Gregory Gloor, PhD
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1 Expertise and Research Interests

Composition and function of the human and other microbiomes. We 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 for the analysis of high throughput experiments that generate counts per sequence tag: 16S rRNA gene sequencing, transcriptomics and selex-type experiments.

2 Education and Training

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

1988 Ph.D, University of Western Ontario, Department of Biochemistry. Supervisor: Dr. George Chaconas

1983 HBSc, University of Western Ontario, Genetics

3 Employment

2002-present, Professor, University of Western Ontario - Biochemistry

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

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

1990-1992, Assistant Professor, Memorial University of Newfoundland - Medicine

4 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.

5 HQP Training Summary

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

6 Scholarly and Professional Activities Summary

6.1 Grants and Awards Panels, Editorial

2015-present, 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
1995-2001, Peer review organizer for the Foundation for Gene and Cell Therapy
1997-1999, OGS Biochemistry/Biophysics panel
1999, Chair OGS Biochemistry/Biophysics panel
1997–2000, NCIC Virology and Molecular Biology Committee,

6.2 Recent Presentations and Invitations

2016, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2015, Cambridge, UK
2016, Invited workshop organizer at Exploring Human Host-Microbiome Interactions in Health and Disease 2015, Cambridge, UK
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, Tromso, 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, Berkley, CA

6.3 Peer Reviewed Papers since 2010:

H-index: 31.
Erdos number 3 (two ways).

1) 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*, accepted, 2016.

2) Gregory B Gloor and Gregor Reid. Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data. *Can J Microbiol*, pages 1–12, Apr 2016.

3) 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.

4) 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. *J Gastroenterol*, Jun 2016.

5) Camilla Urbaniak, Gregory B Gloor, Muriel Brackstone, Leslie Scott, Mark Tangney, and Gregor Reid. The microbiota of breast tissue and its association with tumours. *Appl Environ Microbiol*, Jun 2016.

6) 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.

7) 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, 2016.

8) 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*, http://dx.doi.org/10.1080/10618600.2015.1131161, 2016.

9) 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. *Scientific Reports*, 5:14174 EP –, 09 2015.

10) 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.

11) 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), 2015.

12) 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.

13) N St Denis, M Gabriel, J P Turowec, G B Gloor, S S-C Li, A-C Gingras, and D W Litchfield. Systematic investigation of hierarchical phosphorylation by protein kinase CK2. *J Proteomics*, 118(6):49–62, Nov 2014.

14) 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.

15) 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.

16) 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.

17) 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 Kavere, Johanna Lindahl, Amee 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.

18) 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.

19) 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.

20) 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.

21) 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.

22) 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.

23) Russell J Dickson and Gregory B Gloor. Bioinformatics identification of coevolving residues. *Methods Mol Biol*, 1123:223–43, 2014.

24) 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.

25) Jordan E Bisanz, Megan K Enos, Joseph R Mwanga, John Changalucha, 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.

26) 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.

27) Lance F DaSilva, Samantha Pillon, Julie Genereaux, Megan J Davey, Gregory B Gloor, Jim Karagiannis, 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.

28) 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.

29) 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.

30) 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.

31) 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.

32) 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.

33) 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.

34) 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.

35) 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.

36) 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.

37) 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.

38) 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.

39) 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.

40) 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.

41) 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.

42) 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.

43) 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.

44) 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.

45) 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.

46) 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.

47) James S Duncan, Jacob P Turowec, Kelly E Duncan, Greg Vilk, 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.

48) 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.

49) 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.

50) 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 homoplasic nor conserved in clades. *Mol Biol Evol*, 27(5):1181–91, May 2010.

51) 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.

52) 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.

53) James S Duncan, Jacob P Turowec, Greg Vilk, 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.

54) 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.

55) 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.

56) 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.

6.4 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.

6.5 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 Sept, 2014

Languages and utilities: R, bash, Perl, awk, LaTeX, Markdown, HTML, git, svn

7 Research Funding

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

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

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

7.1.1 Total:522169, direct to Gloor: 25000

Abstract: Fatty liver disease is a fat buildup in the liver with or without inflammation. The disease can damage the liver and sometimes requires liver transplantation. Almost all people who are morbidly obese and require weight-loss surgery have fatty liver. New research shows that the kind of bacteria in the gut might contribute to the development of obesity, fatty liver and inflammation. Weight-loss surgery clearly changes the gut bacteria, probably because of the surgical changes to the gut, the weight loss and the food intake, which is very different after surgery. We think that differences in the gut bacteria could influence fatty liver in morbidly obese patients before and after weight-loss surgery. Therefore, we would like to measure the bacteria in the stool of patients with fatty liver undergoing weight-loss surgery A) at the time of the surgery, to see, if there is a difference between those who have fatty liver without inflammation and those who have the more severe form of fatty liver with inflammation. We are also planning to measure bacterial products in the stool and in the blood of our patients. B) We then want to follow the same patients for one year after their weight loss surgery to find out, whether changes in the gut bacteria are connected to improvement or worsening of their fatty liver disease. This study is new and important, as it could lead to new treatments for patients with fatty liver disease

7.2 Intestinal microbiome and extremes of atherosclerosis. CIHR, 2014-2016

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

Keywords: ATHEROSCLEROSIS; BIOCHEMISTRY; INTESTINAL MICROBIOME; METABONOMICS; MICROBIOLOGY; NUTRITION; RENAL FUNCTION; ULTRASOUND

7.2.1 Total:211600, direct to Gloor: 25000

Abstract: Atherosclerosis is the underlying cause of heart attacks, and of a substantial proportion of strokes. Our project will lead to an entirely new approach to treating atherosclerosis to prevent heart attacks, strokes, and dementia due to strokes: replacement of harmful intestinal bacteria with beneficial bacteria. Meat and egg yolks are harmful to the arteries. Besides cholesterol and saturated fat (in meat), they contain nutrients (lecithin and L-carnitine) that are converted by the bacteria in the intestine to trimethylamine, which in turn is converted in the liver to trimethylamine n-oxide (TMAO). In this project we plan to study patients with extremes of carotid atherosclerosis not explained by traditional risk factors. The 250 with unexplained atherosclerosis have far more plaque than would be expected from their age, sex, blood pressure, cholesterol, smoking and diabetes; the 250 with protection have little or no plaque despite high levels of risk factors. These two extremes are very powerful for genetic studies and studies of new risk factors; they reduce by ¾ the number of patients who need to be studied. We plan to: 1. Identify patterns of intestinal bacteria associated with high levels of TMAO and other bacterial metabolic products in the blood and urine 2. identify patterns of intestinal bacteria that are associated with excess carotid plaque not explained by traditional coronary risk factors, and patterns of bacteria associated with protection from traditional risk factors, 3. study the relationship between usual diet and high levels of TMAO and other bacterial metabolic products in the blood and urine, 4. Study the relationship of impaired kidney function to high levels of TMAO and other bacterial metabolic products in the blood and urine, 5. Collect blood for extraction and banking of DNA and plasma for future genetic studies as funding becomes available.

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

Investigators: ALLARD, Johane P (PI), co-investigators: COMELLI, Elena M; GLOOR, Gregory B; LOU, Wen-Yi W

Keywords: BIFIDOBACTERIA; ENDOTOXIN; FISH-OIL; INFLAMMATION; INTESTINAL MICROBIOTA; NON- ALCOHOLIC FATTY LIVER DISEASE; NUTRITION; POLYUNSATURATED FATTY ACIDS; SHORT- CHAIN FATTY ACIDS

7.3.1 Total:363051, direct to Gloor: 17000

Abstract: About 20-30% of Canadians have non-alcoholic fatty liver disease, which is a fat buildup in the liver with or without inflammation. The disease can damage the liver and sometimes requires liver transplantation. Our team has received a grant from the Canadian Institute of Health Reseaearch (CIHR) to examine the role of diet, especially antioxidant vitamins and fat, in fatty liver disease. We also give fish oil to patients with fatty liver to see if this is beneficial for their liver. This project is almost completed. In addition, we have collected stool from our patients, as the latest research shows that the kind of bacteria in the gut could also influence the course of fatty liver disease. We are now seeking funding to characterize the bacteria in the stool and to measure bacterial products in stool and blood of patients with fatty liver compared to healthy controls. This study is new and important, as it could lead to new treatments for patients with fatty liver disease. If the gut bacteria are different in patients with fatty liver, we might in the future try to treat fatty liver with beneficial bacteria (probiotics) or carbohydrates that promote the growth of these ”good” bacteria (prebiotics). Nobody has ever tested, whether fish oil could change human gut bacteria. Therefore we would also like to measure gut bacteria before and after 1 year treatment with fish oil in patients with fatty liver.

7.4 The Vaginal Microbiome Project Team CIHR, 2010-2015

Investigators: 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

Keywords: BACTERIAL VAGINOSIS; GYNECOLOGY; INFECTION; MICROBIOME; PRETERM BIRTH; WOMEN'S HEALTH

7.4.1 Total:1745341, direct to Gloor: 15000

Abstract: Recent advances in genomic sequencing and bioinformatics have provided adequate tools to investigate the human microbiome, and the opportunity for Canadian research teams to uniquely contribute to deciphering the role that microbes play in health and disease. Studies of the human vaginal microbiome represent a niche area where Canada has significant expertise, research capacity, and pre-existing infrastructure upon which to build. The Vaginal Microbiome Project Team - VMPT - will place Canada at the forefront of research into the role of vaginal bacterial communities in health and disease. While our current collaboration represents an established scientific and clinical program, success in this competition will allow the extended team to not only identify the bacterial species present under various conditions over a woman's lifespan, but develop novel diagnostic tools and interventions to restore and retain health. Major research themes will continue with understanding of the core vaginal microbiome, but also explore the associations behind vaginal microbiota and preterm delivery, genital tract infection, and reproductive health. Conditions associated with an imbalance in vaginal microbiota afflict several million Canadian women each year, and accumulate health care costs of billions of dollars annually. The Emerging Team Grant will lead to significant breakthroughs in the care of women in Canada and around the world.

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

Investigators: PETROF, E (PI), coinvestigators: ROPELSKI, Mark, ALLEN-VERCOE, Emma, GLOOR, Gregory

Keywords: CLOSTRIDIUM DIFFICILE, ECOSYSTEM THERAPEUTICS, INTESTINAL MICROBIOTA, FECAL TRANSPLANT

7.5.1 Total:92000, direct to Gloor: 14000

Abstract: Clostridium difficile infection (CDI) of the colon is a major cause of morbidity and mortality for patients and can disrupt the hospital's ability to provide its full range of care. A patient being treated for a first episode of CDI has a 10-25% chance of developing recurrent CDI, and patients who have had one episode of recurrent CDI have a 50-65% chance of developing multiple episodes of recurrent CDI1. Treatment options for recurrent CDI are very limited as oral vancomycin, the drug of choice, carries a failure rate of around 70%. Recurrent infection despite antibiotics has thus become a key clinical dilemma but recently fecal microbial therapy (FMT) or "stool transplant" (infusing donor stool into the intestine of the recipient to re-establish normal bacterial flora) was recently shown in a randomized clinical trial to be highly effective for recurrent CDI2. There is a direct link between recurrent disease and intestinal dysbiosis i.e. there is an inability of certain individuals to "re-establish" their normal protective bacterial flora3-5, and FMT is effective at re-establishing this colonization resistance against C.difficile.

7.6 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

7.6.1 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.

7.7 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

7.7.1 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 Glenny, 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 (endopytic), 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 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.

7.8 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

7.8.1 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 Glenny, 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 (endopytic), 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 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.

7.9 Molecular covariation in protein families Current NSERC Discovery grant, 2010-2015

Investigators: GLOOR, Gregory

Keywords: Proteins, molecular coevolution, computational biology, molecular biology, protein evolution, epistasis, molecular evolution, mutual information, yeast genetics, phosphoglycerate kinase

7.9.1 Total:155000, direct to Gloor: 155000

Abstract: Proteins are one of the fundamental building blocks of the cells in our bodies. They are composed of long chains of 20 amino acids, and the sequence of the amino acids along the protein direct the shape and function of the protein. The same protein in different organisms usually have a dramatically amino acid order and composition, demonstrating that the same protein can be constructed in many different ways. We are seeking to understand how the sequence of amino acids directs the folding and function of the protein by studying the positions that vary among the proteins with the same function in different organisms. We have generated a series of tools that find pairs of positions in the sequence that covary, that is, if one position changes the other position changes. We propose to examine how these covarying positions affect the structure and function of the protein.

7.10 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

7.10.1 Total:1,500,000, direct to Gloor: 80000

7.11 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 Bioligicals 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

7.11.1 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 bets methods to mange 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.