Dr. André M. COMEAU

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Education

1998-2005	**Doctor of Philosophy (PhD) – Microbiology**	University of British Columbia (UBC), Vancouver BC
1994-1998	**Bachelor of Science – Honors Biology**	Acadia University, Wolfville NS

Relevant Work Experience

2014+	**Manager**	Integrated Microbiome Resource (imr.bio), Dalhousie University, Halifax NS
2014+	**Research Associate**	Department of Pharmacology, Dalhousie University, Halifax NS
2013	**Research Associate**	Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec QC
2009-2013	**Post-Doctoral Fellow**	Institut de Biologie Intégrative et des Systèmes (IBIS)/Québec-Océan and Centre d'Étude de la Forêt (CEF), Université Laval, Québec QC
2005-2009	**CNRS and Fondation des Treilles Post-Doctoral Fellow**	Laboratoire de Microbiologie et Génétique Moléculaires (LMGM) – Centre National de la Recherche Scientifique (CNRS), Toulouse FR
1998-2005	**Academic Webmaster (part-time)**	Faculty of Science – UBC
1998	**Scientific Program Coordinator / Volunteer Coordinator (summer)**	8th International Symposium on Microbial Ecology (ISME-8), Halifax NS
1995-1997	**Quality Control Technician (summer)**	Nova West Laboratory, Clare NS

Professional/Academic Development

2006+	***Ad hoc* Reviewer (granting agencies in bold)**	**Agence Nationale de la Recherche** (France, 2011-2012) *Applied and Environmental Microbiology* (2010+) *Aquatic Microbial Ecology* (2009+) *Archives of Virology* (2024+) *ASLO Methods* (2009) *Biogeosciences* (2012+) *Biology and Fertility of Soils* (2010+) *BMC Genomics* (2019+) *Canadian Journal of Microbiology* (2008+) **CONICYT** (Chile, 2019) *Continental Shelf Research* (2016+) *Deep-Sea Research* (2011+)

Environment International (2024+)
Environmental Microbiology (2006+)
European Journal of Protistology (2016+)
Frontiers in Microbiology (2014+)
ISME Journal (2017+)
Journal of Bacteriology (2012+)
Journal of Molecular Biology (2009+)
Journal of Plankton Research (2010+)
Journal of Virology (2018+)
Marine Environmental Research (2024+)
mBio (2017+)
Microbial Ecology (2014+)
Microbiology Spectrum (2025+)
Microbiome (2023+)
Molecular Microbiology (2007+)
mSystems (2016+)
National Science Foundation (USA, 2009)
npj Viruses (2025+)
NSERC/CRSNG (Canada, 2021)
PeerJ (2019+)
PLoS ONE (2011+)
Polar Biology (2010+)
Polar Research (2014+)
Research in Microbiology (2008+)
*Science of the Total Environmen*t (2024+)
Scientific Reports (2021+)
Soil Biology and Biochemistry (2008+)
US-Israel Binational Science Foundation (USA-Israel, 2007)
Virology Journal (2023+)
Water Research (2024+)

1999+ **Scientific Research Collaborations**

Diagnosing novel crop pathogens:
- Dalhousie University (*Z.Cheng, S.Stone*; 2025+)

AMR in foodborne isolate genomes:
- Université Ste.-Anne (*R.BenSallem*; 2024+)

Crop fungal endophyte genomes:
- AAFC-Kentville (*S.Ali*; 2024+)

SNP analysis in yeast expression system:
- Dalhousie University (*C.McMaster*; 2024+)

Alkenone genomics in marine eukaryotes:
- Dalhousie University (*M.Kienast*; 2024-2025)

Crop flavin-secreting bacterial genomes:
- USDA/WSU (*S.Yurgel*; 2023+)

Toxic cyanobacteria and invasive plant impacts on lakes:
- Dalhousie University (*R.Jamieson*; 2021+)

Onion bacterial pathogen genomes:
- AAFC-Kentville (*S.Ali*; 2020+)

Inflammatory Bowl Disease (IBD) microbiomes:
- University of Amsterdam (*J.VanLimbergen*; 2019+)

Soil restoration microbiomes in Spain:
- Universidad de Almeria (*I.Miralles*; 2019+)

Human forensic microbiome:
- Western Carolina University (*S.O'Connell*; 2019-2021)

Microbial diversity in Canadian and Indian lakes:
- Université Laval (*D.Khasa*; 2017-2022)

Helicobacter pylori microevolution:
- Universitat de Barcelona (*D.Miñana-Galbis*; 2017-2020)

Influenza A genomics:
- Dalhousie University (*P.Slaine, D.Khaperskyy*; 2016-2018)

Microbial diversity and diazotroph genomics in the Atlantic:
- Dalhousie University (*J.LaRoche*; 2015-2024)

Chronic kidney disease (CKD) and the gut microbiome:
- University of California, Irvine (*K.Whiteson*; 2015-2018)

Chemerin and the gut microbiome:
- Dalhousie University (*C.Sinal*; 2015-2018)

River microbiomes in South Africa:
- North-West University (*C.Bezuidenhout*; 2013-2019)

Human microbiome of CF and COPD patients:
- Université Laval (*R.Lévesque*; 2013-2018)

Spruce budworm microbiome:
- Université Laval (*R.Lévesque*; 2013-2015)

Fungal pathogen (Dutch Elm Disease) genomics:
- Université Laval (*L.Bernier*; 2013-2015)

Microbial diversity in the Canadian Arctic:
- Université Laval (*C.Lovejoy*; 2013-2019)
- University of Victoria (*D.Varela*; 2010-2016)
- Canadian Museum of Nature (*M.Poulin*; 2010-2012)
- Centre d'Études Nordiques (*W.Vincent*; 2010-2012)
- Université de Québec à Rimouski (*M.Gosselin*; 2010-2012)

Phage genome sequencing/characterization:
- Dalhousie University (*L.Murray, Z.Cheng*; 2016+)
- D.K. Zabolotny Institute (*A.Kushkina, F.Tovkach*; 2011-2013)
- CNRS-UPS Toulouse III (*H.Krisch*; 2010-2014)
- Université Laval (*H.Ackermann, S.Moineau*; 2010-2012)

		▪ George Eliava Institute (*R.Adamia, M.Kutateladze*; 2005-2010) ▪ Tulane University (*J.Karam*; 2005-2006) ▪ University of Texas (*S.Hardies, P.Serwer*; 2001-2003) ▪ Pittsburgh Bacteriophage Institute (*G.Hatfull, R.Hendrix*; 2000-2005)
		Bacterial predator characterization: ▪ Université Laval (*R.Lévesque, S.Charrette, C.Landry*; 2012-2013) ▪ University of British Columbia (*C.Suttle*; 2005-2013)
		Ecology of bacteria and viruses within Pacific oysters (*Crassostrea gigas*): ▪ Canadian Food Inspection Agency (*E.Buenaventura*; 1999-2005)
2013	**Contracted Hands-on Workshops**	Responsible for designing/conducting hands-on workshops on-campus for internal and external clients (listed below) on behalf of the IBIS Bioinformatics/Sequencing Core: *"Analysis of 454 16S amplicons – The mothur pipeline"* ▪ 02/2013: INAF – Université Laval ▪ 02/2013: Agriculture & Agri-Food Canada ▪ 05/2013: CEF – Université Laval ▪ 05/2013: IBIS – Université Laval ▪ 05/2013: Institut Armand-Frappier – INRS ▪ 07/2013: CRH – Université Laval
2007-2009	**Member – Laboratory Advisory Council**	Representative for non-permanent members on the LMGM-CNRS council.
2007-2008	**Special Issue Co-editor**	Co-editor of a special issue of Research in Microbiology (June 2008, vol.159, n°5) following the Les Treilles conference.
2005-2007	**Co-organizer – Les Treilles Foundation Meeting**	"The evolution, diversity and ecology of the dark matter of the biosphere: Bacteriophages", Fondation des Treilles, Tourtour FR (March 2007)
2003-2005	**Member – Academic Committees**	Information Technology Standing Committee, UBC (2003-2005); Teaching and Learning Enhancement Fund Proposal Review Committee, UBC (2004)
2002-2004	**Associate Editor – Undergraduate Research Journal**	UBC *Journal of Experimental Microbiology and Immunology* (JEMI) which contains undergraduate research conducted during senior-level laboratory courses (now open internationally).
1999-2004	**Oceanographic Expeditions**	Six one-week cruises on the in-shore waters of coastal British Colombia (1999-2004); One six-week Arctic research cruise in the Gulf of Amundsen (CASES 2003)

Teaching/Supervisory Experience

2016 **BScH Primary Student Mentor – Dalhousie University**

Responsible for mentoring the following student conducting a research project at the BScH level, under the supervision of M.G.I. Langille and L. Murray:

- C. Trim (2016) Project: Classification and comparative genomics of seven bacteriophages which infect *Streptomyces griseus*.

2014+ **BScH, MSc and PhD General Student Mentor – Dalhousie University**

Responsible for mentoring various internal and visiting students conducting research projects at the MSc and PhD levels, under the supervision of M.G.I. Langille.

2013 **Guest Lecturer (Graduate) – Université Laval**

Invited lecture to graduate students on the following subject:

- 16S, Metagenomics and the *mothur* Analysis Pipeline (2/2013)

2009-2013 **BScH, MSc and PhD General Student Mentor – Université Laval**

Responsible for mentoring various internal and visiting students conducting research projects at the BScH, MSc and PhD levels, under the supervision of C. Lovejoy and L. Bernier.

2009-2011 **Replacement/Guest Lecturer (Undergraduate) – Université Laval**

Invited lectures to 4th-year undergraduate students on the following subjects:

- Southern Hybridization (11/2009); Marine Viruses (11/2009); Marine Microbial Ecology (03/2011 and 11/2011)

2009-2011 **PhD Committee Member – UPMC, Paris FR / Laboratoire Arago, Banyuls-sur-Mer FR**

R. Thomas (2009-2011) UPMC PhD student. Project: Impact of Phycodnaviruses on the diversity and adaptation of phytoplankton populations (Prasinophytes).

2005-2009 **MSc and PhD Primary Student Mentor – Université Paul Sabatier (UPS), Toulouse FR**

Responsible for mentoring the following students conducting research projects at the MSc (French M1/2R) and PhD levels, under the supervision of H.M. Krisch:

- S. Trojet (2006-2011) UPS PhD student. Project: Functional study of the adhesins: Key proteins in the phage-host interaction.
- C. LeBlanc (2007-2008) UPS M2R. Project: Isolation and characterization of novel T4-like phage-host systems.
- C. Arbiol (2006-2008) UPS M2R student. Project: Defining the most rapidly evolving loci in T4-type bacteriophage genomes.
- C. LeBlanc (2007) U. de Caen M1 student. Project: Isolation of novel T4-like phage-host systems from aquatic environments.
- S. Trojet (2005-2006) UPS M2R student. Project: Genetic engineering of predators of pathogenic bacteria.

1999-2005 **Education Technology Teaching Assistant – UBC**

Responsible for assessing teaching technology needs and implementing/administering on-line course components for 21 courses with the Dept. of Microbiology and Immunology.

1999-2004 **BSc/BScH Primary Student Mentor – UBC**

Responsible for mentoring the following internal and visiting students conducting research projects at the BSc/BScH levels, under the supervision of C. Suttle:

- L. Raggi-Hoyos (2003-2004) Exchange student from Mexico. Project: Characterization of a novel marine predatory bacterium isolated from the Strait of Georgia.

- D. Kessler (2002) Exchange student from Germany. Project: Genetic characterization of *Vibrio parahaemolyticus* viruses.
- K. Liu (2001) UBC Student. Project: Assessment of automated image analysis for the enumeration of marine viruses.
- E. Chu (1999-2000) UBC Student. Project: Photoreactivation of *Vibrio parahaemolyticus* viruses (VpVs).

1998-2004 **Graduate Student Teaching Assistant – UBC**
Responsible for teaching and evaluation of undergraduate students in the following courses:

- BIOL 334 – Basic Genetics – 3rd-year fundamental genetics tutorial (1998).
- MICB 421 – Experimental Microbiology – 4th-year Majors and Honours self-directed, project-based laboratory course (2002-2004).

Publications and Presentations

Journal Articles

#. **Comeau AM**, Kwawukume A, Quinn DP, Langille MGI. **202X.** Quantification of sequence bleed-through in Illumina sequencing platforms. In preparation.

#. Trim C, Murray L, Stoltz M, **Comeau AM**. **202X.** Complete genome sequencing of 8 novel *Streptomyces griseus* phages isolated from soil. In preparation.

#. Godin X, Parmar NR, **Comeau AM**, Ali S. **202X.** Complete long-read sequencing of 20 novel endophytic fungal genomes. In preparation.

#. Verburgt CM, van der Kruk N, Dunn KA, Bielawski JP, Otley AR, de Meij T, Sylvester F, **Comeau AM**, Langille MGI, de Jonge WJ, van Limbergen JE. **202X.** Personalized AZithromycin/metronidAZole (PAZAZ) in combination with dietary therapy, to achieve a fecal microbiome community structure and metagenome changes associated with sustained remission in pediatric Crohn's Disease (CD): Results of a pilot study. *Inflammatory Bowel Diseases*, submitted.

#. Villafuerte AB, **Comeau AM**, Ortega R, Wright RJ, Miralles I. **202X.** Linking microbial taxonomy and function in N and P metabolism: A study of organic amendments in semiarid restored soils. *Environmental Microbiome*, submitted.

57. Valadez-Cano C, Reyes-Prieto A, Johnston L, Huang Y, Morris H, Zamlynny L, **Comeau AM**, Beach DG, Jamieson RC, Lawrence J. **2025.** The co-existence of *Microcoleus* strains with gene variations in the anatoxin-a biosynthesis cluster can explain the different toxin profiles observed in freshwater benthic mats. *Toxicon*, **264:**108461.

56. Villafuerte AB, López J, Soria R, **Comeau AM**, Ortega R, Miralles I. **2025.** Exploring the long-term impact of organic amendments on restored quarry soil microbial communities by shotgun metagenome sequencing. *IOP Conference Series: Earth and Environmental Sciences*, **1455:**012002.

55. Rose S, Robichaud BM, Tolman J, Fonseca-Batista D, Rowland E, Desai D, Ratten J-M, Kantor EJH, **Comeau AM**, Langille MGI, Jerlstrom-Hultqvist J, Devred E, Sarthou G, Bertrand EM, LaRoche J. **2024.** Nitrogen-fixation in the widely distributed model marine γ-proteobacterial diazotroph *Candidatus* Thalassolituus haligoni. *Science Advances*, **10:**eadn1476.

54. Johnston L, Huang Y, Bermarija TD, Rafuse C, Zamlynny L, Bruce MR, Graham C, **Comeau AM**, Valdez-Cano C, Lawrence JE, Beach DG, Jamieson RC. **2024.** Proliferation and anatoxin production of benthic cyanobacteria along a stream-lake continuum. *Science of the Total Environment*, **917:**170476.

53. Verburgt CM, Dunn KA, Otley AR, Heyman MB, Verstraete S, Sunseri W, Sylvester F, de Meij T,

Comeau AM, Langille MGI, de Jonge WJ, Benninga MA, van Limbergen JE. **2023.** Personalized azithromycin/metronidazole (PAZAZ), in combination with standard induction therapy, to achieve a faecal microbiome community structure and metagenome changes associated with sustained remission in paediatric Crohn's Disease (CD): Protocol of a pilot study. *BMJ Open*, **13:**e064944.

52. Wright RJ, **Comeau AM**, Langille MGI. **2023.** From defaults to databases: Parameter and database choice dramatically impact the performance of metagenomic taxonomic classification tools. *Microbial Genomics*, **9:**000949.
51. Bermarija T, Hiscock A, Johnston L, Huang Y, **Comeau AM**, Jamieson R. **2022.** Performance and ecological impacts of benthic barriers for the control of an invasive plant in a small urban lake. *Ecological Engineering*, **184:**106784.
50. Obieze CC, Wania GA, Shash MA, Reshi ZA, **Comeau AM**, Khasa DP. **2022.** Anthropogenic activities and geographic locations regulate microbial diversity, community assembly and species sorting in Canadian and Indian freshwater lakes. *Science of the Total Environment*, **826:**154292.
49. Nearing JT, Douglas GM, Hayes M, MacDonald J, Desai D, Allward N, Jones CMA, Wright R, Dhanani A, **Comeau AM**, Langille MGI. **2022.** Microbiome differential abundance methods produce disturbingly different results across 38 datasets. *Nature Communications*, **13:**342.
48. Miralles I*, Ortega R, **Comeau AM***. **2021.** Functional and taxonomic effects of organic amendments on the restoration of semiarid quarry soils. *mSystems*, **6:**e00752-21. *contributed equally
47. Ashe EC, **Comeau AM**, Zejdlik K, O'Connell SP. **2021.** Characterization of bacterial community dynamics of the human mouth throughout decomposition via metagenomic, metatranscriptomic, and culturing techniques. *Frontiers in Microbiology*, **12:**689493.
46. Nearing JT, **Comeau AM**, Langille MGI. **2021.** Identifying biases and their potential solutions in human microbiome studies. *Microbiome*, **9:**113.
45. Palau M, Piqué N, **Comeau AM**, Douglas GM, Ramírez-Lázaro MJ, Lario S, Calvet X, Langille MGI, Miñana-Galbis D. **2020.** Detection of *Helicobacter pylori* microevolution and multiple infection from gastric biopsies by housekeeping gene amplicon sequencing. *Pathogens*, **9:**97.
44. Jones CMA, Moore-Connors J, Dunn KA, Bielawski JP, **Comeau AM**, Langille MGI, van Limbergen J. **2020.** Bacterial taxa and functions are predictive of sustained remission following exclusive enteral nutrition in pediatric Crohn's disease. *Inflammatory Bowel Diseases*, **26:**1026-1037.
43. **Comeau AM**, Lagunas M, Scarcella K, Varela D, Lovejoy C. **2019.** Nitrate consumers in Arctic marine eukaryotic communities: Comparative diversities of 18S rRNA, 18S rRNA genes, and nitrate reductase genes. *Applied and Environmental Microbiology,* **85:**e00247-19.
42. Jordaan K, **Comeau AM**, Khasa DP, Bezuidenhout CC. **2019.** An integrated insight into the response of bacterial communities to anthropogenic contaminants in a river: A case study of the Wonderfonteinspruit catchment area, South Africa. *PLoS ONE,* **14:**e0216758.
41. Zorz J, Willis C, **Comeau AM**, Langille MGI, Li WKW, Johnson C, LaRoche J. **2019.** Drivers of regional bacterial community structure and diversity over depth and time in the Northwest Atlantic Ocean. *Frontiers in Aquatic Microbiology*, **10:**281.
40. Lau WL, Vaziri ND, Nunes A, **Comeau AM**, Langille MGI, England W, Khazaeli M, Suematsu Y, Phan J, Whiteson K. **2018.** The phosphate binder ferric citrate alters the gut microbiome in rats with chronic kidney disease. *Journal of Pharmacology and Experimental Therapeutics,* **367:**452-460.
39. Dranse H, Zheng A, **Comeau AM**, Langille MGI, Zabel B, Sinal C. **2018.** The impact of chemerin or chemokine-like receptor 1 loss on the mouse gut microbiome. *PeerJ,* **6:**e5494.
38. Nearing JT, Douglas GM, **Comeau AM**, Langille MGI. **2018.** Denoising the denoisers: An independent evaluation of microbiome sequence error-correction approaches. *PeerJ,* **6:**e5364.

37. Slaine PD, MacRae C, Kleer M, Lamoureux E, McAlpine S, Warhuus M, **Comeau AM**, McCormick C, Hatchette T, Khaperskyy DA. **2018.** Adaptive mutations in influenza A/California/07/2009 enhance polymerase activity and infectious virion production. *Viruses*, **10:**272.
36. Jubinville E, Veillette M, Milot J, Maltais F, **Comeau AM**, Levesque RC, Duchaine C. **2018.** Exacerbation induces a microbiome shift in sputa of COPD patients. *PLoS ONE*, **13:**e0194355.
35. Douglas GM, Hansen R, Jones C, Dunn K, **Comeau AM**, Bielawski JP, Tayler R, El-Omar EM, Russell RK, Hold GL, Langille MGI, van Limbergen J. **2018.** Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. *Microbiome,* **6:**13.
34. Yurgel SN, Douglas GM, **Comeau AM**, Mammoliti M, Dussault A, Percival D, Langille MGI. **2017.** Variation in bacterial and eukaryotic communities associated with natural and managed wild blueberry habitats. *Phytobiomes,* **1:**102-113.
33. Onda DF, Medrinal E, **Comeau AM**, Thaler M, Babin M, Lovejoy C. **2017.** Seasonal and interannual changes in ciliate and dinoflagellate species assemblage in the Arctic Ocean (Amundsen Gulf, Beaufort Sea, Canada). *Frontiers in Marine Science*, **4:**16.
32. **Comeau AM**, Douglas GM, Langille MGI. **2017.** Microbiome Helper: A custom and streamlined workflow for microbiome research. *mSystems*, **2:**e00127-16.
31. **Comeau AM**, Vincent WF, Bernier L, Lovejoy C. **2016.** Novel chytrid lineages dominate fungal sequences in diverse marine and freshwater habitats. *Nature Scientific Reports,* **6:**30120.
30. Landry M, **Comeau AM**, Derome N, Cusson M, Levesque RC. **2015.** Composition of the spruce budworm (*Choristoneura fumiferana*) midgut microbiota as affected by rearing conditions. *PLoS ONE,* **10:**e0144077.
29. **Comeau AM**, Dufour J, Bouvet G, Jacobi V, Nigg M, Henrissat B, Laroche J, Levesque RC, Bernier L. **2015.** Functional annotation of the *Ophiostoma novo-ulmi* genome: Insights into the phytopathogenicity of the fungal agent of Dutch Elm Disease. *Genome Biology and Evolution,* **7:**410-430.
28. Bernier L, Aoun M, Bouvet G, **Comeau AM**, Dufour J, Naruzawa ES, Nigg M, Plourde KV. **2014.** Genomics of the Dutch elm disease pathosystem: Are we there yet? *iForest,* **8:**149-157.
27. **Comeau AM**, Arbiol C, Krisch HM. **2014.** Composite conserved promoter-terminator motifs (PeSLs) that mediate modular shuffling in the diverse T4-like myoviruses. *Genome Biology and Evolution*, **6:**1611-1619.
26. Kushkina A, Tovkach FI, **Comeau AM**, Kostetskii IE, Lisovski I, Ostapchuk AM, Voichuk SI, Gorb TI, Romaniuk LV. **2013.** Complete genome sequence of *Escherichia* phage Lw1, a new member of the RB43 group of Pseudo T-even bacteriophages. *Genome Announcements*, **1:**e00743-13.
25. Monier A, Terrado R, Thaler M, **Comeau AM**, Medrinal E, Lovejoy C. **2013.** Upper Arctic Ocean water masses harbor distinct communities of heterotrophic flagellates. *Biogeosciences*, **10:**4273-4286.
24. **Comeau AM**, Philippe B, Thaler M, Gosselin M, Poulin M, Lovejoy C. **2013.** Protists in Arctic drift and land-fast sea ice. *Journal of Phycology*, **49:**229-240.
23. Charvet S, Vincent WF, **Comeau AM**, Lovejoy C. **2012.** Pyrosequencing analysis of the protist communities in a High Arctic meromictic lake: DNA preservation and change. *Frontiers in Extreme Microbiology*, **3:**422.
22. **Comeau AM**, Harding T, Galand P, Vincent WF, Lovejoy C. **2012.** Vertical distribution of microbial communities in a perennially-stratified Arctic lake with saline, anoxic bottom waters. *Nature Scientific Reports*, **2:**604.
21. **Comeau AM**, Tremblay D, Moineau S, Kushkina A, Tovkach FI, Rattei T, Krisch HM, Ackermann H-A. **2012.** Phage morphology recapitulates phylogeny: The comparative genomics of a new group of myoviruses. *PLoS ONE*, **7**:e40102.
20. **Comeau AM**, Li WKW, Tremblay J-E, Carmack EC, Lovejoy C. **2011.** Changes in Arctic Ocean

microbial community structure following the 2007 record sea ice minimum. *PLoS ONE*, **6:**e27492.

19. Trojet SN, Caumont-Sarcos A, Perrody E, **Comeau AM**, Krisch HM. 2011. The gp38 adhesins of the T4 superfamily: A complex modular determinant of the phage's host specificity. *Genome Biology and Evolution*, **3:**674-686.
18. Ackermann H-W, Krisch HM, **Comeau AM.** 2011. Morphology and genome sequence of phage ϕ1402: A dwarf myovirus of the predatory bacterium *Bdellovibrio bacteriovorus*. *Bacteriophage*, **1(3):**1-5.
17. **Comeau AM**, Arbiol C, Krisch HM. 2010. Gene network visualization and quantitative synteny analysis of more than 300 marine T4-like phage scaffolds from the GOS metagenome. *Molecular Biology and Evolution*, **27:**1935-1944.
16. Arbiol C*, **Comeau AM***, Kutateladze M, Adamia R, Krisch HM. 2010. Mobile regulatory cassettes mediate modular shuffling in T4-type phage genomes. *Genome Biology and Evolution,* **2010:**140-152. *co-first authors
15. Leblanc C*, Caumont-Sarcos A*, **Comeau AM***, Krisch HM. 2009. Isolation and genomic characterization of the first phage infecting Iodobacteria: ϕPLPE, a myovirus having a novel set of features. *Environmental Microbiology Reports*, **1:**499-509. *co-first authors
14. **Comeau AM**, Krisch HM, Mann NH, Prangishvili D. 2008. Editorial. *Research in Microbiology*, **159:**305.
13. **Comeau AM**, Hatfull GF, Krisch HM, Lindell D, Mann NH, Prangishvili D. 2008. Exploring the prokaryotic Virosphere. *Research in Microbiology*, **159:**306-313.
12. Krisch HM, **Comeau AM.** 2008. The immense journey of bacteriophage T4 – From d'Hérelle to Delbrück and then to Darwin and beyond. *Research in Microbiology*, **159:**314-324.
11. **Comeau AM**, Krisch HM. 2008. The capsid of the T4 phage superfamily: The evolution, diversity, and structure of some of the most prevalent proteins in the biosphere. *Molecular Biology and Evolution*, **25:**1321-1332.
10. **Comeau AM**, Tétart F, Trojet SN, Prère M-F, Krisch HM. 2008. La découverte d'un phénomène naturel, la « synergie phages-antibiotiques » - Un enjeu pour la phagothérapie. *Médecine/Sciences,* **24:**449-451.
9. **Comeau AM***, Tétart F*, Trojet SN, Prère M-F, Krisch HM. 2007. Phage-Antibiotic Synergy (PAS): β-lactam and quinolone antibiotics stimulate virulent phage growth. *PLoS ONE*, **2:**e799. *co-first authors
8. **Comeau AM**, Suttle CA. 2007. Distribution, genetic richness and phage sensitivity of *Vibrio* spp. from Coastal British Columbia. *Environmental Microbiology*, **9:**1790-1800.
7. **Comeau AM**, Bertrand C, Letarov A, Tétart F, Krisch HM. 2007. Modular architecture of the T4 phage superfamily: A conserved core genome and a plastic periphery. *Virology*, **362:**384-396.
6. **Comeau AM**, Chan AM, Suttle CA. 2006. Genetic richness of vibriophages isolated in a coastal environment. *Environmental Microbiology*, **8:**1164-1176. [Faculty of 1000 citation]
5. Filée J, **Comeau AM**, Suttle CA, Krisch HM. 2006. Les bactériophages de type T4: Des composants prépondérants de la « matière noire » de la biosphère. *Médecine/Sciences*, **22:**111-112.
4. **Comeau AM**, Buenaventura E, Suttle CA. 2005. A persistent, productive and seasonally dynamic vibriophage population within Pacific oysters (*Crassostrea gigas*). *Applied and Environmental Microbiology*, **71:**5324-5331.
3. **Comeau AM**, Krisch HM. 2005. War is peace – Dispatches from the bacterial and phage killing fields. *Current Opinion Microbiology*, **8:**488-494.
2. **Comeau AM**, Short SM, Suttle CA. 2004. The use of degenerate-primed random amplification of polymorphic DNA (DP-RAPD) for strain-typing and inferring the genetic similarity among closely related viruses. *Journal of Virological Methods*, **118:**95-100.

1. Hardies S, **Comeau AM**, Serwer P, Suttle CA. **2003.** The complete sequence of marine bacteriophage VpV262 infecting *Vibrio parahaemolyticus* indicates that an ancestral component of a T7 viral supergroup is widespread in the marine environment. *Virology*, **310:**359-371. [Faculty of 1000 citation]

Books/Chapters

Douglas GM, **Comeau AM**, Langille MGI. **2018.** Processing a 16S rRNA sequencing dataset with the Microbiome Helper workflow. In *Methods in Molecular Biology – Microbiome Analysis: Methods and Protocols*. Beiko R, Parkinson J, Hsiao W (eds.). Humana Press. [ISBN 978-1-4939-8726-9; DOI 10.1007/978-1-4939-8728-3]

Gosselin M, Mundy CJ, Ardyna M, Belt ST, Brown T, **Comeau AM**, Alou Font E, Larouche P, Lovejoy C, Massé G, Medrinal E, Nozais C, Philippe B, Poulin M, Sallon A, Roy S, Terrado R, Thaler M. **2012.** Chapter 3: Light, nutrients and primary production. In *On the Edge: From Knowledge to Action during the Fourth International Polar Year Circumpolar Flaw Lead System Study (2007-2008).* Barber D, Tjaden T, Leitch D, Barber L, Chan W (eds.). University of Manitoba. [ISBN 978-0-9813265-1-1]

Comeau AM, Noble RT. **2010.** Preparation and application of fluorescently-labeled virus particles, p. 19-29. In *Manual of Aquatic Viral Ecology*. Wilhelm SW, Weinbauer MG, Suttle CA (eds.). American Society for Limnology and Oceanography. [DOI 10.4319/mave.2010.978-0-9845591-0-7.19]

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89. Verburgt CM, van der Kruk N, Dunn KA, Bielawski JP, Otley AR, de Meij T, Sylvester F, Comeau AM, Langille MGI, de Jonge WJ, **van Limbergen JE**. **2025.** Personalized AZithromycin/metronidAZole (PAZAZ) in combination with dietary therapy, to achieve a fecal microbiome community structure and metagenome changes associated with sustained remission in pediatric Crohn's Disease (CD): results of a pilot study. *PIBD2025*. Sorrento IT, October 2025. [poster]
88. Boneh RS, van der Kruk N, Ghiboub M, Dunn KA, Bielawski JP, de Meij TGJ, de Jonge WJ, D'Haens GRAM, Parmar NR, Comeau AM, Langille MGI, Wine E, **van Limbergen JE**. **2025.** Establishment of an open repository of Proteobacteria-signatures from metagenome assembled-genomes of paediatric CD: responders vs. non-responders to nutritional therapy. *PIBD2025*. Sorrento IT, October 2025. [poster]
87. **DeClercq V**, Comeau AM, Kwawukume A, Murphy R, Parmar NR, Quinn DP, Wright R, Wallace A, Langille MGI. **2025.** Challenges in acquiring reliable microbiome profiles from blood and tumour samples. *IMPACTT 2025*. Canmore AB, September 2025. [poster]
86. **Soria R**, Ortega R, Comeau AM, Miralles I. **2025.** Influence of organic amendments on genes related to polysaccharide production and soil structural stability in restored Technosols. *EUROSOIL2025*. Sevilla ES, September 2025. [poster]
85. **Shin K**, Dobranowski P, Li J, Tanabe G, Zhang L, Comeau AM, Langille MGI, Singleton R, Mack D, Stintzi A. **2025.** Bridging the gap in bacterial taxonomic identification between 16S and shotgun sequencing. *uOttawa BMI Poster Day*. Ottawa ON, February 2025. [poster]
84. **Ortega R**, Soria R, Comeau AM, Villafuerte AB, López J, Miralles I. **2024.** Functionality assessment of bacterial communities in short-term restored soils: A metagenomic sequencing study in semi-arid ecosystems. *ISADAE2024*. Reims FR, October 2024. [poster]
83. **Villafuerte AB**, López J, Soria R, Comeau AM, Ortega R, Miralles I. **2024.** Exploring the long-term

impact of organic amendments on restored quarry soil microbial communities by shotgun metagenome sequencing. *ISADAE2024*. Reims FR, October 2024. [poster]

82. **Ortega R**, Soria R, Comeau AM, Villafuerte-Acuña A, Lopez J, Miralles I. **2024.** Functionality assessment of bacterial communities in short-term restored soils: A metagenomic sequencing study in semi-arid ecosystems. *SERE24*. Tartu EE, August 2024. [poster]
81. **Villafuerte-Acuña A**, Lopez J, Soria R, Comeau AM, Ortega R, Miralles I. **2024.** Assessing the long-term impact of organic amendments on taxa and functions of restored quarry soil microbial communities through shotgun metagenomics. *SERE24*. Tartu EE, August 2024. [poster]
80. **Wright R,** Fisher B, Comeau AM, Langille MGI. **2024.** Reducing false-positive taxa in metagenomes by coverage validation of reference genomes. *ISME19*. Cape Town RSA, August 2024. [seminar]
79. **Villafuerte-Acuña A**, Comeau AM, Ortega R, Miralles I. **2024.** Estudio de las funciones potenciales en el ciclo del fósforo de las comunidades bacterianas en suelos restaurados con enmiendas orgánicas en un clima semiárido. *CONDEGRES 2024*. Burgos ES, June 2024. [poster]
78. **DeClercq V,** Comeau AM, Parmar NR, Murphy R, Wright R, Wallace A, Langille MGI. **2024.** Body site-specific microbiomes hold predictive value for lung cancer outcomes. *IMPACTT 2024*. Camore AB, June 2024. [poster]
77. **Wright R,** Fisher B, Comeau AM, Langille MGI. **2024.** Reducing false-positive taxa in metagenomes by coverage validation of reference genomes. *IMPACTT 2024*. Camore AB, June 2024. [seminar]
76. **Villafuerte-Acuña A**, Comeau AM, Ortega R, Miralles I. **2024.** Analysis of phosphonate and phosphinate metabolism in restored soils in semiarid climate by shotgun metagenomic sequencing. *CONDEGRES 2024*. Burgos ES, January 2024. [poster]
75. **Rose S**, Robichaud BM, Tolman J, Fonseca-Batista D, Rowland E, Desai D, Ratten J-M, Kantor EJH, Comeau AM, Langille MGI, Bertrand EM, LaRoche J. **2023.** Nitrogen-fixation in the widely distributed model marine gamma-proteobacterial diazotroph *Candidatus* Thalassolituus haligoni. *2023 ICG Biodiversity Symposium*. Halifax NS, November 2023. [poster]
74. **Desai D**, Comeau AM, Langille MGI. Visualising taxa-function relationships from meta-omic data. **2023.** Microbial biodiversity at the Harrison Lewis Coastal Discovery Centre (Nova Scotia, Canada). *2023 ICG Biodiversity Symposium*. Halifax NS, November 2023. [poster]
73. Sangster S, Phelan E, Chung D, Dunn K, Kantor E, Mastrangelo B, Baldwin I, Barkhouse K, Blais C, Brask N, Breglia S, Haro R, Hosmer M, Maclean C, Madaan A, Martijn J, Matar S, MacMillan N, McCarthy C, Mora Collazos A, Myles S, Roberts M, Rowland E, Shao J, Stevens-Green R, Tymoshenko D, Weston L, Zhao D, Comeau AM, Dlutek M, Rohde JR, Roger AJ, Sterling SM, Slamovits CH, Westwood A, Bertrand EM, LaRoche J, Langille MGI, Simpson AGB, **Archibald JM**. **2023.** Microbial biodiversity at the Harrison Lewis Coastal Discovery Centre (Nova Scotia, Canada). *2023 ICG Biodiversity Symposium*. Halifax NS, November 2023. [poster]
72. **Desai D**, Comeau AM, Langille MGI. **2023.** Visualizing taxa-function relationships from meta-omic data. *72nd Annual Conference of the Canadian Society of Microbiologist*. Halifax NS, June 2023. [poster]
71. **Johnston L**, Huang Y, Bermarija TD, Rafuse C, Zamlynny L, Graham C, Bruce MR, Comeau AM, Valdez-Cano C, Lawrence JE, Beach DG, Jamieson RC. **2023.** Proliferation and Toxin Production of Benthic Cyanobacteria along a Stream-Lake Continuum. *IFHAB 2023*. Montréal QC, May 2023. [poster]
70. **Filloramo GV**, Comeau AM, Fennessey E, Gallot-Lavallée L, Spinney K, Dlutek M, Archibald JM, Langille MGI. **2022.** Integrated Microbiome Resource: Recent advances in microbiome sequencing & bioinformatics. *Microbiome 2022*. Cold Spring Harbor NY, October 2022. [poster]

69. **Verburgt CM**, Dunn KA, Otley AR, Heyman MB, Verstraete S, Sunseri W, Sylvester F, de Meij T, Comeau AM, Langille MGI, de Jonge WJ, Benninga MA, van Limbergen JE. **2022.** Personalized AZithromycin/metronidazole (PAZAZ), in combination with standard induction therapy, to achieve a faecal microbiome community structure and metagenome changes associated with sustained remission in paediatric Crohn's Disease (CD): Initial results of a pilot feasibility study. *United European Gastroenterology Week 2022*. Online+Vienna AT, October 2022. [poster]

68. **Verburgt CM**, Dunn KA, Otley AR, Heyman MB, Verstraete S, Sunseri W, Sylvester F, de Meij T, Comeau AM, Langille MGI, de Jonge WJ, Benninga MA, van Limbergen JE. **2022.** Personalized AZithromycin/metronidazole (PAZAZ), in combination with standard induction therapy, to achieve a faecal microbiome community structure and metagenome changes associated with sustained remission in paediatric Crohn's Disease (CD): Initial results of a pilot feasibility study. *6th International Symposium on Paediatric Inflammatory Bowel Disease*. Edinburgh UK, September 2022. [poster]

67. **Wright RJ**, Comeau AM, Langille MGI. **2022.** From defaults to databases: Parameter and database choice dramatically impact the performance of metagenomic taxonomic classification tools in low microbial biomass samples. *Having IMPACTT: Advancing Microbiome Research 2022*. Canmore AB, June 2022. [seminar]

66. **Nearing JT**, Douglas GM, Hayes M, MacDonald J, Desai D, Allward N, Jones CMA, Wright R, Dhanani A, Comeau AM, Langille MGI. **2021.** Microbiome differential abundance methods produce strikingly different results across 38 datasets. *Having IMPACTT: Advancing Microbiome Research 2021*. Online, June 2021. [poster]

65. **Wright RJ**, Kwawukume A, Dhanani AS, Comeau AM, LeBlanc JJ, Langille MGI. **2021.** Leveraging the microbiome to predict COVID-19 susceptibility, severity and transmissibility. *Microbiome Data Congress 2021*. Online, June 2021. [poster]

64. **Nearing JT**, Douglas GM, Hayes M, MacDonald J, Desai D, Allward N, Jones CMA, Wright R, Dhanani A, Comeau AM, Langille MGI. **2021.** Microbiome differential abundance methods produce disturbingly different results across 38 datasets. *Microbiome Data Congress 2021*. Online, June 2021. [poster]

63. **Callaghan B**, Comeau AM, Langille MGI. **2020.** Reconstructing unculturable microbial genomes from clinically relevant stool samples using mixed sequencing and bioinformatic approaches. *28th Conference on Intelligent Systems for Molecular Biology (ISMB)*. Online, July 2020. [poster]

62. **Rodriguez-Berbel N**, Soria R, Ortega R, Comeau AM, Zornoza R, Miralles I. **2020.** Recovery of microbiological status with organic amendments on soils affected by mining activity in a decadal temporal scale. *Global Symposium on Soil Biodiversity*. Rome IT, March 2020. [poster]

61. **Ortega R**, Soria R, Rodriguez-Berbel N, Sánchez B, Comeau AM, Zornoza R, Miralles I. **2020.** Intercrop management as a tool to increase soil microbial diversity on rainfed almond cultivations. *Global Symposium on Soil Biodiversity*. Rome IT, March 2020. [poster]

60. **Borza T**, Al-Mughrabi T, Comeau AM, Sanderson L, Singh M, Prithiviraj B. **2019.** Assessment of potato early dying complex in New Brunswick fields using classical and molecular techniques. *Northeast Potato Technology Forum.* Charlottetown PEI, March 2019. [poster]

59. **Getz LJ**, Comeau AM, Langille MGI, Thomas NA. **2018.** Linking phenotype and pathogen genomics: Tn-Seq and Next Generation DNA sequencing. *23rd Annual Infectious Diseases Research Day & 10th Annual Canadian Center for Vaccinology Symposium*. Halifax NS, April 2018. [poster]

58. Leuschen K, Douglas G, Jones C, Comeau AM, Hansen R, Russell R, Hold G, van Limbergen J, **Langille MGI**. **2018.** Combining microbiome taxonomic and functional profiles for precision medicine. *Keystone Symposia Series: Microbiome, Host Resistance and Disease (X4)*. Banff AB, March 2018. [poster]

57. **Hansen R**, Douglas G, Jones C, Dunn K, Comeau AM, Bielawski J, Tayler R, El-Omar EM, Russell R, Hold G, Langille MGI, van Limbergen J. **2017.** Shotgun metagenomics, 16S rRNA gene sequencing, and human genetics differentially classify paediatric Crohn's disease state and treatment outcome. *4th International Symposium on Pediatric Inflammatory Bowel Disease*. Barcelona ES, September 2017. [E-poster]
56. **Palau M**, Comeau AM, Piqué N, Ramírez-Lázaro MJ, Lario S, Calvet X, Langille MGI, Miñana-Galbis D. **2017.** Detection of *H. pylori* microevolution and multiple infection from gastric biopsies by amplicon sequencing. *FEMS 2017 – 7th Congress of European Microbiologists.* Valencia ES, July 2017. [poster]
55. **Stadnyk AW**, Douglas G, Comeau AM, Jain U, Schwaeble WJ, Stover CM, Bieko R, Langille MGI. **2017.** Properdin deficiency does not impact the mouse response to DSS-induced colitis despite differences in colonic microbiome. *Canadian Digestive Diseases Week 2017*. Banff AB, March 2017. [poster]
54. Jones C, Douglas G, Comeau AM, Hansen R, Russell R, Hold G, van Limbergen J, **Langille MGI**. **2016.** Assessing the relative contribution of genetics and micro-omics for predicting pediatric Crohn's Disease. *6th International Human Microbiome Congress*. Houston TX, November 2016. [seminar+poster]
53. Jones C, Douglas G, Comeau AM, Hansen R, Russell R, Hold G, Langille MGI, **van Limbergen J**. **2016.** An integrated microbiome and genetic analysis of pediatric Crohn's disease. *5th World Congress of Pediatric Gastroenterology, Hepatology and Nutrition*. Montréal QC, October 2016. [poster]
52. **Comeau AM**, Ratten J-M, Tolman J, LaRoche J, Langille MGI. **2016.** Evaluation of standard and hybrid assembly methods for de novo sequencing of a novel marine bacterium representing a widespread clade of North Atlantic diazotrophs. *ISME 2016.* Montréal QC, August 2016. [poster]
51. Jones C, **Douglas G**, Comeau AM, Hansen R, Russell R, Hold G, Langille MGI, van Limbergen J. **2016.** Assessing the relative contribution of genetics and the microbiome for predicting pediatric Crohn's disease. *ISME 2016.* Montréal QC, August 2016. [poster]
50. **LaRoche J**, Ratten J-M, Tolman J, Comeau AM, Langille MGI. **2016.** The genome of a novel marine heterotrophic diazotroph isolated from the North West Atlantic Ocean sheds light on its life style. *ISME 2016.* Montréal QC, August 2016. [invited seminar]
49. Comeau AM, **Langille MGI**. **2016.** Integrated Microbiome Resource (IMR): Developing an open and streamlined experimental and analysis pipeline for microbiome research. *American Society for Microbiology Microbe*. Boston MA, June 2016. [poster]
48. **Jones C**, Douglas G, Comeau AM, van Limbergen J, Hansen R, Russell R, Hold G, Langille MGI. **2016.** Host-microbe interactions influence the development of Inflammatory Bowel Disease. Crossroads Conference 2016. Halifax NS, March 2016. [seminar]
47. Comeau AM, **Langille MGI**. **2015.** Microbiome: From samples to statistics in a workweek. *American Society for Microbiology General Meeting*. New Orleans LA, May 2015. [poster]
46. **Lovejoy C**, Comeau AM, Lagunas M, Varela D. **2015.** Nitrogen uptake and community structure at the Canada Basin ice edge. *ASLO Aquatic Sciences Meeting*. Granada ES, February 2015. [seminar]
45. **Nigg M**, Comeau AM, Landry CR, Bernier L. **2014.** *Ophiostoma novo-ulmi*: A new model species for dimorphism studies? *Gordon Conference on Cellular and Molecular Fungal Biology*. Holderness NH, June 2014. [poster]
44. **Jordaan K**, Hamman D, Comeau AM, Khasa D, Bezuidenhout CC. **2014.** Correlations between

physico-chemical water quality and 454-pyrosequencing bacterial community data: A case study in the lower Wonderfonteinspruit. *Water Institute of Southern Africa (WISA) Biennial Conference & Exhibition*. Mbombela SA, May 2014. [poster]

43. Jeukens J, Boyle B, Kukavica-Ibrulj I, Laroche J, Comeau AM, 18 others, **Levesque RC**. **2013**. Clinical exploitation of genomics data produced by the *Pseudomonas* International Consortium: the 1000 genomes project. *14th International Conference on Pseudomonas*. Lausanne CH, September 2013. [seminar]
42. **Comeau AM**, Forgetta V, Dewar K, Henrissat B, Dufour J, Levesque RC, Bernier L. **2013**. Séquençage et annotation du génome du champignon *Ophiostoma novo-ulmi*, principal agent de la maladie hollandaise de l'orme (MHO). *ACFAS*. Québec QC, May 2013. [poster]
41. **Comeau AM**. **2013**. Les recherches sur la maladie hollandaise de l'orme à l'ère de la génomique. Partie 2: Détails du génome d'*Ophiostoma novo-ulmi* H327. Centre d'Étude de la Forêt (CEF), Université Laval. Québec QC, February 2013. [invited seminar]
40. **Comeau AM**. **2012**. Use of mothur to analyze pyrosequencing data – from raw sequences to finished analysis. Université du Québec à Rimouski (UQAR). Rimouski QC, September 2012. [invited hands-on workshop]
39. **Comeau AM**. **2012**. Amplicon pyrosequencing in microbial ecology: Practical aspects, analysis methodology and concrete research examples. Université du Québec à Rimouski (UQAR). Rimouski QC, September 2012. [invited seminar]
38. Comeau AM, Philippe B, Thaler M, Gosselin M, **Poulin M**, Lovejoy C. **2012.** Diatom communities from Arctic drift and land-fast ice as revealed by high-throughput pyrosequencing. *22nd International Diatom Symposium*. Ghent BE, August 2012. [poster]
37. Comeau AM, Tremblay D, Moineau S, Rattei T, Kushkina A, Tovkach FI, **Krisch HM**, Ackermann H-A. **2012.** Phage morphology recapitulates phylogeny: The comparative genomics of a new group of myoviruses. *EMBO Viruses of Microbes Conference*. Brussels BE, July 2012. [poster]
36. **Lovejoy C**, Comeau AM. **2012.** The where and withal of sea ice protists. *ASLO Summer Meeting*. Lake Biwa JP, July 2012. [seminar]
35. **Charvet S**, Comeau AM, Vincent WF, Lovejoy C. **2012**. Spatial and seasonal variations of protist communities in a High Arctic meromictic lake. *International Polar Year Conference*. Montréal QC, April 2012. [seminar]
34. **Comeau AM**. **2012**. Use of mothur to analyze pyrosequencing data – from raw sequences to finished analysis. *Canada Healthy Oceans Network (CHONe) Université Laval Workshop*. Québec QC, March 2012. [invited hands-on workshop]
33. **Comeau AM**. **2012**. Amplicon pyrosequencing in microbial ecology: Practical aspects, analysis methodology and concrete research examples. *Canada Healthy Oceans Network (CHONe) Université Laval Workshop*. Québec QC, March 2012. [invited seminar]
32. **Lovejoy C**, Comeau AM, Medrinal E, Gratton Y, Monier A. **2012.** Protist communities through the deep chlorophyll maxima layer of the Mackenzie Canyon, Beaufort Sea, Arctic Ocean. *ASLO Ocean Sciences Meeting*. Salt Lake City UT, February 2012. [poster]
31. **Comeau AM**, Lovejoy C. **2011**. Pyroséquençage dans l'Arctique Canadien: Étude des communautés microbiennes avec la technique de séquençage nouvelle-génération. *Québec-Océan Annual General Assembly*. Lac Delage QC, November 2011. [seminar]

30. **Charvet S**, Comeau AM, Vincent WF, Lovejoy C. **2011**. Variations saisonnières et spatiales des protistes dans un lac méromictique du haut arctique canadien. *Québec-Océan Annual General Assembly*. Lac Delage QC, November 2011. [poster]
29. **Medrinal E**, Terrado R, Thaler M, Comeau A, Lovejoy C. **2011**. Arctic extremes: Follow the sun and the endless summer versus surviving winter darkness? *ASLO Ocean Sciences Meeting*. San Juan PR, February 2011. [poster]
28. **Comeau AM. 2011**. Pyroséquençage dans l'Arctique Canadien: Étude des communautés microbiennes avec la technique de séquençage nouvelle-génération. Québec-Océan, Université du Québec à Rimouski (UQAR). Rimouski QC, February 2011. [invited seminar]
27. **Comeau AM. 2011**. Pyroséquençage dans l'Arctique Canadien: Étude des communautés microbiennes avec la technique de séquençage nouvelle-génération. Québec-Océan, Université Laval. Québec QC, January 2011. [invited seminar]
26. **Lovejoy C**, Galand P, Comeau AM, Kirchman D. **2010**. How many and what picoplankton are in the Arctic Ocean. *13th International Symposium on Microbial Ecology (ISME-13)*. Seattle WA, August 2010. [poster]
25. **Comeau AM**, Lovejoy C. **2010**. Bar-code pyrosequencing of arctic microbial communities. *13th International Symposium on Microbial Ecology (ISME-13)*. Seattle WA, August 2010. [poster]
24. Arbiol C, Comeau AM, **Krisch HM. 2010**. Mobile regulatory cassettes mediate modular shuffling in T4-type phage genomes. *Viruses of Microbes Meeting*. Institut Pasteur. Paris FR, June 2010. [invited seminar]
23. **Comeau AM. 2008**. The immense journey of bacteriophage T4: From molecular guinea pig to environmental dominance. Institut Pasteur. Paris FR, December 2008. [invited seminar]
22. **Comeau AM. 2008**. La biologie intégrative des bactériophages marins : Des macromolécules, aux nanomachines, aux populations naturelles. Laboratoire Arago. Banyuls-sur-Mer FR, November 2008. [invited seminar]
21. **Comeau AM. 2008**. T4 phage superfamily capsid proteins: Diversity, evolution and structure of the marine majority. *Genomics and Ecology of Aquatic Viruses.* Laboratoire Arago. Banyuls-sur-Mer FR, February 2008. [seminar]
20. **Comeau AM. 2007**. Phage-Antibiotic Synergy (PAS): Antibiotics stimulate virulent phage production. *Meeting on Bacterial Infectology: Which Role for Phage Therapy?* Institut Pasteur. Paris FR, November 2007. [invited seminar]
19. **Comeau AM. 2007**. Écologie, diversité et évolution des virus marins. Laboratoire d'Évolution et Diversité Biologique – CNRS/UPS. Toulouse FR, July 2007. [invited seminar]
18. **Comeau AM**, Tétart F, **Trojet SN**, Prère M-F, Krisch HM. **2007**. Phage-Antibiotic Synergy (PAS): Antibiotics that block cell division stimulate phage growth. *MicrobioToul Meeting*. Toulouse FR, April 2007. [poster]
17. **Arbiol C, Comeau AM**, Kutateladze M, Adamia R, Krisch HM. **2007**. Initial genome divergence in the T4-like phages: Comparison of the complete genome sequences of two closely related coliphages, Φ1 and RB49. *MicrobioToul Meeting*. Toulouse FR, April 2007. [poster]
16. **Comeau AM**, Tétart F, Trojet SN, Prère M-F, Krisch HM. **2007**. Antibiotics and phage – Phage-Antibiotic Synergy (PAS). *Les Treilles Meeting on The Evolution Diversity and Ecology of the Dark Matter of the Biosphere: Bacteriophages*. Fondation des Treilles. Tourtour FR, March 2007.

[invited seminar]

15. **Comeau AM**, Bertrand C, Letarov A, Tétart F, Krisch HM. 2007. 2 Mb of phage DNA – What is it telling us?: Comparative genomics of the T4-type phages. *Les Treilles Meeting on The Evolution Diversity and Ecology of the Dark Matter of the Biosphere: Bacteriophages*. Fondation des Treilles. Tourtour FR, March 2007. [invited seminar]
14. Comeau AM, Bertrand C, Letarov A, Petrov V, Tétart F, Nolan JM, Karam JD, **Krisch HM.** 2006. Modular architecture of the T4 superfamily: A conserved core genome and a plastic periphery. *EMBO Molecular Microbiology Meeting*. EMBL. Heidelberg DE, October 2006. [invited seminar]
13. Comeau AM, Bertrand C, Letarov A, Petrov V, Tétart F, Nolan JM, Karam JD, **Krisch HM.** 2006. Modular architecture of the T4 superfamily: A conserved core genome and a plastic periphery. *MicrobioToul Meeting*. Toulouse FR, April 2006. [poster]
12. **Comeau AM**, Suttle CA. 2005. Ecology and diversity of marine vibriophage. *MicrobioToul Meeting*. Toulouse FR, May 2005. [poster]
11. **Comeau AM.** 2004. Distribution and diversity of *Vibrio parahaemolyticus* Viruses (VpVs) and their hosts. Canadian Food Inspection Agency. Burnaby BC, December 2004. [invited seminar]
10. **Comeau AM.** 2004. Principles and applications of polymerase chain reaction (PCR) and other emerging technologies. Canadian Food Inspection Agency. Burnaby BC, December 2004. [invited seminar/workshop]
9. **Comeau AM.** 2004. Distribution and diversity of *Vibrio parahaemolyticus* Viruses (VpVs) and their hosts. Department of Microbiology and Immunology, UBC. Vancouver BC, November 2004. [seminar]
8. **Suttle CA**, Lang AS, Tai V, Hardies S, St. John TM, Frederickson CF, Reid K, Culley AI, Comeau AM. 2004. Sequence analysis indicates most viruses in the sea belong to unknown groups. *ASLO Ocean Sciences Meeting*. Honolulu HI, February 2004. [invited seminar]
7. **Comeau AM**, Short SM, Suttle CA. 2003. Strain-typing of viruses using degenerate-primer random amplification of polymorphic DNA (D-RAPD). *American Society for Microbiology General Meeting*. Washington DC, May 2003. [poster]
6. **Comeau AM.** 2002. Vibrio-vibriophage dynamics in the Pacific Oyster (*Crassostrea gigas*). Canadian Food Inspection Agency. Burnaby BC, August 2002. [invited seminar]
5. **Comeau AM**, Suttle CA. 2002. Diversity of a Vibrio-vibriophage system. *ASLO Summer Meeting*. Victoria BC, June 2002. [seminar]
4. Hardies S, Comeau AM, Sewer P, **Suttle CA**. 2002. Genome sequence of a novel marine phage infecting *Vibrio parahaemolyticus*. *ASLO Ocean Sciences Meeting*. Honolulu HI, February 2002. [poster]
3. **Comeau AM.** 2001. *Vibrio parahaemolyticus* and VpVs - Seasonal dynamics and diversity. Canadian Food Inspection Agency. Burnaby BC, August 2001. [invited seminar]
2. **Comeau AM.** and C.A. Suttle. 2001. Seasonal abundance and host range of phages infecting *Vibrio parahaemolyticus* in oysters, sediments, and seawater. *14th Evergreen International Phage Biology Meeting*. Olympia WA, August 2001. [seminar]
1. **Comeau AM.** 1998. BIOLOG kinetics of *E. coli* supplemented communities: Manipulations in species evenness. *8th International Symposium on Microbial Ecology (ISME-8)*. Halifax NS, August 1998. [poster]

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Comeau AM. 1998. Use of the BIOLOG system to characterize changes in species diversity in two freshwater aquatic communities. Acadia University, BScH thesis.

Published Genomes/Sequence Databases

14. Rose SA, Robicheau BM, Tolman J, Fonseca-Batista D, Rowland E, Desai D, Ratten JM, Kantor EJH, **Comeau AM**, Langille MGI, Jerlstrom-Hultqvist J, Devred E, Sarthou G, Bertrand EM, LaRoche J. **2024.** *Candidatus* Thalassolituus haligoni strain BB40. GenBank: NZ_CP139482.
13. Lovejoy C, **Comeau AM**, Thaler M. **2016.** Curated reference database of SSU rRNA for northern marine and freshwater communities of Archaea, Bacteria and microbial eukaryotes, v. 1.1 (2002-2008). *Nordicana D23*, doi: 10.5885/45409XD-79A199B76BCC4110.
12. **Comeau AM**, Arbiol C, Krisch HM. **2013.** *Yersinia* phage PST. GenBank: KF208315.
11. **Comeau AM**, Arbiol C, Krisch HM. **2013.** Vibriophage nt-1. GenBank: HQ317393.
10. Kushkina AI, Tovkach FI, **Comeau AM**, Kostetskii IE, Lisovskiy I, Ostapchuk AM, Voychuk SI, Gorb TY, Romanyuk LV. **2013.** Enterobacteria phage Lw1. GenBank: KC801932.
9. **Comeau AM**, Tremblay D, Moineau S, Krisch HM, Ackermann H-W. **2011.** Vibriophage vB_VchM-138. GenBank: JQ177064.
8. **Comeau AM**, Tremblay D, Moineau S, Krisch HM, Ackermann H-W. **2011.** Vibriophage CP-T1 (vB_VchM-CP-T1). GenBank: JQ177061.
7. **Comeau AM**, Tremblay D, Moineau S, Krisch HM, Ackermann H-W. **2011.** *Aeromonas* phage vB_AsaM-56. GenBank: JQ177063.
6. **Comeau AM**, Kushkina A, Tovkach FI, Krisch HM, Ackermann H-W. **2011.** *Pectobacterium* phage ZF40 (vB_PcaM-ZF40). GenBank: JQ177065.
5. **Comeau AM**, Krisch HM, Ackermann H-W. **2011.** Bdellovibriophage ϕ1422. GenBank: JQ177062.
4. **Comeau AM**, Krisch HM, Ackermann H-W. **2011.** Bdellovibriophage ϕ1402. GenBank: NC_015721.
3. Leblanc C, **Comeau AM**, Sarcos A, Krisch HM. **2008.** Iodobacteriophage phiPLPE. GenBank: NC_011142.
2. Arbiol C, Kutateladze M, Tétart F, Adamia R, Krisch HM, **Comeau AM.** 2007. Enterobacteriophage phi1. GenBank: NC_009821.
1. Hardies S, **Comeau AM**, Serwer P, Suttle C. 2002. Vibriophage VpV262. GenBank: NC_003907.

Awards / Distinctions

2008	**Fondation des Treilles Scientific Prize**	20,000 €
1999	**UBC Faculty of Science Grant Supplement Award**	$12,000 over 12 months
1999	**NSERC Postgraduate Scholarship (PGS A)**	$34,600 over 24 months
1999	**UBC University Graduate Fellowship**	rescinded due to above PGS A
1994	**Le Club de Lions de Clare Bursary**	$500

1993	**Interchange on Canadian Studies Delegate**	Selected as one of 12 Nova Scotian high-school representatives

Languages

Fluent in French (paternal), English (maternal), and Spanish. Rudimentary ability in Italian and German (1st-year university level).

Relevant Skills

Experimental

- Culture of microorganisms – bacteria, viruses, phytoplankton, fungi
- Environmental microbial ecology – isolations, molecular techniques (PFGE, DGGE), ultrafiltration
- Molecular biology and genetics techniques – PCR, qPCR, dPCR, cloning, expression systems, Southern hybridization, separation gradients, etc.
- Sequencing – traditional Sanger and NGS pyrosequencing/Illumina/PacBio/MinION
- Epifluorescent and transmission electron microscopy – sample preparation and observation
- Liquid-handling robotics (QIAGEN+Hamilton) – operation and programming

Related

- Bioinformatics – genomic and network (Cytoscape) analyses, protein modeling (Chime, Swiss-Model), phylogeny, NGS metagenomics (ex: Kraken2, MMseqs2, etc.), NGS analysis for microbial ecology (Mothur, QIIME2), genomics (ex: assembly, hybrid assembly, SNP analysis, etc.) and bash scripting
- Chemical and biohazard safety training (Level 2)
- Oceanographic research cruise equipment operation (CTD, coring, etc.) and planning
- PC-based software – word processors, spreadsheets, statistical packages, databases, etc.
- Programming HTML; Retool + mySQL design; operational/server Linux; developing/maintaining websites; PC construction, maintenance and repair

Personal Interests

Architectural and landscape photography; Astronomy and astrophotography; Digital painting, design and 3D printing; World history and politics; Egyptology; Acadian culture and genealogy; Language studies; Website design; Exploring new software and computer construction; Strategy games; Recreational curling and golf.