





Workshop on Next Generation Sequencing of Viruses

Auditorium F Jacob, Institut Pasteur, Paris, France 20 & 21 May 2015

Programme

DAY 1 – WEDNESDAY 20TH MAY

8:00 – 9:00	Registration
9:00 – 9:15	Welcome/Objectives Sylvie van der Werf and Alan Hay
SESSION 1:	Objectives of NGS/Deep Sequencing – Possibilities & Limitations Chairs: John McCauley and Peter Walker
9:15 – 9:40	The Evolution and Epidemiology of Virus Epidemics from Genome Sequencing Andrew Rambaut, Institute of Evolutionary Biology, Edinburgh, UK
9:40 – 10:05	Virus Discovery Ron Fouchier, Erasmus MC, Rotterdam, The Netherlands
10:05 – 10:30	Outbreak Detection and Investigation with NGS Martin Beer, Friedrich Loeffler Institute, Isle of Riems, Germany
10:30 – 10:45	Discussion
10:45 – 11:15	Tea/Coffee Break
10.45 - 11.15	Tearconee Dieak
SESSION 2:	Sequencing Technologies - Current & Future Developments Chairs: David Wentworth and Nicholas Loman
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SESSION 2: 11:15 – 11:40	Sequencing Technologies - Current & Future Developments Chairs: David Wentworth and Nicholas Loman Platforms and Pipelines (Now and in the Future) David Wentworth, CDC, Atlanta, GA, USA Respiratory Virus RNA Detection with RNA-Seq Using Capture Technology
SESSION 2: 11:15 – 11:40 11:40 – 11:55	Sequencing Technologies - Current & Future Developments Chairs: David Wentworth and Nicholas LomanPlatforms and Pipelines (Now and in the Future) David Wentworth, CDC, Atlanta, GA, USARespiratory Virus RNA Detection with RNA-Seq Using Capture Technology Gary Schroth, Illumina, San Diego, CA, USABacterial and Viral Sequencing with Ion Torrent NGS Technology

12:30 – 13:30	Lunch
SESSION 3:	Sample Preparation, Data processing, Assembly, Analysis Chairs: Marco Vignuzzi and Elodie Ghedin
13:30 – 13:55	Sample Preparation & Analysis Saskia Smits, Erasmus MC, Rotterdam, The Netherlands
13:55 – 14:20	Data Processing, Assembly, Analysis Simon Watson, Sanger Institute, Hinxton, UK
14:20 – 14:35	Consensus Iterator: a Hybrid Algorithm for Consensus Sequence Determination in the Presence of Noisy Short-Read Shotgun Sequence Data Robert Carter, St. Jude Children's Research Hospital, Memphis, TN, USA
14:35 – 14:55	Optimising the Reconstruction of Whole Genomes, for HIV and Other Diverse Viruses, from NGS Data Chris Wymant, Imperial College London, UK
14:55 – 15:10	Discussion
15:10 – 15:30	Tea/Coffee Break
SESSION 4:	Examples of Different Virus Pipelines Chairs: Ron Fouchier and Martin Beer
15:30 – 15:50	RSV and Other viruses Matthew Cotten, Sanger Institute, Hinxton, UK
15:50 – 16:10	MERS Coronavirus Sequences Detected in Dromedary Camels from a Single Farm Leo Poon, The University of Hong Kong, Hong Kong, SAR China
16:10 – 16:30	Intrinsic Genetic Diversity of Rabies Virus and Host Adaptation Hervé Bourhy, Institut Pasteur, Paris, France
16:30 – 16:50	Prospective, Real-Time Nanopore Sequencing for Ebola Genomic Epidemiology under Outbreak Conditions Nicholas Loman, Birmingham University, Birmingham, UK
16:50 – 17:00	Discussion
17:00 – 17:30	General Discussion Chairs: David Wentworth and Elodie Ghedin
19:30	Dinner at Restaurant "L'entrepôt"

DAY 2 - THURSDAY 21ST MAY

SESSION 4:	Examples of Different Virus Pipelines – Continued Chairs: Gavin Smith and Hervé Bourhy
9:00 – 9:20	Are Arthropods at the Heart of Virus Evolution? Yong-Zhen Zhang, China-CDC, Beijing, China
9:20 – 9:40	Virus Identification in Biological Samples by NGS: Validation and Examples of Use in Clinical Cases Marc Eloit, Institut Pasteur, Paris, France
09:40 – 09:55	Full-Length HIV-1 env Deep Sequencing in a Donor with Broadly Neutralizing V1/V2 Antibodies Melissa Laird, Pacific Biosciences, Menlo Park, CA, USA
09:55 – 10:10	European Mobile Lab NGS Pipeline David Matthews, Bristol University, Bristol, UK
10:10 – 10:30	Discussion
10:30 – 11:00	Tea/Coffee Break
SESSION 5:	Advances in Understanding of Viral Infections from NGS data Chairs: Andrew Rambaut and Maria Zambon
11:00 – 11:25	Going Viral: NGS Platform Integration for Analysis of Virus Diversity and Population Dynamics Elodie Ghedin, New York University, New York, NY, USA
11:25 – 11:50	Data to Knowledge: Data Integration and Big Data Maria Giovanni, NIAID, Rockville, MD, USA
11:50 – 12:05	Lessons from Developing a New Influenza Annotation Pipeline Benjamin Turner, QIAGEN Custom Informatics Solutions, Hilden, Germany
12:05 – 12:20	Discussion
12:20 – 13:20	Lunch
SESSION 5:	Advances in Understanding of Viral Infections from NGS data – Continued Chairs: Monica Galiano and Nancy Cox
13:20 – 13:40	Metagenomic Detection of Immunogenic Parasites in Bat Feces Gavin Smith, Duke NUS, Singapore
13:40 – 13:55	Reconstruction of an Empirical Fitness Landscape Reveals the Mutational Robustness and Evolvability of RNA Viruses Marco Vignuzzi, Institut Pasteur, Paris, France

13:55 – 14:10	The Intrinsic Heterogeneity of Human Influenza A Viruses Evaluated by Deep Sequencing the Virus Directly in Nasal Swabs Cyril Barbezange, Institut Pasteur, Paris, France
14:10 – 14:25	Testing for Drug Resistance in Influenza: Taking It to Another Level? Larisa Gubareva, Influenza Division, CDC, Atlanta, GA, USA
14:25 – 14:35	Use of Next Generation Sequencing for the Detection of Antiviral Resistant Influenza Viruses Aeron Hurt, WHO CC, Melbourne, Australia
14:35 – 14:55	Whole-Genome Deep Sequencing of Longitudinal Samples from HIV-1 Patients Followed from Early into Chronic Infection Richard Neher, Max-Planck-Institute for Developmental Biology, Tubingen, Germany
14:55 – 15:10	Discussion
15:10 – 15:30	Tea/Coffee Break
SESSION 6:	Significance and Communication of Information Chairs: Sylvie van der Werf and Maria Giovanni
15:30 – 15:55	The Public Health Importance of Timely Sharing of Sequence Data Nancy Cox, GISAID Scientific Advisory Council
15:55 – 16:20	Public Health Perspective (Surveillance; Zoonotic Risk) Maria Zambon, Public Health England, London, UK
16:20 – 16:45	Applications of NGS in Animal Health Peter Walker, CSIRO, Geelong, Victoria, Australia
16:45 – 17:00	Discussion
17:00 – 17:30	General Discussion (Conclusions) Chairs: Andrew Rambaut and Maria Giovanni
17:30	Close of Workshop