Keynote Lecture

Dr. Ed Yong, Science Writer for the Atlantic. Author of “I Contain Multitudes: The Microbes Within Us and a Grander View of Life.”

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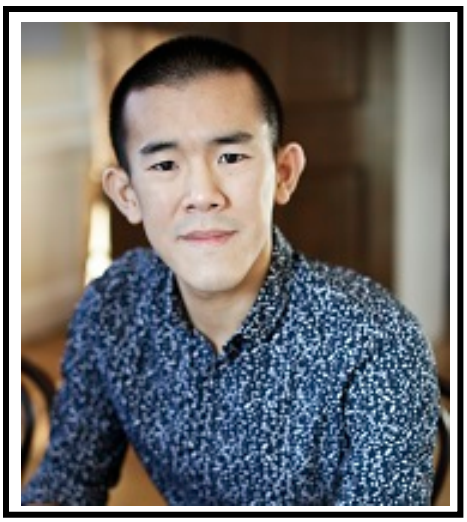

Ed Yong is a science writer who reports for The Atlantic, on topics such as microbes, animal behavior, science policy, paleontology, and reproducibility in science. His writing has also appeared in National Geographic, New Yorker, Wired, Nature, New Scientist, Scientific American, and more. He has won the National Academies Keck Science Communication Award in 2010, the Byron H. Waksman Award for Excellence in the Public Communication of Life Sciences in 2016, and 10 other awards. "I CONTAIN MULTITUDES", his first book, looks at the amazing partnerships between animals and microbes. It was a New York Times bestseller, and was listed in best-of-2016 lists by the New York times, NPR, the Economist, the Guardian, and more.

No One Has To Read This Crap: A Guide to Telling Stories About Science

Ed YONG, Science Writer for the Atlantic, Washington, USA

Science writing isn't about translating papers. It's about telling stories. Science writer **Ed Yong** will deconstruct some of his own work to show why good science writing matters, why it's hard, and how to do it.

Keynote Lecture

Dr. Barbara Sherwood Lollar, University of Toronto, Toronto, ON
2016 NSERC John C. Polanyi award recipient; 2016 Companion to the Order of Canada

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Dr. Barbara Sherwood Lollar, C.C. FRSC is a University Professor in Earth Sciences at the University of Toronto. She is Research Chair in Isotopes of the Earth and Environment, Director of the Stable Isotope Laboratory, and Past-President of the Geochemical Society. She was named a Fellow of the American Geophysical Union in 2015. Sherwood Lollar has published extensively in research on stable isotope geochemistry and hydrogeology, the fate of carbon-bearing fluids and gases such as CO_2, CH_4, and H_2 in ancient fracture waters in the Earth's crust, and the role of deep subsurface microbial populations in carbon cycling. She has been a recipient of many academic awards (including the NGWA Darcy Lecturer, Steacie, Killam and NSERC Accelerator Awards) and most recently the 2012 Eni Award for Protection of the Environment, 2012 Geological Society of America Geomicrobiology and Geobiology Prize, and 2016 NSERC John Polanyi Award. Sherwood Lollar was selected in 2000 by Time Magazine Canada for their feature on "Leaders for the 21st Century" and by Canadian Geographic in 2013 for their list of Ten Canadians "Changing the World", along with and Astronaut Chris Hadfield.

"Follow the Water": Exploring the deep hydrogeosphere and the subsurface terrestrial biosphere

Barbara SHERWOOD LOLLAR, University of Toronto, Toronto, ON

Although the deep subsurface biosphere in the oceans and marine crust has been investigated for decades, the subsurface microbiology of terrestrial systems is undergoing a recent expansion, in particular to include the > 70% of the continental lithosphere comprised of Precambrian rocks - the oldest rocks on Earth. Rich in reduced dissolved gases such as CH_4 and H_2, fracture waters in Precambrian rocks on the Canadian Shield, Fennoscandian Shield, and Southern Africa have been shown to host extant microbial communities of chemolithoautotrophs dominated by H_2-utilizing sulfate reducers and, in some cases, methanogens. Recent estimates of global H_2 production via water-rock reactions (including radiolysis and hydration of mafic/ultramafic rock, e.g. serpentinization) show that the Precambrian continents are a source of H_2 for life, on par with H_2 production estimates for water-rock reactions from the marine lithosphere. To date, this extensive deep terrestrial habitable zone has been significantly under-investigated compared to the marine deep biosphere. Underground research laboratories and mines provide access to the deep subsurface in Precambrian settings worldwide, and targets for investigation of extant microbial ecosystems. Kidd Creek Mine located in Timmins Ontario on the Canadian Shield is an iconic site. Investigation of fracture fluids here to 3 km revealed H_2 production via radiolysis and serpentinization; production of methane and higher hydrocarbons via abiotic organic synthesis; and fracture fluids with mean residence times on the order of a billion years. Recently, investigation of the sulfur cycle in these fluids has revealed a mass independent sulfur isotope signature in the dissolved sulfate, whereby oxidants from radiolysis oxidize Archean sulfide minerals, providing a mechanism to supply both electron donors (H_2) and electron acceptors (sulfate) to fuel a deep microbial biosphere. Recent MPNs results demonstrate the presence of sulfate-reducing bacteria in these waters in the present day. The deep levels at this site are providing access to international teams of researchers to collaborate with the University of Toronto in a multi-year program to characterize the deep carbon, hydrogen, nitrogen, and sulfur cycles, as terrestrial geobiology continues to expand our understanding of the habitability of the Earth.

Fisher Award Recipient

Dr. Étienne Yergeau, INRS-Institut Armand Frappier, Laval, QC

Étienne Yergeau completed his B.Sc. in biological sciences with a specialization in plant biology and biotechnology at the Université de Montréal in 2002. He then obtained a M.Sc. under the supervision of Marc St-Arnaud at the Université de Montréal for his research on the fungal diseases of asparagus. He then joined the team of George Kowalchuk in the Netherlands where he obtained his Ph.D. from the Free University of Amsterdam in 2008 for his thesis on the consequences of global warming on Antarctic soil microorganisms. Étienne joined the team of Charles Greer as a postdoctoral fellow and worked on the microorganisms involved in the remediation of contaminated soils. In 2013, he was recruited as a research scientist by the National Research Council of Canada. He later joined the faculty of the Centre INRS-Institut Armand-Frappier in January 2016. The vision of "Le Labo Yergeau" is that the plant microbiota can be reengineered to promote specific plant phenotypes, potentially generating solutions to many real-life problems like climate change, contaminated soils, and declining food production. In the mid-term, the research program of “Le Labo Yergeau” is aimed at finding new approaches to purposefully, reliably, and sustainably enhance the beneficial microbiota of important crops.

Understanding and manipulating the plant holobiont

Étienne YERGEAU, INRS-Institut Armand Frappier, Laval, Quebec

Plants and their microbiota form and inseparable entity known as a holobiont. The concept of the hologenome (all the genomes of the holobiont) as an evolutionary unit suggests mechanisms that could be harnessed to rapidly evolve/adapt holobionts. For this presentation, I will discuss recent studies aimed at understanding and manipulating the microbial part of the plant holobiont. More specifically, I will: 1) compare the capacity of various plant genotypes to recruit beneficial microorganisms under stressful conditions, 2) contrast the effects of the plant genotype and the environment on the stress response, and 3) show that manipulating the microbiota can modify the phenotype of the host plant. Globally, my research shows that it is possible to modify the plant holobiont through microbiota manipulation, highlighting the central role of microbes in plant phenotypic plasticity. More research will be however necessary to completely understand the mechanisms involved and apply them for increasing crop yields, for example.

Armand-Frappier Outstanding Student Award Recipient

Dr. George diCenzo, McMaster University, Hamilton, ON

Sponsored by Candian Society of Microbiologists

Dr. George diCenzo completed his B.Sc. in Molecular Biology and Genetics at McMaster University in 2012. He has completed his PhD training in the lab of Dr. Turlough Finan at McMaster University. He is now beginning a postdoctoral fellowship in the group of Dr. Alessio Mengoni at the University of Florence in Italy. His research focuses on understanding the genetics and metabolism of the bacterium *Sinorhizobium meliloti*, a model species for the study N_2-fixing plant symbionts. His work has involved the use individual genes, and *in silico* genome-scale metabolic network reconstruction. Using this multi-faceted approach, his work has contributed to the understanding of the evolution and role of the complex *S. meliloti* genome structure, characterization of genes important for an effective symbiotic relationship or for competitive fitness as a free-living organism, and the development of wet-lab and *in silico* genomic resources for further characterization of these processes. In the long term, he hopes to develop novel strategies for engineering of rhizobium – legume symbioses, as well as for producing synthetic N_2-fixing symbioses with non-legume plants.

Experimental and *in silico* guided approaches to engineering the rhizobium – legume symbiosis.

George DICENZO, McMaster University, Hamilton, ON

Rhizobia are bacterial species capable of fixing atmospheric nitrogen gas to ammonium in symbiosis with a plant host. Symbiotic nitrogen fixation (SNF) is an agriculturally and ecologically important process, but unfortunately we are unable to harness the full power of this biological process in agricultural systems. Our group studies *Sinorhizobium meliloti*, a symbiont of legumes such as alfalfa, whose genome consists of a 3.7 Mb chromosome as well as the secondary 1.7 Mb pSymB and 1.4 Mb pSymA replicons. In this talk, I will describe our development of experimental and *in silico* resources for the study and engineering of SNF. We have developed a genetic background strain for identification of the core genetic chassis required for SNF. This involved the cloning and stable re-introduction of a 69-kilobase region into the *S. meliloti* chromosome that translocated to the pSymB replicon in a recent ancestor, followed by the reduction of the *S. meliloti* genome by 45% through the complete removal of pSymA and pSymB. In order to localize all single-copy genes essential for SNF on pSymA/pSymB, we produced a library of large-scale (50-800 kilobases) defined deletion on these replicons, and screened these deletion mutants for symbiotic phenotypes with alfalfa. We found that most regions of pSymA could be removed with no apparent effect on the rate of SNF, and we have constructed deletions of greater than 50% of each replicon without abolishing symbiotic abilities. Indeed, less than 12% of each replicon was absolutely essential for SNF with alfalfa, and these regions are currently serving as our initial target of a minimal symbiotic genome. Through the above described screen and follow-up genetic studies, a previously uncharacterized gene (smb20752) encoding a putative 3-hydroxyisobutyryl-CoA hydrolase, was identified as required for efficient SNF. Strikingly, deletion of the orthologous gene in *Sinorhizobium fredii* NGR234 completely abolished SNF. Moreover, the screen described above led us to determine that the BacA protein of *S. meliloti* is specialized to support symbiosis with plants of the genus *Medicago*, and that the BacA proteins of the closely related species (*S. fredii* or *Rhizobium leguminosarum*) cannot fulfil this function. Complementing this experimental approach, we performed a S. meliloti genome-scale metabolic network reconstruction for modelling metabolism and metabolic consequences of gene mutations in free-living and symbiotic cells. The metabolic reconstruction accounts for 1575 genes, it is constantly being improved through manual curation, and can serve as a platform for the coherent integration of systems-level datasets. Through growth simulations with flux balance analysis, we have examined the genetics involved in high fitness colonization of bulk soil, the rhizosphere, and SNF. Ongoing work involves using *in silico* simulations to identify targets for biotechnological manipulation to improve the symbiosis.

CSM Murray Award for Career Achievement Recipient

Dr. Sylvain Moineau, Université Laval, Quebec, QC

Professor Sylvain Moineau graduated with a BSc degree in Microbiology from the Université Laval in 1987. He continued at the same university but in Food Sciences, where he obtained his PhD in 1993 for his studies investigating phages biology. During his PhD, he also spent 18 months at North Carolina State University. He then undertook an industrial postdoc in Florida within a division of the multinational Unilever. In 1996, he moved back to Canada and the University Laval as an Assistant Professor in Microbiology to work on phage biology and resistance mechanisms in lactic acid bacteria. His was appointed full Professor of Microbiology in 2005 and since 2011, he holds the Canada Research Chair in Bacteriophages. Since 2002, he is also the Curator of the Félix d'Hérelle Reference Center for Bacterial Viruses, the world largest collection of reference phages (www.phage.ulaval.ca). Over the years, Professor Moineau has won numerous teaching and research awards and he has developed one of the leading international phage research programs. Prof. Moineau's team has made a number of landmark discoveries that have changed our views of phage-host interactions, including his work on CRISPR-Cas systems. In 2016, Prof. Moineau was awarded the Flavelle Medal by the Royal Society of Canada for his outstanding contribution to biological sciences. In 2017, he won the NSERC John C. Polanyi Award for his Canadian-based research that led to an outstanding advance in natural sciences. Professor Moineau was also on Thomson Reuters's list of highly cited researchers in the Microbiology Category for the last three years (2014, 2015, 2016).

CRISPR-Cas systems: from humble beginnings to today's headlines

Sylvain MOINEAU, Université Laval, Quebec, QC

This year marks the 100th anniversary of the publication by Félix d'Hérelle entitled: An invisible microbe that is antagonistic to the dysentery bacillus (Comptes Rendus de l'Académie des Sciences 165:373-375). With it, the field of phage biology was born. Viruses are now recognized at the most abundant biological entities on the planet and display a remarkable genetic diversity. Not surprisingly, bacteria have a plethora of diverse defense mechanisms to combat their phages. Four decades after the discovery of one such defense mechanism, restriction enzymes, another bacterial anti-phage system that cleaves foreign DNA was identified—one that acts as an adaptive immune system. Clustered regularly interspaced short palindromic repeats (CRISPR) and their associated *cas* genes protect microbial cells against infection by foreign nucleic acids, including phage genomes and plasmids. Bacterial CRISPR-Cas type II systems function by first incorporating short DNA "spacers", derived from invading phage genomes or plasmid sequences, into a CRISPR array located in their genome. This step is known as adaptation or vaccination. The CRISPR array is then transcribed and matured into short RNAs (the maturation step), which, by recruiting a Cas endonuclease, act as surveillance complexes that recognize and cleave invading matching sequences (the interference step). The cleavage occurs near a short motif, called the PAM, adjacent to the sequence targeted by the spacer. Phages can bypass the protection provided by CRISPR-Cas through point mutations, deletions, or the production of anti-CRISPR proteins. Exploiting this system has also resulted in the development of the much-publicized CRISPR-Cas9 technology for precise genome manipulation of various organisms. This presentation will recall the roles played by phages in the discovery and understanding of CRISPR-Cas systems. In addition, I will highlight the use of CRISPR-Cas9 technology for viral genome editing in order to better understand phage-host interactions.

CSM Recognition Award Recipient

Dr. Raina Fyson, University of Ottawa, Ottawa, ON

Raina Fyson (nee Yanda) (1929 Saskatoon SK). Received from University of Alberta BSc (Chemistry) in 1950, MSc (Medical Bacteriology) in 1952. Instructor in Bacteriology (Medicine) (1952-53), responsible for laboratory teaching and course for nurses. A predominately academic career was initiated, focusing on human pathogens, immunity and microbiota. Lecturer, Regina College, University of Saskatchewan, (1953-57), taught comprehensive 10 month Bacteriology course (basic, human pathogens, clinical, mycology, parasitology) to BSc (Med Lab Tech) students and nurses. University of Ottawa Microbiology and Immunology (1962-90). TA for med student labs. PhD (1966-72/73) re antigenic relationships and reservoirs of influenza A viruses (human, animal, avian) using IDD. Avian (duck) virus cross reacted broadly with other strains.MRC Postdoctoral trainee (1973-74) in M. Richter's Lab for CMI research. Assistant Professor in Microbiology and Immunology (1975-83). Introduced South African problem solving approach to med student labs. Resumed influenza research (1976-83). Initiated by colleague Dr. E Perry, "Response to Influenza Vaccines in the Aged", in St. Vincent Hospital, Ottawa (1976-1983) revealed that annual influenza immunization of the aged and chronically ill was >90% protective on epidemic challenge in 1982-83, promoting adoption by Canadian health authorities of annual immunization for this group. Consulting Microbiologist, Ethiopian Central Public Health Laboratory, NAHRI (1984). Part time Academic, Biology Department, University of Ottawa (1986-90). Conducted introductory and applied microbiology courses. Canadian Government Contracts for Biotechnology (1989-95): Environment- (1) for safety guidelines in labs; Health- (6) for effect on human health focusing on risk assessment and potential pathogens. Worked with founders of Biological Implications of Pathogenicity (B.I.O.P.), Drs. M. Goldner and J. De Repentigny (1978-2005), to further understand pathogenicity through annual symposia and collaboration. CCM member and Director (1988-90,-92-93) (editorial, education, awards, exam committees). ASM (emeritus). Career Mentorship (1995-2008), University of Ottawa, promoting microbiology to students. Follow microbial tenets: opportunistic – adaptable – persistent for success and survival.