA detection.

**Results:**
A DNAzyme motors responding to a microRNA was constructed by conjugating hundreds of substrate strands, and decades of inactive DNAzyme strands to a single gold nanoparticle (AuNP). In the presence of target microRNA, the DNAzyme is activated to cleave the substrate strands on the AuNP, initiating autonomous, stepwise movement of DNAzyme along AuNP. The motor is able to translate a single binding event into cleavage of hundreds of substrates from a single AuNP, resulting in enhanced detection capability. This DNAzyme motor was used for amplified detection and imaging of specific microRNA in living cells.

**Conclusions:**
We demonstrate, for the first time, the accomplishment of the operation of a synthetic DNA motor in living cells. We envision many applications of the DNAzyme motor strategy, such as sensing intracellular molecules, imaging live cells, regulating cellular functions and facilitating drug delivery.
Title: Alberta Physician Assistance in Dying, a Review of Deaths during the First Year.

Authors: Joseph Andrews, M.D.¹, Seth H. Weinberg, Ph.D.², Mitchell Weinberg, M.D.³  
¹. Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, Alberta.  
². Department of Biomedical Engineering, Virginia Commonwealth University, Richmond, Virginia.  
³. Office of the Chief Medical Examiner, Edmonton, Alberta.

Background and Aim:  
In the 2015 case Carter v Canada, the Supreme Court of Canada deemed a provision in the Canadian Criminal Code, which prohibited medical assistance in dying (MAID), as contradicting the Canadian Charter of Rights and Freedom. Therefore, in June 2016 the Canadian government implemented Bill C-14, which legalizes MAID for terminally ill patients. In Alberta, MAID involves a strict stepwise protocol and after death a forensic pathologist examines the deceased. The objective of this presentation is to provide an overview of the data acquired from the Office of the Chief Medical Examiner for all MAID deaths during 2016 and early 2017.

Material and Methods:  
We collected demographic data including date of death; age; gender; location of death (rural vs urban); and the patient’s underlying medical reason for obtaining MAID.

Results:  
Between April 2016 and February 2017, 95 MAID deaths occurred in Alberta: the underlying medical condition for seeking MAID was terminal cancer in 63 patients (66%), degenerative neurological disease in 21 patients (22%), and other medical illnesses in 11 patients (12%). The number of males and females was almost equivalent (49 females and 46 males). Most patients (62%) resided in either the cities of Edmonton or Calgary versus in a rural location (38%). On a population basis, there have been 24.4 MAID deaths per million residents per year in Alberta thus far.

Conclusions:  
MAID is a new, yet controversial, option for terminally ill patients and this presentation will overview the current trends of MAID deaths in Alberta.
Title: Molecular Injury and Repair Assessment of Ex Vivo Perfused Swine Lung Transplants.

Authors: P Dromparis, S Wagner, N Abelnaz, S Himmat, J Luc, D Freed, J Nagendran, M Mengel, and B Adam.

Background and Aim:
Due to acute lung injury (ALI), only 20% of donated lungs are suitable for transplant. Evidence suggests ex vivo lung perfusion (EVLP) may improve lung quality over the current gold-standard, cold static preservation (CSP), but the molecular mechanisms driving this are unclear. We aim to define and validate a set of molecular markers that quantify ALI to monitor lung quality before, during and after EVLP.

Material and Methods:
Swine lung biopsies were collected from lungs exposed to EVLP (N=34) or CSP (N=7) treatments at 0 hours (T0) and 12 hours (T12). RNA expression of 53 ALI-associated genes were quantified with the NanoString nCounter system. Histological analysis was performed on H&E slides. Functional parameters were documented during EVLP. Data were analyzed with nSolver and R.

Results:
Heat map analysis demonstrated differing gene expression between treatment groups. Volcano plot analysis identified 10 'repair' genes and 2 'injury' genes significantly different between EVLP-T12 and all other groups (Figure 1). 'Repair' genes were significantly increased in EVLP-T12 but not CSP-T12 group compared to respective T0 controls. 'Repair' gene expression inversely correlated with interstitial edema (r=-0.379; p=0.012), interstitial inflammation (r=-0.531; p=0.001), and interstitial neutrophils/HPF (r=-0.361; p=0.021). 'Injury' gene expression inversely correlated with PaO2/FiO2 ratio (r=-0.521; p=0.004), lung compliance (r=-0.539; p=0.003) and pulmonary artery pressure (r=0.395; p=0.037).

Conclusions:
We identified gene sets for ALI quantification that may be used for molecular monitoring of tissue repair during EVLP, a potential tool for tailoring ex vivo protocols in human transplant lungs.
**Title:** Sweetened Swimming Pools and a Taste of Global Media Attention

**Authors:** Lindsay K. Jmaiff Blackstock and Xing-Fang Li

**Background and Aim:**
Acesulfame-K (ACE) is a widely consumed artificial sweetener. It is rapidly excreted, exclusively in urine. Compounds in urine can react with disinfectants (e.g. chlorine) to form nitrogenous disinfection byproducts (N-DBPs) that may negatively affect health. Trichloramine is a volatile N-DBP, eye irritant, and is linked to asthma in professional swimmers. We aimed to determine occurrence of ACE in pools and verify if ACE can be used as a urinary indicator in recreational water.

**Material and Methods:**
Investigating occurrence and variability of ACE, we sampled 29 pools and tubs then monitored two sized swimming pools over three weeks. We pooled 20 Canadian urine samples for ACE analysis. Samples were analyzed using high performance liquid chromatography tandem mass spectrometry in multiple-reaction-monitoring mode.

**Results:**
ACE occurrence was 100%, ranging from 30-7110 ng/L. Average ACE in the small and large pools were 156 and 210 ng/L with %RSDs of 15 and 18%, respectively. Average ACE in Canadian urine was 2360 ng/mL. We estimated approximately 30 and 75 L of urine in each pool.

Within 24 hours of publication, over 100 news outlets in several countries and languages covered our research. Unfortunately many headlines misrepresented the data; calling the study “gross” or broadcasting “how much pee in your pool?” An immense effort ensued during interviews to emphasize the health benefits of swimming over risks of urine in pools.

**Conclusions:**
The global attention was used to promote good swimmer hygiene for public health: continue swimming but rinse off and go pee before entering pools and everyone will benefit.

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**Figure 1:** Altmetric score for our recently published paper Sweetened Swimming Pools and Hot Tubs [https://www.altmetric.com/details/16888238](https://www.altmetric.com/details/16888238) [accessed 10 Mar 2017]
**Title:** Simple and Sensitive Detection of Biomarkers via Binding-induced Formation of DNA Enzyme

**Authors:** Yiren Cao, Hongquan Zhang, X. Chris Le

**Background and Aim:**
Detection of biomarkers can contribute to both diagnosis of diseases and assessment of human exposure to environmental contaminants. However, conventional methods are laborious, time-consuming and not sensitive for the detection of trace amount of protein target. Therefore, the aim of this project is to use the DNA enzyme to achieve a simple and sensitive detection of proteins.

**Material and Methods:**
We designed two partial DNA enzymes which are inactive to substrates. In the presence of the target protein, binding-induced formation of full DNA enzyme restores the catalytic activity and enables the cleavage of substrates conjugated with fluorophores. Real-time monitoring of fluorescence was used to analyze the signal amplification generated from released fluorophores.

**Results:**
Research results demonstrated that amplified fluorescence signal was proportional to the concentration of a model protein ranging from 5 to 500 pM. Sensitivity of protein detection was improved greatly because of DNA enzyme-mediated isothermal amplification.

**Conclusions:**
This assay exhibits high sensitivity and avoids the separation steps in traditional methods. By changing affinity ligands on partial DNA enzymes, the proposed method has potential applications on point-of-care detection and on-site analysis of various targets.
**Title:** Germline Copy Number Variations harboring small non-coding RNA genes and their role in conferring Breast cancer risk

**Authors:** M Kumaran¹, P Krishnan¹, Y Yasui², C Cass³, S Damaraju¹

1. Departments of Laboratory Medicine and Pathology
2. School of Public Health
3. Oncology, University of Alberta, Edmonton, Canada,

**Background and Aim:**
The role of germline Copy Number Variants (CNVs) in genetic predisposition of Breast Cancer (BC) is still evolving. We hypothesize that germline CNVs harbor small RNA genes (miRNA, piRNA, tRNA and snoRNA) and these genes show expression in breast tumors, and affect regulation of downstream target genes to confer BC risk.

Objectives are to 1) Identify CNVs associated with BC risk; 2) Identify small RNA regions within the CNVs; 3) Demonstrate breast tumor specific expression of small RNAs mapping to CNV regions; 4) Predict the miRNA regulated mRNA targets in breast tumors and affected pathways.

**Materials and Methods:**
Genome-wide CNVs were profiled using Affymetrix Human SNP 6 array for 722 samples (in-house) and 495 TCGA samples. All data analysis was performed using Partek Genomics Suite. NGS data (small RNA and mRNA) was accessed for 85 TCGA breast tissue samples (subset of 495) for expression and correlation analysis. miRNA target genes were predicted using Target Scan. Associated pathways were identified using Ingenuity Pathway Analysis.

**Results:**
We have identified 1829 germline CNVs with embedded small RNA genes associated with BC. 34 small RNAs showed breast tissue specific expression. Of these, 10 miRNAs potentially target 156 genes. Genes enriched in pathways such as mismatch repair, protein ubiquitination, BRCA1, hereditary BC signaling, and telomerase extension were identified.

**Conclusion:**
This study offers functional insights of germline CNVs and their role in BC etiology, and we show that expressions of small RNAs embedded within CNVs potentially regulate mRNAs in a tissue specific manner.
Title: Effects of isomeric structures on cytotoxicity, formation of reactive oxygen species, and genotoxicity of halobenzoquinones, an emerging class of disinfection byproducts

Authors: Jinhua Li, Birget Moe, and Xing-Fang Li

Background and Aim:
Halobenzoquinones (HBQs) are a structurally diverse class of emerging water disinfection byproducts (DBPs). However, the effects of isomeric structures on HBQ-toxicity are unclear. This study examined the effects of isomeric structure of HBQs on their cytotoxicity, formation of reactive oxygen species (ROS), and genotoxicity.

Material and Methods:
Two pairs of HBQ isomers were studied, including 2,6-dichloro-1,4-benzoquinone (2,6-DCBQ) and its isomer 2,5-dichloro-1,4-benzoquinone (2,5-DCBQ), 2,6-dibromo-1,4-benzoquinone (2,6-DBBQ) and its isomer 2,5-dibromo-1,4-benzoquinone (2,5-DBBQ). The cytotoxic effects of HBQ isomers on Chinese hamster ovary (CHO-K1) cells were determined using an impedance-based real-time cell analysis (RTCA) method. In parallel, cellular ROS and p53 protein induced by HBQs were measured.

Results:
Dynamic responses and IC50 histograms were obtained using RTCA, clearly ranking the cytotoxicity of the HBQs in CHO-K1 cells. Strong isomeric structure effects were shown with 2,5-HBQ isomers inducing greater cytotoxicity than their corresponding 2,6-HBQ isomers (P<0.05). Determination of HBQ-induced ROS further supports isomeric structure effects. HBQ-induced genotoxicity was shown as increased levels of p53 protein, and this also supports isomeric structure effects. Pearson correlation analysis of the HBQ toxicity measurements with their physicochemical parameters demonstrates that dipole moment is the major structural influences on isomer toxicity.

Conclusions:
This study suggests that formation and occurrence of highly toxic 2,5-HBQs warrant further investigation to fully assess the impact of HBQs in drinking water.
Title: A Universal Fluorescence Assay for Homogeneous Detection of Aflatoxin B_1

Authors: Lin Xu, Hongquan Zhang*, Zhaowei Zhang*, Peiwu Li*, X. Chris Le*

Background and Aim:  
Aflatoxin B_1 (AFB_1), a common food contaminant, is a toxic secondary metabolite mainly produced by Aspergillus flavus and A. parasiticus. Due to its toxicity and carcinogenicity, reliable and sensitive methods are required to detect AFB_1 contamination. Here, we demonstrate an universal binding-induced fluorescence turn-on assay for AFB_1. This assay combines antibody-antigen recognition, binding-induced DNA assembly, and the fluorescence quenching property of gold nanoparticles (AuNP).

Material and Methods:  
Scheme 1 shows the principle. It is based on binding-induced fluorescence recovery and competition between AFB_1 and fluorophore-labeled antigen. In the absence of AFB_1, antibody immobilized on AuNP specifically captures fluorophore-labeled antigen, allowing for the complementary DNA sequence to hybridize due to the increased local concentration. This hybridization brings the fluorophore into close proximity to the AuNP, resulting in quenching of the fluorescence. In the presence of AFB_1, the AFB_1 binds to the antibody immobilized on the AuNP, competing off the fluorophore-labeled antigen. Released from the AuNP, the fluorophore-labeled antigen in solution is fluorescent.

Results:  
The length of complementary fluorophore-labeled sequence, the antibody density on AuNP, and antibody to antigen ratio were optimized to achieve the highest signal-to-background ratio. The method showed a linear dynamic range of 5-50 nM and a detection limit of 2.3 nM.

Conclusions:  
We demonstrated a novel, universal binding-induced fluorescence turn-on assay for AFB_1. This homogeneous fluorescence assay can be extended to other mycotoxin targets by simply changing the specific antibody.
Poster Presentations
**Title:** Evaluating the Pilot of Electronic Performance Tracking Forms for Medical Laboratory Science Students in Clinical Rotations

**Authors:** Andrea Whyte, Lisa Purdy, Valentin Villatoro

**Background and Aim:**
Technology is an integral part of education and its use to enhance education is an emerging area of research. This study evaluated the pilot of electronic performance tracking forms (EPTF) for the hematology clinical rotation of Medical Laboratory Science (MLS) students at the University of Alberta.

**Material and Methods:**
Multi-methods were used to evaluate the EPTF. MLS clinical students and trainers completed email surveys. Two trainers that used the forms more than once, clinical educators and a lab supervisor at a participating clinical site were interviewed. Interview responses were transcribed and anonymized, and data was analyzed using thematic analysis. Descriptive statistics were applied to Likert scale responses.

**Results:**
There is a clear desire amongst educators, students, and trainers to implement an online learning management system for MLS students in clinical rotations. The EPTF removed the worry of losing papers and allowed educators to track student progress in real time. Themes such as challenges and benefits of implementing the forms, transferability beyond hematology, and communication were identified. Areas for future improvement such as ease of accessing forms were also identified.

**Conclusions:**
This study demonstrated a desire for electronic progress tracking and the benefits and challenges involved in implementing it. This pilot had a small sample size and was specific to the MLS program in Edmonton; however, these findings can provide guidance for others aiming to adopt more technology into educational systems.
Title: Transfusion reactions to red cells – are there donor issues at play?

Authors: Carol Chan, Heather Blain, Jason Acker, Gwen Clarke, Susan Nahiriak

Background and Aim:
It has been shown donor characteristics and unit processing methods are associated with patient outcome after transfusion with red blood cell (RBC) units. The aim of the study is to determine if there is a relationship between donor characteristics (age and sex) and processing methods to the types and severities of transfusion reactions after a RBC unit is transfused in the Edmonton zone. Additional Variables examined for association are patient age, patient sex, unit modifiers, other products issued and sex-match/mismatch units.

Material and Methods:
Data was obtained from the Edmonton Zone’s Sunquest and Canadian Blood Services (CBS) from 2014 to 2016. The data was split into 2 cohorts, one without combination of transfusion reactions/severities and one with combination of the outcomes. Data was entered into the SPSS statistical program to perform Chi-square tests and descriptive statistics for analysis.

Results:
A higher proportion of red cell filtered (top/bottom) RBC products were implicated in transfusion reactions than for whole blood filtered (bottom/bottom) RBC products. There was no significant association seen between donor sex, patient sex, unit modifiers, donor recipient sex match/mismatch and the types and severity of transfusion reaction.

Conclusions:
The method of blood component manufacturing may be affecting the incidence and severity of transfusion reactions. However differences in the proportion of RBC filtered and whole blood cell filtered products transfused in the Edmonton Zone need to be considered for future analysis.
Title: Standardizing the Medical Laboratory Staff Training Curriculum Using Competency Based Assessments within the Edmonton Zone

Authors: Granley C, Lyon B, Villatoro V

Background and Aim:
Newly hired laboratory staff requires training on site-specific procedures if they are expected to produce and report accurate patient results. Current training curricula assesses clinical competence at a basic level but are not standardized. A formal, standardized training curriculum offers several advantages. Trainers can ensure that all relevant knowledge is covered; trainees’ competency can be verified and if required, augmented; misunderstandings can be minimized, enhancing patient care. This project aims to create a standardized curriculum to train and assess laboratory staff in the Edmonton Zone. The curriculum will address the information staff require to be competent. It will give trainers and supervisors a tool for assessing staff competency and provide a record of this information.

Material and Methods:
Edmonton Zone laboratories were surveyed to assess the current training curriculum to discover any of improvement. A standardized format was created for UAH laboratory staff utilizing these survey results. The new curriculum was reviewed by Edmonton Zone laboratory staff. Feedback was collected through surveys.

Results:
Our initial survey showed that there is a need for standardization and improvement of training curricula in the Edmonton Zone. Evaluation of the new training curriculum showed that it assess the knowledge of staff, enables feedback to trainees to enhance professional growth, identifies areas needing improvement and documents staff training and competency consistently.

Conclusions:
Standardized medical laboratory training curriculums can be created using existing methods and tools to ensure all laboratory staff working in a medical lab are competent to produce and report quality patient results.
Title: Comparing the alloimmunization rates using phenotype matched units in the chronically transfused population


Background and Aim:
Individuals dependent on red cell transfusions have a higher risk of alloimmunization. Previous studies have focused on implementing phenotype matching in order to reduce the rates of alloimmunization, however, in the Edmonton zone, phenotype matching for chronically transfused patients has been implemented since a previous study done in 2013. This study aimed to determine whether or not phenotype matching has reduced the alloimmunization rate since its implementation.

Material and Methods:
Chronically transfused patients were identified through 2016 RBC transfusion data. Patient antibodies and phenotype information was collected and compared to information from 2013 to 2015. We found dates were non-phenomatched transfusions were issued and compared the dates of the non-phenomatched transfusions to the dates when antibodies were discovered.

Results:
There was an initial drop in the alloimmunization rate from 40% in 2013 to 30% in 2014, but has stayed steady since 2014. Phenotype matching has increased steadily during the study period, with full phenotypes becoming more prevalent. 58% of 51 patients in 2016 with phenotype data had 192 non-phenomatched transfusions. 10% of those patients developed an antibody as a result of that non-phenomatched transfusion.

Conclusions:
The alloimmunization rate has dropped and the number of patients with phenotype data has increased, suggesting phenotype matching has improved the alloimmunization rate. However, there are a significant number of patients receiving non-phenomatched units, but only a small proportion of those patients develop an antibody that is a direct result of the non-phenomatched transfusions. Review of phenotyped inventory stock may further improve management of these chronic patients.
Title: An Assessment of Discovery Learning in Medical Laboratory Science

Authors: Jenna Smith, Roberta Martindale, Meagan Homer, Lisa Purdy

Background and Aim:
Discovery Learning (DL) is a learning style that allows small student groups to work through a case study guided by a facilitator. Specific group roles of scribe and leader are assigned while the entire group creates learning objectives to research to solve the case. DL is said to increase a student's ability to think critically, and problem-solve.1 DL is well studied in nursing and medicine; however, no academic evaluation has been conducted in Medical Laboratory Science (MLS). The aim of this study was to assess if there is a perceived increase in critical thinking and problem solving among MLS students and alumni as a result of DL.

Material and Methods:
Surveys were sent to current students and alumni (2007-2016). Two faculty who utilize DL in their courses were interviewed, and course evaluations exploring DL were examined. Data was analyzed using a combination of statistical and thematic analysis.

Results:

![Bar Chart: DL Increases Critical Thinking and Problem Solving Compared to TL]

Figure 1: 22 alumni (48%) and 10 students (27%) agree that DL increases their ability to think critically and problem solve. These values are lower than other health professions; studies reported in the literature cite as high as 85% agreement.1 TL is defined as traditional lecture.

Conclusions:
From this study, it is concluded that although alumni report higher critical thinking and problem-solving learned from DL compared to current students, both remain lower than other health professions. To further study why the disparity exists a California Critical Thinking Skills Test (CCTST) could be employed.

References:
**Title:** Assessment of Bacterial Growth on Clothing Fabrics

**Authors:** Jessica Kilgour, Rachel McQueen

**Background and Aim:**
Bacteria can colonize clothing fabrics through direct contact and sweat, resulting in infection control and industrial concerns. For example, potentially pathogenic bacteria can colonize healthcare provider’s clothing; certain bacteria can be odour-causing as well as cause deterioration and discoloration of textiles. There have been some conflicting results in the literature on the effect of fibre type on bacterial growth with suggestions of a possible time-dependent difference in the rate of growth on different fabric types. This study was aimed at comparing the selective growth of common skin flora on a variety of natural and synthetic fabrics to find any time-dependent differences in growth and persistence of bacteria.

**Material and Methods:**
Micrococcus luteus, Bacillus cereus, and Staphylococcus aureus strains were incubated on nylon, wool, polyester, and cotton fabric samples. Bacterial extractions were carried out and colony counts performed at 3 to 4 day intervals for 31 days to assess the bacterial growth.

**Results:**
Wool had significantly higher bacterial counts than the other fabrics, best supporting the persistence of bacteria over time. Time-dependent growth was observed on wool with Micrococcus. Time-dependent inhibition was observed on polyester with Micrococcus and Staphylococcus. Although some decreased counts were observed, all bacterial strains persisted across all fabric types for the entire 31 days.

**Conclusions:**
Inherent chemical and physical properties including hygroscopicity result in time-dependent differences in bacterial colonization of fabrics.
Title: Development of hypersensitive tandem amplification assay for protein detection

Authors: Jingyang Xu, Albert Zuehlke, Hongquan Zhang

Background and Aim:
Detection of biomarker play an important role in the diagnosis and determination of disease such as cancer. In this investigation we aim to develop a simple, homogenous, isothermal tandem amplification assay using the principal of Binding-Induced DNA assembly (BINDA). BINDA is the spontaneous favorable assembly of double stranded DNA when 2 complement single stranded DNA when they bind to a common target via probes that would normally be unfavorable if both stands are free floating in solution. This investigation aim to optimize the first step of the tandem amplification assay through improvement of signal to noise ratio.

Material and Methods:
Combine labeled gold nanoparticle, 20nM Probe, 10X NEB buffer, and Streptavidin Substrate with varying amount of deionized water for a final volume of 90uL in multi-well plate. Incubate at room-temperature for 20 minutes to allow for substrate-probe binding and BINDA interaction to occur. The Nicking Enzyme is combined with 1X NEB buffer at a 1 in 10 ratio, and incubated for 10 minutes before transferring a 10 uL aliquot into each well. Read the fluorescence measurement at 5 minutes interval at physiological temperature for 2 hours or plateau is reached.

Results:
Through initial detection we are able to detect as low as 50pM of streptavidin substrate. Signal to background ratio can be improved by decreasing the enzyme amount to 1 uL. A difference of 20% is observed between the BSA blank signal and No enzyme control suggest there are non-specific signal form no specific binding by probe and non-specific release of labeled DNAzyme.

Conclusions:
Using just a single step detection we are able to detect distinct signal for 50 pM streptavidin substrate. This detection limited can be improved when a second amplification is introduced. Signal to noise ratio can be further improved through the use of blocker sequence and altering enzyme amount.
**Title:** Quality Improvement Assessment of the Utilization of Fibrinogen Concentrate in the Edmonton Zone (EZ)

**Authors:** Kelsey Dacosta, Heather Blain, Susan Nahiriak, Hanan Gerges

**Background and Aim:**
Since introduction in 2013 fibrinogen concentrate (FC) has shown an increase in utilization. FC is licensed for patients with congenital fibrinogen deficiencies. Congenital deficiencies are rare disorders, unlikely to cause the increase in FC utilization. Off-label use for acquired hypofibrinogenemia is likely behind the increase in utilization. This study will identify clinical indications responsible for increased utilization. Cryoprecipitate is another agent used to treat hypofibrinogenemia so its utilization will be compared to FC use. Possible adverse events (AE) will also be examined. Data will be used to inform local guidelines and improve inventory management of FC.

**Material and Methods:**
A retrospective data analysis of the FC and cryoprecipitate utilization between 2013-2016 was performed using the EZ Transfusion Service’s Laboratory Information System and the FC and Massive Hemorrhage databases. AEs were extracted from the FC database. All data was entered into an EXCEL spreadsheet and analyzed using an unadjusted univariate data analysis and descriptive statistics.

**Results:**
Since 2013 there has been a 92% increase in the number of grams FC while number of cryoprecipitate units over the same time period increased only by 33%. 52% of FC requests were in cardiovascular patients. Figure 1 demonstrates the utilization associated with MHPs. Table 1 demonstrates the AEs with FC.

**Conclusions:**
FC increase has outpaced cryoprecipitate but has not replaced cryoprecipitate completely. Guidelines for use in CV surgery and MHPs need to be refined to improve standardization. FC is not without AE so risk benefit analysis must be considered.
Title: Simulated Urgent Release of Fibrinogen, Platelets and other Blood Products for Bleeding Patients in Hospital Setting


Background and Aim:
To evaluate current Edmonton Zone Standard Operating Procedures (SOPs) for the handling of urgent blood product requests using simulated scenarios. Specifically, we evaluated the preparation and release of blood type-irrelevant products. This type of high acuity, low opportunity situation is amenable to simulation because it increases familiarity with the process in a safe environment. By implementing simulated scenarios, not only does laboratory staff gain experience, but the process can be evaluated for shortcomings.

Material and Methods:
We performed 46 in situ simulations in 5 transfusion medicine laboratories in Edmonton region hospitals with medical laboratory technologists (MLTs), Registered Nurse callers and Transfusion Medicine Physicians in their normal roles. All simulations maintained bleeding urgency before a Type and Screen/Crossmatch request was complete, followed by a request for red blood cells, fresh frozen plasma and fibrinogen concentrate. Simulated products, paperwork and samples were used for each simulation and an on-site observer recorded resources consulted and tasks performed until issue.

Results:
The average time from fibrinogen concentrate (FIB) request to issue for all 41 simulations was 19.4 minutes with a range of 8 to 42 minutes. Major causes of delays for issue for FIB release are LIS glitches, TM physician delays and SOP interpretation delays.

Conclusions:
Using simulation allows identification of causes for delayed and/or problematic release of urgent blood products through a better understanding of factors that affect the process in situ. Standard Operating Procedure updates are necessary to decrease site variability and fibrinogen release delays.

Figure 1: Fibrinogen Concentrate Time from Product Request to Release by Hospital Laboratory

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Table 2: Comparison of Factors Affecting Mean Fibrinogen Release

<table>
<thead>
<tr>
<th>Factor</th>
<th>N</th>
<th>Mean time to FIB Issue (min)</th>
<th>Difference from Mean time to FIB issue (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Obstetrical</td>
<td>20</td>
<td>19.7</td>
<td>+0.3 min (2% increase)</td>
</tr>
<tr>
<td>Gastrointestinal</td>
<td>8</td>
<td>15.6</td>
<td>-3.8 min (20% decrease)</td>
</tr>
<tr>
<td>Gastrointestinal with historic Anti-K</td>
<td>13</td>
<td>21.5</td>
<td>+2.1 min (11% increase)</td>
</tr>
<tr>
<td>SOP interpretation with confusion</td>
<td>17</td>
<td>22.2</td>
<td>+2.8 min (14% increase)</td>
</tr>
<tr>
<td>SOP Interpretation without confusion</td>
<td>5</td>
<td>16.8</td>
<td>-2.6 min (13% decrease)</td>
</tr>
<tr>
<td>Difficulty locating Plasma Products</td>
<td>11</td>
<td>22.7</td>
<td>+3.3 min (17% increase)</td>
</tr>
<tr>
<td>Processing procedure</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No difficulty locating correct SOP for FIB</td>
<td>11</td>
<td>19.3</td>
<td>-0.1 min (1% decrease)</td>
</tr>
<tr>
<td>Consulted SOP looking for FIB guidelines</td>
<td>28</td>
<td>20.6</td>
<td>+1.2 min (6% increase)</td>
</tr>
<tr>
<td>Released FIB without consulting SOP</td>
<td>13</td>
<td>16.9</td>
<td>-2.5 min (13% decrease)</td>
</tr>
<tr>
<td>Consulted TM physician</td>
<td>32</td>
<td>20.1</td>
<td>+0.7 min (4% increase)</td>
</tr>
<tr>
<td>Released FIB without consulting TM Physician</td>
<td>9</td>
<td>17.0</td>
<td>-2.4 min (12% decrease)</td>
</tr>
<tr>
<td>Encountered LIS Glitch/Errors causing delay</td>
<td>6</td>
<td>17.2</td>
<td>-2.2 min (11% decrease)</td>
</tr>
<tr>
<td>TFiB ordering code unfamiliarity</td>
<td>15</td>
<td>20.7</td>
<td>+1.3 min (7% increase)</td>
</tr>
</tbody>
</table>
Title: Frequency of AT1R-Autoantibodies in Pediatric Heart Transplant Patients: Investigating Positive Reactions

Authors: Abou-Zeki, S,1 Halpin, A,1,2,3,4 Larsen, I,2,4 Campbell, P,1,4,5 Urschel, S,2,3,4 West, L2,3,4

1. University of Alberta, Dept. of Laboratory Medicine and Pathology
2. University of Alberta, Dept. of Pediatrics
3. Canadian National Transplant Program
4. Alberta Transplant Institute
5. University of Alberta, Dept. of Nephrology

Background and Aim:
Donor-specific-antibodies to human leukocyte antigens (HLA) are associated with reduced transplant survival. Recently, non-HLA/auto-antibodies have been suggested to be relevant in transplantation. There are currently no published studies on AT1R-antibodies in pediatric heart transplant (PHTx) patients.

Material and Methods:
Our study population included 42 patients (n=154 samples) for whom pre- and post-transplant sera and HLA antibody status were available. AT1R-antibodies were measured by ELISA (One Lambda™ Inc.). Age-matched, sex-balanced controls (n=27) were chosen from cardiac-catheterization laboratory to determine frequency in non-transplanted pediatric population. Results are: positive (>17U/mL), at risk (AR) (10-17U/mL), or negative (<10U/mL). To investigate specificity, 52/84 positive samples were treated with Adsorb Out™ (One Lambda™ Inc.).

Results:
The control population yielded 56%(n=15) positive and 33%(n=9) results. The frequencies of AT1R-antibody in 42 PHTx patients were 55% (84/154) positive, 36% (56/154) negative, and 9% (14/154) AR. Figure-1A illustrates AT1R-antibody interpretation changes pre-to post-transplant. Of the 55%(84/154) positive samples, 38%(59/154) were strongly positive. In the 52/84 positive samples (29 patients) chosen for adsorb treatment, 39/52 (75%) of adsorbed sera were now negative and therefore considered false positive in the original assay (Figure -1B).

Conclusions:
Control and test populations showed high frequency of AT1R-autoantibody. We identified the need for more controls for false positivity in this assay. It appears important to rule out non-specific reactivity to fully investigate AT1R-autoantibody’s true association with graft injury. Future analysis will investigate true and false positive reactivity in relation to transplant outcomes and include HLA antibody analysis.

*cont’d on next page
Figure 1A: AT1R antibody interpretation of pre-to post-transplant in pediatric heart patients (n=42)

<table>
<thead>
<tr>
<th></th>
<th>Negative Post-Tx</th>
<th>Positive Post-Tx</th>
<th>At Risk Post-Tx</th>
</tr>
</thead>
<tbody>
<tr>
<td>Negative Pre-Tx</td>
<td>9</td>
<td>5</td>
<td>1</td>
</tr>
<tr>
<td>AR Pre-Tx</td>
<td>2</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Positive Pre-Tx</td>
<td>2</td>
<td>21</td>
<td>1</td>
</tr>
</tbody>
</table>

Figure 1B: Increased AT1R antibody presence in non-adsorb treated sera (n=84) in contrast to adsorb treated sera (n=52).
Title: Predefined Criteria for Cancellation of Low Clinical Utility Peripheral Smear Requests

Authors: Sarah Sy1, Salwa El Malti1, 2, Susan Nahiriak1, 2, Hanan Gerges1, 2
University of Alberta1, Alberta Health Services2

Background and Aim:
Many peripheral smears (PSs) ordered by physicians may not have high clinical utility and can delay reporting of other interpretative testing. The aim of this study is to develop and validate safe criteria for screening and cancellation of PS orders providing no additional clinical information. This will improve efficiency and cost effectiveness by reducing turn-around-time for laboratory testing.

Material and Methods:
Ninety-five consecutive PSs were retrospectively analyzed. Additional information collected: Patient demographics, clinical history, complete blood count and differential (CBCD), analyzer flag induced technologist screening and previous PS in the preceding 30 days. PSs were evaluated using patients’ electronic health records, PS morphologic findings and significant CBCD changes to subdivide them by clinical utility. Two-tailed T-Tests were used in comparing the clinical utility status to each parameter.

Results:
Three rules were identified that predicted no additional clinical utility:

1. No technologist screen AND no clinical history provided
2. History containing the words micro/macrocytosis, anemia NYD, or hemoglobinopathy
3. Previous PS report within 30 days and no morphologic/CBCD changes

Using these rules as the predefined criteria allowed cancellation of 60% (38/63) of PSs without additional clinical utility. However, this also resulted in cancellation of 9% (3/32) of PSs with possible utility.

Conclusions:
These preliminary findings showed the value of using these predefined criteria for cancelling PSs but additional ones should be developed to avoid missing those providing additional information. Validation of these rules will be performed on prospective PS requests in addition to other jurisdictions’ criteria.
**Title:** Reducing the Length of Stay in the Rural Emergency Department with Point of Care Testing

**Authors:** Ursal Williams, BSc, and Laura Jensen*, CLXT and The SZ Point of Care Tech II.
*Alberta Health Services

**Background and Aim:**
Point of care testing (POCT) can reduce the turnaround time (TAT) which allows quicker patient management decisions. So, TAT is decreased there is potential for the emergency department (ED) length of stay (LOS) to also decrease resulting in decreased waiting time and increased bed availability.

**Material and Methods:**
The objective of this study is to compare the ED LOS between patients who receive POCT versus laboratory testing (LT) with subgroup analysis to type of disposition and types of tests. The retrospective study compared 4 EDs in the South Zone of Alberta Health Services where sites with like ED annual visits were compared. And sites with both POCT and LT were compared internally. The LOS was the primary outcome; secondary outcomes were subgroup analysis to disposition and type of test.

**Results:**
Analysis comparing 2 different sites was inconsistent. Comparing the POCT and LT internally found at site 3 the LOS to admissions decreased by a mean of 2.94 hours. At site 4, the mean LOS and LOS to admissions decreased by a mean difference of 0.74 and 4.43 hours, respectively. Site 4 also found that the LOS for troponin decreased by mean difference of 1.51 hours.

**Conclusions:**
In conclusion, the retrospective study design found that the POCT in the ED varied the LOS between ED settings.
**Title:** Assessment of HLA Expression on Organ Donor Lymphocytes: Impact to Pre-Transplant Compatibility Assessment

**Authors:** W Tsoi\(^1\), A Halpin\(^{1,2,3,4}\), L Hidalgo\(^1,3\), D Manna\(^1\), P Campbell\(^{1,3,5}\)

1. Department of Laboratory Medicine, University of Alberta  
2. Canadian National Transplant Research Program  
3. Alberta Transplant Institute  
4. Department of Pediatrics, University of Alberta  
5. Department of Nephrology, University of Alberta

**Background and Aim:**  
Histocompatibility laboratories perform flow cytometric crossmatches (FCXM) in pre-transplant assessment to evaluate immunogenic risk. Variation in HLA expression may affect FCXM interpretation. The objectives of this study are to a) measure the variation in HLA class I, II, and HLA-DQ expression on lymphocytes, b) compare the differences in HLA expression between cell source, donor type, and cell isolation and c) investigate the impact of HLA expression on FCXM.

**Material and Methods:**  
HLA expression was measured with monoclonal FITC-conjugated antibodies performed along with FCXM. Cells isolated from living (LD-PBL) & deceased donor (DD-PBL) whole blood, and spleen were evaluated for degree of HLA expression. Cells were isolated by immunomagnetic depletion and pronase treated prior to HLA measurements. Data were collected by the HLA laboratory and analyzed.

**Results:**  
PBL T- and B-cells showed comparable HLA class I and II expression. Splenic T- and B-cells showed lower levels of HLA overall. HLA-DQ expression was lower on all DD B-cell when compared to B-cells from LD-PBL. LD cells showed the highest overall HLA expression while DD-spleen was lowest (Figure 1). Pronase treatment resulted in higher T-cell HLA class I and B-cell HLA Class II detectable expression in all donor sources (Table 1). No significant correlation between HLA expression and FCXM reactivity, as measured by positive control, was observed.

**Conclusions:**  
Cell source, donor type, and pronase treatment impacted HLA expression in FCXM. Correlation between HLA expression and FCXM reactivity was not fully explored in this study but these observations warrant further investigation.

<table>
<thead>
<tr>
<th>Source</th>
<th>HLA Class</th>
<th>Total Cells</th>
<th>T Cells</th>
<th>B Cells</th>
<th>EasySep/Easy Sep Direct</th>
<th>Untreated Cells</th>
<th>Pronase-treated Cells</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>I</td>
<td>II</td>
<td>Neg control</td>
<td>I</td>
<td>Change</td>
<td>I</td>
<td>Change</td>
</tr>
<tr>
<td>Spleen</td>
<td>507</td>
<td>5</td>
<td>63</td>
<td>189</td>
<td>66</td>
<td>46</td>
<td>57</td>
</tr>
<tr>
<td>PBL1</td>
<td>504</td>
<td>1</td>
<td>63</td>
<td>475</td>
<td>58</td>
<td>58</td>
<td>3</td>
</tr>
<tr>
<td>PBL2</td>
<td>505</td>
<td>2</td>
<td>63</td>
<td>507</td>
<td>58</td>
<td>58</td>
<td>7</td>
</tr>
</tbody>
</table>

Table 1: Impact of pronase treatment on HLA expression in T and B cells.

*cont’d on next page*
Figure 1: HLA class I, II & HLA-DQ expressions on T and B cells isolated from different cell sources and donor types performed along with 66 clinical FCXMs
Title: Quality Assurance in Red Cell Components – Does Number and Total Time of Transportation Event Affect Level of Hemolysis?

Authors: X. Han, J. P Acker, S. Nahiriak, A. Howell, D. Clarke, H. Blain

Background and Aim:
Despite maintenance of cold chain storage, increased levels of hemolytic markers were observed in red cell units involved in the Fort McMurray fire. One hypothesis was that the increased number of transports and storage environments impacted the hemolytic parameters. The aim of this study is to test whether frequency and total time of transportation increases hemolysis.

Material and Methods:
A total of 124 expired units were received from three different sites (University of Alberta Hospital, Calgary Canadian Blood Service (CBS) and Edmonton CBS) from January to March, 2017. Percent hemolysis was measured using the gold standard Drabkin’s method to observe the correlation between percent hemolysis and the frequency and/or total time of transportsations. The results were separated into categories for comparison, and also compared to the CBS quality control reference data.

Results:
Little to no correlation existed between percent hemolysis and either the frequency or total time of transportation. 65% of all units exceed the reference percent hemolysis range. However, only four units were considered to be clinically significant with levels above 0.8% hemolysis.

Conclusions:
There is no evidence from this study to suggest that the frequency or total time of transportation events will lead to increased percent hemolysis. This allows hospitals and CBS centers to continue to redistribute red cells to help preserve inventory. Future research is required to determine the etiology behind the increased hemolysis that was seen in the Fort McMurray units.
Title: Are we using the right red cell units and plasma components for transfusion?

Authors: Kim Y, Blain H, Gerges H, Nahimiak S

Background and Aim:
O negative red blood cell units (RBCUs) and AB plasma units are in high demand because of compatibility. Some group O RBCUs are also pre-irradiated for our congenital cardiac program. The aim of this study is to evaluate utilization of O negative RBCUs and AB plasma, and irradiated stock.

Material and Methods:
Retrospective review of the Sunquest Laboratory Information System to obtain transfusion data of the following components:
a) O-negative RBCUs to non-O patients; b) AB plasma units transfused to non-AB patients and c) irradiated RBCUs that were transfused in patients with no indication for irradiation. All instances were categorized according to their usage reasons. Categories a and b were evaluated between July and December 2016 but irradiation data was only available between September and December.

Results:
1092 O negative units were transfused. 119 units (10.9%) were emergency unmatched but 973 units (89.1%) were non-emergent situations: Hemobank stock, administration to avoid expiry (internal and external), phenotyping requirements, no confirmatory ABO group and neonatal transfusion. 376 AB plasma units were transfused. 85 units (22.6%) were group specific. 73 units (19.4%) were uncrossmatched; 168 units (44.7%) transfused to neonates and 50 units (13.3%) were initially thawed as either unmatched or group specific but transfused to a different patient to avoid discard. 1201 irradiated RBCUs were transfused. 930 units (77.4%) were given to patients who required irradiation but 271 units (22.6%) were given to patients with no indication for irradiation.

Conclusions:
Areas for improvement were recognized to better utilize O negative RBCUs, AB plasma units and irradiated RBCUs.
Title: The identification of variables for measuring the impact of near-patient respiratory virus testing in an emergency department: A literature review

Authors: Fiona Ko, Steven Drews

Background:
Influenza season brings a large volume of patients to the emergency department. Current flu diagnostic procedures are lengthy and require extensive resources. The development of newer molecular near-patient tests offers opportunities to improve patient care and decrease health care system costs. However, the data on patient outcomes and system benefit is limited.

Aim:
To identify key patient outcomes and health system benefits from molecular and non-molecular near patient testing as a foundation for further research.

Material and Methods:
Studies that examined direct and indirect effects of rapid flu diagnostics were searched in PubMed from 2000-2016 using the terms impact, effect, management, influenza, and rapid test. Though the diagnostic test of interest was XpertFlu®, other rapid diagnostic tests, including newer molecular point-of-cares, were included. Study inclusion and criteria was performed by one reviewer.

Results:
The search strategy found 33 relevant articles, including RCTs, cohort and observational studies. Four studies in the last six years focused on molecular assays. A majority (63%) of articles found an association between rapid diagnostic tests and prescription of antibiotics, and therapeutic timing of antivirals. Studies also identified a significant improvement in patient flow indicators such as length-of-stay, isolation and a decrease in additional microbiology and virology laboratory testing.

Conclusions:
Future studies should focus on prescription patterns and lab resource impacts as measurable outcomes for near-patient test implementation strategies. Other more difficult to measure impacts may include improved patient management, decreased health care costs, and the reduction of viral transmission in health care settings.
Title: Fluorescent in situ hybridization detection of viable Helicobacter pylori from spiked untreated river water samples

Authors: Oanh Nguyen, Homun Yee, Monika Keelan and the CANHelp Working Group

Background and Aim:
Remote Canadian Arctic communities have ~60% prevalence of H. pylori, a causative agent of gastritis, peptic ulcers and gastric cancer. Community members have concerns that water may be a source of H. pylori infection. A fluorescent in situ hybridization (FISH) assay on H. pylori exposed to low dose novobiocin is proposed to detect viable H. pylori in lake/river water. Aim: To optimize a novobiocin-FISH assay for H. pylori detection in spiked river water.

Material and Methods:
Five 1 L water samples were collected from the North Saskatchewan River; four spiked with H. pylori (103, 104, 105, 106 CFU/L) and one unspiked control. Each 1 L sample was collected onto 0.22 um filters, eluted and divided into aliquots for novobiocin (50 mg/L)-FISH, as well as highly selective agar culture (colony counts) and PCR to detect viable/non-viable H. pylori DNA. After exposure to novobiocin overnight, bacteria were prepared for hybridization with green fluorescent universal bacterial probe (EUB388) or red fluorescent H. pylori specific (Hpy-1) probe and visualized by fluorescent microscopy.

Results:
Novobiocin-FISH detected viable H. pylori from river samples containing 104 to 106 CFU of H. pylori. In comparison, both highly selective agar culture and PCR on DNA extracts detected H. pylori from river water samples containing 105 to 106 CFU of H. pylori.

Conclusions:
Novobiocin-FISH is able to detect viable H. pylori in spiked river water, despite the presence of particulates and other solutes. Future studies will investigate detection of viable H. pylori from northern environmental water samples.
Title: Evaluation of the functional properties of cryopreserved buffy-coat derived monocytes for monocyte monolayer assay

Authors: Betty J. Kipke1, Luciana da Silveira Cavalcante1,2, Donald R. Branch3,4, Jason P. Acker1,2, Jelena L. Holovati1,2

1. University of Alberta
2. Canadian Blood Services, Edmonton, AB, Canada
3. University of Toronto
4. Canadian Blood Services, Toronto, ON, Canada

Introduction:
Monocyte monolayer assay (MMA) is a compatibility testing method for evaluating clinical significance of red blood cell alloantibodies. However, current MMA practices involve tedious processing of fresh peripheral blood monocytes. The aim of this study was to develop effective monocyte isolation and cryopreservation protocols then, evaluate the utility of cryopreserved buffy-coat derived monocytes for MMA.

Materials and Methods:
Peripheral blood mononuclear cells (PBMCs) were isolated from buffy-coats or peripheral blood (Histopaque-10771), pooled, suspended in cryopreservation media and cryopreserved in liquid nitrogen. PBMC membrane integrity was determined by trypan blue exclusion. Monocytes were cultured on poly-L-lysine-treated coverslips and incubated with either anti-D-sensitized RBCs, anti-Scianna-2 sensitized RBCs or lipopolysaccharide (LPS). Phagocytic index (PI) was determined microscopically. Cell supernatants were analyzed for cytokines using multiplex fluorochrome assay.

Results:
On average, 67 ± 6% and 76 ± 8% of PBMCs were isolated from buffy-coats and peripheral blood respectively with low contamination (RBCs ≤ 5%, platelets < 15%, neutrophils < 5%). Freshly isolated PBMCs were 100% intact whereas cryopreserved PBMCs showed 93.9 ± 1.2% membrane integrity. For anti-D sensitized RBCs, cryopreserved monocytes resulted in a PI of 79.6 ± 5.9% compared to both fresh buffy-coat (PI; 76.7 ± 10.9%) and peripheral blood monocytes (PI; 82.4 ± 10%). A PI of 9.4 ± 2.3% was obtained with anti-Scianna-2 sensitized RBCs. TNF-α, IL-8, IL-1β, IL-6, MIP-α and MIP-β secretion was significantly higher in cryopreserved buffy-coat monocytes.

Conclusion:
We show that cryopreserved buffy-coat derived monocytes can used reliably to assess phagocytic responses of sensitized red blood cells.
**Title:** Estrogen induces G1 phase cell cycle arrest in “luminal-A-like” breast cancer cells while promoting growth in luminal B breast cancer cells.

**Authors:** Brittney Loney, Xiuying Hu, Lacey Haddon, and Dr. Judith Hugh

**Background and Aim:**
80% of invasive breast cancers are Estrogen Receptor (ER) positive and are subtyped into luminal A or luminal B which differ in level of ER expression, proliferative gene expression, and response to hormone therapy. Currently, treatment of both subtypes is the same and patients with luminal B tumors have a poor prognosis. The aim of this research is to investigate the role of the level of ER expression in the differential response of the two subtypes to hormone therapy.

**Material and Methods:**
MCF-7 cells were transduced to create luminal B (low-ER) and “luminal-A-like” (high-ER) cell line models. The cells were treated with estrogen or a control for 24 hours and lysed for protein extraction. Western blot was performed to compare expression of specific cell cycle phase proteins in both cell types.

**Results:**
Expression of G1 phase proteins was elevated, while expression of S and G2/M proteins was reduced in high-ER cells following estrogen treatment. The opposite was observed for low-ER cells. Flow cytometry confirmed an estrogen induced G1/S cell cycle block in high-ER cells and a G1/S transition in low-ER cells.

**Conclusions:**
High-ER and low-ER cells have an opposing response to estrogen mediated by the level of ER expression. These findings have the potential to contribute to novel diagnostic and therapeutic approaches for ER+ breast cancers which is especially critical for improving the treatment and prognosis of patients with luminal B tumors.
**Title:** The detection of surface phosphoglycerate kinase (PGK) on distinct Group A *Streptococcus* (GAS) strains

**Authors:** Hirji FH, Tyrrell GJ

**Background and Aim:**
GAS is a human bacterium affiliated with greater than 600 million incident pharyngitis cases per year and approximately 660 000 incident invasive disease cases per year globally. GAS pharyngitis is mild but can lead to acute rheumatic fever if not treated. Invasive diseases result in approximately 160 000 incident deaths per year globally. GAS PGK is a glycolytic enzyme that can be found on the bacterial surface. It demonstrates human immunoglobulin reactivity and causes activation and degranulation of neutrophils when secreted for instance. Therefore, it seems that PGK has a role in GAS pathogenesis. However, the presence of surface PGK amongst numerous and a variety of GAS strains is unknown. The purpose of this study is to assess surface PGK presence in different GAS strains.

**Material and Methods:**
Sixteen clinical GAS strains underwent testing for surface PGK using enzyme linked immunosorbent assay (ELISA) in triplicate. These strains are from the Edmonton Provincial Laboratory for Public Health and from years between 2008 and 2015. The GAS strains are distinct in terms of their *emm* type, *emm* pattern group and/or specimen source.

**Results:**
Out of the sixteen GAS strains tested, fifteen have PGK detectable on their surfaces. The GAS strain with no detectable surface PGK is GAS *emm* 59 MGAS15252. In addition, no relationship seems to exist between surface GAS PGK presence and *emm* pattern group or specimen source.

**Conclusions:**
Surface PGK is present amongst the majority of distinct GAS strains tested.
Title: Process-Affected Water in the Oil Sands Industry of Alberta: Toxicity Attribution and Evaluating Aging as a Remediation Strategy

Authors: Gault I.G.M., Moe, B., Sun, C., Martin J.W.; University of Alberta

Background and Aim:
Oil sands process-affected water (OSPW) is a by-product of the industrial method for recovering bitumen in the oil sands industry. OSPW contains a complex dissolved organic mixture that is toxic, persistent, and largely uncharacterized, with thousands of chemical species detected in positive and negative mode with mass spectrometry. Suspected contamination of surrounding natural water by OSPW today, combined with a need to release OSPW from reclamation sites in the future raises many unknowns about risks to surrounding wildlife and human settlements. This investigation compared the cytotoxicity of OSPW of different ages to evaluate the effectiveness of natural aging as a remediation strategy, and to further understand the toxicity of isolated OSPW chemical classes.

Material and Methods:
A fractionation technique separated groups of chemical classes in OSPW, and samples from differentially aged sources were characterized by high resolution orbitrap mass spectrometry. Real-Time Cell Analysis of human hepatocellular carcinoma cells (HepG2) measured cytotoxicity, while the yeast estrogenic/androgenic screens will assess endocrine disruption.

Results:
OSPW organics were cytotoxic up to 12.5-fold natural concentrations, with different toxicity (IC50) profiles depending on sample age. A fraction containing naphthenic acids was the most cytotoxic, while the non-acidic fraction, speculated to contain steroid-like chemicals, was not.

Conclusions:
OSPW organics are cytotoxic in a human cell line, with naphthenic acids largely responsible, and potency decreasing with increasing age. Identifying the most hazardous chemicals in OSPW can improve the understanding of apical toxic effects and help research into targeted remediation of OSPW before its inevitable release.
Title: Assessing ionic liquids as novel precursors of N-nitrosamines during water disinfection

Authors: Ian Vander Meulen, Jianye Zhang and Xing-Fang Li

Background and Aim:
Ionic liquids (ILs) are a novel class of solvents branded as “green” due to their unique advantages over traditional solvents. While no releases have been reported yet, laboratory studies have shown that many ILs are water soluble and have limited biodegradability, with predicted half-lives up to a month, depending on water depth and sunlight exposure. If ILs were accidently released to the environment, they may contaminate drinking water sources. Many ILs contain quaternary amines, a structural similarity to other known nitrosamine precursors. Nitrosamines are disinfection by-products and confirmed animal carcinogens. Therefore, this study examines the formation potential of nitrosamines from ILs during chloramination.

Material and Methods:
1-ethyl-1-methypyrrolidinium bromide (EMImBr) and 1-ethyl-3-methylimidazolium bromide (EMPyrBr) were chosen as model ILs. Dissolved EMImBr and EMPyrBr were treated with chloramines, and then analyzed for nitrosamines by liquid chromatography-tandem mass spectrometry. Nitrosamine productivity at varied molar ratios of disinfectant-to-precursors was examined, and factors such as pH and temperature will later be examined.

Preliminary Results:
Repeated chloramination treatments of both ILs at millimolar concentrations generated N-nitrosomethylethylamine (NMEA) up to 0.9 µg/L after 72 hours. Reactions at 1:1 molar ratios of disinfectant-to-precursors maximized yields, at 1.0 ± 0.04% and 0.32 ± 0.04% from EMPyrBr and EMImBr, respectively.

Conclusions:
When treated with chloramines, selected ILs can generate NMEA (a known carcinogen), emphasizing the need to responsibly dispose of IL-impacted waste to protect drinking water sources. This is a useful starting point for future studies further evaluating potential impacts of ILs on drinking water quality.
**Title:** A DNAzyme-motor for Detection of Intracellular ATP

**Authors:** Jeffrey Tao, Hanyong Peng, Hongquan Zhang, X. Chris Le

**Background and Aim:**
DNA nanotechnology has advanced diagnostics for various diseases with its ultrasensitive capabilities. One particular nanomachine, the DNA-walker, involves an oligonucleotide that traverses DNA tracks to release payloads for molecular detection. However, the nanomachine cannot detect intracellular targets because its components are unable to enter cells. Thus, we functionalized gold nanoparticles (AuNPs) with a DNAzyme-motor to permit cellular entry and detection of a common intracellular biomolecule, adenosine triphosphate (ATP).

**Material and Methods:**
1. Annealed DNAzyme with AA to block catalytic activity.
2. Conjugated DNAzyme-AA and FAM-sub onto 20nm AuNPs
3. Centrifuged and washed AuNPs
4. Activated AuNPs with ATP, Mn2+, and Mg2
5. Recorded fluorescence over time using a fluorometer

**Results:**
Initially, the DNAzyme is blocked by an ATP aptamer (DNA sequence capable of strongly binding with ATP) (Figure 1A). ATP competitively displaces the ATP aptamer from the DNAzyme (Figure 1B), allowing the DNAzyme to hybridize with fluorescein-labelled substrate (FAM-sub) strands (Figure 1C). Activation by Mn2+ cofactor (Figure 1D) allows the DNAzyme to cleave substrates, releasing FAM from AuNP fluorescence quenching (Figure 1E). These steps are repeated for multiple FAM-sub strands to produce an amplified fluorescence response (Figure 1F).

Conclusions:
This novel DNAzyme-motor design has successfully detected physiological concentrations of ATP in tubes. Conducting in vitro studies will confirm whether intracellular detection of biomolecules is achievable with this design. Future perspectives include ultrasensitive assays for a variety of intracellular disease markers and targeted drug therapies with drugs as payloads.

**Figure 1:** Schematic of DNAzyme-motor
Title: The University of Alberta Hospital Anatomical Pathology (UAH AP) Turnaround Time (TAT) Improvement Initiative

Authors: Nikhita Arora¹
¹Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada

Background and Aim:
TAT is regarded as an important quality indicator of the efficiency of medical services. The College of Physicians and Surgeons of Alberta (CPSA) requires that the UAH AP laboratory establish and meet the TAT of surgical pathology reports for small/simple cases (HL4’s), and large/complex cases (HL5/6’s). The aim of this study was to identify points at which delays in TATs occur from the time between the assembly of surgical pathology case slides and the generation of a preliminary/final case report.

Material and Methods:
TATs were calculated for HL4 cases (n=100), and HL 5/6 cases (n=50) selected at random over 30 day period using Vantage and CoPath databases. A Value Stream Map of the analytic surgical pathology workflow process was generated. Data for cases with special procedure requests (n=147) was extracted and included the accession number, procedure order date/time, and case assembled date/time.

Results:
The UAH AP department is not meeting the expected TAT targets for HL4, 5 and 6 cases. Areas of the analytic surgical pathology workflow which largely contributed to the delays in TAT included various pathologist interruptions, and special procedure requests such as immunohistochemistry stains, special stains, reblocks, and levels.

Conclusions:
The accuracy of diagnosis and providing complete reports in a timely manner is one of the main quality indicators in surgical pathology. Collective efforts to improve the TAT of surgical pathology reports will eventually be instrumental in avoiding delays in treatment, ensuring appropriate patient management, and enhancing patient care.
Title: Identification and characterization of heat resistant Escherichia coli clinical isolates possessing the locus of heat resistance

Authors: Angela Ma, Linda Chui

Background and Aim:
Pathogenic Escherichia coli strains, particularly Shiga toxin-producing E. coli, are etiologic agents of hemorrhagic colitis. Ingestion of undercooked, contaminated meat contributes to a significant portion of E. coli related outbreaks. Non-pathogenic, environmental E. coli strains have been reported to survive heat inactivation measures at 71°C, raising the question of whether heat resistant E. coli is a potential threat to food safety.

Material and Methods:
Three qPCR assays using hydrolysis probes were developed to identify heat resistant E. coli. D60- and D71-values were calculated from survival curves generated for the heat resistant strains grown in varying salt concentrations upon heat inactivation at 60 and 71°C. To assess the survival of heat resistant E. coli in cooked foods, ground beef patties were inoculated with cultures of each isolate and grilled to an internal temperature of 71°C.

Results:
From a collection of 613 clinical E. coli isolates, 3 were identified as heat resistant by the qPCR assays. Phenotypic heat resistance was confirmed by heat inactivation at 60 and 71°C. D60- and D71-values of heat resistant isolates were determined to exceed 10 and 0.20 minutes, respectively. Cell counts were recovered from grilled patties inoculated with the heat resistant isolates, whereas the heat sensitive E. coli isolate was no longer detectable after cooking.

Conclusions:
The identification of heat resistant E. coli clinical isolates indicates a novel risk factor to food safety and human foodborne disease. Furthermore, the ability of these organisms to survive in meat cooked to 71°C, suggests that current cooking practices may not be sufficient at eliminating foodborne pathogens.
Title: CIP-1, a calcium sensor protein, encodes an important component of the p53-mediated stress response pathway.

Authors: Ao Ma and Roger Leng

Background and Aim: p53 is a crucial tumor suppressor gene that controls many functions with many downstream genes such as p21WAF1 and MDM2. Recently, our lab discovered a gene encoding a neuronal calcium sensor named CIP-1 is a novel p53 target gene. CIP-1 is involved in calcium signal transduction pathways, it has been demonstrated that CIP-1 plays roles in the genesis of Alzheimer's disease and tumor. My goal is to determine whether CIP-1 encodes an important component of the p53-mediated stress response pathway. By characterizing CIP-1 as a novel p53 target gene in the regulation of Ca2+ signaling, we open up new options in tumor and Alzheimer's disease therapy.

Material and Methods: p53-null and wild-type p53 expressing cells were treated with γ-irradiation or drug to activate p53. The expression levels of p53 and CIP-1 (both in mRNA and protein) were examined by using quantitative real time-PCR and Western Blotting, respectively. To determine if p53 activates the transcription of CIP-1, luciferase assay and chromatin immunoprecipitation assays (ChiP) will be performed. CIP-1 functions will be investigated through RNAi and CRISPR/cas9 techniques.

Results: CIP-1 mRNA levels increased in response to p53 activation; but not in p53-null cells. This pattern of expression was similar to that of the p53-inducible gene p21WAF1, MDM2, and UBE4B. Similarly, expression of the CIP-1 protein is induced by the activations in a p53-dependent manner.

Conclusions: My findings demonstrated that CIP-1 is a p53 inducible gene. This is the first report that p53 is involved in the regulation of calcium signaling through the calcium sensor protein, CIP-1.
**Title:** Development of a Novel DNA-Based Bioanalytical Assay for the Detection of a Mitochondrial Disease

**Authors:** Ashley M. Newbigging, Hongquan Zhang, X. Chris Le

**Background and Aim:**
Mitochondrial diseases are caused by genetic mutations. Because of the heteroplasmic distribution of afflicted mitochondria throughout the body, symptoms are nonspecific. Currently, there is no reliable means to diagnose mitochondrial disease. Although DNA sequencing provides a reliable diagnosis, it is impractical for high-throughput patient screening. Therefore, there is a need for an inexpensive and rapid assay capable of detecting mitochondrial mutations.

**Material and Methods:**
A DNA hairpin with a long 5’ overhang conjugated to a fluorescence quencher was designed. A second strand, conjugated to a fluorophore on its 3’ end, is hybridized to the overhang. The fluorophore and quencher are brought into close proximity such that fluorescence is quenched. If present, the target hybridizes to the loop of the hairpin and opens the stem, which initiates DNA polymerization. The target and fluorophore strands are both displaced, and fluorescence is produced. Exponential amplification of the detection signal is achieved by designing the displaced fluorophore strand to also trigger the same reaction.

**Results:**
Reaction conditions such as temperature and polymerase concentration were optimized. A limit of detection of 10 fM was achieved within 45 minutes in a total volume of 20 µL.

**Conclusions:**
Synthetic DNA was used to construct a complex where, when triggered by the presence of the target mutated DNA, fluorescence is produced. This complex provides a rapid and sensitive bioanalytical assay for the detection of a mitochondrial DNA mutation. This assay can be adapted for applicability in the detection of other nucleic acids or proteins.
**Title:** Diverse roles of Small RNAs: Piwi-interacting RNAs (piRNAs) and their role in cancer cachexia

**Authors:** Bhumi Bhatt, Ashok Narasimhan, Preethi Krishnan, Vickie Baracos^ and Sambasivarao Damaraju

Departments of Laboratory Medicine and Pathology, and ^Oncology, Edmonton, AB, Canada

**Background and Aim:**
Cancer Cachexia (CC) is a multifactorial syndrome, affects ~50% of advanced cancer patients, and is characterized by loss of skeletal muscle with/without fat loss. Expression of coding genes, mRNAs and miRNAs (small non-coding (nc) RNAs) were shown to be dysregulated in CC. Another class of ncRNAs, piRNAs (26-32 nt) also regulate gene expression. However, piRNA expression in muscle and their role in CC are not elucidated. We hypothesize that dysregulation of piRNAs contributes to etiology of CC. Objectives of this study are to i) profile piRNAs in human skeletal muscle biopsies and ii) identify differentially expressed (DE) piRNAs associated with CC.

**Material and Methods:**
Cachectic cases and non-cachectic controls were defined according to the international consensus diagnostic framework (based on weight loss history, and/or sarcopenic status and BMI). RNA isolation from muscle biopsies was performed using Trizol method. Illumina-MiSeq was used to profile piRNAs and analysed using Partek Genomics Suite. Raw data was filtered using cut-off >5 read counts in at least 80% samples and normalized using Reads per Kilobase per Million method. piRNAs with fold-change ≥1.2 and p<0.1 (one-way ANOVA) were considered DE.

**Results:**
274 piRNAs were expressed in muscle and 28 piRNAs were retained after applying stringent filtering criteria. We identified 9 DE piRNAs, of which 3 were up-regulated and 6 were downregulated in cachectic cases compared to non-cachectic controls.

**Conclusions:**
We identified piRNAs associated with the pathophysiology of CC and their role in gene regulation (targets regulated) needs to be ascertained using model systems.
**Title:** Regulation of p53 and its E3/E4 ubiquitin ligases by Wip1

**Authors:** Yasser Abuetabh and Roger Leng

**Background and Aim:**
UBE4B is an ubiquitin chain assembly factor that binds to Hdm2 and promotes the poly-ubiquitination and proteasomal degradation of the tumor suppressor p53. UBE4B is an emerging oncogene implicating the outcomes of several cancers, including brain, breast and liver cancers. Recently, our group demonstrated that UBE4B could independently co-immunoprecipitate with phosphorylated (active) p53 at different serine residues, which led to its poly-ubiquitination and degradation. Nonetheless, UBE4B regulation is still largely unknown. Wild-type p53-induced protein 1 phosphatase (Wip1) is an essential main known phosphatase that targets phosphorylated p53. Moreover, Wip1 is found to target most of the negative and positive regulators of p53, including ATM, ATR, Hdm2 and Chk1/2. Thus, we wondered if Wip1 could also target UBE4B.

**Material and Methods:**
We investigated the endogenous UBE4B protein levels in response to Wip1 over-expression or silencing in different cancer cell lines with or without IR exposure.

**Results:**
The initial results indicated that UBE4B protein levels in response to Wip1 overexpression showed differential responses based on p53 status. Interestingly, UBE4B protein levels were decreased in response to Wip1 down regulation. Moreover, half-life assay demonstrated that Wip1 might stabilize UBE4B.

**Conclusions:**
Our preliminary data showed that Wip1 could directly or indirectly impact the expression of UBE4B. Our aim is to explore this potential relationship between Wip1 and UBE4B. Thus, we are currently conducting several experiments including co-immunoprecipitation and ubiquitination assays. Consequently, revealing the possible regulators of UBE4B may lead to development of novel therapeutic strategies to battle cancer.
**Title:** Myeloma cells acquire STAT3 activity and dependence in established three-dimensional reconstructed bone matrix (3D/rBM) model

**Authors:** Yung-Hsing Huang, Moinul Haque and Raymond Lai

**Background and Aim:**
It is known that three-dimensional (3D) cultures better represents the in vivo growth conditions of tumor cells. A 3D reconstructed bone matrix (3D/rBM) model was published before that allow prolong survival and proliferation of primary bone marrow cells. 3D/rBM has been utilized for assessing the efficacy of novel therapeutics on treating multiple myeloma (MM) in vitro. However, the molecular biology of MM cells in 3D/rBM and it differs from conventional two-dimensional (2D) cell culture remains a puzzle. In this study, we aim to study the STAT3 activation in 3D/rBM cells as a therapeutic target for MM.

**Material and Methods:**
We used 2 MM cell lines, U266 and RPMI8226 for this study. The morphology, cell growth, drug accessibility, cancer-related gene expression and signaling pathway activity of 2D versus 3D/rBM cells was compared. The efficacy of 2 STAT3 inhibitors in 3D/rBM cells were evaluated by MTS assay. The synergy of STAT3 inhibition and conventional MM therapeutic (bortezomib) was assessed by MTS assay.

**Results:**
We found that 3D/rBM cells formed spheroid structure, slower cell growth and less drug uptake. 3D/rBM cells showed expression changes in genes related to STAT3. Among all signaling pathways we investigated, STAT3 was always activated in 3D/rBM. We found that STAT3 is activated 2 days and 1 day after seeding into 3D/rBM, respectively (see figure below). MM cells in 3D/rBM became more sensitive to STAT3 inhibition. Moreover, it is found that STAT3 inhibition sensitizes MM in response to bortezomib.

**Conclusions:**
STAT3 is activated in MM cells cultured under close-to-in vivo conditions, hence a valid therapeutic target.
Title: Regulation of tumor suppressor PTEN and its E3 ligase NEDD4-1 by selected microRNAs

Authors: Chengsen Chai, Roger Leng

Background and Aim:
In cancer cells, tumor suppressor PTEN was one of most frequently inactivated genes and its ubiquitination E3 ligase NEDD4-1 can negatively regulate PTEN through degradation by proteasome. MicroRNA involved regulation of genes by binding to the target messenger RNAs and impeding their translation. In this project, we aim to find and confirm new microRNAs that bind to PTEN mRNA and lead to PTEN inactivity or microRNAs that bind to NEDD4-1 mRNA, and enhance PTEN activity.

Material and Methods:
20 predicted microRNAs targeting PTEN / 15 predicted microRNAs targeting NEDD4-1 were constructed and transfected into breast cancer cell MCF7. Endogenous PTEN / NEDD4-1 level were examined in whole cell lysates by immunoblotting. Next co-transfection of microRNA and its target PTEN ORF&3'UTR or NEDD4-1 ORF&3'UTR were performed in HEK 293 cell to check the effect of microRNAs on exogenous PTEN or NEDD4-1. By luciferase assay, the binding sites of microRNAs on target mRNA were confirmed.

Results:
microRNA #14 can down regulate both endogenous and exogenous PTEN level. MicroRNA #33 can down regulate both endogenous and exogenous NEDD4-1. MicroRNA #14 bound to PTEN mRNA 3UTR and microRNA #33 bound to NEDD4-1 mRNA 3UTR, negatively regulating target protein translation. microRNA #14 promoted BCa cell proliferation, while microRNA #33 suppressed BCa cell proliferation.

Conclusions:
MicroRNA #14 was found to negatively regulate PTEN and played an oncogenic role. MicroRNA #33 was found potentially to negatively regulate NEDD4-1 but enhance PTEN, acting as tumor-suppressing role.
Title: Differences in the Biliary Excretion of Arsenic by Rat and Human Sandwich-Cultured Hepatocytes

Authors: Gurnit Kaur, Barbara A. Roggenbeck, X. Chris Le and Elaine M. Leslie

Background and Aim:
Arsenic is a proven human carcinogen, causing cancers of the skin, lung and bladder. More than two hundred million people worldwide are exposed to levels of arsenic above the World Health Organization guideline of 10 ppb. Yet, the cellular handling of arsenic remains inadequately understood. In the liver, the ATP-binding cassette transporter, multidrug resistance protein 2 (human MRP2/ABCC2 and rat Mrp2/Abcc2) is localized to the apical surface of hepatocytes. In rats, Mrp2 has been shown to be responsible for 99% of arsenic biliary excretion and arsenic triglutathione [As(GS)3] and the diglutathione conjugate of monomethylarsonous acid [MMA(GS)2] are the transported forms. Our studies using sandwich cultured primary human hepatocytes (SCHH) indicate that arsenic undergoes biliary excretion more extensively in rats than humans. Using vesicular transport assays we have shown that human MRP2 can transport As(GS)3, while its ability to transport MMA(GS)2 is unknown. We hypothesize that differences in the biliary excretion of arsenic between human and rat are due to differences in arsenic transport by MRP2 and Mrp2. Our objectives are to 1) To characterize the hepatobiliary transport of arsenic using sandwich cultured rat hepatocytes (SCRH) for direct comparison with published SCHH data. 2) To determine any differences in transport of As(GS)3 and MMA(GS)2 by rat and human Mrp2/MRP2-enriched membrane vesicles.

Material and Methods:
Biliary excretion of arsenic will be characterized using SCRH, which are primary rat hepatocytes cultured between two layers of collagen. SCRH are treated with 73AsIII (1 μM) for 24 hours and then efflux across the basolateral and apical membranes measured and the biliary excretion index (BEI) calculated. Plasma membrane enriched vesicles of human embryonic kidney cells transfected with MRP2/Mrp2 are used to carry out vesicular transport experiments. Arsenic vesicular transport is quantified using inductively coupled plasma mass spectrometry.

Results:
Preliminary experiments with SCRH show a higher arsenic BEI (range 44-76%) compared with SCHH (BEI range 0-31%). Using vesicular transport assays MMA(GS)2 was found to be transported by both human and rat MRP2/Mrp2. Future work will characterize kinetic differences in rat and human Mrp2/MRP2 transport of As(GS)3 and MMA(GS)2.

Conclusions:
There is a large volume of arsenic studies done in rat models, despite the marked species differences in the cellular handling of arsenic between species, as well as between individuals. This study facilitates interpretation of in vivo arsenic data from rat models in context with human exposures. In addition, it provides insight into the mechanism of action of MRP2, thereby leading us to better understand inter-individual differences in the handling of arsenic.
**Title:** Using Chromatin Loops to Unravel the Paradox of Diagnosing ER+ Breast Cancers

**Authors:** Lacey Haddon, Hosna Jabbari, Xiuying Hu, Kirstin Arnold, Judith Hugh

**Background and Aim:**
Estrogen receptor positive (ER+) breast cancer is divided into two luminal subtypes, A and B. Clinically, luminal A patients have higher ER levels and an excellent response to hormone therapy whereas luminal B patients have low ER expression and require additional chemotherapy. The inaccuracy of current diagnostic tests results in poor differentiation between the luminal subtypes and can often cause luminal A patients to receive unnecessary chemotherapy. Since ER is a major regulator of gene transcription in breast cancer cells, we hypothesized that increased ER expression enables a novel chromatin reconfiguration that promotes a differential transcriptional response to hormones.

**Material and Methods:**
Next Generation Sequencing (NGS) experiments were done using MCF-7 cells with (MCF7-ER) or without (MCF7-EM) an inducible ESR1 plasmid treated +/- 10nM estrogen (E2) to detect genome-wide changes in ER-DNA-binding using chromatin immunoprecipitation (ChIP) and differential gene expression using extracted mRNA. ChIA-PET data for long-range ER-chromatin interactions from MCF-7 cells treated with E2 was obtained from the public database.

**Results:**
Increased ER expression leads to novel ER binding at several well-defined ER target genes, in the presence and absence of E2. Differential gene expression analysis shows an increase in basal activation in MCF7-ER cells that is suppressed in the presence of E2. Validation against the MCF-7 ChIA-PET dataset show these novel ER DNA binding sites correspond to long-range chromatin loops.

**Conclusions:**
Our results suggest that increased ER expression promotes a novel chromatin configuration which may serve as the biological mechanism that differentiates the luminal subtypes.
Title: Group B Streptococcal virulence is enhanced in the presence of erythritol, a polyol (sugar alcohol).

Authors: Maram Hulbah and Greg Tyrrell

Background and Aim:
Group B streptococci (GBS) causes invasive disease in neonates resulting in pneumonia, sepsis and possibly meningitis. A cofactor we hypothesize to be associated with GBS virulence in neonates are polyols. Polyols (of which erythritol is a member) are sugar alcohols that have been found in coelomic and amniotic fluids of humans. In this study, the effect erythritol has on GBS virulence was investigated.

Material and Methods:
GBS were grown in varying concentrations of erythritol (0%, 1%, 2% and 4%), bacteria then harvested and various virulence phenotypes assayed. The expression of phosphoglycerate kinase (PGK – a plasminogen binding protein on the surface of GBS) was determined by ELISA. The antiphagocytic properties of GBS were examined by measuring the bacteria's ability to multiply in fresh human blood during a 3-h incubation period. In addition, the effect erythritol has on the invasion by GBS of epithelial cells (HeLa 229 cells) was investigated.

Results:
The bacteria showed no statistically significant difference in growth in the various concentrations of erythritol used (P=0.69 with 1%, P=0.63 with 2% and P=0.51 with 4%). GBS growth in the presence of 1%, 2% and 4% erythritol enhanced the expression of GBS-PGK compared to 0% erythritol (120%, 122 and 134%, respectively). The antiphagocytic activity of GBS in the presence of 1%, 2% and 4% erythritol was significantly increased compared to 0% (P=0.026, P=0.019 and P=0.0002, respectively). The epithelial cell invasion assay revealed that in the presence of 1% of erythritol, GBS invaded the HeLa cells (164%) at a rate higher than when GBS was grown in 0% erythritol.

Conclusions:
This study demonstrates that the presence of erythritol (a polyol) in culture media enhances the virulence of this bacterium. This further suggests that erythritol may play a role in GBS pathogenesis during neonatal infection.
Title: Characterization of Extracellular Vesicles Is Influenced by Method of Detection, Blood Manufacturing Processes and Storage Duration

Authors: Ruqayyah J. Almizraq¹, Jelena Holovati¹,², Jason P. Acker¹,²
1. Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada
2. Centre for Innovation, Canadian Blood Services, Edmonton, AB, Canada

Background:
Extracellular vesicles (EVs) are small phospholipid vesicles (≤1 µm) that are present in blood products, accumulate during storage, and have a potential transfusion-related immunomodulatory role. Characterizing these heterogeneous submicron-sized vesicles is difficult. This study assessed the impact of different methods to characterize EVs in stored and differently manufactured red cell concentrates (RCC).

Methods:
Leukoreduced packed RCC units (n=3/group) produced from whole blood using whole blood filtration (WBF) and buffy coat (BC) methods, were analyzed in triplicate. Quantification and size-profiling of EVs in RCC products were examined on day 3, 7, 21, and 42 of storage using tunable resistive pulse sensing (TRPS), flow cytometer (FC), and dynamic light scattering (DLS) methods.

Results:
On day 3, the TRPS results indicate that WBF products have a different EVs size-profile (smaller EVs in comparison to BC products, (p<0.0001). The concentration of EVs < 200 nm increase throughout storage until day 21 then dramatically and significantly decrease by day 42 (BC: p=0.005, WBF: p=0.0001). The EV concentration changes are not detectable with FC or DLS due to limitations in the resolution of particles < 200 nm and/or accurate determination of concentration. However, TRPS and FC show that the concentration of EVs/MVs ≥ 200 nm in BC and WBF significantly increase on day 42 vs. day 3 (p<0.0001).

Conclusion:
EV size and concentration in RCC products is significantly influenced by the blood manufacturing methods and storage length. Overall, this study shows that not all RCCs are equivalent when it comes to EV size and concentration.
Title: A history of Bacillus Calmette–Guérin (BCG) vaccine is associated with sustained reduced mycobacterial load and transiently increased interferon-γ production in an eight day in vitro model of Mycobacterium tuberculosis H37Ra infection

Authors: Sudha Bhavanam, Gina R. Rayat, Monika Keelan, Dennis Kunimoto, Steven J. Drews

Background and Aim:
Donor Bacillus Calmette-Guérin (BCG) vaccine history (BCG+) or lack of (BCG-) impacts clinical interferon-γ concentration [IFN-γ] in IFN-γ release assays. BCG+ imparts variable vaccine efficacy. Few studies have assessed the impact of BCG+ on in vitro models of Mycobacterium tuberculosis H37Ra (MtbRa) infection using donor peripheral blood mononuclear cell (PBMCs) Aim: To determine the impact of BCG+ vs BCG- on; colony forming units (CFUBCG+ vs CFU BCG-) and IFN-γ concentration ([IFN-γ]BCG+ vs [IFN-γ]BCG-) using donor PBMCs in a previously validated 8 day in vitro MtbRa infection model.

Material and Methods:
PBMCS from BCG+ donors (n=3) and BCG- donors (n=3) were infected with MtbRa in the 8 day infection model. MtbRa CFUBCG+ and CFUBCG- were measured at days 0, 3, 5, 8. An enzyme-linked immunosorbance assay measured ([IFN-γ]BCG+ vs [IFN-γ]BCG-) from model supernatants at days 0, 3, 5 and 8. The Mann-Whitney U (MWU) test was used to compare medians.

Results:
Models using BCG+ donor PBMCs had decreased median MtbRa CFUs compared to models using BCG- donors PBMCs at day 5 (MtbRa CFUBCG+ 1 log10 less than MtbRa CFUBCG- [p<0.05, MWU] and day 8 (MtbRa CFUBCG+ 2 log10 less than MtbRa CFUBCG- [p<0.01, MWU]). Median IFN-γ production was higher in models using BCG+ PBMCs (median 18610.9 pg/ml) than BCG- PBMCs (5245.9 pg/ml) (P<0.001, MWU) at day 3 post- infection but not at other times.

Conclusions:
Compared to infections using BCG- PBMCs , infections with BCG+ PBMCs showed; a sustained reduction in Mtb load, and transiently increased INF-γ concentrations.
**Title:** Detection of proteins using a DNA three-way junction and gold nanoparticle amplification by ICP-MS

**Authors:** Yanwen Lin†, Hongquan Zhang‡, and X. Chris Le,†,‡

**Background and Aim:**
Proteins are important biomarkers, but direct detection at ultra-trace level has proven to be a great challenge. High background signals are easily generated because of the complex matrix of biological systems. We have developed a new method to measure proteins at low concentrations by using gold nanoparticle amplification with inductively coupled plasma mass spectrometry (ICP-MS) detection.

**Material and Methods:**
DNA three-way junctions (TWJs), one of the most common structures used in building DNA structures, are designed as dynamic DNA devices for protein detection. In the presence of a target protein, the binding-induced TWJs can facilitate displacement of the double-stranded DNA beacon, resulting in the release of output DNA. The output DNA is a linker that hybridizes with two short complementary probes that are each functionalized to a magnetic bead (MB) on one end and a gold nanoparticle (AuNP) on the other end. After washing away free AuNPs, excess complementary nucleic acids are added to displace the output DNA, and the AuNPs are separated from the MBs.

**Results:**
Using ICP-MS, the AuNPs are directly atomized, allowing for any matrix interference to be avoided, enhancing specificity. The sensitivity is also increased by using large AuNPs, which amplifies the gold signal. A low pM limit of detection is achieved.

**Conclusions:**
We have improved a TWJ DNA devices for detection of proteins. We will apply this technique to the detection of thrombin at trace concentrations.
Title: Molecular epidemiology of Norovirus Outbreaks in Alberta, Canada: 2012-2016

Authors: Eloisa Hasing1, Bonita Lee2, Yuanyuan Qiu1, Ming Xia3, Graham Tipples4,5, Xi Jiang3, Xiaoli Pang1,5

1. Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada
2. Department of Pediatrics, University of Alberta, Edmonton, AB, Canada
3. Division of Infectious Diseases, Cincinnati Children’s Hospital Medical Centre, Cincinnati, OH, USA
4. Department of Medical Microbiology and Immunology, University of Alberta, Edmonton, AB, Canada
5. Provincial Laboratory for Public Health (ProvLab) Edmonton, AB, Canada

Background and Aim:
The emergence of new norovirus strains of genotype GII.4 has been associated with gastroenteritis pandemics worldwide, prompting molecular surveillance for early detection of novel strains. In this study, we aimed to characterize the outbreak activity of norovirus in Alberta occurring between July 2012 and June 2016.

Material and Methods:
Norovirus gastroenteritis outbreak investigations were performed by the Provincial Public Health Laboratory as part of a routine program. One positive specimen per outbreak was sequenced at the 5’ end (region C) of the major capsid gene using Sanger’s method and genotypes were assigned using NoV Genotyping Tool.

Results:
A total of 420 norovirus outbreaks were identified in the four-year period. The number of NoV outbreaks showed a gradual annual decrease (148, 102, 92 and 78 outbreaks, respectively) and two novel strains emerged: GII.17 Kawasaki in July 2014-June 2015, and a novel GII.P16/GII.4 Sydney recombinant in July 2015-2016. GII.4 Sydney strains were the most predominant between July 2012 and June 2015 (201/342, 58%) whereas July 2015-2016 had increased genetic diversity characterized by a high prevalence of GII.P16/GII.4 Sydney recombinant, GI.3 and GII.17 Kawasaki strains.

Conclusions:
The activity of norovirus outbreaks in Alberta has been in decline while the genetic diversity of norovirus has increased. There are several novel strains currently in circulation; future studies should be aimed to evaluate their differences in antigenicity compared to past pandemic strains as well as their potential to become predominant in future winter seasons.
Title: Nuclear Acids Modifications in Type 2 Diabetes Mellitus (T2dm): A Human and a T2dm Animal Model

Authors: Fan Shen, Consolato Sergi
Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, Canada

Objective:
Nuclear acid modifications are related to the development of T2DM. Fat mass- and obesity-associated (FTO) protein, an RNA demethylase, has been associated with T2DM and obesity. Here, we investigated the RNA methylation in T2DM patients and a T2DM animal model.

Materials and Methods:
Whole blood samples (WBSs) from T2DM patients (n=88) and healthy individuals (n=92) as well as T2DM Sprague-Dawley (T2DMSD) rats were collected. The liquid chromatography-electrospray ionization-tandem mass spectrometry (LC-ESI-MS/MS) method was performed to detect the N6-methyladenosine (m6A) content in RNA from the WBSs. RT-qPCR was used to examine the mRNA levels of FTO, alkB homolog 5 (ALKBH5), methyltransferase-like-3 (METTL3), -like-14 (METTL14) and Wilms tumor-1-associated protein (WTAP) genes. We screened for 4 FTO single-nucleotide polymorphisms (SNPs).

Results:
In T2DM, the m6A content in the RNA from T2DM was lower compared to controls (P=2.6×10-24). Similar results were seen in T2DMSD-rats (P=0.001). FTO mRNA was higher in T2DM than the controls (P=0.0007). We found no difference in the distributions of the four SNPs. METTL3, METTL14 and WTAP mRNAs were higher in T2DM than controls. METTL3 and METTL14 mRNAs only were also higher in T2DMSD-rats (P<0.001). METTL14 mRNA level was negatively correlated with m6A contents (r=-0.258, P=0.001).

Conclusions:
M6A can characterize T2DM and the increase of FTO could be responsible for the reduction of m6A in T2DM. FTO mRNA may be a novel potential biomarker of T2DM and METTL14 seems to play a central role in the methyltransferase complex.
Title: Mass Spectrometry Identification of N-chlorinated Dipeptides in Drinking Water

Authors: Guang Huang, Ping Jiang, Jianye Zhang, Xing-Fang Li

Background and Aim:
Proteins, peptides, and amino acids are relatively abundant in surface water, and the majority <10 kDa are not removed by common coagulation. These diverse nitrogenous compounds could react with disinfectants to form complex halogenated disinfection byproducts (DBPs). Little is known about halogenated peptides, a potentially very large group of DBPs, in drinking water, primarily because of lack of appropriate analytical methodology. N-Cl-peptides and N,N-di-Cl-peptides are suspected to form during chlorination, but their presence in drinking water remains unclear. In this study, we aimed to develop a strategy for the identification of N-Cl-DBPs and N,N-di-Cl-DBPs resulting from specific peptides in drinking water.

Material and Methods:
Three model dipeptides, tyrosylglycine (Tyr-Gly), tyrosylalanine (Tyr-Ala), and phenylalanylglycine (Phe-Gly), reacted with sodium hypochlorite, and these reaction solutions were analyzed. To enable sensitive detection of N-Cl-dipeptides in authentic water, we developed a high-performance liquid chromatography–tandem mass spectrometry (HPLC-MS/MS) method with multiple reaction monitoring (MRM) mode. The stability of these N-Cl-dipeptides was also evaluated.

Results:
N-Cl-Tyr-Gly, N,N-di-Cl-Tyr-Gly, N-Cl-Phe-Gly, N,N-di-Cl-Phe-Gly, N-Cl-Tyr-Ala, and N,N-di-Cl-Tyr-Ala were identified as the major products. These identified N-Cl-dipeptides were synthesized and found to be stable in water over 10 days except N,N-di-Cl-Phe-Gly. N-Cl-Tyr-Gly, N,N-di-Cl-Tyr-Gly, N-Cl-Phe-Gly, N-Cl-Tyr-Ala, and N,N-di-Cl-Tyr-Ala along with their corresponding dipeptides were detected in authentic tap water samples. The dipeptides were clearly detected in the raw water but the N-Cl-dipeptides were at background levels.

Conclusions:
The N-chlorinated dipeptides are produced by chlorination, and may also be new DBPs in drinking water. Our strategy can be used to identify chlorination products of other peptides in drinking water.
**Title:** Oxidative stress induces the acquisition of cancer stem-like phenotype in ER+ breast cancer

**Authors:** Nidhi Gupta, Keshav Gopal, Abdulraheem Alshareef, Afsaneh Lavasanifar, Raymond Lai.

**Background and Aim:**
We have previously identified a novel intra-tumoral dichotomy in breast cancer based on the differential responsiveness to a Sox2 reporter (SRR2), with cells responsive to SRR2 (RR) being more stem-like than unresponsive cells (RU). Here, we assessed if RR cells have a higher tolerance to oxidative stress, a phenotype known to be associated with cancer stemness.

**Material and Methods:**
RU/RR cells derived from MCF7 and ZR751 were used for all the experiments. H2O2 was used as an inducer of oxidative stress. Flow analysis, luciferase assay and probe pull-down experiments were carried out.

**Results:**
RR cells exhibited a significantly higher tolerance to H2O2 than RU cells. Sox2 is directly implicated, since siRNA knockdown of Sox2 in RR cells leveled this difference. Interestingly, H2O2 converted a proportion of RU cells into RR cells, as evidenced by their expression of luciferase and GFP, markers of SRR2 activity. Compared to RU cells, converted RR cells showed a significant increase in their mammosphere formation and tolerance to H2O2. Converted RR cells ‘adopted’ the biochemical features of RR cells, as the RU/RR conversion correlated with a significant increase in Sox2-SRR2 binding and the expression of 3 signature genes of RR cells (CD133, GPR49 and MUC15).

**Conclusions:**
To conclude, our findings have further supported that RR cells are stem-like in breast cancer. The H2O2-induced RU/RR conversion has provided a novel model to study the acquisition of cancer stemness and plasticity.
Title: Construction of functional DNA-protein conjugates of precise 1:1 stoichiometry

Authors: Xiaowen Yan, Hongquan Zhang, Xing-Fang Li, X. Chris Le*

Background and Aim:
DNA-protein conjugates combining the unparalleled programmability of DNA with the tremendous diversity of protein functions, have found great potential in applications ranging from protein immobilization and bioanalysis to fluorescence imaging and targeted delivery of therapeutics. For a majority of the applications based on DNA-protein conjugates, a 1:1 stoichiometry of DNA:protein is required to introduce the DNA functionality and minimize the interference of DNA conjugation on the normal properties of proteins. Here we present a binding-facilitated conjugation method for the coupling of DNA to native proteins with 1:1 stoichiometry.

Material and Methods:
We label an affinity ligand and a reactive group respectively to the terminals of a pair of complementary oligonucleotides (ONs). When affinity ligand binds to a target protein, the complementary ONs bring the reactive group in close proximity to the protein surface, leading to high local concentration and specific labeling of the target proteins. Thus, the conjugation reaction is manipulated in a spatial and temporal controllable manner.

Results:
Gel electrophoresis and electrospray mass spectrometry analyses of the DNA:protein conjugates showed the desirable 1:1 stoichiometry. The generality of this method was demonstrated through conjugation of different proteins facilitated by different types of affinity ligands. We demonstrated that the purified DNA-protein conjugates possess promising potential for various applications that cannot be achieved by using either DNA or protein alone. An example application is the precise introduction of a small drug molecule to inhibit a specific enzyme.

Conclusions:
We successfully achieved the synthesis of functional DNA-protein conjugates with 1:1 stoichiometry through binding-facilitated conjugation.
Title: Primary EBV positive diffuse large B cell lymphoma of prosthetic aortic valve

Authors: Ashish Rajput, MDa, Claribeth Ruano, MDa, Sabin Bozso, MDb, Safwat Girgis, MD, FRCPCa, Julinor Bacani, MD, FRCPCa, Anthea Peters, MD, FRCPCc, Brittney Loney, MSca, Mireille Kattar, MDa, Michael Moon, MD, FRCSCb, Jean Deschenes, MD, FRCPCa

Background and Aim: Primary cardiac diffuse large B cell lymphoma arising in bioprosthetic valve (PCLAV) is very rare.

Material and Methods: We present one such unique case developing 9 years after aortic valvular replacement in an otherwise immunocompetent patient, who presented with minor symptoms despite significant disease burden.

Results: As usually described, this tumor contained Epstein-Barr virus, was confined to the site of its origin, and has behaved non-aggressively after excision so far. Suggestions have been made to classify this unique disease as prosthesis-associated DLBCL in view of its favorable clinical course.

Conclusions: Despite its rarity, knowledge of this neoplasm`s distinct clinical and pathological features is clinically useful.
**Title:** Nanostring Copy Number Variation Assay Is Very Sensitive in Identifying EGFR Amplification but Is Less Sensitive in Identifying Deletions in 1p/19q Compared to FISH in Brain Tumors Samples

**Authors:** Hanan Armanious, Iyare Izevbaye

**Background and Aim:**
CNV (copy number variation) is frequently detected in neuro-oncologic tumors and provide important diagnostic, prognostic and predictive information. These changes include EGFR amplification and 1p/19q co-deletion. FISH remains the gold standard for CNV detection in current molecular pathology practice. However, as FISH is costly and time consuming and requires significant manpower, newer copy number variation techniques such as Nanostring may provide a superior testing methodology.

**Material and Methods:**
We used the Nanostring CNV assay, which detects CNV by interrogating hundreds of loci across different regions in each chromosome in a single reaction. DNA was extracted from 23 archival FFPE neuro-oncologic specimen with histologic diagnosis by a neuropathologist and confirmed FISH results. The histologic types include oligodendroglioma and glioblastoma. FISH results include 16 cases for EGFR amplification and 16 cases for 1p/19q co-deletion. 3 samples of normal brain tissue were used as controls. Samples were run on the nCounter CNV assay and analyzed by the nSolver software. Ratio of target to normalized control was used to identify copy number changes. The results were compared with FISH to determine assay sensitivity and specificity.

**Results:**
Comparison of CNV nanostring assay vs FISH showed 100% concordance for EGFR amplification (6/6 positive and 8/8 negative) with sensitivity, specificity and positive predictive values of 100%; 1p/19q deletion vs FISH showed (10/12 positive and 3/4 negative) with sensitivity of 83%, specificity of 75% and positive predictive value of 91%.

**Conclusions:**
These results demonstrate the ability of the CNV nanostring assay to detect copy number variations particularly EGFR amplification, with comparable sensitivity to the reference FISH technique in brain tumor samples. The assay also demonstrated rapid TAT, high throughput and cost effectiveness in assessing copy number changes. However, more assay optimization is required especially to improve deletion detection.
**Title:** Toxic cyanobacteria monitoring in Alberta lakes from 2012-2016

**Authors:** Yuanyuan Qiu, Xiaoli Pang

**Background and Aim:**
Cyanobacterial bloom in freshwaters has become a major ecological and water quality problem worldwide because of the toxins they produce. Alberta has many eutrophic lakes and reservoirs where cyanobacterial blooms occur frequently in summer. Microcystin, the most common cyanotoxin in the world, is also prevalent in Alberta lakes. Therefore, monitoring microcystin-producing cyanobacterial blooms in Alberta lakes is essential for safe use and better management of recreational beaches. The aim of this study is to use qPCR method for early detection and monitoring of toxic cyanobacteria in lake waters.

**Material and Methods:**
A total of 2619 water samples were collected from 80 Alberta lakes during the open water season of 2012-2016. qPCR was used to detect and quantify the microcystin synthetase E gene (mcyE) that synthesizes microcystin. Three species that produce microcystin, including Microcystis, Anabaena and Planktothrix were differentiated.

**Results:**
Among all the samples tested, 1439 samples (55%) were positive for mcyE gene. 111 samples had the mcyE gene copy number greater than 1 x 10^5 copies/ml, which is equivalent to the Canadian recreational water guideline for microcystin of 20 µg/L. The highest mcyE gene copy number (8 x 10^7 copies/ml) was found in Moose Lake in 2014. Microcystis is the dominant species found in Alberta lakes. MycE gene was detected in 63 out of the 80 lakes (79%). There is only one lake named 40 mile lake that was completely negative for mcyE gene during the 5-years monitoring period.

**Conclusions:**
Microcystin-producing cyanobacteria are frequently found in many recreational lakes in Alberta. Continuous monitoring toxic cyanobacterial bloom is important for public health protection and risk management. This study also provides evidence that qPCR may be used as a promising indicator for cyanotoxin in freshwater.
**Title:** Utility and utilization of urine HCG qualitative testing in a community lab setting

**Authors:** Asifa Amin, Deb Holmes, Dylan Thomas, Trefor Higgins, Mathew P. Estey, Karina Rodriguez-Capote.

**Background and Aim:**
Pregnancy tests can be performed on urine (uHCG) or serum (sHCG). Selection of the optimal test is influenced by analytical performance, convenience, and turnaround time. While sHCG is more sensitive, sample collection for uHCG is less invasive and results may be available sooner. In the community setting however, physicians often request uHCG concurrently with sHCG and/or other bloodwork. In addition, turnaround time is not significantly different between the two tests when sample transport time to the laboratory is considered. This study aims to dissect the community ordering patterns for HCG to assess if order substitutions can be implemented to improve patient care.

**Material and Methods:**
Ad hoc analysis of all physician-ordered qualitative urine HCG tests performed at DynaLIFE from January 23 to February 03, 2017. Accessions numbers were extracted from the Laboratory Information System, and requisitions were reviewed to determine whether other tests were requested.

**Results:**
356 physician-ordered qualitative uHCG tests were performed during the study period. Blood was simultaneously drawn from 225 (63%) of these patients. 77 of these patients had sHCG requested.

**Conclusions:**
More than 60% of uHCG requests were accompanied by either sHCG or other bloodwork. In such instances, the uHCG test offers no advantage over sHCG as a blood specimen has already been collected and turnaround times are similar. Substitution of these uHCG for sHCG would provide more sensitive, quantitative results.
Title: Falsely low HbA1c due to a hidden hemoglobin variant

Authors: Bryce Macek, Mathew P. Estey, Karina Rodriguez-Capote, Trefor Higgins, Dan Beriault, Dylan Thomas.

Background and Aim:
More than 400 million people live with diabetes, a risk factor for ophthalmic, renal, neurologic and cardiovascular disease. Glycemic control is assessed, in part, by measurement of hemoglobin A1c (HbA1c), the glycated form of hemoglobin A (HbA). Measurement of HbA1c by high performance liquid chromatography (HPLC) can be affected by variant hemoglobin’s that co-elute with HbA or HbA1c. Our study characterizes a variant that interferes with specific HPLC methodology, Hb Tacoma, and demonstrates its effect on several different methods of HbA1c measurement.

Material and Methods:
HbA1c was measured in six patients using several methods (three HPLC, capillary zone electrophoresis, two immunoassays). Hb variant identification was performed by HPLC, gel electrophoresis, capillary zone electrophoresis and DNA sequencing.

Results:
Our index patient HbA1c measured with HPLC on our Bio-Rad Variant II was 4.7% in contrast to immunoassay, which reported 7.3%. Subsequent HbA1c analysis on different platforms gave results of 7.2%, 6.8% and 7.5%. This discrepancy prompted characterization of the patient’s hemoglobin via a secondary HPLC method, which revealed no variant. However, gel electrophoresis identified a band near the J region at alkaline pH. Capillary electrophoresis resolved a variant hemoglobin in the Z11 zone representing 38.6%. PCR analysis confirmed a mutation consistent with Hb Tacoma trait, which is now shown to interfere with HbA1c measurement, and is invisible on the Variant-II Turbo hemoglobinopathy program.

Conclusions:
This study demonstrates how the presence of an unrecognized hemoglobin variant can method dependently affect the measurement of HbA1c. The Bio-Rad VARIANT-II Turbo 2.0 underestimates HbA1c measurement in the presence of Hb Tacoma.

<table>
<thead>
<tr>
<th>Instrument</th>
<th>DCA</th>
<th>Variant II</th>
<th>Capillarys 2</th>
<th>Tosoh</th>
<th>Integra</th>
<th>D100</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1C %</td>
<td></td>
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<tr>
<td>Patient 1</td>
<td>7.3</td>
<td>4.7</td>
<td>7.2</td>
<td>7.5</td>
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<td>Patient 3</td>
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<td>Patient 6</td>
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</table>
Title: Agriculture Related Fatalities in Alberta from 2000 - 2015.

Authors: Joseph Andrews, M.D.1, Elizabeth Brooks-Lim, M.D.2
   1. Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, Alberta
   2. Alberta Office of the Chief Medical Examiner, Edmonton, Alberta

Background and Aim:
In 2016, the Alberta government implemented Bill 6, a piece of legislation introducing occupational health and safety regulations and workers’ compensation board insurance for hired farm workers. This legislation, however, does not cover unpaid workers or non-paid family members of the farm owner. This poster will examine the demographics, characteristics, and trends of accidental farm deaths in the sixteen years prior to implementation of Bill 6.

Material and Methods:
We collected data surrounding demographics, circumstances of death, and cause of death in individuals that died of farm accidents in Alberta from the beginning of 2000 to the end of 2015.

Results:
A total of 308 accidental farm deaths occurred in Alberta during the examined period; 63 deaths occurred in individuals under the age of 18, 137 deaths occurred in people between the ages of 18 - 64, and 108 deaths occurred in individuals over the age of 65. Males comprised 89% of deaths and almost 80% of the deaths occurred during work related activities. Of the total number of deaths 173 were the owner, 63 deaths were children of the owner, and 29 deaths were a hired worker. Tractors were the deadliest object on the farm, accounting for 47 deaths.

Conclusions:
During the sixteen-year period prior to implementation of Bill 6, the large majority of agricultural deaths involved a male farm owner, in sunlight hours, during work related activities. Overall, this data from this poster presentation will assist in future analysis of agriculture related fatalities within Alberta.
**Title:** Death certification in northern Alberta: error categorization and occurrence rate based on physician speciality

**Authors:** Kimberly A. Wood\textsuperscript{a}, Seth H. Weinberg\textsuperscript{b}, Mitchell L. Weinberg\textsuperscript{c}
\textsuperscript{a} Laboratory Medicine and Pathology, University of Alberta Hospital, Edmonton, AB
\textsuperscript{b} Department of Biomedical Engineering, Virginia Commonwealth University, Richmond, VA
\textsuperscript{c} Alberta Office of the Chief Medical Examiner, Edmonton, AB

**Background:**
Death certificates (DCs) are important documents used not only for end-of-life matters but also to gather data for epidemiologic studies that monitor health trends and disease surveillance. Prior studies have shown that DCs are fraught with errors\textsuperscript{1-3}; but no previous studies have examined DC errors by specialty.

**Aim:**
This study was performed to evaluate DCs completed by Albertan physicians for types of errors and their frequency based on physician specialty.

**Methods:**
A retrospective review of 1500 DCs completed by Albertan physicians between August and November of 2015 was performed to categorize errors and determine physician speciality and interest in palliative care.

**Results:**
Due to illegible physician name, 108 DCs were excluded. Of the 1392 remaining death certificates, 73\% (n=1020) were completed by family physicians, 18\% (n=251) by internists, 3\% (n=44) by surgeons, 2\% (n=28) by emergency physicians, 1\% by neurologists (n=18) and 2\% (n=31) by other specialties. Error occurrence (EO) rate ranged between 32 and 75\% based on specialty (26-68\% excluding formatting errors). Family physicians experienced in palliative care (FAM-PC) had a significantly lower (P<0.001) EO rate (32\%) than family physician (62\%), internists (62\%) and surgeons (75\%). The most common errors were use of abbreviations (Abbr, 26\%), mechanism used as underlying cause of death (McUCoD, 23\%) and no underlying cause of death recorded (NoUCoD, 22\%). Co-incidence analysis showed that when McUCoD occurred, 95\% of the time, NoUCoD also occurred (P<0.05). A total of 15 wrong manner of death errors were found.

**Conclusion:**
This data shows a need for postgraduate medical education in death certification.

**References:**
Title: Death certification in northern Alberta: educational intervention

Authors: Kimberly A. Wood, Seth H. Weinberg, Mitchell L. Weinberg

Laboratory Medicine and Pathology, University of Alberta Hospital, Edmonton, AB
Department of Biomedical Engineering, Virginia Commonwealth University, Richmond, VA
Alberta Office of the Chief Medical Examiner, Edmonton, AB

Background:
A variety of educational interventions have shown to improve death certificate (DC) error rate, with greatest improvements from interactive case-based sessions. A needs assessment performed by this group demonstrated that family physicians complete the majority (73%) of DCs with the most common errors being use of abbreviations (26%), mechanism used as underlying cause of death (23%) and no underlying cause of death recorded (22%).

Aim:
To evaluate the effectiveness of a didactic/case-based seminar targeting the most common and important errors in DCs.

Methods:
A 60 minute didactic/case-based seminar delivered to family medicine residents and staff physicians at Grand Rounds with administration of pre-, immediate post, and 2-month post surveys.

Results:
Pre-survey (n=72) demonstrated an overall error occurrence (EO) rate of 71.5% (64% without formatting errors), with no statistical significance between staff (n=9) and residents (n=63) frequency of DC competition. A lower EO rate (P<0.05, without formatting errors) was observed for persons with formal DC education (54%) or electives in pathology (56%) and palliative care (60%) compared to those with informal DC education (67%) or no electives (71%) in pathology/palliative care, respectively. Immediate post (n=75) and 2 month post (n=24) surveys demonstrated a lower overall EO rate (without formatting errors) of 34% (12%) and 24% (15%), compared to the pre-survey (P<0.05). The majority of participants found the seminar to be useful or very useful (n=61), were more confident in completing DCs (n=61), and recommended repetition (n=71).

Conclusion:
A 60-minute didactic/case-based seminar on DC can significantly reduce EO rate with long-term effects.

References:
Title: Thromboelastography Platelet Mapping Assay: Interference Remediation Using Eptifibatide

Authors: Tara Dixon MD, Lorraine Petryk MLT, Linda Stang MLT, Artur Szkotak MD PhD FRCPC

Background and Aim:
The Thromboelastography Platelet Mapping Assay (TEG-PM) is used to monitor anti-platelet therapy. Occasionally, interference attributed to platelet hyper-reactivity precludes accurate interpretation of results. We hypothesize that the platelet GpIIb/IIIa inhibitor eptifibatide may resolve this interference.

Material and Methods:
Parallel TEG-PM with and without an eptifibatide adjunct was performed on 22 control and 41 patient samples using TEG® 5000 Analyzer (TEG-PM, Haemonetics, Braintree, MA). A Clauss fibrinogen level was obtained for comparison (STA Fibrinogen 5, Diagnostica Stago, Asnières Sur Seine, France).

Results:
7/41 of patient samples showed assay interference. Eptifibatide adjunct eliminated 84% of the interference, which was statistically significant. However, a small but statistically significant amount of bias remained (ANCOVA P-value=0.03 with df=2, 115). Eptifibatide adjunct also significantly improved correlation with the Clauss fibrinogen level (r=0.09 vs r=0.50) (ANCOVA p-value=0.005 with df=1, 11).

Eptifibatide adjunct did not have a statistically significantly effect on any TEG-PM parameter in controls (P-value >0.40), or normal patient samples (34/41) (P-value>0.39, paired student’s T-test). Pooled data (controls + normal patient samples) showed reasonable linear correlation with the Clauss fibrinogen level (r=0.59), and no significant difference in slope or y-intercept with an eptifibatide adjunct (ANCOVA P-value>0.67 with df=1, 108).

Conclusions:
Assay interference attributed to platelet hyper-reactivity precludes accurate TEG-PM interpretation and does not correlate with the Clauss fibrinogen level. Eptifibatide adjunct significantly improves accuracy in samples with interference and improves correlation with the Clauss fibrinogen level. Eptifibatide adjunct does not cause interference in the TEG-PM assay.


**Title:** Applying LEAN / 6S methodology to MOD lab organization and SOP maintenance.

**Authors:** Navkiran Randhawa, Candace Betiku, Dena Adachi, and Carmen Charlton

**Background and Aim:**
In the Molecular Diagnostics Department (MOD), Standard Operating Procedures (SOP) are used for all testing and general procedures routinely executed to ensure standardization and quality. Overtime, MOD SOP’s have become less effective. Staff have reported difficulty finding and using SOPs due to the poor organization and inadequate upkeep of documents. Similarly, the lack of organization of the materials and equipment within the lab has caused routine work to becoming increasingly challenging.

The goal of this project is to reduce distress and physical strain while increasing efficiency within the lab by implementing the LEAN principle and 6S methodology.

**Material and Methods:**
Staff concerns regarding SOPs were documented during staff meetings, and the strengths and weaknesses of the SOP system was assessed using Swimlane analysis. SOPs were re-organized and physical SOPs were re-located according to staff discussions. Departmental workflow was determined by tracking staff travel patterns with spaghetti diagrams during routine testing. To improve ease of access, items in the laboratory were categorized as (1) ‘Red Tag’/‘Green Tag’, (2) donate, (3) discard or (4) store unused items. Laboratory reorganization grouped similar supplies and distribution items in close proximity location of use. Staff were encouraged to provide feedback and further suggestions to improve the process.

The success of the project was measured by surveying staff before and after and comparing several parameters.

**Results:**

<table>
<thead>
<tr>
<th>Measurements</th>
<th>Before</th>
<th>After</th>
</tr>
</thead>
<tbody>
<tr>
<td>Timely revision of SOPs</td>
<td>25%</td>
<td>90%</td>
</tr>
<tr>
<td>Ability to troubleshoot effectively with SOPs</td>
<td>50%</td>
<td>85%</td>
</tr>
<tr>
<td>Time needed to locate SOPs, materials and equipment</td>
<td>avg. of 10 minutes</td>
<td>avg of 1 minute</td>
</tr>
<tr>
<td>Ability to complete tech responsibilities within work hours</td>
<td>50%</td>
<td>100%</td>
</tr>
<tr>
<td>Incidences of distress and physical strain</td>
<td>avg of 3 / week</td>
<td>0 / week</td>
</tr>
<tr>
<td>Staff moral and ease of work</td>
<td>Fair</td>
<td>Very Good</td>
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</table>

**Conclusions:**
The efforts to create positive change through this project were successful in improving workflow, ergonomic/lab safety, as well as the general work environment.
Title: Cost Savings following Stamp Utilization

Authors: Lillian Wirth, Shannon Robinson, Melodie Barnett, Seema Kailey, Anita Vishnu, and Carmen L. Charlton

Background and Aim:
The stamp utilization project was piloted to reduce test duplication between DynaLIFE and ProvLab. Previously, samples requiring testing at DynaLIFE and ProvLab were tested at DynaLIFE first, and then forwarded to ProvLab for the remainder of the testing. However, no system was in place to determine which tests had already been performed. To ensure no testing was missed, all tests requested were tested by ProvLab. This resulted in significant test duplication.

Material and Methods:
As a collaborative effort between DynaLIFE and ProvLab, testing was streamlined by using a stamp. It was agreed each requisition received by DynaLIFE for ProvLab testing will be stamped with all the tests performed at DynaLIFE (including serology markers for Hepatitis A and B and syphilis). ProvLab will consequently only perform the tests not indicated on stamp.

Results:
After data was analyzed it was determined that:

a) Quantity of all markers included on the stamp decreased from time of implementation onwards.
b) Largest decreases were seen in Syphilis, HBsAg, and HBsAb.
c) Substantial savings were realized in reagents, instrumentation costs, technologist, and lab assistant time

Conclusions:
The development of the ‘stamp’ proved to be an effective and efficient tool for communication between DynaLIFE and ProvLab. This inexpensive method resulted in cost savings, increased clientele satisfaction, removed indecision on whether to test, and improved collaboration between DynaLIFE and ProvLab. Due to the success of this pilot project, the stamp will now become an operational-best-practice for microbiology testing in Northern Alberta.