SECOND INTERNATIONAL CONFERENCE ON CLINICAL METAGENOMICS (ICCMg)

Campus Biotech, Geneva, October 19-20, 2017
www.clinicalmetagenomics.org

Welcome

Welcome to Geneva for the second edition of the International Conference on Clinical Metagenomics! Last year in October, we hold the first ICCMg which was a success with more than 150 attendees from all over the world and a panel of internationally-renowned speakers. Truly, a new field that we refer to as clinical metagenomics is emerging, and the objective of ICCMg is to accompany this wave. ICCMg indeed aims at being the place where every year, clinicians, microbiologists, scientists, bioinformaticians, private companies and others shall meet, present their work, discuss, network and create new grounds for developing clinical metagenomics. Such opportunities are hard to create in international, multidisciplinary meetings that currently leave little space for clinical metagenomics. Hence, we believe that ICCMg fills the needs for the emerging clinical metagenomics community.

For this second edition, we kept what had worked for ICCMg1 i.e. a panel of excellent speakers, the location at Campus Biotech easily accessible from the airport and the train station, not forgetting the wonderful dinner at Vieux-Bois restaurant. In addition, we listened to the expectations of ICCMg1 attendees and introduced lectures from selected abstracts. We are also proud to offer the first ICCMg prize with the support of the Swiss Society of Microbiology and another prize offered by the American Society for Microbiology. Also, we are delighted to offer sponsorship for early career scientists with the support of the Federation of European Microbiology Societies (FEMS).

We hope that ICCMg2 will contribute to the development of clinical metagenomics at different levels, since several scientific and regulatory obstacles have to be tackled before it can enter in routine laboratories. Nonetheless, we are getting closer and closer so let's see how the future of clinical metagenomics looks like during these two days, and let's meet next year for ICCMg3!

For the International Society of Clinical Metagenomics

Jacques Schrenzel

Etienne Ruppé

Program
Thursday 19 October

10.45 **Welcome speech**
Welcome speech from Jacques Schrenzel, head of the bacteriology laboratory of the Geneva University Hospitals and co-organizer of the ICCMg2.
Jacques Schrenzel, Geneva, Switzerland

Update in sequencing and bioinformatics

11.00 **From yesterday to tomorrow: past, present and future of sequencing**
An overview of the thrilling advances in sequencing during the last decade by Laurent Farinelli, a co-inventor of the DNA sequencing method currently used in Illumina sequencers.
Laurent Farinelli, Geneva, Switzerland

11.30 **Critical Assessment of Metagenome Interpretation**
Always wondered whether an assembler or a taxonomy classifier was performing better over another one? Some responses from the CAMI project.
Alice McHardy, Düsseldorf, Germany

12.00 **On the importance of databases**
Clinical metagenomics relies on bioinformatic tools that dig into various databases. How to cure, update and maintain them? What are the right reference set for clinical studies? Answers from the Swiss Institute of Bioinformatics.
Philippe Lemercier, Geneva, Switzerland

12.30 **Lunch break**
After an introduction to sequencing and bioinformatics, let's enjoy the buffet and get ready for the afternoon.

Regulatory issues raised by clinical metagenomics

14.00 **Experience of the development of iDTECT, the first NGS based CE-IVD test for pathogen detection**
Setting up a clinical metagenomic pipeline is not just a scientific issue. Quality is crucial! The experience of a clinical metagenomics start-up.
Pascale Beurdeley, Paris, France

14.30 **Experience from an academic: QC in clinical metagenomics pipeline**
The experience of an academic laboratory.
Steve Miller, San Francisco, USA

15.00 **Potential approaches to validation of sequencing based assays (video-conference)**
The point of view from regulatory agencies.
Kristian Roth, Rockville, USA

15.30 **Coffee break**
If the video conference has worked without trouble, we shall have some time to grab a bit of cafeine before the last session.

Clinical metagenomics (I)

16.15 **Clinical metagenomics: our real-life experience**
Feedback from a pioneer on validation and implementation of a clinical metagenomic assay for diagnosis of infectious diseases in acutely ill hospitalized patients.
Charles Chiu, San Francisco, USA

16.45 **Selected abstract:**
Rapid metagenomic diagnosis of pneumonia
First talk about clinical metagenomics of pneumonia (there will be others).
Justin O'Grady, Norwich, UK

17.00 **Clinical metagenomics of dermohypodermitis**
The application of deep sequencing to dermohypodermitis samples: comparison with conventional methods and 16S profiling.
Christophe Rodriguez, Créteil, France

17.20 **Title not communicated yet (surprise!)**
Rita Colwell, Rockville, USA

17.50 **ICCMg awards!**
The ICCMg/SSM and ASM prizes for best posters will be awarded.

17.55 **ICCMg/SSM prize lecture: Virus transmission during kidney transplantation assessed by virome analysis of living donor and recipient**
Among submitted abstracts, this one has been selected to get the ICCMg/SSM prize and has the hard task to be the last presentation before drinks.
Verena Kufner, Zurich, Switzerland

18.10 **Poster session**
Let's discover the ICCMg2 posters, discuss with their authors and network. Wine, other drinks and apetizers will be served.

20.00 **Dinner at the Vieux Bois restaurant**
We will have dinner at the Vieux Bois restaurant, located at a 10-minute walk from ICCMg. Conveniently located next to the United Nations, in the beautiful Ariana's park. Let's hope that it will not rain on the way like it did last year (bring your umbrella).

Program
Friday 20 October

Antibiotic resistance

9.00 **Understanding and Combatting Resistome Exchange Across Commensal, Environmental, and Pathogenic Microbes**
Let's start the day with the exploration of the antibiotic resistome from various environments.
Gautam Dantas, Saint Louis, USA

9.30 **Wrap up of the NGS/EUCAST consultation**
Is next-generation sequencing a realistic approach for inferring an antibiogram from genomic data today? Tomorrow? for all bacteria/antibiotics?
Matthew Ellington, London, UK

10.00 **Selected abstract: NGS for characterization of clinical class 1 integrons from hospital effluents**
How integrons have invented mass tourism for antibiotic resistance genes.
Olivier Barraud, Limoges, France

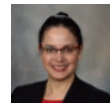
10.13 **Selected abstract: clinical metagenomics in endophthalmitis**
Let's keep our eyes wide open for this presentation.
Sünje Johanna Pamp, Lyngby, Denmark

10.26 **Selected abstract: Detection of previously missed pathogens in immunocompromised children with suspected pulmonary infections by a fully-validated metagenomics-based test**
Clinical metagenomics in pneumonia again! And not the last one.
Robert Schlaberg, San Francisco, USA

10.40 **Coffee break**
Let's charge batteries with drinks and sweets.

Clinical metagenomics (II)

11.15 **Clinical metagenomics in bone and joint infections**
How the next-generation sequencing of bone and joint infection samples can support or even replace conventional methods.
Robin Patel, Rochester, USA



11.45 **Nanopore sequencing of urine samples**
How the Nanopore technology allows the ultra-fast sequencing of urine samples and the identification of pathogens and their antibiotic resistance traits.
Katarzyna Schmidt, Norwich, UK

12.05 **Clinical metagenomics of hospital-acquired pneumonia**
The last talk about clinical metagenomics in pneumonia (promised!)
Sébastien Hauser, Grenoble, France

12.30 **Lunch break**
Let's enjoy the buffet under the amazing glass roof of the Campus Biotech.

Microbiota and metagenomics

14.30 **So what? Clinical impact of microbiome studies**
More than ten years after after the next-generation sequencing revolution and the thrilling advances in the understanding of our microbiota, what are the concrete consequences in medicine that can be expected?
Oluf Pedersen, Copenhagen, Denmark

15.00 **The blood microbiome in health and disease**
Bugs in blood? New insights from metagenomics.
Peter Gyarmati, Peoria, USA

15.30 **Metagenomics: Think before you speak**
Metagenomics generate tremendous amount of data, but what about interpretation? We shall still have some work to do.
Patrick Veiga, Palaiseau, France

16.00 **Selected abstract: Clinical Metagenomics applied to human mummified remains – Reconstruction of a 5,300-year-old Helicobacter pylori genome from the Iceman's stomach**
Introducing paleo-clinical metagenomics.
Frank Maixner, Bolzano, Italy

16.20 **Conclusive speech**
Etienne Ruppé co-organizer of the ICCMg2 closes the conference in wrapping up the main messages given during ICCMg2.
Etienne Ruppé, Paris, France

The FEMS sponsorships laureates

The Federation of European Microbiology Societies (FEMS) supported the attendance of ICCMg2 for 23 early career scientists.

Here they are:
Mr Olivier Barraud, Limoges France
Mr Sylvère Bastien, Lyon, France
Ms Coralie Bouchiat, Lyon, France
Ms Oana Dumitrescu, Lyon, France
Ms Christina Gabrielsen, Trondheim, Norway
Mr Christophe Ginevra, Lyon, France
Mr Thomas Gurry, Cambridge, Usa
Ms Iva Kotaskova, Brno, Czech Republic
Mr Jason Kwong, Melbourne, Australia
Mr Sacha Laurent, Lausanne, Switzerland
Ms Patrícia Martins Simoes, Lyon, France
Mr Andre Mu, Melbourne, Australia
Ms Saskia Neuert, Norwich, UK
Mr Justin O'grady, Norwich, UK
Mr Onya Oppota, Lausanne, Switzerland
Ms Sünje Johanna Pamp, Lyngby, Denmark
Mr Francesco Paroni Sterbini, Roma, Italy
Mr Gianenrico Rizzati, Rome, Italy
Mr Venkat Subramaniam Rathinakannan, Turku, Finland
Ms Adriana Sananria-Moreno, Tromsø, Norway
Mr Leonard Schuele, Groningen, Netherlands
Ms Petra Videnska, Brno, Czech Republic
Ms Fathiah Zakham, Lausanne, Switzerland

Congratulations to all of them!

The awards:
congrats to our laureates!

ICCMg/SSM award

The first ICCMg/SSM (Swiss Society for Microbiology) prize was awarded to Ms Verena Kuffner (Zurich, Switzerland) for her work entitled "Virus transmission during kidney transplantation assessed by virome analysis of living donor and recipient".

Verena Kufner is a PhD student in Prof. Alexandra Trkola's group at the Institute of Medical Virology at the University of Zurich. Her work focuses on metagenomic high-throughput sequencing of viral pathogens applied to clinical specimens. More specifically, by establishing and validating the metagenomic approach for virus analysis in diverse clinical samples, virome characteristics associated with immunocompromised individuals can be analyzed for improved infectious disease diagnostics and management.

Ms Kufner will receive her 1,000 CHF prize on October 19 at 5.50 pm and will present her work.

ASM Award

The ASM award was awarded to Ms Mónika Számel (Szeged, Hungary) for her work entitled "Genetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiome".

Mónika Számel got her bachelor's degree as a cell and molecular biologist at the University of Szeged. In 2014, she joined the Synthetic and Systems Biology Unit of Csaba Pál at the Biological Research Centre of the Hungarian Academy of Sciences where she started working in the topic of antimicrobial resistance. In 2016, she obtained her Master's degree as a molecular and immunobiologist. In this September, she just started her PhD at the University of Szeged with the supervision of Csaba Pál and Bálint Kintses. Her main fields of interests are antimicrobial resistome research and antimicrobial peptides.

Ms Számel will receive a 200 USD credit on the ASM bookstore and a complimentary ASM membership on October 19 at 5.50 pm.

AMERICAN SOCIETY FOR MICROBIOLOGY

Invited Speakers

Pascale Beurdeley (Paris, France)
Dr. Pascale Beurdeley is the Chief Scientific Officer of Pathoquest. She has 20 years experience in the biotechnology industry. Prior to joining PathoQuest, Dr. Beurdeley held several positions at DiaxonHit (formerly ExonHit Therapeutics) with increasing responsibilities from Group Leader R&D to Executive Director R&D, Genomics. Prior to joining ExonHit Therapeutics, Dr. Beurdeley held a researcher position in the translational medicine department at the Curie Institute. Dr. Beurdeley is graduated from the University Louis Pasteur (Strasbourg) and holds a Ph.D in Molecular and Cell Biology. She completed her training as a postdoctoral fellow at Magainin Pharmaceuticals Inc, focusing on her interest in antimicrobial peptides.

Charles Chiu (San Francisco, USA)
Charles Chiu, M.D./Ph.D. is an Associate Professor of Laboratory Medicine and Medicine, Division of Infectious Diseases at University of California, San Francisco, Director of the UCSF-Abbott Viral Diagnostics and Discovery Center (VDDC), and Associate Director of the UCSF Clinical Microbiology Laboratory. He is a board-certified consulting infectious diseases physician at UCSF, and a practicing infectious diseases physician and clinical microbiologist. Dr. Chiu obtained an MD and PhD in biophysics from UCLA and subsequently completed an internal medicine residency, infectious diseases fellowship, and postdoctoral research at UCSF.He heads a translational research laboratory engaged in clinical next-generation sequencing assay development for diagnosis of infectious diseases, pathogen discovery, bioinformatics software development, nanopore sequencing, and characterization of emerging infections (Lyme disease, enterovirus D68, and Zika virus).

Rita Colwell (Rockville, USA)
Rita Colwell is a Distinguished University Professor both at the University of Maryland at College Park and at Johns Hopkins University Bloomberg School of Public Health, senior advisor and chairman emeritus at Canon US Life Sciences, Inc., and president and CEO of CosmosID, Inc. Her research interests are focused on global infectious diseases, water, and health. Pr. Colwell is currently developing an international network to address emerging infectious diseases and water issues, including safe drinking water for both the developed and developing world. She has held many advisory positions in the U.S. government, nonprofit science policy organizations, and private foundations, as well as in the international scientific research community. Colwell is a nationally-respected scientist and educator, and has authored or co-authored 17 books and more than 750 scientific publications. She produced the award-winning film, "Invisible Seas," and has served on editorial boards of numerous scientific journals. She founded the company CosmosID in 2008.

Gautam Dantas (Saint Louis, Missouri)
Gautam Dantas is associate professor of pathology and immunology, and biomedical engineering at the Washington University School of Saint Louis. Using metagenomics and functional metagenomics, he studies the ecology, evolution and transmission dynamics of microbes and their antibiotic resistance genes across multiple habitats, towards building better predictive models of resistance selection and dissemination. He conducts such investigations in both resource-rich and resource-poor settings in the U.S., Central America, South America and Africa, to elucidate the impact of features such as geography, cultural traditions, access to clean water, food and health care, population density, and disease endemicity on the exchange of microbes and their resistance genes between interconnected ecologies.

Matthew Ellington (London, UK)
Dr Ellington is a research active clinical scientist with broad experience in HCAI organisms. He has 15 years experience at the clinical / research interface in reference and frontline clinical laboratories with a specific and consistent focus on the molecular epidemiology of antimicrobial resistance among "ESKAPEE" pathogens. Dr Ellington's expertise in investigating the factors underpinning antimicrobial resistance and supports his involvement with the European Committee on Antimicrobial Susceptibilty Testing (EUCAST) subcomittee on WGS for AST, as well as his recent appointment to the British Society for Antimicrobial Chemotherapy (BSAC) standing committee on antimicrobial susceptibility testing.

Laurent Farinelli (Geneva, Switzerland)
Laurent Farinelli was the co-inventor in the mid 90s of the DNA clustering technology that was essential for the development of next-generation sequencing. Then, he founded Fasteris, a pioneering sequencing company based near Geneva. Fasteris was the first service provider in the world to acquire an Illumina sequencer in 2006 (then called Solexa). Today, Fasteris provides services for research laboratories, industries and pharma clients as well as offering services in medical diagnostics. Fasteris shares co-author of more than 100 publications since 2007 and is cited in hundreds.

Peter Gyarmati (Peoria, USA)
Peter Gyarmati is Assistant Professor at the University of Illinois College of Medicine at Peoria, currently focusing on microorganisms (bacteria, fungi, viruses) in patients with childhood leukemia, with the aim of identifying and characterizing infectious agents in systemic infections with metagenomics. Before, he did several post-doc fellowships at Karolinska Institutet, the University of Kentucky and the Science for Life laboratory.

Sébastien Hauser
Sébastien HAUSER (PhD) is staff scientist in molecular biology at bioMérieux in Grenoble (France). After his PhD, he spent 7 years in service laboratories and small companies to develop protocols and standards for application of real-time PCR and DNA Chip to clinical diagnostics and food safety control. He joined bioMérieux in 2007 where he evaluated the feasibility of various molecular technologies for the development of clinical diagnostic. Since 2015 he is working on the feasibility of clinical metagenomics for the diagnostic of Hospital Acquired pneumonia in collaboration with the Hôpitaux Universitaires de Genève (HUG).

Alice McHardy (Düsseldorf, Germany)
Alice McHardy studied biochemistry from 1995 to 2000 at Bielefeld University. She obtained a PhD in computational biology in 2004 and then worked as a postdoc at the Center for Biotechnology at Bielefeld University. From 2005-2007 she worked as a postdoc and then as a permanent staff member in the Bioinformatics and Pattern Discovery Group at the IBM T.J. Watson Research Center in Yorktown Heights, USA. She then became the head of "Computational Genomics and Epidemiology" group at the Max Planck Institute for Computer Science in Saarbrücken. In 2010 Alice McHardy became the chair of the Department for Algorithmic Bioinformatics at Heinrich Heine University in Düsseldorf. Since 2014 she is the head of the Computational Biology of Infection Research Group at the HZI.

Steve Miller (San Francisco, USA)
Steve Miller MD, PhD is Director of the Clinical Microbiology Laboratory at the University of California San Francisco and Associate Professor in the Department of Laboratory Medicine. Dr. Miller trained at the Albert Einstein College of Medicine in Bronx, New York. His research involves translation of novel molecular methods for diagnosis and monitoring of clinical infectious disease, with over 40 publications. Dr. Miller has received several grants to provide clinically actionable results from large sequence data sets, including the California Initiative to Advance Precision Medicine project for clinical implementation of metagenomic next-generation sequencing for precision diagnosis of acute infectious diseases.

Robin Patel (Rochester, USA)
Robin Patel, M.D., is the director of the Infectious Diseases Research Laboratory. In the research laboratory, she and her colleagues focus on biofilms. Biofilms cause a large number of infections in modern clinical practice, such as prosthetic joint infection and endocarditis. Dr. Patel and her team are unraveling the process of biofilm formation and resistance of biofilms to antibiotics. They are developing new and improved diagnostic tools and treatment strategies for biofilm-associated infections. Her group uses in vitro studies as well as animal models of infection for their studies. Dr. Patel is also the chair of the Division of Clinical Microbiology and the director of its Bacteriology Laboratory. In this state-of-the-art clinical facility, she and her colleagues develop and deploy cutting-edge assays for clinical detection of bacteria, identification of bacteria, and characterization of antimicrobial resistance and susceptibility.

Oluf Pedersen (Copenhagen, Denmark)
Oluf Pedersen is a group Leader at Section of Metabolic Genetics, Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Denmark (DK) (www.metabol.ku.dk) and Professor of Metabolic Genetics, Faculty of Health and Medical Sciences, University of Copenhagen. Oluf Pedersen and his research team contribute to gain novel insights into the complex and multifactorial aetiology of type 2 diabetes, obesity and cardiovascular disorders – scientific efforts that aim for novel approaches to prevent and treat these common disorders which are in epidemic growth.

Christophe Rodriguez (Créteil, France)
Christophe Rodriguez is associate professor in the microbiology laboratory of the Henri Mondor hospital near Paris, where he leads the next-generation sequencing platform. He is now moving to the application of metagenomics for identifying bacterial, fungal and viral pathogens from clinical samples.

Kristian Roth (Rockville, USA)
Kristian Roth, Ph.D. is the Branch Chief in the Bacterial Respiratory and Medical Countermeasures Branch FDA/CDRH/OIR/DMD. He received his Ph.D. in analytical chemistry from the University of California Riverside then completed a postdoc at the University of California Santa Barbara. Afterward he moved to the Seattle area to join CombiMatrix, a startup diagnostics company targeting infectious diseases using DNA microarray detection. There, he worked on developing nucleic acid amplification assays for the detection and differentiation of influenza using microarrays. Dr. Roth then moved to the Maryland area to join Meso Scale Discovery developing lab based and POC capable platforms for the detection of influenza antigen, Hepatitis and radiation biodosimetry. In 2011 he started at FDA as a scientific reviewer and was involved in the writing of guidance documents for assay migration and multiplex infectious disease detection then later served as Branch Chief in the Multiplex Bacteriology and Medical Countermeasures branch in the Division of Microbiology (DMD). The branch has been challenged with recent clearances utilizing mass spectrometry identification of clonal isolates, endogenous biomarkers of infection and ever increasing numbers of syndromic infectious disease panels. Dr. Roth has also been a stakeholder in the emergency response to the recent Ebola and Zika outbreaks.

Katarzyna Schmidt (Norwich, UK)
Katarzyna (Kasia) Schmidt is working as a Biomedical Scientist in the microbiology laboratory at The Norfolk and Norwich University Hospital. She obtained an M.Sc. Degree in Biotechnology from The Poznan University of Life Sciences, Poland. Currently she is finishing her doctoral studies at The University of East Anglia in Norwich. Her research focused on evaluation of new technologies for rapid detection of urinary pathogens and their antibiotic resistance. She previously worked at the Institute of Biochemistry and Biophysics in Warsaw, Poland and as a laboratory diagnostician in the genetics laboratory of the DNA Research Centre in Poznan, Poland, where she gained experience in clinical microbiology and molecular diagnostics.

Patrick Veiga (Palaiseau, France)
Patrick Veiga received his PhD from the Université of Orsay - Paris XI in 2007. He joined Danone Nutricia Research in 2008 with the mission to investigate the interplay between probiotics and gut microbiota, an emerging field at that time. Among other collaborators, he specifically worked with the Laboratories of D. Ehrlich and J. Doré (Institut National de le Recherche Agronomique, France). In 2011, he was assigned as a visiting scientist to the Laboratory of the Prof. W. Garrett (Harvard School of Public Health, Boston, MA) where he spent 3 years identifying "probiotic effectors" able to modulate the immune system in a context of intestinal inflammation. In 2014, he took the position of Gut Microbiota Research Axis co-leader within the Life Science (LS) Dept of Danone Nutricia Research (Palaiseau, France). Lately (2017), he was appointed Head of the "Microbes & Foods for Health" science team and Scientific Advisor for the Dairy Division, a position that entails the lead of the Life Science Dpt scientific strategy of the Dairy division.

Posters at a glance

1 Xavier Argemi, France
Identification of an enterotoxin-bearing pathogenicity island in two clinically virulent strains of Staphylococcus epidermidis producing a type C enterotoxin

2 Antonin Bal, France
Quality controls implementation for universal characterization of DNA and RNA respiratory viruses using single metagenomic Next Generation Sequencing workflow.

3 Francisco Brito, Switzerland
Transfusion safety - A characterization of the virome of platelet concentrates using shotgun metagenomics

4 Ian Cohn, United States
Depletion of human DNA from infectious joint aspirates results in loss of pathogen DNA

5 Stéphane Cruveiller, France
PathoTRACK: Toward a complete analytical chain of NGS data for the detection and identification of pathogenic organisms in complex samples

6 Anna Cusco, Spain
Using MinION to characterize dog skin microbiota through full-length 16S rRNA gene sequencing approach

7 Thomas Gurry, United States
Reproducibility of the human gut microbiota's metabolic and compositional response to prebiotic dietary supplementation

8 Andre Kahles, Switzerland
Scalable Reference Graphs for Clinical Metagenomics

9 Mohamed Kassam, Switzerland
From gene to activity - Analytics pipeline to exploit the potential of the Nestlé Culture Collection

10 Michel Christoph Koch, Switzerland
Identification of novel enterotropic astroviruses in cattle

11 Iva Kotaskova, Czech Republic
Comparison of ready-to-use bioinformatic tools for 16S rRNA amplicon next-generation sequencing data analysis

12 Sacha Laurent, Switzerland
Building a portable and reproducible bioinformatics pipeline for the analysis of high throughput sequencing data in a microbiological diagnostic lab context

13 Vladimir Lazarevic, Switzerland
Hepatic brucelloma assessed by next-generation sequencing

14 Andre Mu, Australia
Metagenomic reconstruction of KPC-producing Klebsiella pneumoniae uncovers unsuspected colonization with a second high-risk antimicrobial resistant pathogen

15 Yueqiong Ni, Hong Kong
A cohort study of human gut microbiota in different metabolic status of Type 2 Diabetes and Obesity

16 Alban Ramette, Switzerland
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17 Chris Rands, Switzerland
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18 Etienne Ruppé, Switzerland
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19 Nicholas Sanderson, United Kingdom
Real time analysis of metagenomic sequencing from prosthetic joint infections using an Oxford Nanopore MinIon sequencer

20 Neuert Saskia, United Kingdom
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21 Leonard Schuele, Netherlands
Shotgun metagenomics approach for identification and typing of pathogens in clinical samples

22 Mónika Számel, Hungary
Genetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiome

23 Petra Videnska, Czech Republic
Comparison of sampling kits and DNA isolation kits for the 16S rDNA sequencing analysis of microbiome from stool samples

24 Yaxin Xue, Norway
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25 Daniel Manoil, Switzerland
Identification of the Microbiota from Infected Dental Root Canals Based on 16S rRNA Gene Amplicon Sequencing

Posters

Poster #1

Identification of an enterotoxin-bearing pathogenicity island in two clinically virulent strains of Staphylococcus epidermidis producing a type C enterotoxin

Xavier Argemi *et al.*, France

Background

Staphylococcus epidermidis is a coagulase negative staphylococci (CoNS) that belongs to the normal skin flora. It is involved in nosocomial infections as it produces several adhesion factors and biofilm. Rarely, S. epidermidis produces superantigens and we recently described two clinical strains involved in bacteremia and septic schock that produced a type C enterotoxin, a toxin that, firstly, was identified in Staphylococcus aureus. The objective of this study was to confirm the presence of the gene coding for this toxin and describe its genomic environment.

Methods

We performed de novo sequencing and annotation of the two enterotoxin producing strains. The genomes were sequenced using Illumina paired end sequencing (GATC Biotech, Germany) and assembled with SPAdes 3.8. Contigs ordering, orientation, gaps closing and scaffolding were achieved using PAGIT (Post-assembly genome improvement kit). Mobile genetics elements as plasmids, pathogenicity islands and prophages were identified using de novo annotation, Phaster, and Islandviewer3 software.

Results

One final chromosome was obtained for each strain and allowed identification of the sec3 gene coding for type C enterotoxin, but also another gene, sel, coding for type L enterotoxin. Those 2 virulence factors were situated in a 20 kb pathogenicity island, inserted at the tmRNA, downstream of the SsrA binding protein. This pathogenicity island displays 85% nucleotide identity with SePI, the first and only enterotoxin-bearing pathogenicity island identified in CoNS. We identified two prophages that did not bear any virulence factors, and 7 plasmids sequence, some bearing antibiotic resistance genes.

Discussion

This study allowed identification of an entorotxin-bearing pathogenicity island in two clinically virulent S. epidermidis strains. It confirms the existence of such mobile virulent structure in CoNS; a matter of debate since several years. In addition, this observation argues for the possibility of stable horizontal acquisition of virulence-associated mobile elements originating from S. aureus in a CoNS.

Poster #2

Quality controls implementation for universal characterization of DNA and RNA respiratory viruses using single metagenomic Next Generation Sequencing workflow

Antonin Bal *et al.*, France

Background

Metagenomic Next Generation Sequencing (NGS) is now considered as an efficient unbiased diagnosis tool in clinical virology. However the complex genetic heterogeneity of viruses has impaired the development of a unique workflow. The lack of standardization and control also limit routine use of this technology in clinical lab. The objective of this study was to validate a single metagenomic protocol for universal characterization of respiratory viruses including the implementation of internal and external quality controls (IQC, EQC).

Methods

DNA and RNA viral strains were used as EQC. MS2 bacteriophage was selected as IQC. Two QC checkpoints were implemented throughout the process: post amplification and post NGS steps. Metagenomic NGS workflow was then evaluated on clinical respiratory samples tested by viral RT-PCR: 8 negative samples and 22 samples tested positive for a broad panel of DNA and RNA viruses including multiple viral infections.

Results

The correct dilution of IQC was determined in order to both be detected and have limited interference with other viruses present in the sample. QCs were detected at 2 steps allowing process and results validation. All targeted viruses as well as anelloviruses and prokaryote viruses were successfully identified after metagenomics analysis. A wide range of viral load was covered (semi-quantitative RT-PCR Ct values were from 15 to 36). Viral genome coverage ranged from 6,2% to 100%, depending on the Ct value.

Discussion

The widespread use of metagenomic process in clinical virology led to a substantial increase in published protocols but without systematic evaluation on clinical samples and validation by QCs. QCs are widely used in RT-PCR assay and should also be implemented in clinical metagenomic studies to ensure the quality of the generated sequences. We provide an efficient standardized protocol successfully evaluated for the characterization of DNA and RNA respiratory viruses.

Poster #3

Transfusion safety - A characterization of the virome of platelet concentrates using shotgun metagenomics

Francisco Brito *et al.*, Switzerland

Background

Shotgun metagenomic sequencing gives us an in depth overview of the microbial genomics of a patient (bacteria, viruses, archaea, etc) all in one go. Contrary to routine assays, which only test for the presence of specific organisms, metagenomic sequencing is an open approach that characterizes the whole content of a sample, making it suitable to the detection of previously uncharacterized emergent infectious diseases.

Methods

In order to assess the safety of platelet concentrates for transfusion, we shotgun sequenced total RNA and DNA from 10 platelet pools (30 donors each) and used our metagenomics analysis pipeline, ezVIR, to detect viruses based on a comprehensive and curated database of clinically relevant pathogens.

Results and Discussion

Unlike our recently published metagenomic analysis of red blood cells and plasma from donors, where we found a case of an overlooked pathogen in a donor (Astrovirus MLB2), recently associated with cases of meningitis in immunocompromised patients, we do not find any clinically relevant viruses in platelet concentrates, which are often transfused to immunocompromised patients. Though these results could be affected by the loss of sensitivity on pooled data, as positive controls we found, as expected, several commensal viruses: Anellovirus, Pegivirus, human Papillomavirus and Merkel cell Polyomavirus, which confirm the quality of these libraries. We also identified several expected false positive results of different origin (same lane cross-talk, reagent contaminants and ambiguous reads). Our current findings suggest the donor pools to be safe, presenting only viruses that aren't a major risk to patients.

Poster #4

Depletion of human DNA from infectious joint aspirates results in loss of pathogen DNA

Ian Cohn *et al.*, United States

Background

A major limitation in diagnosing infections with metagenomic sequencing is the low ratio of pathogen:human DNA in patient samples, which require ultradeep sequencing for high-confidence microbial identification. Following joint replacements, small numbers of bacteria can initiate an infection, which recruit massive numbers of immune cells. Targeted depletion of human DNA may then increase the pathogen:human DNA ratio, thereby aiding in metagenomic diagnosis of peri-prosthetic joint infections (PJI).

Methods

Aspirates from three prosthetic joints were treated with a human DNA depletion kit (MolYsis Basic (Molzym)) designed to selectively lyse human cells and digest the DNA, while preserving bacteria and fungi. This kit was also tested on a bacterial mock community (Zymo Research) spiked into human immune cells. Each sample was split to be processed with or without the human DNA depletion kit, which were then subjected to column-based DNA purification (QIAamp BIOstic Bactermia Kit (Qiagen)). Prokaryotic DNA recovery was initially measured by 16S qPCR, with human DNA measured by ACTB. The purified DNA was then analyzed by metagenomic sequencing (Nextera XT DNA Library Preparation Kit, Illumina HiSeqX sequencer).

Results

The human depletion kit successfully reduced the yield of human DNA from the samples. However, the total yield of prokaryotic DNA was also reduced in all samples. Addition of a carrier nucleic acid to the samples undergoing depletion did not improve bacterial DNA yield. In 1/3 of the synovial fluid samples, there was detectable bacterial DNA via qPCR after the human DNA depletion kit. Metagenomic sequencing will demonstrate if the improved pathogen:human DNA ratio impacts diagnostic confidence.

Discussion

Our results indicate that human DNA depletion reduces prokaryotic DNA yield, possibly due to unintentional pathogen lysis and subsequent DNA degradation. This necessitates further investigation of methods to increase the pathogen:human DNA ratio beyond strategies involving targeted lysis of human cells.

Poster #5

PathoTRACK: Toward a complete analytical chain of NGS data for the detection and identification of pathogenic organisms in complex samples

Stéphane Cruveiller *et al.*, France

Background

In addition to being time consuming and irrelevant for detection of a wide panel of pathogenic targets, current diagnostic methods for pathogens detection (microbial cultures, PCR-RFLP, test strips…) are almost useless in case of complex biological threats (e.g. several pathogens in a mixed sample). To date, Next Generation Sequencing technologies (NGS) seem to be the only promising tools in such a context since they can theoretically deliver the complete list of organisms included in a sample within a few hours.

Methods

PathoTRACK is a collaborative program involving the French Alternative Energies, Atomic Energy Commission (CEA), and the French Bioinformatics Institute (IFB). The original goal of this initiative was the development of an innovative bioinformatics pipeline that automatically screens for Select Agent organisms based on analyses of large amounts of genomic data obtained from complex samples sequencing. Since last year, thanks to a new partnership developed with the Centre National de Recherche en Génomique Humaine (CEA-CNRGH), a wet lab part has been included in the project allowing us:
i) to build up our own test samples and
ii) to test several NGS technologies.

Results

We present here a first comparison of complex samples sequenced with the main NGS machines available on the market, namely Illumina MiSeq™, Ion Torrent PGM™ and Oxford Nanopores Technologies MinION™ and subsequently analyzed by the PathoTRACK platform.

Discussion

Those various data will be used to validate and enhance the PathoTRACK platform, keeping in mind that the rapid identification and characterization of pathogens from environmental and clinical samples is critical for informed diagnosis, treatment selection and reactive responses to bioterrorism threats.

Poster #6

Using MinION to characterize dog skin microbiota through full-length 16S rRNA gene sequencing approach

Anna Cusco *et al.*, Spain

Introduction

The most common strategy to assess microbiota is sequencing specific hypervariable regions of 16S rRNA gene using 2nd generation platforms. Despite obtaining high-quality reads, many sequences fail to be classified at the genus or species levels due to their short length. This pitfall can be overcome sequencing the full-length 16S rRNA gene (1,500bp) by 3rd generation sequencers. We aimed to assess the performance of nanopore sequencing using MinION on complex microbiota samples.

Methods

First set-up was performed using a staggered mock community (HM-783D). We amplified full-length 16S rRNA gene by duplicate (M1 and M2). Nanopore sequencing was performed on MinION™ using 1D PCR barcoding sequencing protocol to pool different samples in the same run. Data was pre-processed and analyzed using QIIME v1.9.1 and NanoOK. Then, we sequenced a pool of skin microbiota samples of healthy dogs following the same procedure and compared the results with those obtained by IonTorrent PGM.

Results

Nanopore sequencing of the full-length 16S rRNA gene with MinION™ allowed us inferring microbiota composition from the mock community and the dog skin microbiota samples. Besides, we were able to obtain some of the taxonomic assignments down to species level. Long-reads and degenerated primers were able to retrieve increased richness estimates at high taxonomic level (Bacteria and Archaea) unveiling the presence of previously unseen phyla on dog skin microbiota.

Discussion

The full-length 16S rRNA gene using MinION allowed us inferring microbiota composition of a complex microbial community to lower taxonomic levels than short-reads from 2nd generation sequencers. However, the assignment down to species level was not always feasible due to: i) incomplete database; ii) primer set chosen; iii) low taxonomic resolution of 16S rRNA gene within some genera; and/or iv) sequencing errors. Future studies should be relying on the new 1D2 kit that presents higher accuracy.

Poster #7

Reproducibility of the human gut microbiota's metabolic and compositional response to prebiotic dietary supplementation

Thomas Gurry *et al.*, United States

Background

A promising avenue for modulating the composition and metabolic output of the human gut microbiota for clinical purposes is dietary supplementation with rationally selected prebiotics. It remains to be shown that these prebiotics result in reproducible effects across different patients, both in terms of their effects on microbial community composition and metabolic output.

Methods

A human cohort of 60 subjects was placed on a constant liquid diet, and prebiotic supplements were spiked-in against this background. Daily stool samples were collected, from which we sequenced the 16S rRNA gene for taxonomic analyses and performed shotgun metagenomic sequencing for functional and strain-level analyses. In addition, we probed the output of Short Chain Fatty Acids (SCFAs) from subjects' fecal material in response to challenge with different prebiotics using an anaerobic ex vivo assay.

Results

We show that certain bacterial species respond in a reproducible manner to specific prebiotics, driven by the presence of genomic carbohydrate-active enzymes, with evidence of strain-level selection in some cases. Introduction of the constant liquid diet appears to result in stress on the patients' microbiomes, with increased phage abundances and a flattening of the fitness landscape within most bacterial clades as observed by increased genomic SNP heterozygosity. We also show that the fecal microbiota have different SCFA production profiles in response to the same prebiotic.

Discussion

Using metagenomic sequencing coupled with SCFA analysis, we show that specific constituents of the human gut microbiome reproducibly respond to particular prebiotics in vivo, but that the resulting SCFAs produced differ from subject to subject as a function of initial community composition. Using these insights, we outline a strategy for tailoring specific diets to an individual's microbiota for clinical purposes.

Poster #8

Scalable Reference Graphs for Clinical Metagenomics

Andre Kahles *et al.*, Switzerland

Background

Technological advancements in high-throughput sequencing have ushered in a new era of clinical genomics. Full human genomes and metagenomes of complex microbial communities can now be sequenced at the scale of several thousands. Traditional methods for storage and analysis of biological sequencing data increasingly fail to keep up with this growth. New approaches to analyze samples in an integrative manner that make use of the thousands of already-sequenced genomes are needed. Our motivation is to capture rare or hitherto unseen genetic variation, as it is commonly observed in the analysis of microbial metagenomes, addressing the problem of incomplete and biased reference data-repositories.

Methods

Using techniques from genome-assembly and text-compression, we encode sequence information and associated metadata in a succinct colored assembly graph, which represents single genomes and captures inter- and intra-genome variability. The graph representation is structured as a self-index that can be used for alignment and classification of reads arising from sequencing of novel samples.

Results

Our graph structure can leverage information from reference genomes and sequenced samples and it provides access to rare observations not yet present in reference databases. It is designed to dynamically integrate further knowledge over time (accumulating information over many heterogeneous data-sources), to provide greater sensitivity to detect unseen or rarely seen variants. We can encode a human genome and all sequence variants from the gnomAD project in under 2 hours, resulting in a fully indexed reference of only 3GB. We will present applications in clinical metagenomics, encoding over 50,000 viral sequences and show strategies to visualize and query the large data structures.

Discussion

We present a novel, highly efficient approach to combine large sets of (meta-)genomes with raw sequencing data and known variation into a sparse representation that can be comprehensively annotated and efficiently queried, addressing an unmet analysis-need for clinical metagenomics.

Poster #9

From gene to activity - Analytics pipeline to exploit the potential of the Nestlé Culture Collection

Mohamed Kassam *et al.*, Switzerland

Background

One of the main Nestlé objectives is to provide nutritious, healthy and sustainably produced food. A culture collection of more than 3000 food grade strains (Nestlé Culture Collection, NCC), is available through an R&D network whose expertise covers genomics, microbiology, fermentation, food processing, nutrition and health. This network also enables clinical trials to develop and produce new functional foods containing beneficial microbes.

Methods

We established a complete workflow to sequence, assemble and annotate the genomes of the NCC. Sequencing of the entire NCC was performed with a combination of short- and long-read sequencing technologies. For assembly and annotation, we have implemented an internal webserver toolset to check the quality of the produced data. In a first pilot phase, a subset of 75 strains representative of the diversity of the collection were sequenced with both short- and long-read technologies to define and develop the necessary methods required for the further processing of the entire collection. To this end, a dedicated workflow was then implemented based on these findings starting from assembly, identification and reference search, to annotation and final quality evaluation of the data.

Results

The integrated quality checks and manual inspections allowed to identify samples with contaminated data or with a lower sequencing quality, which represents less than 3% of the whole dataset. Assembled genomes were integrated in the MicroB database together with RefSeq genomes to create the NCC genome database, which can be accessed and searched using the web-based comparative genomic software Wallgene.

Discussion

Integration of 2692 genomes in the developed infrastructure enables to perform comparative analysis of those organisms and to reveal their metabolic potentials. This will enable to develop novel concepts around biotransformation (enzymes, fermentation and probiotics) to deliver nutritious, healthy and sustainably produced food.

Poster #10

Identification of novel enterotropic astroviruses in cattle

Michel Christoph Koch *et al.*, Switzerland

Background

Astroviruses are single-stranded positive-sense RNA viruses with a genome size of 6.2-7kb. The genome includes at least three open reading frames (ORF): ORF1a and ORF1b encode the non-structural protein nsp1ab; ORF2 encodes the capsid protein precursor. In humans and mammalian animals, astroviruses are mainly enterotropic. Recently, our lab has identified a divergent bovine astrovirus (BoAstV-CH13) in brain tissues of cattle. We do not know whether this virus is shed by subclinical infected cattle via the feces, similarly to what is the case for known enterotropic BoAstV strains.

Methods

148 bovine stool samples were analyzed with a pan-astrovirus RT-PCR. Consequently, nine RT-PCR positive samples were subjected to Next-Generation Sequencing (NGS). RNA libraries were prepared and sequenced using an Illumina HiSeq2500 machine. Between 64'523'947 and 100'111'185 reads per sample were generated and then analyzed using an in-house pipeline.

Results

Amplicon sequences of all 11 RT-PCR positive samples revealed highest similarities to known enterotropic BoAstV and not to BoAstV-CH13. Scaffolds displaying similarities to Mamastrovirus sequences were found in all nine NGS sequenced samples, 14 of them longer than 5'500 nucleotides and with three identified ORF. Deduced amino acid sequences were aligned to the Genbank Viral Protein database. The best hits for nsp1ab sequences in all scaffolds were to known Astroviruses with an identity of >90%. In nine scaffolds, the capsid precursor protein sequence identity to those of known astroviruses was only between 74,1% and 88.5%.

Discussion

The neurotropic BoAstV-CH13 was not found in our study, suggesting that it does not occur at a high frequency in feces of cattle in Switzerland. However, we identified astrovirus sequences with high similarity to known enterotropic BoAstVs. Nine of the putative astrovirus genomes encode divergent capsid proteins, which may indicate recombination events with so far unknown astrovirus genotype species.

Poster #11

Comparison of ready-to-use bioinformatic tools for 16S rRNA amplicon next-generation sequencing data analysis

Iva Kostakova *et al.*, Czech Republic

Background

Although Next-Generation Sequencing (NGS) technologies enable simultaneous broad-range detection of all microbiota presented in a clinical sample, automated data analysis and results interpretation remains challenging for routine use. We aimed to map and evaluate available ready-to-use bioinformatic tools for .fastq file analysis and taxonomical results acquisition in not-deep 16S rRNA Illumina amplicon sequencing.

Methods

Data from shallow Illumina paired-end V3-V5 targeted 16S rRNA sequencing of 20 common low-diverse polybacterial clinical samples were intentionally selected for analysis. Demultiplexed and merged .fastq or gunzipped files were analyzed by several publicly available tools (OneCodex; BaseSpace 16S Metagenomics application; Taxonomer.iobio; Blast2Go; and finally MG-RAST pipeline). Results were compared to QIIME results, and various parameters were evaluated: analytical results (e.g., OTUs, abundance), computing knowledge and requirements (e.g., the necessity of pre-processing), and user experience (e.g., duration, user interface). Taxonomical results considering species abundance were assessed by Simpson´s index and tested by ANOVA, and finally by Bray-Curtis index.

Results

A critical aspect of duration time varied from seconds (Taxonomer.iobio) to minutes (BaseSpace, Onecodex) and up to dozens of hours (Blast2Go, MG-RAST). Blast2Go and Taxonomer.iobio results were excluded from taxonomical comparison because of long duration and absence of tabelarized results, respectively. The vast majority of reads were binned and mapped to bacterial 16S rRNA genes. The highest OTUs (genus and higher level OTUs) richness was achieved by BaseSpace application, the lowest by MG-RAST, surprisingly. All tested tools provided comparable taxonomical results. The most frequently, taxonomical discordances were observed in case of Enterobacteriaceae family, as expected.

Discussion

Multiple algorithms and pipelines can be used to perform data analysis. We present a comparison and characteristics of available ready-to-use bioinformatic tools for amplicon sequencing analysis and evaluate them for use in the clinical context.

Poster #12

Building a portable and reproducible bioinformatics pipeline for the analysis of high throughput sequencing data in a microbiological diagnostic lab context

Sacha Laurent *et al.*, Switzerland

Background

Bioinformatic analysis of high throughput sequencing data comes with a variety of hurdles that must be dealt with in a diagnostic context. Reproducibility, availability, portability and ergonomy all have to be addressed in order to build reliable tools. In this work, we aim at developing a prototype workflow enabling genome assembly, basic annotation and comparative genomics of a microbiological isolate.

Methods

We used the workflow management language Snakemake to create our bioinformatics pipeline, together with conda, a light package management system, that creates independent virtual environments for each steps of the workflow. Using bioconda, most of the standard bioinformatic tools are already available for easy inclusion in our workflow.

Results

The source code of our workflow is available at https://github.com/Cashalow/diag_pipelines and can be deployed on any Unix machine. We use it to generate reports on the assembly of any strain sequenced by our diagnostic lab and to perform comparative analyses with already sequenced genomes available in RefSeq.

Discussion

This work is a first step towards developing reproducible pipelines for various analysis performed in our diagnostic lab and this pipeline might easily be implemented in similar clinical microbiology genomics laboratories.

Poster #13

Hepatic brucelloma assessed by next-generation sequencing

Vladimir Lazarevic, Switzerland

Backgound

Human infections caused by Brucella (brucellosis) are among the most common zoonoses worldwide. However, hepatic abscess, as a complication of chronic brucellosis, is rarely encountered in the clinical practice. We aimed at identifying Brucella by whole metagenome shotgun sequencing (WMGS) of a patient with a suspicion of chronic hepatic brucelloma.

Methods

We extracted DNA from the leftover of the patient's necrotic hepatic lesion. The extraction procedure included bacterial/fungal DNA enrichment procedure based on degradation of DNA released from host cells after their selective lysis. DNA was sequenced (2x250 b) on an Illumina MiSeq instrument.

Results

Nearly all (>99.99%) taxonomically classified reads corresponded to human genome sequence. Of 25 reads classified as bacterial, 23 were assigned to the genus Brucella and two corresponded Beijerinckia and Propionibacterium which are known reagent contaminants.

Discussion

To the best of our knowledge, this is the first report of the use of WMGS on a hepatic brucelloma sample. Our data show that WMGS may be used together with other diagnostic procedures to strengthen the diagnosis of hepatic brucelloma.

Poster #14

Metagenomic reconstruction of KPC-producing Klebsiella pneumoniae uncovers unsuspected colonization with a second high-risk antimicrobial resistant pathogen

Andre Mu *et al.*, Australia

Background

Culture-independent metagenomic methods have shown promise in identifying pathogens, but applications in tracking transmission in outbreak investigations require high-level reconstruction of microbial genomes for typing – a challenging task from microbiologically complex samples. Here, using short-read metagenomic sequencing of a faecal sample from a patient colonised with KPC-producing Klebsiella pneumoniae, we investigated whether reconstruction of individual antimicrobial resistant strains from the metagenome could be used infer transmission for outbreak investigation.

Methods

Genomic DNA extracted directly from patient faecal sample was sequenced on the Illumina MiSeq. An emergent self-organizing map was used to reconstruct bacterial genomes from the patient's sample using tetranucleotide frequencies. Metagenomic k-mers were assigned to representative PacBio reference genomes from three local transmission clusters in a custom Kraken database. Metagenomic reads mapping to K. pneumoniae were also phylogenetically compared to publicly available ST258 genomes in GenBank, based on core genome SNPs from read alignment to a single local PacBio reference K. pneumoniae genome.

Results

blaKPC was detected, as was a full vanB operon encoding vancomycin resistance, suggesting vancomycin-resistant enterococci (VRE) colonisation. Metagenomic binning reconstructed distinct K. pneumoniae, and Enterococcus faecium bins, with sufficient reconstruction of the reference genomes to perform rudimentary typing. Through k-mer assignment to the custom local KPC Kraken database, we were able to determine the most closely related local reference genome. This was reaffirmed by phylogenetic comparisons based on core genome SNPs, and corresponding epidemiological data to identify the probable transmission network.

Discussion

Our results demonstrate that faeces metagenomics can identify detailed information to distinguish highly related K. pneumoniae strains and allow assignment to a transmission network, independent of the parallel epidemiological investigation. These proof-of-principle results provide new insights into potential applications of culture-independent whole-genome sequencing and genome-reconstruction of pathogens to perform surveillance, investigate outbreaks of multidrug-resistant organisms, and inform public health responses.

Poster #15

A cohort study of human gut microbiota in different metabolic status of Type 2 Diabetes and Obesity

Yueqiong Ni *et al.*, Hong Kong

Background

Numerous studies have revealed the association of gut microbiota to the development of two human metabolic disorders, obesity and type 2 diabetes (T2D). Medical research has found a positive correlation between the two diseases, and previous metagenomic studies have reported potential metagenomic markers linked with them. However, few metagenomic studies have been designed to investigate two related diseases interactively. Our objective here is to investigate how the gut microbiota contribute to the development and the differentiation of people into different metabolic status of obesity and T2D.

Methods

A well-controlled cohort of 182 Chinese subjects were collected and further classified into four phenotypes based on host metadata: non-diabetic lean control (NL), metabolically unhealthy diabetic lean (TL), non-diabetic obese (NO) and diabetic obese (TO). Shotgun metagenomic sequencing was performed for host fecal samples. In house pipelines were applied to characterize the taxonomic and functional profiles of the gut microbiota.

Results

We found that the TL group had distinct gut microbiota composition compared to TO group, while NO and TO subjects shared highly similar gut microbiota composition. The same conclusion was also drawn from the microbial functional profiles. Several species had significantly different abundances among the four different phenotypes. In addition, we identified certain microbes showing significant correlations with clinically important measures for obesity, insulin resistance and insulin secretion.

Discussion

Our study based on gut microbiota suggests the possibly different pathology of T2D in lean and obese patients, and implies that metabolic-healthy obese people might be at a risky transitional stage as obese diabetic people. A reliable identification of key bacteria or bacteria cocktail in different status of metabolic diseases could lead to different prevention and treatment strategies.

Poster #16

Direct RNA sequencing of clinical samples using nanopore technology

Alban Ramette *et al.*, Switzerland

Background

High-throughput, short-read technologies often cannot assemble complex genomes satisfactorily due to the presence of repetitive elements or genomic rearrangements, and are often not competitive when compared to faster and cheaper methods in the routine diagnostic laboratories. For human viruses, PCR-based detection is still the mostly used method for routine diagnostics, and is often complemented by Sanger sequencing for genotype determination. Yet, point mutations and recombination events are frequent and can potentially lead to false negative results. Here, we developed a wet lab solution and assessed bioinformatic pipelines to obtain whole genomes of viruses from clinical samples within a minimum amount of time.

Methods

We used nanopore sequencing to obtain genome-wide information of enteroviruses (RNA viruses), and assessed the feasibility of direct RNA sequencing from stool samples. The MinION apparatus is a pocket-size instrument that sequences long strands of nucleic acids. The nanopore technology offers the unique opportunity of direct RNA sequencing, besides the traditional sequencing of reverse transcribed and PCR-amplified DNA molecules.

Results

We sequenced viral cDNA and RNA molecules directly from stool of RT-qPCR EV-positive patients using the MinION platform. cDNA sequencing provided >95% coverage of EV genomes, with >99% consensus accuracy when compared to Sanger sequencing. Direct RNA sequencing provided the fastest sample-to-answer turnaround time, as no amplification step was needed for the production of the sequences. Noticeably, near-complete RNA genomes of EV isolates could be retrieved.

Discussion

Here we demonstrate that nanopore sequencing of cDNA molecules may be used successfully with clinical samples for the rapid production of good quality, long DNA reads that cover most of the target genomes, while direct RNA sequencing offers the fastest identification of viral genomes, in a timeframe that is amenable to actionable clinical and public health diagnostics.

Poster #17

Antibiotic resistance and virulence genes harboured by phages in the human gut

Chris Rands *et al.*, Switzerland

Background

The spread of antibiotic resistance (AR) and virulent pathogen strains are major global public health issues. Horizontal gene transfer of AR and virulence genes can occur by several mechanisms, including via phages (bacterial viruses).

Methods

We scanned 1,302 human gut metagenomes and metaviromes, in addition to 2,090 phage whole genome sequences, to look for examples of where phages have carried bacterial AR or virulence genes. To achieve this, we developed catalogs of profile Hidden Markov Models (HMMs) with model-specific thresholds annotated for AR and virulence function, and a sliding window approach to identify clusters of phage genes annotated via HMMs.

Results

We identify and characterise several good candidates of possible AR gene mobilisation by phages in the human gut microbiome, including efflux pumps, tetracyclines, and beta-lactams. Otherwise, we find that AR genes are rarely co-located with phages. We are able to annotate known virulence genes, such Shiga toxin and Panton–Valentine leukocidin operons, in phage whole genome sequences, and we predict a small number of possible virulence genes, including effector proteins, in human gut metaviromes.

Discussion

Previous pioneering studies have searched for phages linked to AR and virulence genes, but the availability of more metagenomic data and annotations, combined with our novel methods, allowed us to conduct arguably the most comprehensive search yet. The rare cases we identify where phages may mobilize AR or virulence genes in the human gut are worthy of further investigation.

Poster #18

Clinical metagenomics for the microbiological diagnostic of infective endocarditis: lessons from 5 cases

Etienne Ruppé *et al.*, Switzerland

Background

Clinical metagenomics (CMg) is a culture-independent method that refers to the application of next-generation sequencing (NGS) to clinical samples with the dual purpose of identifying infective agents and of predicting their susceptibility to antimicrobials. CMg applied in the context of IE could improve the microbiological diagnostic of IE. Our objective was to study the feasibility of applying CMg to clinical samples obtained in the context of IE.

Methods

We sequenced (Illumina MiSeq 2x250b) five samples obtained in the context of IE suspicion. Two were negative in both culture and 16S PCR, the three others respectively yielding Streptococcus gallolyticus, Enterococcus faecalis and Staphylococcus aureus in culture. A specific DNA extraction method aiming at depleting human DNA (Molzym) was tested against a conventional DNA extraction method (MagCore). Bacteria were identified using MetaPhlAn2 and Kraken. Antibiotic resistance determinants (ARDs) were identified directly from reads using ARIBA and the Resfinder database. Two negative controls (one per DNA extraction method) were sequenced.

Results

No pathogen was identified by CMg in the two negative samples while the bacteria were correctly identified in the three positive samples, except that the S. gallolyticus was identified by CMg as S. pasteurianus. No other pathogen was found in the three positive samples. The Molzym extraction protocol increased by 3.8, 4.0 and 58 folds the abundance of bacterial reads in the three positive samples. Despite a limited number of reads per sample used for this proof-of-concept study (range 2-6M), bacterial genomes could be assembled at 4.6% for S. pasteurianus, 30.3% for S. aureus and 38.1% for E. faecalis. No acquired ARDs but Tet(L) in S. pasteurianus were found, in consistence with the observed phenotypes.

Discussion

CMg appears to be suitable for the microbiological diagnostic of IE. Further studies with an increased number of reads per samples should now be implemented.

Poster #19

Real time analysis of metagenomic sequencing from prosthetic joint infections using an Oxford Nanopore MinIon sequencer

Nicholas Sanderson *et al.*, United Kingdom

Background

Prosthetic joint infections (PJI) are clinically difficult to diagnose and treat. Previously we demonstrated metagenomic sequencing on an Illumina Miseq replicates the findings of current diagnostic techniques (Street et al 2017). Nanopore sequencing offers advantages in speed of detection over MiSeq. Here, we compare direct-from-clinical-sample metagenomic Illumina sequencing with Nanopore sequencing, and report a novel analytical pathway for Nanopore sequence data.

Methods

DNA extracts from nine PJI sonication fluids were sequenced on an Oxford Nanopore Technologies MinION sequencer using either the 1D genomic DNA by ligation protocol or a PCR-based protocol for low input DNA. Samples were sequenced on FLO-MIN105(v.R9) or FLO-MIN106(v.R9.4) flowcells. Extraction and processing for Miseq was as previously described (Street et al 2017). Analysis of Minion sequencing data was via a Nextflow workflow incorporating basecalling (Albacore), read classification (Centrifuge) and reference genome alignment (BWA mem). The workflow was contained within a singularity image and can be executed across a distributed cluster or local installation. Results were filtered on thresholds calculated from negative controls.

Results

Nine PJI samples, including two negative controls, were sequenced and analyzed. The majority of DNA classified (>90%) was host contamination and discarded. Using negative control cutoff thresholds, the species identified corresponded with both microbiological diagnosis and MiSeq results, with greater taxonomic resolution in some samples. The Nanopore sequence analytical pathway was reliable, reproducible and scalable.

By analyzing sequences in real time, causes of infection were robustly detected within ten minutes from onset of sequencing.

Discussion

We demonstrate initial proof of concept that metagenomic nanopore sequencing can provide rapid, accurate diagnosis for PJI. We demonstrate a novel, scalable pipeline for real-time analysis of nanopore sequence data. The high proportion of human DNA in extracts prevents further genotyping, and methods to reduce this could increase genome depth and allow AMR profiling.

Poster #20

Application of -omics technologies for the identification of characteristic changes in gut microbiota composition and function during infectious intestinal disease

Saskia Neuert *et al.*, United Kingdom

Background

Despite a decline in associated mortality, infectious intestinal diseases (IID) and their potential long-term adverse consequences remain a major healthcare problem, even in industrialised countries. Routinely used diagnostic methods are often time-consuming and require isolation of pathogens from faecal matter prior to identification. Even the most advanced rapid approaches fail to detect the aetiological agent of IID in 40% of cases referred for laboratory diagnostics. We believe there is huge potential in culture-free approaches that make use of advances in high-throughput technologies.

Methods

To detect signature changes in microbiota composition associated with specific pathogens, which can aid their identification, we performed 16S rRNA gene sequencing on 170 faecal samples obtained from the enteric laboratory of the Norfolk and Norwich University Hospital. Of these, 131 had tested positive for bacterial pathogens and 39 for protozoan parasites using standard diagnostic techniques. Furthermore, we investigated the metabolite profiles of the IID samples using 1H NMR spectroscopy on faecal water extracts to identify characteristic functional differences in the microbiota.

Results

Infections with bacterial and protozoan parasites resulted in distinct states of microbiota dysbiosis affecting the relative abundances of key genera such as Bacteroides and Ruminococcus to varying extents. Bacterial infection seemed to lead to a larger decrease in bacterial diversity than protozoan infection. Distinct compositional profiles were accompanied by different functional consequences as illustrated by changes in the concentrations of important metabolites such as tyrosine.

Discussion

Based on these findings new culture-free diagnostics pipelines can be developed that will take into account ecological consequences of IID instead of focussing on the aetiological agent in isolation. In cases where routinely used.

Poster #21

Shotgun metagenomics approach for identification and typing of pathogens in clinical samples

Leonard Schuele *et al.*, Netherlands

Background

Faster methodologies that lead to reliable and accurate detection of pathogens, e.g., associated with outbreaks, are needed to further speed the appropriateness of treatment, especially within the hospital. shotgun metagenomics may provide further information on the microorganisms present in patients' samples (e.g. virulence factors, antimicrobial resistance genes, epidemiological information).

Methods

We have recently performed shotgun metagenomics on different types of patients' samples, including fluids and tissues. DNA was extracted using human DNA depletion kits. Libraries were prepared with the Nextera XT Library Preparation kit (Illumina), combined in equimolar ratios and sequenced on a MiSeq instrument (Illumina). The data was analysed with CLC Genomics Workbench v10.0.1 (Qiagen), Taxonomer (IDbyDNA), CosmosID, BaseSpace tools and several Linux-based tools. The samples were also subjected to standard culturing and susceptibility testing methods.

Results

On average, about 75.3% of the reads were mapped against the human genome (hg19). Most of the pathogens identified by culture were identified through shotgun metagenomics. Moreover, additional bacteria were detected, mainly anaerobes. In three samples, we were able to determine the sequence type of the most abundant species, several plasmids and antimicrobial resistance genes, compatible with the antimicrobial susceptibility profiles of the respective bacteria.

Discussion

Although most of the bacteria identified by classical culturing were also identified by the tools used in this study, human DNA background or insufficient sequencing depth could explain the lack of sensitivity in some samples. The identification of antimicrobial resistance genes, plasmids and typing shows how powerful shotgun metagenomics can be for clinical microbiology.

Poster #22

Genetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiome

Mónika Számel *et al.*, Hungary

Background

Antimicrobial peptides (AMPs) are the ancient effector molecules of the innate immune system also controlling the composition of the human gut microbiome. Since these molecules are considered as future therapeutics against multiresistant pathogens, exploring horizontal transfer of resistance mechanisms against them is a crucial and yet unexplored issue.

Methods

We adapted functional metagenomic screens, cultivation of the gut microbiome and analysis of the mobile gene pools in order to characterize the resistome of the human gut microbiota against a comprehensive set of AMPs and clinically relevant small-molecule antibiotics.

Results

We found various novel genes that provide resistance against polymyxin B, a clinically important AMP. However, for most of the AMPs, the resistance reservoir available for horizontal gene transfer was very limited compared to what we observed for antibiotics. This is unexpected, as microbiome culturing revealed that phylogenetically diverse gut bacterial species display resistance to AMPs, similarly to antibiotics. However, transfer of AMP resistance genes generally provides only low levels of resistance in the new bacterial host.

Discussion

Our findings highlight major differences in the mobilization of resistance genes as a result of antibiotic and AMP perturbations, respectively. These results are in line with differences in the presence / absence patterns of AMP and antibiotic resistant genes in the mobile gene pools of the human gut microbiome. Based on the differences in AMP resistance level between the host and the recipient strains, we conclude that resistance against AMPs is highly dependent on the genetic background.

Poster #23

Comparison of sampling kits and DNA isolation kits for the 16S rDNA sequencing analysis of microbiome from stool samples

Petra Videnska *et al.*, Czech Republic

Background

Microbiome plays a key role in shaping human health. In large cohort microbiome studies a comfortable sampling kit is crucial for good compliance of volunteers. The kit should also provide material of good quality for sequencing. In addition, different DNA isolation kits provide varying results due to different lysis procedures. We compared multiple sampling and DNA isolation kits to select the best combination for cohort studies.

Methods

The study involved testing of sampling kits by 16 volunteers, who answered short questionnaires. The quality of the DNA was determined by measurements of DNA yield (NanoDrop) and DNA integrity (Fragment Analyser). Presence of PCR inhibitors and human DNA was tested by qPCR. The library of 16S rDNA was prepared and sequenced with MiSeq (Illumina).

Results

Stool container (against swabs) was chosen by volunteers as the most comfortable for use. The QIAamp DNA Stool Mini Kit (QS kit) gave the highest yield of isolated DNA while PowerLyzer® PowerSoil® DNA Isolation kit (PS kit) produced the highest DNA integrity. For both DNA isolation kits we observed higher quantity of PCR inhibitors in comparison to control DNA. The human DNA to bacterial DNA ratio was approximately 1/20 000 in both kits. Isolation using QS kit resulted in higher abundance of G- bacteria. The abundance of representatives of Bacteroidetes, Actinobacteria and Firmicutes phyla had the highest impact on sample clustering at phylum, order and family taxa level as well as on inter-individual variability in genus, strain and OTU taxa.

Discussion

Based on these results we selected stool container as the best sampling kit for healthy volunteers and PS kit as more suitable isolation kit providing the best trade-off between the performance and efficiency in lysis of the G+ cell walls.

Poster #24

Analysis the stability and variability of airway microbiome among repeated samples in Chronic Obstructive Pulmonary Disease (COPD) patients

Yaxin Yue *et al.*, Norway

Background

Increasing evidence indicates that microbiomes have been associated with lung disease or play a functional role in the development disease severity, like chronic obstructive pulmonary disease (COPD). Bergen COPD microbiome study (MicroCOPD) is a large, ongoing study that aims to investigate the relationship between airway and respiratory microbiome with COPD development and progression systemically. One major issue of COPD microbiome is if the airway microbiome is stable over time. In this paper, our aim was identifying if airway microbiome is stable when sampled repeatedly with or without intercurrent events, such as drugs, or antibiotics, etc.

Methods

We surveyed 896 samples collected with 97 subjects underwent bronchoscopy through all working channels, 60 subjects examined twice, 11 of them three times. 16S rRNA amplicon sequencing was performed on the samples using Illumina Miseq NGS platform. OTUs were generated with DADA2 workflow, and downstream analysis was achieved by our in-house scripts. We tracked the microbiome variation of the same subjects with multiple factors, including time point, COPD stage, sampling position, the use of antibiotics, etc.

Results

5840 taxa and 880 samples were kept after preliminary analysis with DADA2 workflow. The overall microbiome community was dominated by Firmicutes, Actinobacteria, Bacteroidetes and Proteobacteria phylum, and alpha diversity was relative similar, in same subjects among different COPD stage and antibiotics usage. Antibiotics seemed have more influenced on beta diversity. We calculated distance across all the samples firstly, then picked pair-wise distance which from same subjects but different time point and COPD stage. We found that airway microbiome tended to be more stable when antibiotics was used in some channels.

Discussion

Our analysis indicated that the airway microbiome in subjects was relatively stable over time in terms of alpha and beta diversity; however, there were still some variations among them.

Poster #25

Identification of the Microbiota from Infected Dental Root Canals Based on 16S rRNA Gene Amplicon Sequencing

Daniel Manoil *et al.*, Switzerland

Background

Apical periodontitis is an inflammatory disease of the dental peri-radicular tissues resulting from the bacterial invasion of the root canal system. Primary root canal infections are caused by the microbial colonization of necrotic pulp tissues. In contrast, secondary infections result from a recontamination of the root canal after treatment, or the persistence of bacteria from the primary infection. The aim of this study was to characterize the microbiota present in primary and secondary intra-radicular infections associated with apical periodontitis.

Methods

Freshly extracted teeth associated with peri-radicular lesions and exhibiting either necrotic pulps or pre-existing radicular treatments, were collected for microbial sampling. From each tooth, a dentin sample and the intra-radicular content were collected and subjected to DNA extraction. PCR amplicons of the V3-V4 region of the bacterial 16S rDNA were pooled and sequenced (2x300) on an Illumina MiSeq instrument. The bioinformatics analysis pipeline included quality filtering, merging of forward and reverse reads, clustering of reads into operational taxonomic units (OTUs), removal of potentially contaminant OTUs and assigning taxonomy.

Results

The most prevalent OTUs were assigned to known anaerobic oral bacteria, Fusobacterium nucleatum, Dialister invisus and Parvimonas micra. The relative abundance of Veillonella parvula was significantly higher in dentin samples than in root canals. Multivariate analysis showed clustering of microbiota by sample type (dentin vs root apex) and by pathology (primary vs secondary infection). Notably, in root canal samples, the proportions of Enterobacter faecalis and Fusobacterium nucleatum were respectively higher and lower when comparing secondary to primary infections. Co-occurrence network analysis provided evidence of microbial interactions specific to both pathology and sample type.

Conclusion

The identification of bacterial taxa differentially abundant in primary and secondary intra-radicular infections provides the basis for targeted therapeutic approaches aimed at reducing the risk of the secondary infection.

The location

Campus Biotech is a new initiative that aims to drive forward the biotechnology sector in the Lake Geneva region, creating new opportunities for scientists and entrepreneurs. Campus Biotech was formed following the announcement by Merck Serono in 2012 that it would be closing its Geneva site. Formerly the global headquarters of Serono, the biotechnology company built over three generations by the Bertarelli family, this site had been the hub for life sciences in the region.

Campus Biotech's mission was to acquire the site from Merck Serono and to ensure that it could be utilized as a focal point for scientists and entrepreneurs in the life sciences sector, rather than be purchased for property development. That mission is now being realized, with, among others, the Human Brain Project and the Bertarelli Professorships in Translational Neuroscience located – or soon to be located – at the emerging hub.

Campus Biotech is nicely located close to the lake and the botanical garden, and is easily accessible by public transportation from the Cointrin airport and the Cornavin train station.

Campus Biotech
Chemin des Mines 9
1202 Genève, Switzerland

Bus 1 and 25 "Mines" stop
Tram 15 "Maison de la Paix" stop

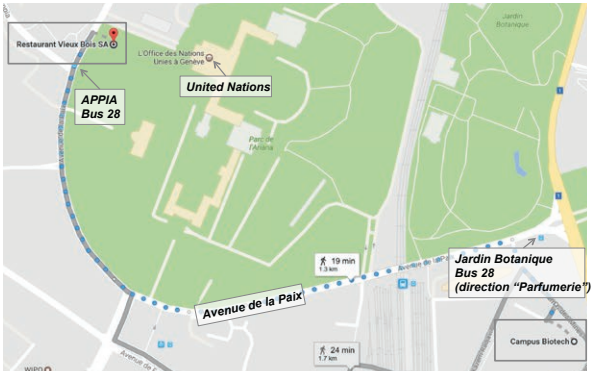
Restaurant Vieux-Bois

The ICCMg dinner will take place at the gourmet restaurant Vieux-Bois ("Old-Wood") that hosts the Hotel School of Geneva. The dinner will start at 8:00 pm.

Conveniently located next to the United Nations, in the beautiful Ariana's park and enjoying a summer terrace, Vieux-Bois restaurant welcomes a demanding clientele, including international delegations, politicians, economic leaders and artists. It opened in 1934 under the name "L'Auberge de Mr. Vieux Bois", honoring one of the main characters of the cartoonist Rudolph Töpffer who lived in the house in the nineteenth century. Today, Vieux-Bois restaurant is a popular address for gourmets who appreciate the excellent cuisine and the high-standards service by students of the Hotel School of Geneva.

How to go there?

The Vieux-Bois restaurant is conveniently located close to Campus Biotech where ICCMg is orgnized. By walking, it takes ~20 minutes through the Avenue de la Paix. By bus (bus stop "Jardin Botanique"), take bus 28 direction "Parfumerie" and stop at "Appia" (just 3 stops ahead).



Restaurant Vieux-Bois
Avenue de la Paix 12
1202 Genève , Switzerland

Institutional Sponsors

Geneva University Hospitals

Founded in 1995, the Geneva University Hospitals (HUG) can draw on a long tradition of medical and scientific excellence. HUG ranks first among Switzerland's university hospitals. It comprises eight public hospitals and 40 outpatient clinics and is also one of the Canton of Geneva's largest employers, with over 10 000 staff and 180 job categories.

Swiss National Science Foundation

Mandated by the federal government, the Swiss National Science Foundation (SNSF) supports basic science in all academic disciplines, from history to medicine and the engineering sciences. The SNSF is Switzerland's foremost research funding organisation and finances over 3,200 projects involving 14,800 researchers each year. To ensure its independence, the SNSF was established as a private foundation in 1952. Its core task is the evaluation of research proposals. In 2014, it allocated CHF 849 million to the best applications. By awarding public research money based on a competitive system, the SNSF contributes to the high quality of Swiss research. In close collaboration with higher education institutions and other partners, the SNSF strives to create optimal conditions for the development and international integration of Swiss research. It pays particular attention to the promotion of young researchers. In addition, it accepts evaluation mandates to ensure that large Swiss research initiatives funded by third parties deliver the highest scientific quality.

Swiss Society for Microbiology

The Swiss Society for Microbiology (SSM) is the professional association of Swiss microbiologists in the fields of medical (human and veterinary), fundamental, environmental and food microbiology, virology, mycology and microbial biotechnology. It promotes the advancement of all microbiological disciplines by organizing annual meetings, workshops, courses in continuous education and by participating in current political and public microbiology related debates for the benefit of our society. The SSM advances the communication and exchange of scientific information among its members. Special attention is drawn on the encouragement and career development of young and promising members by granting an annual SSM promotion award and competitive travel fellowships for PhD students and young postdocs. The SSM currently has more than 700 members and 5 dedicated sections: clinical microbiology, environmental microbiology, mycology, prokaryotic biology and virology.

American Society for Microbiology

The American Society for Microbiology (ASM, established in 1899) is the world's largest scientific society of individuals interested in the microbiological sciences. The Mission of the ASM is to promote and advance the microbial sciences. Membership has grown from 59 scientists in 1899 to more than 50,000 members today. With over 25,000 international members from over 160 countries. ASM's international membership is growing faster than domestic. The ASM Microbe attracts over 12,000 attendees each year (usually held in the month of May). There are over 3,000 posters presented and 300 sessions. Besides, the ASM Press Department publishes over 100 textbooks, reference books, ecosal, periodicals and more. Many are translated into multiple languages. In addition, ASM publishes 18 journals, including 5 (Journal of Microbiology and Biology Educaton, Mbio, Genome Announcements, mSystems and mSphere) that are open access.

Federation of European Microbiology Societies

The Federation of European Microbiology Societies (FEMS) is made up of an active and diverse network of around 30,000 professionals who are committed to advancing microbiology for the benefit of society in the areas of health, energy, food, materials, and the environment. Set up in 1974, today FEMS is a growing coalition of 51 member societies from 36 countries. Around half of those in our network are early career researchers, and others are business partners, scientists or campaigners. FEMS nurtures this network with a variety of knowledge development and network-building activities: publication of five highly regarded journals, organization of a biennial scientific congress (this event is hosted in different European locations and hosts some of the biggest names in microbiology, attracting around 2,000 participants), provision of small research and meeting grants, awards programs and promotion of education and continuing professional development (CPD).

Corporate Sponsors

Gold sponsors

Becton-Dickinson

BD is a global medical technology company that is Advancing the world of health by improving medical discovery, diagnostics and the delivery of care. BD leads in patient and health care worker safety and the technologies that enable medical research and clinical laboratories. The company provides innovative solutions that help advance medical research and genomics, enhance the diagnosis of infectious disease and cancer, improve medication management, promote infection prevention, equip surgical and interventional procedures, optimize respiratory care and support the management of diabetes. The company partners with organizations around the world to address some of the most challenging global health issues. BD has more than 45,000 associates across 50 countries who work in close collaboration with customers and partners to help enhance outcomes, lower health care delivery costs, increase efficiencies, improve health care safety and expand access to health. For more information on BD, please visit www.bd.com.

Danone

Danone is a leading global food company built on four business lines: Essential Dairy and Plant-Based Products, Early Life Nutrition, Waters and Advanced Medical Nutrition.

R&I is at the very heart of Danone's mission: "bringing health through food to as many people as possible".

Danone Nutricia Research combines the research and innovation of Danone, through 1500 researchers and developers all around the world, gathered in 5 research centers and 55 R&I branches.

Danone Nutricia Research delivers safe, healthy and enjoyable food products firmly rooted in scientific and technological knowledge and understanding of the consumers.

Oxford Nanopore Technologies

Oxford Nanopore Technologies has developed the world's first and only nanopore DNA sequencer, the MinION™. The MinION is a portable, real time, long-read, low cost device that has been designed to bring easy biological analyses to anyone, whether in scientific research, education or a range of real world applications such as disease/pathogen surveillance, environmental monitoring, food chain surveillance, self-quantification or even microgravity biology. Already extensively used in the research of pathogens and species identification, it is uniquely positioned to provide real time DNA-based surveillance throughout a food chain, which may provide rich data on food authenticity, composition and deterioration/contamination. Nanopore devices perform DNA/RNA sequencing directly and in real time. The technology is scalable from miniature devices to high-throughput installations. GridION X5™ is a compact benchtop system designed to run and analyse up to five MinION Flow Cells. It is ideal for labs with multiple projects that need the advantages of nanopore sequencing: simple library preparation, real-time analysis and new biological insights from long reads. PromethION™ is a standalone benchtop instrument designed for high-throughput, high sample-number analyses. Its modular design allows a new paradigm of versatile workflow where many different experiments may be run in real time. Read more: www.nanoporetech.com

Roche Diagnostics (Switzerland) Ltd

As a research-focused healthcare company, Roche discovers, develops and provides innovative diagnostic and therapeutic products and services that deliver significant benefits to patients and healthcare professionals – from early detection and prevention of diseases to diagnosis, treatment, and treatment monitoring.

Roche Diagnostics (Switzerland) Ltd is the Swiss sales organisation of the Diagnostics Division of the F. Hoffmann-La Roche Group, with headquarter in Rotkreuz, Canton Zug, and a workforce of over 140 employees.

The broad portfolio of in vitro diagnostics (IVD) encompasses innovative tests and systems for the early detection of disease, targeted screening, and for the diagnosis and monitoring of disease. Some of these IVD play a key role in the pioneering field of Personalised Healthcare.

The Roche NimbleGen next-generation sequencing technologies allow researchers to selectively target DNA or RNA sequences of interest in human or non-human genomes, either through focused exomes, transcriptomes or custom designed gene panels for variant discovery and validation. With tools for targeted DNA sequencing, Roche is enabling the life science community to achieve their research goals more efficiently in

order to understand the association genomics and epigenomics have with diseases and biological processes.

Roche Diagnostics (Switzerland) Ltd helps their customers - patients, private and hospital laboratories, universities, medical practices, life science communities and research institutes in Switzerland - to optimise their success for the benefit of patients by increasing their diagnostics capabilities.

Silver sponsors

Bio-Mérieux

A world leader in the field of in vitro diagnostics for 50 years (celebrated in 2013), bioMérieux provides diagnostic solutions (reagents, instruments, software and services) which determine the source of disease and contamination to improve patient health and ensure product safety. Today, bioMérieux is present in more than 150 countries through 42 subsidiaries and a large network of distributors. bioMérieux employs Over 9,438 employees, with nearly 3000 in 19 production sites and nearly 1400 in 20 R&D sites. Especially, bioMérieux provides a wide range of diagnostic solutions in the fields of infectious diseases, hospital-acquired infections, antibiotic-resistance and cancer. For more information, visit www.biomerieux.com.

Fasteris

Fasteris SA is a sequencing service provider based in Geneva, Switzerland. We offer the longest experience in Next Generation Sequencing (NGS): our co-founder L. Farinelli is co-inventor of DNA clusters (1996).

Our main applications are designed for researchers, industrial and pharma customers as well as medical diagnostics: Transcriptomes, Small RNA, Exomes and panels, Whole genomes, ChIP-SEQ, Metagenomics (PCR 16S/18S/ITS), or Custom projects.

We are equipped with illumina (MiSeq, NextSeq, HiSeq4000) or ThermoFisher (Ion S5 XL) NGS instruments.

Fasteris shares co-authorship of more than 50 publications and is cited in over 500 (see Fasteris website).

Next Generation Sequencing, illumina, ThermoFisher, Sanger DNA sequencing, Bioinformatics

Ferring

Headquartered in Saint-Prex, Switzerland, Ferring Pharmaceuticals is a research-driven, specialty biopharmaceutical group active in global markets. The company identifies, develops and markets innovative products in the areas of reproductive health, urology, gastroenterology, endocrinology and orthopaedics. Ferring has its own operating subsidiaries in nearly 60 countries and markets its products in 110 countries. To learn more about Ferring or its products please visit www.ferring.com.

Institut Mérieux

Institut Mérieux is contributing its experience in biology to improve medicine and public health across the globe. To fight against infectious diseases and cancer, the Institute imagines and develops new approaches in the fields of diagnostics, immunotherapy, food safety, and nutrition. Its three bio-industrial companies (bioMérieux, Transgene and Mérieux NutriSciences), working closely with its entities devoted to innovation (such as ABL Inc. and Mérieux Développement), have contributed to major advances in medicine and public health. Institut Mérieux employs more than 15,000 people around the world and is present in over 40 countries, with close to 2.5 billion euros in sales.

MaaT Pharma

MaaT Pharma (Microbiota as a Therapy) is a French biotech start-up, created at the end of 2014, to treat serious diseases linked to imbalances in the intestinal microbiome. It has developed the first treatment solution based on autologous microbiotherapy. MaaT Pharma envisages a first therapeutic application for patients suffering from leukaemia and bone & joint infections, whose major treatment contributes to dysbiosis. Funded jointly by a team which brings together world-class medical-scientific and entrepreneurial skills, MaaT Pharma has the ambition of becoming a leader in microbiome protection and the treatment of dysbiosis.

Research

Nestlé

We are the leading Nutrition, Health and Wellness Company. We enhance lives with science-based nutrition and health solutions for all stages of life, helping consumers care for themselves and their families. Innovation has been at the heart of our company since its beginning. We have the largest R&D network of any food company in the world, with 34 R&D facilities (3 Science & Research centres and 31 Product Technology Centres and R&D centres worldwide), and over 5,000 people involved in R&D. Behind every one of Nestlé's products there is a team of scientists, engineers, nutritionists, designers, regulatory specialists and consumer care representatives dedicated to earn our consumers' trust with safe products of the highest quality: at Nestlé, safety and quality are non-negotiable. For more information, visit www.nestle.com.

PathoQuest

PathoQuest, a spin-off of Institut Pasteur, offers a game-changing NGS-based metagenomics approach which improves the breadth of pathogen detection. The company's proprietary sample-to-report process, applicable to various biological sample types, addresses current limitations associated with pathogen detection. Major biopharmaceutical companies have chosen Pathoquest's innovative solutions for viral safety. The Company's iDTECT™ Blood test is the first IVD CE marked metagenomic test. This new molecular test provides clinicians an improved method for detecting pathogens and major antibiotic resistance genes in blood samples from immunocompromised patients with suspected infections. It is anticipated to contribute to improved antibiotic stewardship and precision medicine strategies.

Informations

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Post Grade CME

Infectious Diseases, Gastro-Enterology, Oncology, Internal Medicine, Microbiology, Lab Medicine

FAMH (4 + 6 hours)

Société suisse d'infectiologie (4 hours)

Société Suisse de Médecine Interne Générale (8 credits for "formation continue essentielle MIG")