

Gregory Gloor, PhD

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I Expertise and Research Interests

Composition and function of the human and other microbiomes. I use and develop tools to examine 16S rRNA gene composition, gene expression of mixed population samples, and metabolomic analysis of clinical samples. I teach a graduate course on the use of compositional data analysis techniques to examine transcriptomes, microbiomes and other types of complex data sets derived from high throughput sequencing.

Protein evolution. We use and develop tools to examine how protein structure and function is maintained in response to sequences changes. We have a special interest in identifying the role that variable positions play in protein evolution. I teach an undergraduate course in protein sequence alignment and proteins sequence-structure alignment.

Computational biology and that application of techniques for compositional data analysis to the above problems. Our primary contributions so far have been the ALDEx2 tool in Bioconductor for the analysis of high throughput experiments that generate counts per sequence tag: 16S rRNA gene sequencing, transcriptomics and selex-type experiments. I have further tools under development, and have contributed new visualization methods (effect-size plots) to the field.

2 Education and Training

1988-1990 Postdoctoral Fellow. University of Wisconsin - Madison - Laboratory of Genetics. Supervisor: Dr. William Engels.

1988 Ph.D, University of Western Ontario, Department of Biochemistry. Supervisor: Dr. George Chaconas. Dissertation: *Characterization of the Integrative Precursor Protein-DNA Complex of Bacteriophage Mu*.

1983 HBSc, University of Western Ontario, Genetics

3 Employment

2002-present , Professor of Biochemistry
University of Western Ontario, Faculty of Medicine
now the Schulich School of Medicine and Dentistry

1997-2002, Associate Professor of Biochemistry
University of Western Ontario, Faculty of Medicine

1993-1997, Assistant Professor of Biochemistry
University of Western Ontario, Faculty of Medicine

1990-1992, Assistant Professor Medical Genetics
Memorial University of Newfoundland, Faculty of Medicine

4 Faculty Development

- 2014, Five day theory and applied course on Compositional Data Analysis (UdG, Spain)
Accredited by European Statistical Society
- 2007, Leadership Workshop
Offered by Continuing Education of Schulich School of Medicine and Dentistry for Medical School
Accreditation Leaders
- 1995, Course on Teaching at the University Level
Offered through the Faculty of Medicine Development Office.
- 1990, Faculty Orientation Day Memorial University of Newfoundland
This covered teaching tips and grant writing skills for new faculty at MUN

5 Awards, Honours, Fellowships

- 2014, Faculty Development Award: Attended week-long course on Compositional Data Analysis (UdG, Spain)
- 2011-2013, Faculty Scholar
- 2009, University Student's Council Teaching Honor Roll
- 2007, University Student's Council Teaching Honor Roll
- 2005, Schulich School of Medicine Teaching Award
- 2004, WL Magee Teaching Award, Biochemistry, UWO
- 1993 - 1998, Salary Award, Medical Research Council of Canada (MRC)
Development Grant in Molecular Biology
- 1984 -1988, K. M. Hunter Fellowship, National Cancer Institute of Canada.
- 1983, Graduate Entrance Scholarship, UWO.

6 HQP Training Summary

- Graduate Student: 10; Undergraduate Student: 30; Postdoctoral Fellow: 2;
Graduate Advisory Committee: 30; Thesis Defence: 68; Qualifying Examiner: 46.

7 Scholarly and Professional Activities Summary

7.1 Grants and Awards Panels, Editorial membership

- 2017-present, Chair, CIHR Project Grant Scheme (Genomics/Genetics)
- 2017-present, Member, CIHR College of Reviewers (First round invitee)
- 2017, Member, Canadian Crohns and Colitis Review panel
- 2016, Member, Agence Nationale de la Recherche, Preindustrial Biotechnology Demonstrator, Paris, France
- 2016-present, Senior Editor, Microbiome
- 2016, Western Science and Engineering Review Board Member

2016, CIHR Operating Grant Review Panel Chair
2015-2016, Associate Editor, Microbiome
2015, Ontario Genomics Institute: SPARC and Genome Canada review panel
2014-present, CRC College of Reviewers
2012-2015, Editorial Board member Microbiome
2010-2014, Member CIHR Genetics panel
2008-present, IODE Doctoral Scholarship committee
2006-2010, NCIC Model Organisms Panel B2
1998, 1999, 2000, 2003, 2004, 2005, 2006, 2007, 2008 MRC / CIHR BMB / Genetics / Genomics invitee
item 1999, Chair OGS Biochemistry / Biophysics panel item 1997-1999, OGS Biochemistry / Biophysics
panel
1997-2000, NCIC Virology and Molecular Biology Committee
Panel F
1995-2001, Foundation for Gene and Cell Therapy (Jesse's Journey)
Chair and Review Organizer 1995 - 2001

7.2 Board memberships

2001-2002, Member, Board of Directors for Partners in Research
1995-2001 Member, Board of Directors, The Foundation for Gene and Cell Therapy (FFGCT).
I was the lead negotiator for the FFGCT in working out a partnership with the MRC to fund up to 9
post-doctoral fellows in the area of gene therapy. This partnership provided approximately \$900,000
in new money to the MRC.
1995, Member of the Home Team for Jesse's Journey (Internet and Science Advisor).
I posted and updated a World Wide Web map page so that people from around the world could
follow John and Jesse's progress.

7.3 Presentations and Invitations

2017, Keynote, Microbial Ecology 2017, Toronto, Ontario
2017, Workshop, Compositional Data analysis methods, Microbial Ecology 2017, Toronto, Ontario
2017, Invited speaker, EMBL-EBI Industrial Program Workshop - The human microbiome: challenges
and opportunities for novel therapeutics, Hinxton, England
2017, Invited speaker Canadian Society of Microbiology, Waterloo, Ontario
2017, Canadian Statistical Sciences Institute Microbiome Planning Meeting speaker and discussion leader,
Winnipeg, Manitoba
2017, Contributed Oral Presentation (2), Great Lakes Bioinformatics, Chicago, Illinois
2017, Invited speaker in the Microbiology & Immunology Department, Western University, London, CA
2017, Invited speaker in the Health Sciences Department, Carleton University, Ottawa, CA

2016, Invited speaker in the Biostatistics and Epidemiology Department, Western University, London, CA

2016, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2016, Cambridge, UK

2016, Invited workshop organizer at Exploring Human Host-Microbiome Interactions in Health and Disease 2016, Cambridge, UK

2016, Invited speaker at Symposium on Synthetic Biology, Western University, London, CA

2016, Invited workshop presenter, The Human Microbiome and Epidemiology, 2016 Epidemiology Congress of the Americas, Miami, USA

2016, Invited presentation/ workshop, Infection, Inflammation and Immunity course, The Arctic University of Norway, Tromsø, NO

2016, Oral Presentation, Great Lakes Bioinformatics/ Canadian Computational Biology Conference, Toronto, CA

2015, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2015, Cambridge, UK

2015, Invited paper at CoDaWork 2015, Girona, Spain

2015, Applying compositional data framework to microbiome datasets, Canadian Society of Microbiology workshop 2015, Saskatoon, Canada

2015, Invited speaker, University of Guelph Bioinformatics group

2014, Invited seminar, Dept. of Biochemistry, University of Calgary

2014, Invited participant at NIH sponsored Microbiome Quality Control Initiative: only Canadian group invited, Rockville, MD, USA

2013, Invited speaker at Fondation Merieux Conference on Better Foods for Better Health, Annecy, France

2013, Invited speaker at the Institute of Genome Sciences seminar series, University of Maryland, Baltimore, USA

2013, Invited expert participant at African International Conference and Workshop on the Microbiome and Probiotics, Nairobi, Kenya

2011, Invited speaker at the RePOOPulating the gut: therapeutic microbial preparations to eradicate recurrent *C.difficile* infections in Canada, Toronto

2011, Invited expert participant at International Society for the Application of Probiotics and Prebiotics, Berkeley, CA

2010, Invited platform speaker at the Ontario Illumina Users Group, Toronto Ontario

2008, Invited speaker at University of North Carolina-Charlotte Department of Bioinformatics Seminar Series

2003, Invited speaker at First Canadian Workshop on Statistical Genomics, The Fields Institute, Toronto

2000, Department of Genetics seminar series, Harvard Medical School, Boston, Mass.

1999, London and Regional Cancer Center seminar series, London Ontario

1997 Department of Molecular Biology and Genetics seminar series, University of Guelph

1994 Mogenson Research Forum, UWO Faculty of Medicine

1992 Department of Genetics, University of Alberta seminar series
Alberta Heritage Foundation for Medical Research Sponsored Speaker

1992 Lunchtime Seminar Series, Faculty of Medicine, Memorial University of Newfoundland

1992 Department of Biochemistry seminar series, Queens University

1992 Department of Biochemistry seminar series, UWO

1991 Molecular Biology Research Discussion Group seminar series, Faculty of Medicine, MUN

1991 Department of Biochemistry seminar series, MUN

1990 Faculty of Medicine seminar series, MUN

7.4 Peer Reviewed Papers:

Academic trivia

- H-index: 34, i10 index: 75 (Google Scholar)
- Erdos number 3 (two ways)
- Aitchison number 1 (two ways)
- Academic lineage: T.H. Morgan

- [111] Gregory B. Gloor, Jean M. Macklaim, Vera Pawlowsky-Glahn, and Juan J. Egozcue. Microbiome datasets are compositional: And this is not optional. *Frontiers in Microbiology*, 8:2224, 2017.
- [110] Gaorui Bian, Gregory B Gloor, Aihua Gong, Changsheng Jia, Wei Zhang, Jun Hu, Hong Zhang, Yumei Zhang, Zhenqing Zhou, Jiangao Zhang, Jeremy P Burton, Gregor Reid, Yongliang Xiao, Qiang Zeng, Kaiping Yang, and Jiangang Li. The gut microbiota of healthy aged chinese is similar to that of the healthy young. *mSphere*, 2(5):e00327–17, 2017.
- [109] Sarah Lynn Martz, Mabel Guzman-Rodriguez, Shu-Mei He, Curtis Noordhof, David John Hurlbut, Gregory Brian Gloor, Christian Carlucci, Scott Weese, Emma Allen-Vercoe, Jun Sun, Erika Chiong Claud, and Elaine Olga Petrof. A human gut ecosystem protects against c. difficile disease by targeting tcda. *Journal of Gastroenterology*, 52(4):452–465, Apr 2017.
- [108] Amy McMillan, Adebola E. Orimadegun, Mark W. Sumarah, Justin Renaud, Magdalena Muc da Encarnacao, Gregory B. Gloor, Olusegun O. Akinyinka, Gregor Reid, and Stephen J. Allen. Metabolic derangements identified through untargeted metabolomics in a cross-sectional study of nigerian children with severe acute malnutrition. *Metabolomics*, 13(2):13, Dec 2016.
- [107] Grace Ettinger, Jeremy P Burton, Gregory B Gloor, and Gregor Reid. Lactobacillus rhamnosus gr-1 attenuates induction of hypertrophy in cardiomyocytes but not through secreted protein msp-1 (p75). *PLoS One*, 12(1):e0168622, 2017.
- [106] Kait Al, Ousseynou Sarr, Kristyn Dunlop, Gregory B Gloor, Gregor Reid, Jeremy Burton, and Timothy R H Regnault. Impact of birth weight and postnatal diet on the gut microbiota of young adult guinea pigs. *PeerJ*, 5:e2840, 2017.
- [105] Jason M Wolfs, Thomas A Hamilton, Jeremy T Lant, Marcon Laforet, Jenny Zhang, Louisa M Salemi, Gregory B Gloor, Caroline Schild-Poulter, and David R Edgell. Biasing genome-editing events toward precise length deletions with an rna-guided tevCas9 dual nuclease. *Proc Natl Acad Sci U S A*, Dec 2016.
- [104] Joel W G Slade, Yanina Sarquis-Adamson, Gregory B Gloor, Marc-André Lachance, and Elizabeth A MacDougall-Shackleton. Population differences at mhc do not explain enhanced resistance of song sparrows to local parasites. *J Hered*, Dec 2016.
- [103] S Rahat-Rozenbloom, J Fernandes, J Cheng, G B Gloor, and T M S Wolever. The acute effects of inulin and resistant starch on postprandial serum short-chain fatty acids and second-meal glycemic response in lean and overweight humans. *Eur J Clin Nutr*, Dec 2016.

- [102] J W G Slade, M J Watson, T R Kelly, G B Gloor, M A Bernards, and E A MacDougall-Shackleton. Chemical composition of preen wax reflects major histocompatibility complex similarity in songbirds. *Proc Biol Sci*, 283(1842), Nov 2016.
- [101] Mariya I Petrova, Elke Lievens, Tine L A Verhoeven, Jean M Macklaim, Gregory Gloor, Dominique Schols, Jos Vanderleyden, Gregor Reid, and Sarah Lebeer. The lectin-like protein 1 in *Lactobacillus rhamnosus* gr-1 mediates tissue-specific adherence to vaginal epithelium and inhibits urogenital pathogens. *Sci Rep*, 6:37437, Nov 2016.
- [100] Gregory B Gloor, Jean M Macklaim, Michael Vu, and Andrew D Fernandes. Compositional uncertainty should not be ignored in high-throughput sequencing data analysis. *Austrian Journal of Statistics*, 45:73–87, September 2016.
- [99] Gregory B Gloor and Gregor Reid. Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data. *Can J Microbiol*, 62(8):692–703, Aug 2016.
- [98] Camilla Urbaniak, Gregory B Gloor, Muriel Brackstone, Leslie Scott, Mark Tangney, and Gregor Reid. The microbiota of breast tissue and its association with breast cancer. *Appl Environ Microbiol*, 82(16):5039–48, Aug 2016.
- [97] Gregory B Gloor, Jia Rong Wu, Vera Pawlowsky-Glahn, and Juan José Egozcue. It’s all relative: analyzing microbiome data as compositions. *Ann Epidemiol*, 26(5):322–9, May 2016.
- [96] Gregory B. Gloor, Jean M. Macklaim, and Andrew D. Fernandes. Displaying variation in large datasets: a visual summary of effect sizes. *Journal of Computational and Graphical Statistics*, 25(3):971–9, 2016.
- [95] Ruth G Wong, Jia R Wu, and Gregory B Gloor. Expanding the UniFrac toolbox. *PLoS One*, 11(9):e0161196, 2016.
- [94] Camilla Urbaniak, Michelle Angelini, Gregory B Gloor, and Gregor Reid. Human milk microbiota profiles in relation to birthing method, gestation and infant gender. *Microbiome*, 4:1, Jan 2016.
- [93] Asma Asemaninejad, Nimalka Weerasuriya, Gregory B Gloor, Zoë Lindo, and R Greg Thorn. New primers for discovering fungal diversity using nuclear large ribosomal dna. *PLoS One*, 11(7):e0159043, 2016.
- [92] A McMillan, J B Renaud, G B Gloor, G Reid, and M W Sumarah. Post-acquisition filtering of salt cluster artefacts for lc-ms based human metabolomic studies. *J Cheminform*, 8(1):44, 2016.
- [91] David M Walton, James M Elliott, Joshua Lee, Eldon Loh, Joy C MacDermid, Siobhan Schabrun, Walter L Siqueira, Brian D Corneil, Bill Aal, Trevor Birmingham, Amy Brown, Lynn K Cooper, James P Dickey, S Jeffrey Dixon, Douglas D Fraser, Joseph S Gati, Gregory B Gloor, Gordon Good, David Holdsworth, Samuel A McLean, Wanda Millard, Jordan Miller, Jackie Sadi, David A Seminowicz, J Kevin Shoemaker, Gunter P Siegmund, Theodore Vertsegh, and Timothy H Wideman. Research priorities in the field of posttraumatic pain and disability: Results of a transdisciplinary consensus-generating workshop. *Pain Res Manag*, 2016:1859434, 2016.
- [90] Jordan E Bisanz, Praema Suppiah, W Murray Thomson, Trudy Milne, Nigel Yeoh, Anita Nolan, Grace Ettinger, Gregor Reid, Gregory B Gloor, Jeremy P Burton, Mary P Cullinan, and Simon M Stebbings. The oral microbiome of patients with axial spondyloarthritis compared to healthy individuals. *PeerJ*, 4:e2095, 2016.

- [89] Jordan E Bisanz, Megan K Enos, George PrayGod, Shannon Seney, Jean M Macklaim, Stephanie Chilton, Dana Willner, Rob Knight, Christoph Fusch, Gerhard Fusch, Gregory B Gloor, Jeremy P Burton, and Gregor Reid. Microbiota at multiple body sites during pregnancy in a rural tanzanian population and effects of moringa-supplemented probiotic yogurt. *Appl Environ Microbiol*, 81(15):4965–75, Aug 2015.
- [88] Nicole St-Denis, Michelle Gabriel, Jacob P Turowec, Gregory B Gloor, Shawn S-C Li, Anne-Claude Gingras, and David W Litchfield. Systematic investigation of hierarchical phosphorylation by protein kinase ck2. *J Proteomics*, 118:49–62, Apr 2015.
- [87] Lee W Goneau, Thomas J Hannan, Roderick A MacPhee, Drew J Schwartz, Jean M Macklaim, Gregory B Gloor, Hassan Razvi, Gregor Reid, Scott J Hultgren, and Jeremy P Burton. Subinhibitory antibiotic therapy alters recurrent urinary tract infection pathogenesis through modulation of bacterial virulence and host immunity. *MBio*, 6(2), Mar 2015.
- [86] Amy McMillan, Stephen Rulisa, Mark Sumarah, Jean M Macklaim, Justin Renaud, Jordan E Bisanz, Gregory B Gloor, and Gregor Reid. A multi-platform metabolomics approach identifies highly specific biomarkers of bacterial diversity in the vagina of pregnant and non-pregnant women. *Sci Rep*, 5:14174, 2015.
- [85] Sarah-Lynn E Martz, Julie A K McDonald, Jun Sun, Yong-Guo Zhang, Gregory B Gloor, Curtis Noordhof, Shu-Mei He, Teklu K Gerbaba, Michael Blennerhassett, David J Hurlbut, Emma Allen-Vercoe, Erika C Claud, and Elaine O Petrof. Administration of defined microbiota is protective in a murine salmonella infection model. *Sci Rep*, 5:16094, 2015.
- [84] Jean M Macklaim, Jose C Clemente, Rob Knight, Gregory B Gloor, and Gregor Reid. Changes in vaginal microbiota following antimicrobial and probiotic therapy. *Microb Ecol Health Dis*, 26:27799, 2015.
- [83] Siwen Yang, Gregor Reid, John R G Challis, Sung O Kim, Gregory B Gloor, and Alan D Bocking. Is there a role for probiotics in the prevention of preterm birth? *Front Immunol*, 6:62, 2015.
- [82] S Rahat-Rozenbloom, J Fernandes, G B Gloor, and T M S Wolever. Evidence for greater production of colonic short-chain fatty acids in overweight than lean humans. *Int J Obes (Lond)*, 38(12):1525–31, Dec 2014.
- [81] Thomas A McMurrough, Russell J Dickson, Stephanie M F Thibert, Gregory B Gloor, and David R Edgell. Control of catalytic efficiency by a coevolving network of catalytic and noncatalytic residues. *Proc Natl Acad Sci U S A*, 111(23):E2376–83, Jun 2014.
- [80] Camilla Urbaniak, Joanne Cummins, Muriel Brackstone, Jean M Macklaim, Gregory B Gloor, Chwanrow K Baban, Leslie Scott, Deidre M O’Hanlon, Jeremy P Burton, Kevin P Francis, Mark Tangney, and Gregor Reid. Microbiota of human breast tissue. *Appl Environ Microbiol*, 80(10):3007–14, May 2014.
- [79] Xiaohong Tracey Gan, Grace Ettinger, Cathy X Huang, Jeremy P Burton, James V Haist, Venkatesh Rajapurohitam, James E Sidaway, Glynn Martin, Gregory B Gloor, Jonathan R Swann, Gregor Reid, and Morris Karmazyn. Probiotic administration attenuates myocardial hypertrophy and heart failure after myocardial infarction in the rat. *Circ Heart Fail*, 7(3):491–9, May 2014.
- [78] Gregor Reid, Nicholas Nduti, Wilbert Sybesma, Remco Kort, Tobias R Kollmann, Rod Adam, Hamadi Boga, Eric M Brown, Alexandra Einerhand, Hani El-Nezami, Gregory B Gloor, Irene I Kaveri, Johanna Lindahl, Ameer Manges, Wondu Mamo, Rocio Martin, Amy McMillan, Jael Obiero,

- Pamela A Ochieng, Arnold Onyango, Stephen Rulisa, Eeva Salminen, Seppo Salminen, Antony Sije, Jonathan R Swann, William van Treuren, Daniel Waweru, and Steve J Kemp. Harnessing microbiome and probiotic research in sub-Saharan Africa: recommendations from an African workshop. *Microbiome*, 2(1):12, Apr 2014.
- [77] S Rahat-Rozenbloom, J Fernandes, G B Gloor, and T M S Wolever. Evidence for greater production of colonic short chain fatty acids in overweight than lean humans. *Int J Obes (Lond)*, Mar 2014.
- [76] Chantalle Brace, Gregory B Gloor, Mark Ropeleski, Emma Allen-Vercoe, and Elaine O Petrof. Microbial composition analysis of *Clostridium difficile* infections in an ulcerative colitis patient treated with multiple fecal microbiota transplantations. *J Crohns Colitis*, 8:1113–7, Feb 2014.
- [75] Jordan E Bisanz, Shannon Seney, Amy McMillan, Rebecca Vongsa, David Koenig, LungFai Wong, Barbara Dvoracek, Gregory B Gloor, Mark Sumarah, Brenda Ford, Dorli Herman, Jeremy P Burton, and Gregor Reid. A systems biology approach investigating the effect of probiotics on the vaginal microbiome and host responses in a double blind, placebo-controlled clinical trial of post-menopausal women. *PLoS One*, 9(8):e104511, 2014.
- [74] Kristin D Kernohan, Douglas Vernimmen, Gregory B Gloor, and Nathalie G Bérubé. Analysis of neonatal brain lacking ATRX or MeCP2 reveals changes in nucleosome density, CTCF binding and chromatin looping. *Nucleic Acids Res*, 42(13):8356–68, 2014.
- [73] Russell J Dickson and Gregory B Gloor. Bioinformatics identification of coevolving residues. *Methods Mol Biol*, 1123:223–43, 2014.
- [72] Camilla Urbaniak, Amy McMillan, Michelle Angelini, Gregory B Gloor, Mark Sumarah, Jeremy P Burton, and Gregor Reid. Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. *Microbiome*, 2:24, 2014.
- [71] Mariana Rosenthal, Allison E Aiello, Carol Chenoweth, Deborah Goldberg, Elaine Larson, Gregory Gloor, and Betsy Foxman. Impact of technical sources of variation on the hand microbiome dynamics of healthcare workers. *PLoS One*, 9(2):e88999, 2014.
- [70] Jordan E Bisanz, Megan K Enos, Joseph R Mwanga, John Chagalucha, Jeremy P Burton, Gregory B Gloor, and Gregor Reid. Randomized open-label pilot study of the influence of probiotics and the gut microbiome on toxic metal levels in Tanzanian pregnant women and school children. *MBio*, 5(5):e01580–14, 2014.
- [69] Andrew D Fernandes, Jennifer Ns Reid, Jean M Macklaim, Thomas A McMurrough, David R Edgell, and Gregory B Gloor. Unifying the analysis of high-throughput sequencing datasets: characterizing RNA-seq, 16S rRNA gene sequencing and selective growth experiments by compositional data analysis. *Microbiome*, 2:15.1–15.13, 2014.
- [68] Julia M Di Bella, Yige Bao, Gregory B Gloor, Jeremy P Burton, and Gregor Reid. High throughput sequencing methods and analysis for microbiome research. *J Microbiol Methods*, 95(3):401–14, Dec 2013.
- [67] Lance F DaSilva, Samantha Pillon, Julie Genereaux, Megan J Davey, Gregory B Gloor, Jim Karagannis, and Christopher J Brandl. The C-terminal residues of *Saccharomyces cerevisiae* Mec1 are required for its localization, stability, and function. *G3 (Bethesda)*, 3(10):1661–74, Oct 2013.
- [66] A. D. Fernandes, J. M. Macklaim, T.G Linn, G. Reid, and G. B. Gloor. ANOVA-like differential expression (ALDEx) analysis for mixed population RNA-seq. *PLoS ONE*, 8(7):e67019, July 2013.

- [65] Mi Seong Kim, Gregory B Gloor, and Donglin Bai. The distribution and functional properties of Pelizaeus-Merzbacher-like disease-linked Cx47 mutations on Cx47/Cx47 homotypic and Cx47/Cx43 heterotypic gap junctions. *Biochem J*, 452(2):249–58, Jun 2013.
- [64] Roderick A MacPhee, Wayne L Miller, Gregory B Gloor, John K McCormick, Jo-Anne Hammond, Jeremy P Burton, and Gregor Reid. Influence of the vaginal microbiota on toxic shock syndrome toxin 1 production by staphylococcus aureus. *Appl Environ Microbiol*, 79(6):1835–42, Mar 2013.
- [63] E O Petrof, E C Claud, G B Gloor, and E Allen-Vercoe. Microbial ecosystems therapeutics: a new paradigm in medicine? *Benef Microbes*, 4(1):53–65, Mar 2013.
- [62] Piya Lahiry, Lemuel Racacho, Jian Wang, John F Robinson, Gregory B Gloor, C Anthony Rupar, Victoria M Siu, Dennis E Bulman, and Robert A Hegele. A mutation in the serine protease TMPRSS4 in a novel pediatric neurodegenerative disorder. *Orphanet J Rare Dis*, 8:126, 2013.
- [61] M Jean Macklaim, D Andrew Fernandes, M Julia Di Bella, Jo-Anne Hammond, Gregor Reid, and Gregory B Gloor. Comparative meta-RNA-seq of the vaginal microbiota and differential expression by *Lactobacillus iners* in health and dysbiosis. *Microbiome*, 1:15, 2013.
- [60] Kingsley C Anukam, Jean M Macklaim, Gregory B Gloor, Gregor Reid, Jos Boekhorst, Bernadet Renckens, Sacha A F T van Hijum, and Roland J Siezen. Genome sequence of *Lactobacillus pentosus* KCA1: Vaginal isolate from a healthy premenopausal woman. *PLoS One*, 8(3):e59239, 2013.
- [59] Philip A. Wescombe, Jean M. Macklaim, Melissa H. C. Chai, Kyle MacDonald, John D. F. Hale, John Tagg, Gregor Reid, Gregory B. Gloor, and Peter A. Cadieux. Persistence of the oral probiotic *Streptococcus salivarius* M18 is dose dependent and megaplasmid transfer can augment their bacteriocin production and adhesion characteristics. *PLoS ONE*, 8:e65991, 2013.
- [58] Elaine O Petrof, Gregory B Gloor, Stephen J Vanner, J Scott Weese, David Carter, Michelle C Daigneault, Eric M Brown, Kathleen Schroeter, and Emma Allen-Vercoe. Stool substitute transplant therapy for the eradication of *Clostridium difficile* infection: “RePOOPulating” the gut. *Microbiome*, 1:3, 2013.
- [57] Emma Allen-Vercoe, Gregor Reid, Norman Viner, Gregory B Gloor, Susy Hota, Peter Kim, Christine Lee, Kieran O’Doherty, Stephen J Vanner, J Scott Weese, and Elaine O Petrof. A Canadian working group report on fecal microbial therapy: microbial ecosystems therapeutics. *Can J Gastroenterol*, 26(7):457–62, Jul 2012.
- [56] Jean M Macklaim, Craig R Cohen, Gilbert Donders, Gregory B Gloor, Janet E Hill, Groesbeck P Parham, Jacques Ravel, Gregory Spear, Janneke van de Wijgert, and Gregor Reid. Exploring a road map to counter misconceptions about the cervicovaginal microbiome and disease. *Reprod Sci*, May 2012.
- [55] Tao Li, Jack Liang, Alexandre Ambrogelly, Tim Brennan, Guy Gloor, Gjalt Huisman, James Lalonde, Azzeddine Lekhal, Ben Mijts, Sheela Muley, Lisa Newman, Matt Tobin, George Wong, Aleksey Zaks, and Xiyun Zhang. Efficient, chemoenzymatic process for manufacture of the boceprevir bicyclic [3.1.0]proline intermediate based on amine oxidase-catalyzed desymmetrization. *J Am Chem Soc*, 134(14):6467–72, Apr 2012.
- [54] Julie Genereaux, Stephanie Kvas, Dominik Dobransky, Jim Karagiannis, Gregory B Gloor, and Christopher J Brandl. Genetic evidence links the ASTRA protein chaperone component Tti2 to the SAGA transcription factor Tra1. *Genetics*, Apr 2012.

- [53] Stephanie Kvas, Gregory B Gloor, and Christopher J Brandl. Loss of nonsense mediated decay suppresses mutations in *Saccharomyces cerevisiae* TRA1. *BMC Genet*, 13(1):19, Mar 2012.
- [52] Russell J Dickson and Gregory B Gloor. Protein sequence alignment analysis by local covariation: coevolution statistics detect benchmark alignment errors. *PLoS One*, 7(6):e37645, 2012.
- [51] Jacob P Turowec, James S Duncan, Greg B Gloor, and David W Litchfield. Regulation of caspase pathways by protein kinase CK2: identification of proteins with overlapping CK2 and caspase consensus motifs. *Mol Cell Biochem*, 356(1-2):159–67, Oct 2011.
- [50] Ryo Takeuchi, Abigail R Lambert, Amanda Nga-Sze Mak, Kyle Jacoby, Russell J Dickson, Gregory B Gloor, Andrew M Scharenberg, David R Edgell, and Barry L Stoddard. Tapping natural reservoirs of homing endonucleases for targeted gene modification. *Proc Natl Acad Sci U S A*, 108(32):13077–82, Aug 2011.
- [49] Jean M Macklaim, Gregory B Gloor, Kingsley C Anukam, Sarah Cribby, and Gregor Reid. At the crossroads of vaginal health and disease, the genome sequence of *Lactobacillus iners* AB-1. *Proc Natl Acad Sci U S A*, 108 Suppl 1:4688–95, Mar 2011.
- [48] James S Duncan, Jacob P Turowec, Kelly E Duncan, Greg Vilc, Chenggang Wu, Bernhard Lüscher, Shawn S-C Li, Greg B Gloor, and David W Litchfield. A peptide-based target screen implicates the protein kinase CK2 in the global regulation of caspase signaling. *Sci Signal*, 4(172):ra30, 2011.
- [47] Gregor Reid, Jessica A Younes, Henny C Van der Mei, Gregory B Gloor, Rob Knight, and Henk J Busscher. Microbiota restoration: natural and supplemented recovery of human microbial communities. *Nat Rev Microbiol*, 9(1):27–38, Jan 2011.
- [46] Ruben Hummelen, Jean M Macklaim, Jordan E Bisanz, Jo-Anne Hammond, Amy McMillan, Rebecca Vongsa, David Koenig, Gregory B Gloor, and Gregor Reid. Vaginal microbiome and epithelial gene array in post-menopausal women with moderate to severe dryness. *PLoS One*, 6(11):e26602, 2011.
- [45] Stephen M T Hoke, A Irina Mutiu, Julie Genereaux, Stephanie Kvas, Michael Buck, Michael Yu, Gregory B Gloor, and Christopher J Brandl. Mutational analysis of the C-terminal FATC domain of *Saccharomyces cerevisiae* Tra1. *Curr Genet*, 56(5):447–65, Oct 2010.
- [44] Russel J Dickson, Linda M Wahl, Andrew D Fernandes, and Gregory B Gloor. Identifying and seeing beyond multiple sequence alignment errors using molecular covariation. *PLoS ONE*, 5(6):e11082, June:2010 2010.
- [43] Gregory B Gloor, Gaurav Tyagi, Dana M Abrassart, Andrew J Kingston, Andrew D Fernandes, Stanley D Dunn, and Christopher J Brandl. Functionally compensating coevolving positions are neither homoplastic nor conserved in clades. *Mol Biol Evol*, 27(5):1181–91, May 2010.
- [42] Andrew D Fernandes and Gregory B Gloor. Mutual information is critically dependent on prior assumptions: would the correct estimate of mutual information please identify itself? *Bioinformatics*, 26(9):1135–9, May 2010.
- [41] Benjamin P Kleinstiver, Andrew D Fernandes, Gregory B Gloor, and David R Edgell. A unified genetic, computational and experimental framework identifies functionally relevant residues of the homing endonuclease I-BmoI. *Nucleic Acids Res*, 38(7):2411–27, Apr 2010.
- [40] James S Duncan, Jacob P Turowec, Greg Vilc, Shawn S C Li, Gregory B Gloor, and David W Litchfield. Regulation of cell proliferation and survival: convergence of protein kinases and caspases. *Biochim Biophys Acta*, 1804(3):505–10, Mar 2010.

- [39] Ruben Hummelen, Andrew D Fernandes, Jean M Macklaim, Russell J Dickson, John Changalucha, Gregory B Gloor, and Gregor Reid. Deep sequencing of the vaginal microbiota of women with HIV. *PLoS One*, 5(8):e12078, 2010.
- [38] Andrew D Fernandes, Benjamin P Kleinstiver, David R Edgell, Lindi M Wahl, and Gregory B Gloor. Estimating the evidence of selection and the reliability of inference in unigenic evolution. *Algorithms Mol Biol*, 5:35, 2010.
- [37] Gregory B Gloor, Ruben Hummelen, Jean M Macklaim, Russell J Dickson, Andrew D Fernandes, Roderick MacPhee, and Gregor Reid. Microbiome profiling by Illumina sequencing of combinatorial sequence-tagged PCR products. *PLoS One*, 5(10):e15406, 2010.
- [36] Piya Lahiry, Jian Wang, John F Robinson, Jacob P Turowec, David W Litchfield, Matthew B Lanktree, Gregory B Gloor, Erik G Puffenberger, Kevin A Strauss, Mildred B Martens, David A Ramsay, C Anthony Rugar, Victoria Siu, and Robert A Hegele. A multiplex human syndrome implicates a key role for intestinal cell kinase in development of central nervous, skeletal, and endocrine systems. *Am J Hum Genet*, 84(2):134–47, Feb 2009.
- [35] SD Dunn, LM Wahl, and GB Gloor. Mutual information without the influence of phylogeny or entropy dramatically improves residue contact prediction. *Bioinformatics*, 23(3):333–340, 2008.
- [34] A. M. Holmes, K. A. Weedmark, and G. B. Gloor. Mutations in the extra sex combs and Enhancer of Polycomb genes increase homologous recombination in somatic cells of *Drosophila melanogaster*. *Genetics*, 172(4):2367–77, 2006.
- [33] Gregory B Gloor, Louise C Martin, Lindi M Wahl, and Stanley D Dunn. Mutual information in protein multiple sequence alignments reveals two classes of coevolving positions. *Biochemistry*, 44(19):7156–7165, 2005.
- [32] L C Martin, G B Gloor, S D Dunn, and L M Wahl. Using information theory to search for co-evolving residues in proteins. *Bioinformatics*, 21(22):4116–4124, 2005.
- [31] Brian R Dempsey, Mark Wrona, Jana M Moulin, Gregory B Gloor, Farideh Jalilehvand, Gilles Lajoie, Gary S Shaw, and Brian H Shilton. Solution nmr structure and x-ray absorption analysis of the c-terminal zinc-binding domain of the seca atpase. *Biochemistry*, 43(29):9361–71, Jul 2004.
- [30] Hanjuan Qin, Anthony Percival-Smith, Chengjun Li, Christina Y H Jia, Greg Gloor, and Shawn S-C Li. A novel transmembrane protein recruits numb to the plasma membrane during asymmetric cell division. *J Biol Chem*, 279(12):11304–12, Mar 2004.
- [29] Gregory B Gloor. Gene targeting in drosophila. *Methods Mol Biol*, 260:97–114, 2004.
- [28] Angela M Coveny, Tammy Dray, and Gregory B Gloor. The effect of heterologous insertions on gene conversion in mitotically dividing cells in drosophila melanogaster. *Genetics*, 161(1):249–58, May 2002.
- [27] Gregory B Gloor. The role of sequence homology in the repair of DNA double-strand breaks in drosophila. *Adv Genet*, 46:91–117, 2002.
- [26] G B Gloor. Gene-targeting in drosophila validated. *Trends Genet*, 17(10):549–51, Oct 2001.
- [25] Lila Kari, Rob Kitto, and Greg Gloor. A computer scientist’s guide to molecular biology. *Soft Computing*, 5(2):95–101, 2001.

- [24] P Krishna and G Gloor. The hsp90 family of proteins in arabidopsis thaliana. *Cell Stress Chaperones*, 6(3):238–46, Jul 2001.
- [23] Lila Kari, Greg Gloor, and Sheng Yu. Using dna to solve the bounded post correspondence problem. *Theoretical Computer Science*, 231(2):193–203, 2000.
- [22] G B Gloor, J Moretti, J Mouyal, and K J Keeler. Distinct p-element excision products in somatic and germline cells of drosophila melanogaster. *Genetics*, 155(4):1821–30, Aug 2000.
- [21] A S Bassi, D N Ding, G B Gloor, and A Margaritis. Expression of single chain antibodies (scfvs) for c-myc oncoprotein in recombinant escherichia coli membranes by using the ice-nucleation protein of pseudomonas syringae. *Biotechnol Prog*, 16(4):557–63, 2000.
- [20] Mark Daley, Lila Kari, Greg Gloor, and Rani Siromoney. Circular contextual insertions/deletions with applications to biomolecular computation. In *String Processing and Information Retrieval Symposium, 1999 and International Workshop on Groupware*, pages 47–54. IEEE, 1999.
- [19] G B Gloor, T Dray, and K Keeler. Analyzing double-strand repair events in drosophila. *Methods Mol Biol*, 113:425–38, 1999.
- [18] Greg Gloor, Lila Kari, Michelle Gaasenbeek, and Sheng Yu. Towards a dna solution to the shortest common superstring problem. *International Journal on Artificial Intelligence Tools*, 8(04):385–399, 1999.
- [17] Lila Kari, Mark Daley, Greg Gloor, Rani Siromoney, and Laura F Landweber. How to compute with dna. In *International Conference on Foundations of Software Technology and Theoretical Computer Science*, pages 269–282. Springer Berlin Heidelberg, 1999.
- [16] D H Lankenau and G B Gloor. In vivo gap repair in drosophila: a one-way street with many destinations. *Bioessays*, 20(4):317–27, Apr 1998.
- [15] G B Gloor and D H Lankenau. Gene conversion in mitotically dividing cells: a view from drosophila. *Trends Genet*, 14(2):43–6, Feb 1998.
- [14] T Dray and G B Gloor. Homology requirements for targeting heterologous sequences during p-induced gap repair in drosophila melanogaster. *Genetics*, 147(2):689–99, Oct 1997.
- [13] K J Keeler and G B Gloor. Efficient gap repair in drosophila melanogaster requires a maximum of 31 nucleotides of homologous sequence at the searching ends. *Mol Cell Biol*, 17(2):627–34, Feb 1997.
- [12] K J Keeler, T Dray, J E Penney, and G B Gloor. Gene targeting of a plasmid-borne sequence to a double-strand DNA break in drosophila melanogaster. *Mol Cell Biol*, 16(2):522–8, Feb 1996.
- [11] J D Andrews and G B Gloor. A role for the kp leucine zipper in regulating p element transposition in drosophila melanogaster. *Genetics*, 141(2):587–94, Oct 1995.
- [10] N Nassif, J Penney, S Pal, W R Engels, and G B Gloor. Efficient copying of nonhomologous sequences from ectopic sites via p-element-induced gap repair. *Mol Cell Biol*, 14(3):1613–25, Mar 1994.
- [9] G B Gloor, C R Preston, D M Johnson-Schlitz, N A Nassif, R W Phillis, W K Benz, H M Robertson, and W R Engels. Type i repressors of p element mobility. *Genetics*, 135(1):81–95, Sep 1993.
- [8] G B Gloor, N A Nassif, D M Johnson-Schlitz, C R Preston, and W R Engels. Targeted gene replacement in drosophila via p element-induced gap repair. *Science*, 253(5024):1110–7, Sep 1991.

- [7] G Gloor and G Chaconas. Sequence of bacteriophage mu n and p genes. *Nucleic Acids Res*, 16(11):5211–2, Jun 1988.
- [6] G Gloor and G Chaconas. The bacteriophage mu n gene encodes the 64-kda virion protein which is injected with, and circularizes, infecting mu DNA. *J Biol Chem*, 261(35):16682–8, Dec 1986.
- [5] G Chaconas, E B Giddens, J L Miller, and G Gloor. A truncated form of the bacteriophage mu b protein promotes conservative integration, but not replicative transposition, of mu DNA. *Cell*, 41(3):857–65, Jul 1985.
- [4] G Chaconas, G Gloor, and J L Miller. Amplification and purification of the bacteriophage mu encoded b transposition protein. *J Biol Chem*, 260(5):2662–9, Mar 1985.
- [3] E A Faust, G Gloor, M F MacIntyre, and R Nagy. Atp(gtp)-dependent conversion of mvm parvovirus single-stranded DNA to its replicative form by a purified 10 s species of mouse DNA polymerase alpha. *Biochim Biophys Acta*, 781(3):216–24, Apr 1984.
- [2] E A Faust and G Gloor. Characterization of a metastable, partially replicated dimeric intermediate of minute virus of mice. *J Virol*, 49(2):621–5, Feb 1984.
- [1] G Chaconas, G Gloor, J L Miller, D L Kennedy, E B Giddens, and C R Nagainis. Transposition of bacteriophage mu dna: expression of the a and b proteins from lambda pl and analysis of infecting mu dna. *Cold Spring Harb Symp Quant Biol*, 49:279–84, 1984.

7.5 Non Peer Reviewed Manuscripts

Russell J Dickson and Gregory B Gloor. Xorro: Rapid paired-end read overlapper. arXiv preprint arXiv:1304.4620, 2013.

Russell J Dickson and Gregory B Gloor. The MIP toolset: an efficient algorithm for calculating mutual information in protein alignments. arXiv preprint arXiv:1304.4573, 2013.

7.6 Software releases

ALDEx2. ALDEx tool to examine compositional high-throughput sequence data with Welch’s t-test and Wilcoxon rank test. <https://github.com/ggloor/ALDEx2>, and <http://www.bioconductor.org/packages/release/bioc/html/ALDEx2.html> last update Oct 2017

Languages and utilities: R, bash, Perl, awk, L^AT_EX, Markdown, HTML, git, svn

8 Current and Recent Research Funding

NSERC Discovery, 2015-2020: Molecular covariation in protein families

PI: Gloor, GB

Goal is to examine how covarying positions affect the structure and function of protein families that can be used as gene editing reagents.

total: \$155000 - pays for student and supplies

NIH R21 Dec 2015-2017, NIH R33 2017-2018: Microbes that matter

PI: Elaine Petrof (Queen's U), Allen-Vercoe (Guelph), Gloor (UWO)

Developing a synthetic stool substitute for the treatment of recurrent *C. difficile* infection

direct to Gloor: \$70000 - partially pays for one student and sequencing costs

CIHR 2013-2016: Role of intestinal microbiota in non-alcoholic fatty liver disease pre and post bariatric surgery

PI: ALLARD, Johane P (U. Toronto): , Comelli Elena M; GLOOR, Gregory B; JACKSON, Timothy D; LOU, Wen-Yi W; OKRAINEC, Allan

Characterization of the stool microbiota in a cohort of patients undergoing treatment for non-alcoholic fatty liver disease

total: 522169, direct to Gloor: \$25000/yr - partially paid for one student and sequencing costs

CIHR 2014-2016: Intestinal microbiome and extremes of atherosclerosis

PI: SPENCE, J. David , ALLEN-VERCOE, Emma; GLOOR, Gregory B; REID, Gregor

Characterization of the stool microbiota in a cohort of patients screened for risk of atherosclerosis

total: 211600, direct to Gloor: \$25000 - partially paid for one student and sequencing costs

CIHR 2013-2016: Non-Alcoholic Fatty Liver Disease: Role of Intestinal Microbiota and n-3 Polyunsaturated Fatty Acid Supplementation

PI: ALLARD, Johane P , COMELLI, Elena M; GLOOR, Gregory B; LOU, Wen-Yi W

Characterization of the stool microbiota in a cohort of patients treated for non-alcoholic fatty liver disease with fish oils

total 211600, direct to Gloor: \$17000 - partially paid for one student

CIHR Team grant, 2010-2015: The Vaginal Microbiome Project Team

PI: MONEY, Deborah M, BOCKING, Alan D; HEMMINGSEN, Sean M; HILL, Janet E; REID, Gregor (Co-PIs), co-investigators: DUMONCEAUX, Timothy J; GLOOR, Gregory B; LINKS, Matthew G; O'DOHERTY, Kieran C; TANG, Patrick K; VAN SCHALKWYK, Julianne E; YUDIN, Mark H

Collection and analysis of large vaginal microbiota cohorts to identify determinants of health and disease in the Canadian population

total: 1745341, direct to Gloor: 15000/year - partially paid for one student. My role was tool development

Southeastern Ontario Academic Medical Organization 2014-2015: Elucidating the factors that determine success in fecal transplant therapy for *C. difficile* infection

PI: PETROF, E, ROPELSKI, Mark, ALLEN-VERCOE, Emma, GLOOR, Gregory

Identifying mechanisms of microbial ecosystem inhibition of *C. difficile*

total:92000, direct to Gloor: %14000 - paid for sequencing costs

CIHR Network grant 2012-2015 Maternal-Infant Microbiome and Immunity (MIMI) Network

PI: KOLLMANN, Tobias R, GLOOR, Gregory B; REID, Gregor

Team grant to further training and planning of microbiome effects on proper health and development in Africa.

total:600000, direct to Gloor: 200000 - paid for PDF, student and conference costs

8.1 Maternal-Infant Microbiome and Immunity (MIMI) Network CIHR, 2012-2015

Investigators: KOLLMANN, Tobias R(PI) coinvestigators:GLOOR, Gregory B; REID, Gregor

Keywords: GLOBAL HEALTH; IMMUNOLOGY; MATERNAL HEALTH; MICROBIOME; PEDIATRICS

8.1.1 *Total:600000, direct to Gloor: 200000*

Abstract: There are ten times as many bacterial cells in our body than human cells. This community of microorganisms (called the microbiome) plays an important role in influencing human health. For example, in our gut, bacteria aid in the digestion and absorption of nutrients, keeping dangerous microbes in check and directing our defense system's response. Thus, the understanding of how the microbiome contributes to human health is of great importance. Understanding the human microbiome is a daunting task because of its complexity. First, there are very different communities of bacteria present in different parts of the body. Second, these bacterial communities arise from different initial sources and interact with the human defense system in different ways. Third, the human microbiome is affected by a variety of genetic and environmental factors. Finally, people living in different areas of the world have different bacteria living in and on them. These and other factors require that the study of the microbiome should be approached from a global health perspective. We propose the establishment of MIMI, the Maternal-Infant Microbiome and Immunity Network. This network is centered on how the microbiome and immune system interact in the mother and child, as the mother is the initial source of the child's microbiome. MIMI will formalize the collaboration of three groups with expertise in paediatrics and immunology, maternal health and probiotics, and DNA sequencing and data analysis. By bringing these groups with complementary expertise together, MIMI will amplify each group's strength, build research capacity in the field of microbiome analysis, and to transfer knowledge and thus inform maternal and child health policy. MIMI will contribute towards self-sustainability by making Network Members competitive for national and international funding.

Where, years: Title

PI: , co-apps

description

direct to Gloor: \$70000 - partially pays for one student and sequencing costs

8.2 Function of maize endophytic microbiome: NSERC ENGAGE, 2014-2015

Investigators: GLOOR, GREGORY Microbial ecology, plant endophytic organisms, microbial genomics, microbial metatranscriptomics, crop yield enhancement, maize microbiome, RNA-seq, metagenomics

8.2.1 *Total:25000, direct to Gloor: 25000*

Abstract: A&L Biologicals has a mandate to develop and implement agricultural tests that growers can use for the production and maintenance of healthy soil, and the associated high crop yields. A&L Biologicals identified a farmer, Dean Glenney, who has established an extraordinarily productive ecosystem through non-traditional farming methods that produces an average of twice that of adjacent farms. Molecular fingerprinting was used to demonstrate that bacterial species (the microbiome) associated with the soil and internal to the corn plant (endophytic), are different between the high and normal producing fields. The work in this proposal will determine the functional differences between high and normal yield sites by examining the endophytic corn sap microbiome; the microbiome that A&L Biologicals has identified to have the greatest difference between sites. Dr. Gloor has developed approaches that use high throughput sequencing to characterize the molecular functions of entire bacterial communities and their effect on the host. He will apply those methods and identify functional differences between the high and low yield sites in both the microbial community and the corn plant. The results of the functional analysis will be done jointly by scientists from both A&L Biologicals and Dr. Gloor's research unit. The resulting analysis of both the growth-promoting pathways in corn and in the microbiome, will identify key bioindicators of organisms and functions associated with high production agro-ecosystems for future field testing. The analysis will provide detailed information as to which organism should be selected for development of biofertilizer formulations, what functions are required for corn growth in a high yield site, and demonstrate that existing, and developing molecular methods used by A&L Biologicals can provide accurate data for use as a service tool to identify healthy soils/plant tissue.

8.3 Meta-transcriptome of high-yield corn endophytic microbiome Ontario Centre of Excellence, 2014-2015

Investigators: GLOOR, GREGORY

Keywords: Microbial ecology, plant endophytic organisms, microbial genomics, microbial metatranscriptomics, crop yield enhancement, maize microbiome, RNA-seq, metagenomics

8.3.1 *Total:25000, direct to Gloor: 25000*

Abstract: A&L Biologicals has a mandate to develop and implement agricultural tests that growers can use for the production and maintenance of healthy soil, and the associated high crop yields. A&L Biologicals identified a farmer, Dean Glenney, who has established an extraordinarily productive ecosystem through non-traditional farming methods that produces an average of twice that of adjacent farms. Molecular fingerprinting was used to demonstrate that bacterial species (the microbiome) associated with the soil and internal to the corn plant (endophytic), are different between the high and normal producing fields. The work in this proposal will determine the functional differences between high and normal yield sites by examining the endophytic corn sap microbiome; the microbiome that A&L Biologicals has identified to have the greatest difference between sites. Dr. Gloor has developed approaches that use high throughput sequencing to characterize the molecular functions of entire bacterial communities and their effect on the host. He will apply those methods and identify functional differences between the high and low yield sites in both the microbial community and the corn plant. The results of the functional analysis will be done jointly by scientists from both A&L Biologicals and Dr. Gloor's research unit. The resulting analysis of both the growth-promoting pathways in corn and in the microbiome, will identify key bioindicators of organisms and functions associated with high production agro-ecosystems for future field testing. The analysis will provide detailed information as to which organism should be selected for development of biofertilizer formulations, what functions are required for corn growth in a high yield site, and demonstrate that existing, and developing molecular methods used by A&L Biologicals can provide accurate data for use as a service tool to identify healthy soils/plant tissue.

8.4 Exploiting the therapeutic effects of the fecal microbiome in bariatric care CIHR Team grant in Bariatric Care (ranked first in competition), 2014-2019

Investigators: PIs: ALLARD, Johane P ; GAISANO, co-applicants: Herbert Y , BANKS, Kate; COMELLI, Elena M; GLOOR, Gregory B; HOTA, Susy S; JACKSON, Timothy D; LOU, Wen- Yi W; OKRAINEC, Allan; PHILPOTT, Dana J; POUTANEN, Susan M

Keywords: BARIATRIC SURGERY; DIET; INFLAMMATION; LIPOPOLYSACCHARIDE; MICROBIOTA; NON- ALCOHOLIC FATTY LIVER DISEASE; STEATOHEPATITIS

8.4.1 *Total: 1,500,000, direct to Gloor: 80000*

8.5 Developing molecular methods as diagnostic tools to identify biological factors contributing to crop productivity and soil health Agriculture and Agrifoods Canada, Agricultural Innovation Program, 2015-2017

Investigators: A&L Biologicals led by Dr. George Lazarovitz (CSO), GLOOR, G academic co-applicant.

Keywords: soil health, soil ecology, soil microbiology, soilborne disease, disease suppressive soil, ecology, diagnostics, tomato, potato, bacteria, fungi, yield

8.5.1 *Total: 600,000, direct to Gloor: 120000*

Abstract: The population of the planet reached seven billion this year. With more mouths to feed, with declining arable land per capita and with potential crop losses caused by more unpredictable climatic conditions, global agriculture faces new challenges. Increasing costs of petroleum based products continues to force growers to look for crop production technologies that require lower inputs both in cost and energy. Sustainable agriculture and agroecology are two concepts most considered as a means to reduce inputs and maintain high yielding plant agriculture. Soil, with its complex but well understood chemical and physical properties, still requires greater understanding of biology. High yields can sometimes be attributed to healthy biology in the soil, while sub-maximal yields may sometimes be attributed to a detrimental complex of soil organisms reducing growth potential of the plant. Plant disease suppressiveness has been hailed as one of the best methods to manage soilborne diseases which often can only be require highly toxic fumigants. can be transferred to other soils. In order to sustainably manage their soil for optimal plant productivity, farmers must start monitoring and understanding their soil's microbiology.