

## Oral Programme

Tuesday, 10 May 2016

**15:00-19:00** Registration | *Karibu*

**19:00-20:00** Welcome drink

Wednesday, 11 May 2016

**07:00-08:30** Registration | *Health Services Foyer*

**Room** Health Services Auditorium

**08:30-09:30** Opening session

**09:30-10:00** [PI.01] A population genetics view of virus evolution

F. González-Candelas<sup>\*1,2</sup>, M.A. Bracho<sup>1,2</sup>, J.M. Cuevas<sup>1</sup>, N. García-González<sup>1,2</sup>, F.X. López-Labrador<sup>1,2</sup>, J.A. Patiño-Galindo<sup>1,2</sup>, M. Torres-Puente<sup>1,2</sup>, <sup>1</sup>University of Valencia, Spain, <sup>2</sup>FISABIO-Public Health, Spain, <sup>3</sup>CIBERESP, Spain

**10:00-10:30** Coffee break | *Health Services Café*

**10:30-11:00** [PI.02] Pathogens as a driving force in human evolution

M. Sironi, *Bioinformatics - Scientific Institute IRCCS E.MEDEA, Italy*

**11:00-11:30** [PI.03] Origin, spread and global evolution of HIV

M. Peeters<sup>\*</sup>, M. d'Arc, C.J. Villabona-Arenas, A. Ayoub, E. Delaporte, *Institut de Recherche pour le Développement (IRD), France*

**11:30-13:00** Poster session 1 and lunch | *Karibu*

**13:00-15:00** Symposium 1

Room	Aula PG Janssens	Forum 2&3	Auditorium Rochus
	<b>HIV epidemiology and evolution</b> <i>Chairs : Martine Peeters and Dimitrios Paraskevis</i>	<b>Host parameters</b> <i>Chairs : Manuela Sironi and Joey Verdi</i>	<b>Phylogenetics and phylogeography</b> <i>Chairs : Fernando Gonzalez Candelas and Matthew Scotch</i>
<b>13:00-13:17</b>	<b>[S1.A.01] Spatiotemporal characteristics of the CRF02_AG epidemic in Russia and central Asia</b> E. Kostaki <sup>1</sup> , M. Bobkova <sup>2</sup> , M. Oikonomopoulou <sup>1</sup> , G. Magiorkinis <sup>1,3</sup> , A. Hatzakis <sup>1</sup> , D. Paraskevis <sup>*1</sup> , <sup>1</sup> Athens University Medical School, Greece, <sup>2</sup> FSBI "N.F. Gamaleya FRCEM" of the Ministry of Health of the Russian Federation, Russia, <sup>3</sup> University of Oxford, UK	<b>[S1.B.01] Germline transmission of targeted baboon apolipoprotein L-I in mice protects against African trypanosomes</b> J. Verdi <sup>*1,2</sup> , J. Pant <sup>1,2</sup> , D. Kovacsics <sup>1</sup> , M. Yu <sup>3</sup> , S. Kemp <sup>3</sup> , C. Schoenherr <sup>4</sup> , A. Economides <sup>4</sup> , D. Frendewey <sup>4</sup> , V. Lai <sup>4</sup> , J. Raper <sup>1,2</sup> , <sup>1</sup> The Graduate Center at the City University of New York, USA, <sup>2</sup> Hunter College at the City University of New York, USA, <sup>3</sup> International Livestock Research Institute, Kenya, <sup>4</sup> Regeneron Pharmaceuticals, USA	<b>[S1.C.01] Incorporating geospatial observation error in discrete Bayesian virus phylogeography</b> M. Scotch <sup>*1</sup> , R. Beard <sup>1</sup> , T. Tahsin <sup>1</sup> , D. Weissenbacher <sup>1</sup> , M.A. Suchard <sup>2</sup> , G. Gonzalez <sup>1</sup> , <sup>1</sup> Arizona State University, USA, <sup>2</sup> University of California, USA
<b>13:17-13:34</b>	<b>[S1.A.02] Identification of a large, fast-expanding HIV-1 subtype B transmission cluster among men who have sex with men in Valencia, Spain</b> J.A.P. Galindo <sup>*1,2</sup> , M.T. Puente <sup>1,2</sup> , M.A. Bracho-Lapiedra <sup>1,6</sup> , I. Alastrué <sup>3</sup> , A. Juan <sup>3</sup> , D. Navarro <sup>2,4</sup> , M.J. Galindo <sup>4</sup> , E. Ortega <sup>5</sup> , C. Gimeno <sup>2,5</sup> , F. Gonzalez-Candelas <sup>2,6</sup> , <sup>1</sup> FISABIO-Salud Pública, Spain, <sup>2</sup> University of Valencia, Spain, <sup>3</sup> Unidad Prevencia SIDA y otras ITS, Spain, <sup>4</sup> Hospital Clínico Universitario, Spain, <sup>5</sup> Hospital General Universitario, Spain, <sup>6</sup> CIBER Epidemiologia Salud Publica, Spain	<b>[S1.B.02] Red fox in northern Italy and neighbouring countries: Genetic and spatial characterization</b> B. Zecchin <sup>*1</sup> , M. De Nardi <sup>2</sup> , E. Vanek <sup>3</sup> , T. Bedekovic <sup>4</sup> , P. Hostnik <sup>5</sup> , M. Lorenzetto <sup>1</sup> , P. De Benedictis <sup>1</sup> , G. Cattoli <sup>1</sup> , <sup>1</sup> Istituto Zooprofilattico Sperimentale delle Venezie, Italy, <sup>2</sup> SAFOSO AG, Switzerland, <sup>3</sup> Austrian Agency for Health and Food Safety Institute for Veterinary Disease Control, Austria, <sup>4</sup> Croatian Veterinary Institute, Croatia, <sup>5</sup> University of Ljubljana, Slovenia	<b>[S1.C.02] Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation</b> G. Baele <sup>*1</sup> , M.A. Suchard <sup>2</sup> , F. Bielejec <sup>1</sup> , P. Lemey <sup>1</sup> , <sup>1</sup> Rega Institute, Belgium, <sup>2</sup> University of California, USA

13:34-13:51	<p><b>[S1.A.03] Molecular epidemiology HIV-1 in northern Alberta: A combined analysis of viral genetic and public health data</b></p> <p>D. Adachi<sup>1</sup>, B. Vrancken<sup>*2</sup>, M. Benedet<sup>1</sup>, A. Singh<sup>3</sup>, R. Read<sup>4</sup>, S. Shafran<sup>3</sup>, G.D. Taylor<sup>3</sup>, S. Houston<sup>3</sup>, K. Simmonds<sup>5</sup>, C. Sikora<sup>6</sup>, <sup>1</sup>Alberta Provincial Laboratory for Public Health, Canada, <sup>2</sup>Rega Institute for Medical Research, Belgium, <sup>3</sup>University of Alberta,, Canada, <sup>4</sup>University of Calgary, Canada, <sup>5</sup>Alberta Health Services, Canada, <sup>6</sup>Alberta Health Services, Canada</p>	<p><b>[S1.B.03] Human leukocyte antigen-g: a promising marker of predisposition to tropical parasitic diseases?</b></p> <p>D. Courtin<sup>*1,2</sup>, L. Gineau<sup>1,2</sup>, J. Milet<sup>1,2</sup>, A. Sabbagh<sup>1,2</sup>, I. Sadissou<sup>3</sup>, T. D'Almeida<sup>1,2</sup>, P. Sonon<sup>3</sup>, N. Rouas-Freiss<sup>4,5</sup>, P. Moreau<sup>4,5</sup>, E. Donadi<sup>3</sup>, <sup>1</sup>Institut de Recherche pour le Développement, France, <sup>2</sup>Université Paris Descartes, France, <sup>3</sup>University of Sao Paulo, Brazil, <sup>4</sup>Commissariat à l'Energie Atomique et aux Energies Alternatives, France, <sup>5</sup>Université Paris Diderot, France, <sup>6</sup>Centre d'Etude et de Recherche sur le Paludisme Associé à la Grossesse et à l'Enfance, Benin, <sup>7</sup>Institut de Recherche pour le Développement, Benin</p>	<p><b>[S1.C.03] Discovering potential sources of emerging pathogens: South America is a reservoir of generalist avian blood parasites</b></p> <p>M.A.J. Moens<sup>*</sup>, J. Pérez-Tris, <i>Universidad Complutense de Madrid, Spain</i></p>
13:51-14:08	<p><b>[S1.A.04] Phylodynamic analysis of the HIV-1 suboutbreaks among people who inject drugs (PWID) in Athens</b></p> <p>D. Paraskevis<sup>*1</sup>, E. Kostaki<sup>1</sup>, G. Nikolopoulos<sup>2</sup>, A. Flampouris<sup>1</sup>, E. Papachristou<sup>1</sup>, C. Tsiara<sup>2</sup>, V. Sypsa<sup>1</sup>, A. Hatzakis<sup>1</sup>, <sup>1</sup>Athens University Medical School, Greece, <sup>2</sup>Hellenic Center for Disease Control and Prevention, Greece</p>	<p><b>[S1.B.04] Apolipoprotein L1 variant associated with increased susceptibility to trypanosome infection</b></p> <p>B. Cuypers<sup>*1,2</sup>, L. Lecordier<sup>3</sup>, C.J. Meehan<sup>1</sup>, F. Van den Broeck<sup>1</sup>, H. Imamura<sup>1</sup>, P. Büscher<sup>1</sup>, J.-C. Dujardin<sup>1</sup>, K. Laukens<sup>2</sup>, E. Pays<sup>3</sup>, S. Deborggraeve<sup>2</sup>, <sup>1</sup>Institute Of Tropical Medicine, Belgium, <sup>2</sup>University Of Antwerp, Belgium, <sup>3</sup>Université Libre de Bruxelles, Belgium</p>	<p><b>[S1.C.04] Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium</b></p> <p>L. Laenen<sup>*</sup>, S. Dellicour, V. Vergote, I. Nauwelaers, S. De Coster, I. Verbeeck, M. Van Ranst, P. Lemey, P. Maes, <i>KU Leuven-University of Leuven, Belgium</i></p>
14:08-14:25	<p><b>[S1.A.05] Molecular analysis of HIV infected individuals in a network-based intervention (TRIP) in Athens: Phylogenetics identify HIV infected individuals with social links</b></p> <p>E. Kostaki<sup>1</sup>, E. Pavlitina<sup>2</sup>, L. Williams<sup>3</sup>, J. Schneider<sup>4</sup>, B. Skaathun<sup>4</sup>, E. Morgan<sup>4</sup>, M. Psychogiou<sup>5</sup>, V. Sypsa<sup>1</sup>, P. Smyrnov<sup>6</sup>, A. Korobchuk<sup>6</sup>, M. Malliori<sup>7</sup>, A. Hatzakis<sup>1</sup>, S. Friedman<sup>3</sup>, G. Nikolopoulos<sup>2</sup>, D. Paraskevis<sup>*1</sup>, <sup>1</sup>University of Athens, Greece, <sup>2</sup>Transmission Reduction Intervention Project, Greece, <sup>3</sup>National Development and Research Institutes, USA, <sup>4</sup>Center for AIDS Elimination, USA, <sup>5</sup>First Department of Internal Medicine, Greece, <sup>6</sup>Alliance for Public Health, Ukraine, <sup>7</sup>University of Athens, Greece</p>	<p><b>[S1.B.05] Identification of a mannose-binding lectin implicated in the resistance mechanism of Trypanosoma brucei gambiense against the lytic action of the human serum</b></p> <p>J.M. Bart<sup>*1,2</sup>, C. Cordon-Obras<sup>2</sup>, A. Benito<sup>1</sup>, M. Navarro<sup>2</sup>, <sup>1</sup>Instituto de Salud Carlos III, Spain, <sup>2</sup>Consejo Superior de Investigación Científica, Spain</p>	<p><b>[S1.C.05] Flexible inference method to reconstruct phylogenetic and transmission trees from densely sampled outbreaks</b></p> <p>D. Klinkenberg<sup>*</sup>, J. Backer, J. Wallinga, <i>National Institute for Public Health and the Environment, The Netherlands</i></p>
14:25-14:42	<p><b>[S1.A.06] A phylogenetic comparison between Sanger sequencing and 454 pyrosequencing derived HIV-1 pol sequences</b></p> <p>A. Beloukas<sup>*1,2</sup>, H. Papachristou<sup>1</sup>, E. Kostaki<sup>1</sup>, A. Hatzakis<sup>1</sup>, D. Paraskevis<sup>1</sup>, <sup>1</sup>University of Athens, Greece, <sup>2</sup>Institute of Infection and Global Health, University of Liverpool, UK</p>	<p><b>[S1.B.06] When viruses don't go viral: The importance of host phylogeography in the spatial spread of arenaviruses</b></p> <p>S. Gryseels<sup>*1</sup>, S. Baird<sup>2</sup>, R. Makundi<sup>3</sup>, B. Borremans<sup>1</sup>, H. Leirs<sup>1</sup>, J.G. de Bellocq<sup>2</sup>, <sup>1</sup>University of Antwerp, Belgium, <sup>2</sup>Institute of Vertebrate Biology, Czech Republic, <sup>3</sup>Sokoine University of Agriculture, Tanzania</p>	<p><b>[S1.C.06] Effect of RNA substitution models on viroid and RNA virus phylogenetics</b></p> <p>J.A.P. Galindo<sup>*1,2</sup>, O. Pybus<sup>3</sup>, F. Gonzalez-Candelas<sup>1,2</sup>, <sup>1</sup>University of Valencia, Spain, <sup>2</sup>FISABIO-Salud Pública, Spain, <sup>3</sup>University of Oxford, UK</p>

14:42-15:00	<p><b>[S1.A.07] HIV epidemic dynamics in people who inject drugs inferred from data from Russia and Ukraine</b>  T.I. Vasylyeva*<sup>1</sup>, S.R. Friedman<sup>2</sup>, A. Hatzakis<sup>3</sup>, O.G. Pybus<sup>1</sup>, A. Katzourakis<sup>1</sup>, P. Smyrnov<sup>4</sup>, T. Karamitros<sup>1,3</sup>, D. Paraskevis<sup>3</sup>, G. Magiorkinis<sup>1</sup>, <sup>1</sup>University of Oxford, UK, <sup>2</sup>National Development and Research Institutes, USA, <sup>3</sup>Athens University Medical School, Greece, <sup>4</sup>International HIV/AIDS Alliance in Ukraine, Ukraine</p>	<p><b>[S1.B.07] Human geographic population structure and susceptibility to infectious diseases</b>  M. Tibayrenc, <i>IRD Center, France</i></p>	
15:00-15:30	<b>Coffee break   Karibu</b>		
15:30-17:30	<b>Symposium 2</b>		
<b>Room</b>	<b>Auditorium Rochus</b>	<b>Forum 2&amp;3</b>	<b>Aula PG Janssens</b>
	<p><b>Virology of veterinary relevance</b>  <i>Chairs : Daniel Cadar and Fernando Gonzalez Candelas</i></p>	<p><b>Helminth biology and evolution</b>  <i>Chairs : Serge Morand and Thomas J. Crellen</i></p>	<p><b>Ecology and Evolution of Bacteria 1</b>  <i>Chairs : Thierry Wirth and Noémie S. Becker</i></p>
15:30-15:50	<p><b>[S2.A.01] Phylogenetic analysis of BVDV in Canada</b>  A. Chernick*, F. van der Meer, <i>University of Calgary, Canada</i></p>	<p><b>[S2.B.01] Trematode-mitogenomic database with addition of species from Heterophyidae, Echinostomatidae, Opisthorchiidae and Fasciolidae for biomedical studies</b>  T.H. Le*, N.T.B. Nguyen, D.T. Roan, N.T. Khue, D.T.T. Huong, D.T. Dung, <i>Vietnam Academy of Science and Technology, Vietnam</i></p>	<p><b>[S2.C.01] Borrelia burgdorferi sensu lato - the global evolution of a bacterial species complex</b>  N.S. Becker*<sup>1</sup>, G. Margos<sup>2</sup>, H. Blum<sup>1</sup>, S. Krebs<sup>1</sup>, S. Graf<sup>1</sup>, S. Castillo-Ramirez<sup>3</sup>, A. Sing<sup>2</sup>, V. Fingerle<sup>2</sup>, <sup>1</sup>Ludwig Maximilian Universität Munich, Germany, <sup>2</sup>National Reference Centre for Borrelia at the Bavarian Health and Food Safety Authority, Germany, <sup>3</sup>Universidad Nacional Autónoma de México, Mexico</p>
15:50-16:10	<p><b>[S2.A.02] Bluetongue virus spread in Europe is a consequence of host, climatic and landscape factors</b>  M. Jacquot*<sup>1</sup>, K. Nomikou<sup>2</sup>, J. Hughes<sup>1</sup>, M. Palmarini<sup>1</sup>, P. Mertens<sup>2</sup>, R. Biek<sup>1</sup>, <sup>1</sup>University of Glasgow, UK, <sup>2</sup>The Pirbright Institute, UK</p>	<p><b>[S2.B.02] Population genomics of human parasite schistosoma mansoni: Population history and effects of selection</b>  T.J. Crellen*<sup>1,2</sup>, F. Allan<sup>3</sup>, S. David<sup>2</sup>, C. Durrant<sup>2</sup>, T. Huckvale<sup>2</sup>, N. Holroyd<sup>2</sup>, A.M. Emery<sup>3</sup>, D. Rollinson<sup>3</sup>, D.M. Aanensen<sup>1,2</sup>, M. Berriman<sup>2</sup>, <sup>1</sup>Imperial College London, UK, <sup>2</sup>Wellcome Trust Sanger Institute, UK, <sup>3</sup>Natural History Museum London, UK, <sup>4</sup>Royal Veterinary College London, UK</p>	<p><b>[S2.C.02] Two years molecular surveillance of Vibrio cholerae in potable environmental water in cholera endemic region of Central India</b>  M. Jain*<sup>1,2</sup>, P. Kumar<sup>1,3</sup>, A.K. Goel<sup>1</sup>, <sup>1</sup>Defence Research &amp; Development Establishment, India, <sup>2</sup>Jiwaji University, India, <sup>3</sup>National Centre for Disease Control, India</p>
16:10-16:30	<p><b>[S2.A.03] Within-host genetic diversity of an H3N6 avian influenza virus in ferrets</b>  A. Fusaro*, F. Bonfante, E. Mastrorilli, A. Milani, L. Tassoni, A. Salviato, A. Romero, I. Monne, G. Cattoli, <i>Istituto Zooprofilattico Sperimentale delle Venezie, Italy</i></p>	<p><b>[S2.B.03] A link between parasite genotype and host disease phenotype in human schistosomiasis?</b>  N. Boon*<sup>1,2</sup>, F. Van den Broeck<sup>1,2</sup>, L. Meurs<sup>2</sup>, F. Volckaert<sup>1</sup>, K. Polman<sup>2</sup>, T. Huyse<sup>3,2</sup>, <sup>1</sup>KU Leuven, Belgium, <sup>2</sup>Institute of Tropical Medicine, Belgium, <sup>3</sup>Royal Museum for Central Africa, Belgium</p>	<p><b>[S2.C.03] Micro-epidemiological approach to understanding transmission dynamics of Mycobacterium ulcerans in the Ouémé river valley in southern Benin</b>  M. Eddyani*<sup>1</sup>, K. Vandellanoot<sup>1</sup>, C. Meehan<sup>1</sup>, N. Boon<sup>1</sup>, D. Affolabi<sup>2</sup>, J. Aguiar<sup>3</sup>, J. Porter<sup>5</sup>, E. Abatih<sup>1</sup>, J.G. Houezo<sup>4</sup>, G. Sopoh<sup>4</sup>, <sup>1</sup>Institute of Tropical Medicine, Belgium, <sup>2</sup>Laboratoire de Référence des Mycobactéries, Benin, <sup>3</sup>Centre de Dépistage et de Traitement de l'Ulcère de Buruli Gbemotin, Benin, <sup>4</sup>Centre de Dépistage et de Traitement de l'Ulcère de Buruli d'Allada, Benin, <sup>5</sup>University of Melbourne, Australia</p>

16:30-16:50	<b>[S2.A.04] Intraspecific molecular characterization of bovine coronavirus (BCoV)</b> N. Kin <sup>*1,2</sup> , F. Mischczak <sup>1,2</sup> , L. Diancourt <sup>4</sup> , V. Caro <sup>4</sup> , F. Moutou <sup>5</sup> , A. Vabret <sup>2,3</sup> , M. Le Gouil <sup>2</sup> , <sup>1</sup> Normandie Université, France, <sup>2</sup> University of Caen Normandy, France, <sup>3</sup> University Hospital of Caen, France, <sup>4</sup> Institut Pasteur, France, <sup>5</sup> ANSES Boulogne Billencourt, France	<b>[S2.B.04] Gastrointestinal parasite sharing in multi-host primate communities</b> L. Frias*, M. Okamoto, A. MacIntosh, <i>Kyoto University, Japan</i>	<b>[S2.C.04] Molecular epidemiology of carbapenem non-susceptible <i>Acinetobacter baumannii</i> from a university hospital in Egypt</b> A.M. El Banna, N.N. Nawar, R.M. Mohamed, S.T. Salem*, <i>Faculty of Medicine - Cairo University, Egypt</i>
16:50-17:10	<b>[S2.A.05] Bat coronaviruses in France and western palearctic: After mers and sars, are there other candidates to emergence?</b> M. Ar Gouilh <sup>*1,4</sup> , S.J. Puechmaille <sup>2</sup> , L. Diancourt <sup>1</sup> , M. Vandenberghe <sup>1</sup> , V. Caro <sup>1</sup> , J. Serra <sup>1</sup> , A. Vabret <sup>1</sup> , J.C. Manuguerra <sup>1</sup> , <sup>1</sup> Institut Pasteur, France, <sup>2</sup> Université de Caen Normandie, France, <sup>3</sup> Greifswald University, Germany, <sup>4</sup> Universitat de Barcelona, Spain	<b>[S2.B.05] Global change and tropical infectious disease in Europe: The emergence of urinary schistosomiasis in Corsica (France)</b> T. Huyse <sup>*1,2</sup> , N. Boon <sup>2,3</sup> , B. Webster <sup>4</sup> , K. Polman <sup>2</sup> , J. Boissier <sup>5</sup> , <sup>1</sup> Royal Museum for Central Africa, Belgium, <sup>2</sup> Institute of Tropical Medicine, Belgium, <sup>3</sup> University of Leuven, Belgium, <sup>4</sup> The Natural History Museum, UK, <sup>5</sup> Université de Perpignan, France	<b>[S2.C.05] The effect of tick feeding ecology on the distribution of <i>Borrelia burgdorferi</i> OspC major groups</b> S.N. Seifert*, O. Onder, B.A. Garcia, D. Brisson, <i>University of Pennsylvania, USA</i>
17:10-17:30	<b>[S2.A.06] Standardizing bovine sample preparation procedures for viral metagenomics</b> M.R. Garcia*, A. Chernick, R. Dardari, C. Dalton, F. van der Meer <i>University of Calgary, Canada</i>	<b>[S2.B.06] Epidemiology and genetic pattern of the emerging hybrid <i>Fasciola</i> species</b> T.H. Le <sup>*1</sup> , N.T.B. Nguyen <sup>1</sup> , D.T. Roan <sup>1</sup> , N.T. Khue <sup>1</sup> , T.T.H. Doan <sup>1</sup> , P. Dorny <sup>1</sup> , <sup>1</sup> Vietnam Academy of Science and Technology, Vietnam, <sup>2</sup> Institute of Tropical Medicine, Belgium	<b>[S2.C.06] Molecular epidemiology of leprosy in a region of high incidence in the state of Mato Grosso, Brazil</b> L.R. De Lamano <sup>1</sup> , W. Li <sup>2</sup> , A.B. Fontes <sup>3</sup> , L. Fachin <sup>1</sup> , A.F.F. Belone <sup>1</sup> , C. Ghidella <sup>4</sup> , M. Virmond <sup>1</sup> , V. Vissa <sup>2</sup> , P.N. Suffys <sup>3,5</sup> , I.M.F. Dias-Baptista <sup>*1</sup> , <sup>1</sup> Instituto Lauro de Souza Lima, Brazil, <sup>2</sup> Colorado State University, USA, <sup>3</sup> FIOCRUZ, Brazil, <sup>4</sup> Centro de Referencia Jardim Guanabara, Brazil, <sup>5</sup> Institute of Tropical Medicine, Belgium
17:45-20:00	<b>Free walking tour and City Welcome Reception</b>		
<b>Thursday, 12 May 2016</b>			
<b>Room</b>	<b>Health Services Auditorium</b>		
08:30-09:00	<b>[PI.04] Zikavirus 2016: Public Enemy No. 1?</b> R. Huits*, E. Bottieau, L. Cnops, K. Ariën, <i>Institute of Tropical Medicine, Belgium</i>		
09:00-09:30	<b>[PI.05] Use of mycobacterial genomes to measure the impact of man-made problems and solutions for tuberculosis control</b> C.J. Meehan, B. Ofori-Anyinam, L. Rigouts, M. Antonio, S. Niemann, F. Gehre, B.C. de Jong*, <i>Instituut voor Tropische Geneeskunde, Belgium</i>		
09:30-10:00	<b>[PI.06] Darwin's greatest discovery: Design without designer</b> F.J. Ayala, <i>University of California, USA</i>		
10:00-10:30	<b>Coffee break   Health Services Café</b>		
10:30-11:00	<b>[PI.07] Schistosomiasis: From devastating parasitic disease to tractable model system</b> T. Anderson, <i>Texas Biomedical Research institute, USA</i>		
11:00-11:30	<b>[PI.08] When a house is not a home: Innate red cell variants and protection from malaria</b> S.M. Taylor, <i>Duke University Medical Center, USA</i>		
11:30-12:00	<b>[PI.09] Academic versus industrial approaches to tracking of infectious diseases using big data</b> A. van Belkumm <i>bioMerieux Microbiology R&amp;D, France</i>		
12:00-13:50	<b>Poster session 2 and lunch   Karibu</b>		
13:00-13:50	<b>Author Workshop   Aula PG Janssens</b>		

13:50-15:30 Symposium 3			
Room	Auditorium Rochus	Forum 2&3	Aula PG Janssens
	<b>Vector biology and evolution</b> <i>Chairs : Majoline Tchioffo and Jean-Pierre Dujardin</i>	<b>Evolution of parasitic protozoa</b> <i>Chairs : Jean-Claude Dujardin and Thierry de Meeüs</i>	<b>Genomics and next-generation sequencing</b> <i>Chairs : Alex Van Belkum and C.J. Meehan</i>
13:50-14:10	<b>[S3.A.01] Phylogenetic relationship between and within populations of <i>Rhipicephalus appendiculatus</i> from different agro-ecological zones of Democratic Republic of Congo, Rwanda and Burundi</b> S.G. Amzati* <sup>1,2</sup> , R. Pelle <sup>3</sup> , M. Madder <sup>4</sup> , N. Kirschvink <sup>1</sup> , T. Marcotty <sup>1</sup> , <sup>1</sup> University of Namur, Belgium, <sup>2</sup> Université Evangélique en Afrique, Congo, <sup>3</sup> Biosciences Eastern and Central Africa International Livestock Research Institute, Kenya, <sup>4</sup> Institute of Tropical Medicine, Belgium	<b>[S3.B.01] Population genetics, reproductive strategies and taxonomic diversities of african trypanosomes</b> T. De Meeüs* <sup>1</sup> , M. Koffi <sup>2</sup> , M. Séré <sup>3</sup> , W. Weir <sup>4</sup> , <sup>1</sup> IRD, France, <sup>2</sup> Université Jean Lorougnon GUEDE, Cote D'Ivoire, <sup>3</sup> CIRDES, Burkina Faso, <sup>4</sup> Wellcome Centre for Molecular Parasitology, UK	<b>[S3.C.01] Characterising the genomic diversity of the nontuberculous mycobacterial species</b> C.J. Meehan* <sup>1</sup> , T. Fedrizzi <sup>2</sup> , I. Grottola <sup>3</sup> , E. Giacobazzi <sup>2</sup> , G.F. Serpini <sup>3</sup> , S. Tagliacuzzi <sup>3</sup> , O. Jousson <sup>2</sup> , E. Tortoli <sup>4</sup> , N. Segata <sup>2</sup> , <sup>1</sup> Institute of Tropical Medicine, Belgium, <sup>2</sup> University of Trento, Italy, <sup>3</sup> University Hospital Polyclinic, Italy, <sup>4</sup> IRCCS San Raffaele Scientific Institute, Italy
14:10-14:30	<b>[S3.A.02] Database completion and in-silico analysis of anopheles gambiae metabolism to elucidate vital insecticidal targets</b> M. Adebijiyi*, S. Fatumo, E. Adebijiyi, <i>Covenant University, Nigeria</i>	<b>[S3.B.02] Phylogenetic analysis of the <i>Trypanosoma</i> genus based on the heat-shock protein 70 gene</b> J. Fraga* <sup>1</sup> , A.M. Montalvo <sup>1</sup> , I. Maes <sup>2</sup> , S. Deborggraeve <sup>2</sup> , P. Büscher <sup>2</sup> , J.C. Dujardin <sup>2,3</sup> , G. Van der Auwera <sup>2</sup> , <sup>1</sup> Institute of Tropical Medicine Pedro Kouri, Cuba, <sup>2</sup> Institute of Tropical Medicine, Belgium, <sup>3</sup> Antwerp University, Belgium	<b>[S3.C.02] Bovine viral diarrhea virus 1 (BVDV-1) mutation detection by NGS in virus pairs</b> F. Cerutti* <sup>1</sup> , C. Caruso <sup>1</sup> , C. Luzzago <sup>2</sup> , S. Lauzi <sup>2</sup> , P.L. Acutis <sup>1</sup> , L. Masoero <sup>1</sup> , S. Peletto <sup>1</sup> , <sup>1</sup> Istituto Zooprofilattico Sperimentale Piemonte, Liguria e Valle D'Aosta, Italy, <sup>2</sup> University of Milan, Italy
14:30-14:50	<b>[S3.A.03] Bacterial community composition in the malaria mosquito's epithelia (midgut, ovaries and salivary glands)</b> M.T.T. Tchioffo* <sup>1,2</sup> , A.L. Abate <sup>1</sup> , A.B. Boissiere <sup>1</sup> , S.E.N. Nsango <sup>2,3</sup> , A.N.B. Bayibéki <sup>2</sup> , P.A.A. Awono-Ambéné <sup>2</sup> , R.C. Christen <sup>4</sup> , G.G. Gimonneau <sup>2</sup> , I.M. Morlais <sup>1,2</sup> , <sup>1</sup> IRD 224- Centre National de la Recherche Scientifique, France, <sup>2</sup> Laboratoire d'Entomologie Médicale, Cameroon, <sup>3</sup> Université de Douala, Cameroon, <sup>4</sup> Centre National de la Recherche Scientifique, France	<b>[S3.B.03] Atypical human trypanosomoses: An emerging threat?</b> P. Truc* <sup>1</sup> , R. Nzoumbou-Boko <sup>2</sup> , M. Desquesnes <sup>3</sup> , S. Semballa <sup>2</sup> , P. Vincendeau <sup>2</sup> , <sup>1</sup> Institut de Recherche pour le Développement, France, <sup>2</sup> University of Bordeaux, France, <sup>3</sup> CIRAD/Kasetsart University, Thailand	<b>[S3.C.03] Discovering of multiple modes of genomic variation and plasticity in kinetoplastids by whole genome sequencing technologies</b> H. Imamura* <sup>1</sup> , M. Domagalska <sup>1</sup> , E. Tihon <sup>1</sup> , F. Van den Broeck <sup>1</sup> , T. Downing <sup>2,3</sup> , J. Van den Abbeele <sup>1</sup> , J. Arévalo <sup>4</sup> , M. Berriman <sup>2</sup> , J.A. Cotton <sup>2</sup> , J.C. Dujardin <sup>1,5</sup> , <sup>1</sup> Institute of Tropical Medicine, Belgium, <sup>2</sup> Wellcome Genome Campus, UK, <sup>3</sup> Dublin City University, Ireland, <sup>4</sup> Universidad Peruana Cayetano Heredia, Peru, <sup>5</sup> University of Antwerp, Belgium
14:50-15:10	<b>[S3.A.04] Viral diversity as a mechanism for successful infection of the mosquito vector</b> N.L. Forrester*, E.I. Patterson, M. Rojas, T.F. Kautz, Y. Fofanov, <i>University of Texas Medical Branch, USA</i>	<b>[S3.B.04] Babesia microti-like sequences present in wild rodent species in South Africa</b> M. Troskie* <sup>1</sup> , S. Matthee <sup>2</sup> , I. Vorster <sup>1</sup> , R. Jansen <sup>3</sup> , B.L. Penzhorn <sup>1</sup> , M.C. Oosthuizen <sup>1</sup> , <sup>1</sup> University of Pretoria, South Africa, <sup>2</sup> Stellenbosch University, South Africa, <sup>3</sup> Tshwane University of Technology, South Africa	<b>[S3.C.04] Genome-wide association study of carriage versus disease in <i>Neisseria meningitidis</i></b> S.G. Earle*, M.C.J. Maiden, D.J. Wilson, <i>University of Oxford, UK</i>

15:10-15:30	<p><b>[S3.A.05] High fidelity TC-83 has reduced growth rate in RNAi competent mosquito cells</b> T.F. Kautz*, E.I. Patterson, D.I. Auguste, S.C. Weaver, N.L. Forrester, <i>University of Texas Medical Branch, USA</i></p>		<p><b>[S3.C.05] Metagenomic analysis for the detection of an unexpected pathogen in a fatal familial cluster of acute respiratory distress syndrome</b> M. Vandebogaert*<sup>1</sup>, A. Gautheret-Dejean<sup>2</sup>, A.S. Delannoy-Vieillard<sup>1</sup>, V. Sauvage<sup>1,3</sup>, M. Ar Gouilh<sup>1</sup>, V. Lemée<sup>4</sup>, M. Pestel Caron<sup>4</sup>, B. Veber<sup>4</sup>, A. Vabret<sup>5</sup>, A.M. Burguière<sup>1</sup>, <sup>1</sup><i>Institut Pasteur, France</i>, <sup>2</sup><i>Hôpitaux Universitaires La Pitié Salpêtrière-Charles Foix, France</i>, <sup>3</sup><i>Institut National de la Transfusion Sanguine, France</i>, <sup>4</sup><i>CHU Charles Nicolle Rouen, France</i>, <sup>5</sup><i>CHU de Caen, France</i></p>
15:30-16:00	Coffee break   <i>Karibu</i>		
16:00-18:00	Symposium 4		
<b>Room</b>	<b>Auditorium Rochus</b>	<b>Forum 2&amp;3</b>	<b>Aula PG Janssens</b>
	<p><b>Molecular epidemiology and Evolution of <i>Mycobacterium tuberculosis</i></b> <i>Chairs : Bouke de Jong and Igor Mokrousov</i></p>	<p><b>Epidemiology and biology of eukaryotic pathogens</b> <i>Chairs : Frederik Van den Broeck and Irshad M. Sulaiman</i></p>	<p><b>Virus Biology and evolution 1</b> <i>Chairs : Kevin Ariën and Konstantin Chumakov</i></p>
16:00-16:20	<p><b>[S4.A.01] Global phylogeography and phylogeny of Latin-American-Mediterranean lineage of <i>Mycobacterium tuberculosis</i></b> I. Mokrousov*<sup>1</sup>, A. Vyazovaya<sup>1</sup>, T. Iwamoto<sup>2</sup>, Y. Skiba<sup>3</sup>, I. Pole<sup>4</sup>, S. Zhdanova<sup>5</sup>, K. Arikawa<sup>2</sup>, V. Sinkov<sup>5</sup>, V. Valcheva<sup>6</sup>, R. Ranka<sup>4</sup>, <sup>1</sup><i>St. Petersburg Pasteur Institute, Russia</i>, <sup>2</sup><i>Kobe Institute of Health, Japan</i>, <sup>3</sup><i>Aitkhozhin Institute of Molecular Biology and Biochemistry, Kazakhstan</i>, <sup>4</sup><i>Latvian Biomedical Research and Study Centre, Latvia</i>, <sup>5</sup><i>Scientific Center of Family Health and Reproductive Problems, Russia</i>, <sup>6</sup><i>Institute of Microbiology, Bulgaria</i></p>	<p><b>[S4.B.01] Genetic characterization of fungi isolated from environmental swabs collected from various pharmaceutical compounding company premises in the United States: An active surveillance study of public health importance</b> I.M. Sulaiman*, E. Jacobs, S. Simpson, K. Kerdahi, <i>U.S. Food and Drug Administration, USA</i></p>	<p><b>[S4.C.01] Disentangling the heterogeneous transmission dynamics of Middle East respiratory syndrome (MERS) in the Republic of Korea, 2015</b> H. Nishiura, R. Kinoshita*, <i>Hokkaido University, Japan</i></p>
16:20-16:40	<p><b>[S4.A.02] Combining host and pathogen data to reconstruct tuberculosis evolution: Linking back Turkish and Japanese history to modern or Paleolithic era?</b> G. Refregier*<sup>1</sup>, E. Abadia<sup>2</sup>, T. Matsumoto<sup>3</sup>, H. Ano<sup>3</sup>, T. Takashima<sup>3</sup>, I. Tsuyuguchi<sup>3</sup>, E. Aktas<sup>4</sup>, E. Cömert<sup>5</sup>, M. Gomgnimbou<sup>6,7</sup>, S. Panaiotov<sup>8</sup>, <sup>1</sup><i>Institute for Integrative Biology of the Cell (I2BC), France</i>, <sup>2</sup><i>Istituto Venezolano de Investigaciones Cientificas, Venezuela</i>, <sup>3</sup><i>Osaka Prefectural Medical Center for Respiratory and Allergic Diseases, Japan</i>, <sup>4</sup><i>Sisli Etfal and Training Hospital, Turkey</i>, <sup>5</sup><i>Bülent Ecevit University, Turkey</i>, <sup>6</sup><i>Université Polytechnique de Bobo-Dioulasso, Burkina Faso</i>, <sup>7</sup><i>Centre Muraz, Burkina Faso</i>, <sup>8</sup><i>National Center of Parasitic and Infectious Diseases, Bulgaria</i></p>	<p><b>[S4.B.02] Do carnivore scavenging strategies evolve to avoid parasite transmission?</b> W.M. Getz*<sup>1</sup>, M. Moleón<sup>2</sup>, O.C. Muellerklein<sup>1</sup>, J.A. Sánchez-Zapata<sup>2</sup>, <sup>1</sup><i>University of California at Berkeley, USA</i>, <sup>2</sup><i>Universidad Miguel Hernández, Spain</i></p>	<p><b>[S4.C.02] The introduction, spread and reemergence of Ebola virus in Liberia</b> J.T. Ladner*, M.R. Wiley, J.R. Kugelman, S. Mate, M. Sanchez-Lockhart, G. Palacios, <i>US Army Medical Research Institute of Infectious Diseases, USA</i></p>

16:40-17:00	<p><b>[S4.A.03] Host genetic variation underlying resistance to bovine tuberculosis infection in dairy cows</b>  S. Wilkinson<sup>*1</sup>, S.C. Bishop<sup>1</sup>, A.R. Allen<sup>2</sup>, S.H. McBride<sup>2</sup>, M. Birmingham<sup>1</sup>, R.A. Skuce<sup>2,3</sup>, J.A. Woolliams<sup>1</sup>, L. Glass<sup>1</sup>, <sup>1</sup>University of Edinburgh, UK, <sup>2</sup>Agri-Food and Biosciences Institute Stormont, UK, <sup>3</sup>Queen's University Belfast, UK</p>	<p><b>[S4.B.03] Large-scale biochemical and chemical characterization of parasite protein kinases</b>  R. Hui, <i>Structural Genomics Consortium, Canada</i></p>	<p><b>[S4.C.03] Using herpes virus to map the colonization of caribou (<i>Rangifer tarandus</i>) in Canada</b>  C.S. Dalton<sup>*</sup>, F.J. van der Meer, S.J. Kutz, K.E. Ruckstuhl, M.F. Abdul-Careem, <i>University of Calgary, Canada</i></p>
17:00-17:20	<p><b>[S4.A.04] Molecular epidemiology of tuberculosis in goats, pig and sheep in Cameroon</b>  R.A. Guemechieu<sup>*1</sup>, F.K. Koro<sup>1,2</sup>, A.N. Ngane<sup>1</sup>, Y.K. Simo<sup>2</sup>, M. Tchamba<sup>3</sup>, A.T. Onana<sup>1</sup>, J.P.A. Assam<sup>1</sup>, F-X. Etoa<sup>1,4</sup>, <sup>1</sup>International Network of Pasteur Institutes, Cameroon, <sup>2</sup>University of Douala, Cameroon, <sup>3</sup>University of Yaoundé I, Cameroon, <sup>4</sup>University of Montagne, Cameroon</p>	<p><b>[S4.B.04] Human infection with the enteric protozoa <i>Blastocystis</i> sp. is associated with increased diversity of the gut bacterial microbiota</b>  C. Audebert<sup>1</sup>, G. Even<sup>1</sup>, A. Cian<sup>2</sup>, A. Loywick<sup>1</sup>, S. Merlin<sup>1</sup>, F. Delbac<sup>3</sup>, E. Viscogliosi<sup>2</sup>, M. Chabé<sup>*2</sup>, <sup>1</sup>Genes Diffusion, France, <sup>2</sup>Institut Pasteur de Lille, France, <sup>3</sup>University. Blaise Pascal, France</p>	<p><b>[S4.C.04] Algorithmic prediction of virus outbreak locales using past geospatial references</b>  D. Magee<sup>*</sup>, M. Scotch, <i>Arizona State University, USA</i></p>
17:20-17:40	<p><b>[S4.A.05] Is <i>M. africanum</i> still observing a genuine regression in Cameroon: Case of Douala, the most cosmopolitan and economic city in Cameroon</b>  B.M. Fotso<sup>4</sup>, F.K. Koro<sup>1,2</sup>, A.T. Onana<sup>*2</sup>, R.A. Guemechieu<sup>2</sup>, M. Tchamba<sup>4</sup>, R.M. Somo<sup>4</sup>, A.N. Ngane<sup>2</sup>, F-X. Etoa<sup>2,3</sup>, <sup>1</sup>International Network of Pasteur Institutes, Cameroon, <sup>2</sup>University of Douala, Cameroon, <sup>3</sup>University of Yaoundé I, Cameroon, <sup>4</sup>University of Montagne, Cameroon</p>	<p><b>[S4.B.05] Heterokaryon incompatibility and phenotypic characterisation of <i>Aspergillus flavus</i> isolates in low and high risk zones in Kenya</b>  A. Mitema<sup>*1,2</sup>, S. Rafudeen<sup>2</sup>, S. Okoth<sup>1</sup>, R. Iyer<sup>2</sup>, <sup>1</sup>University of Cape Town, South Africa, <sup>2</sup>University of Nairobi, Kenya</p>	<p><b>[S4.C.05] Co-evolution between rabbits and rabbit haemorrhagic disease virus and the important role flies as transporting vectors</b>  N. Schwensow<sup>*</sup>, P. Cassey, <i>University of Adelaide, Australia</i></p>
17:40-18:00	<p><b>[S4.A.06] Mycobacterium tuberculosis East African Indian (EAI)- SNP diversity suggests common ancestry for Brazil-Pará and Malawi isolates potentially linked to slave trade</b>  E.C. Conceição<sup>1,2</sup>, X.O. Daragon<sup>2</sup>, H. Gomes<sup>3</sup>, G. Refrégier<sup>2</sup>, F. Coll<sup>4</sup>, N. Ratovonirina<sup>5</sup>, V. Rasolofo-Razanamparany<sup>6</sup>, M.L. Lopes<sup>6</sup>, K.V. Lima<sup>7</sup>, R. Duarte<sup>1</sup>, C. Sola<sup>*2</sup>, <sup>1</sup>Universidade Federal do Rio de Janeiro, Brazil, <sup>2</sup>Institute for Integrative Biology of the Cell (I2BC), France, <sup>3</sup>Instituto Oswaldo Cruz, Brazil, <sup>4</sup>London School of Hygiene and Tropical Medicine, UK, <sup>5</sup>Institut Pasteur de Madagascar, Madagascar, <sup>6</sup>Instituto Evandro Chagas, Brazil, <sup>7</sup>Institut of Tropical Medicine, Belgium</p>		<p><b>[S4.C.06] Evolution of vaccine-derived polioviruses: Elucidating patterns of intertypic recombination</b>  K. Chumakov<sup>*1,2</sup>, E. Cherkasova<sup>1,3</sup>, E. Rodionova<sup>1</sup>, E. Korotkova<sup>4</sup>, S. Petrovskaya<sup>1</sup>, T. Zagorodnyaya<sup>1</sup>, M. Laassri<sup>1</sup>, O. Ivanova<sup>5</sup>, A. Gmyl<sup>5</sup>, V. Agol<sup>4,5</sup>, <sup>1</sup>FDA Center for Biologics Evaluation and Research, USA, <sup>2</sup>George Washington University, USA, <sup>3</sup>National Institutes of Health, USA, <sup>4</sup>Moscow State University, Russia, <sup>5</sup>Chumakov Institute of Poliomyelitis and Viral Encephalitis, Russia</p>
19:30-22:00	Conference dinner (ticket holders only)   <i>Elzenveld</i>		

Friday, 13 May 2016			
Room	Health Services Auditorium		
09:00-09:30	<b>[Pl.10] Anatomical landmarks, semi-landmarks and pseudo-landmarks in medical entomology</b> J.-P. Dujardin, <i>CIRAD-IRD, France</i>		
09:30-10:00	<b>[Pl.11] Molecular epidemiology and evolution of Ebola virus- new insights from the West African outbreak</b> K.K. Ariën, <i>Institute of Tropical Medicine, Belgium</i>		
10:00-10:30	<b>Coffee break   Health Services Café</b>		
10:30-11:00	<b>[Pl.12] Origin, spread and demography of major human bacterial diseases in a globalizing world</b> T. Wirth, <i>Natural History Museum &amp; Ecole Pratique des Hautes Etudes, France</i>		
11:00-11:30	<b>[Pl.13] Wildlife-borne diseases and habitats in Southeast Asian changing environments</b> S. Morand, <i>Université Montpellier 2, France</i>		
11:30-12:00	<b>[Pl.14] Evolution and revolution in <i>Leishmania donovani</i>: A phylogenomic approach of drug resistance in the Indian sub-continent</b> J.-C. Dujardin <sup>*1</sup> , H. Imamura <sup>1</sup> , F. Van den Broeck <sup>1</sup> , M. Domagalska <sup>1</sup> , G. De Muylder <sup>1</sup> , K. Rai <sup>2</sup> , Suman Rijal <sup>2</sup> , S. Sundar <sup>3</sup> , M. Berriman <sup>1</sup> , J. Cotton <sup>1</sup> , <sup>1</sup> <i>Institute of Tropical Medicine, Belgium</i> , <sup>2</sup> <i>BPKIHS, Nepal</i> , <sup>3</sup> <i>Banaras Hindu University, India</i> , <sup>4</sup> <i>Wellcome Trust Sanger Institute, UK</i>		
12:00-13:00	<b>Lunch   Karibu</b>		
13:00-15:00	<b>Symposium 5</b>		
Room	Aula PG Janssens	Auditorium Rochus	Forum 2&3
	<b>Virus Biology and evolution 2</b> <i>Chairs : Ignacio Bravo and Mattia Calzolari</i>	<b><i>Plasmodium</i> and other apicomplexa parasites</b> <i>Chairs : Steve Taylor and Chris Delgado-Ratto</i>	<b>Mechanisms of drug resistance</b> <i>Chairs : Ralph Huits and Phillip P. Salvatore</i>
13:00-13:20	<b>[S5.A.01] Sympatric circulation of two Usutu virus strains in Northern Italy between 2009 and 2014</b> M. Calzolari*, A. Moreno, L. Baioni, P. Bonilauri, L. Lelli, C. Chiapponi, <i>IZSLER, Italy</i>	<b>[S5.B.01] Next generation sequencing of human-pathogenic <i>Cyclospora cayetanensis</i> parasites from three indigenous geographic regions</b> I.M. Sulaiman <sup>*1</sup> , E. Jacobs <sup>1</sup> , Y. Ortega <sup>2</sup> , S. Simpson <sup>1</sup> , K. Kerdahi <sup>1</sup> , <sup>1</sup> <i>U.S. Food and Drug Administration, USA</i> , <sup>2</sup> <i>University of Georgia, USA</i>	<b>[S5.C.01] Genetic and molecular basis of Isometamidium Chloride resistance in <i>Trypanosoma congolense</i></b> E. Tihon <sup>*1</sup> , H. Imamura <sup>1</sup> , A. Kostense <sup>1</sup> , G. Caljon <sup>1,2</sup> , J.-C. Dujardin <sup>1</sup> , J. Van den abbeele <sup>1</sup> , <sup>1</sup> <i>ITM, Belgium</i> , <sup>2</sup> <i>University of Antwerp, Belgium</i>
13:20-13:40	<b>[S5.A.02] Pathogenesis of the adapted A(H1N1)pdm09 influenza virus in different inner organs of infected mice</b> E.A. Prokopyeva <sup>*1,2</sup> , E.I. Solovyova <sup>1</sup> , I.A. Sobolev <sup>2</sup> , A.V. Glushenko <sup>2</sup> , S.G. Sayfutdinova <sup>2</sup> , M.V. Sivay <sup>2</sup> , M.Y. Shelkanov <sup>3</sup> , A.M. Shestopalov <sup>2</sup> , <sup>1</sup> <i>Novosibirsk State University, Russia</i> , <sup>2</sup> <i>Siberian Division of the Russian Academy of Sciences, Russia</i> , <sup>3</sup> <i>Russian Academy of Sciences, Russia</i>	<b>[S5.B.02] Antigenic diversity of <i>Theileria parva</i> in the great lakes region of central Africa</b> S.G. Amzati <sup>*1,2</sup> , R. Pelle <sup>3</sup> , M. Madder <sup>4</sup> , N. Kirschvink <sup>1</sup> , T. Marcotty <sup>1</sup> , <sup>1</sup> <i>University of Namur, Belgium</i> , <sup>2</sup> <i>Université Evangélique en Afrique, Congo</i> , <sup>3</sup> <i>Biosciences Eastern and Central Africa -International Livestock Research Institute, Kenya</i> , <sup>4</sup> <i>Institute of Tropical Medicine, Belgium</i>	<b>[S5.C.02] The case-control study as a novel tool to quantify the fitness costs of drug resistance mutations</b> P.P. Salvatore <sup>*1,2</sup> , M.C. Becerra <sup>3</sup> , P. Abel zur Wiesch <sup>4</sup> , T. Hinkley <sup>4</sup> , D. Kaur <sup>5</sup> , A. Sloutsky <sup>5</sup> , T. Cohen <sup>4</sup> , <sup>1</sup> <i>Harvard School of Public Health, USA</i> , <sup>2</sup> <i>Johns Hopkins Bloomberg School of Public Health, USA</i> , <sup>3</sup> <i>Harvard Medical School, USA</i> , <sup>4</sup> <i>Yale School of Public Health, USA</i> , <sup>5</sup> <i>University of Massachusetts Medical School, USA</i>



13:40-14:00	<p><b>[S5.A.03] Can the fitness hypothesis explain the limited viral diversity of influenza A virus? A simulation study</b>  J.A. Backer*, O.V. Kuznetsova, D. Klinkenberg, <i>National Institute for Public Health and the Environment, The Netherlands</i></p>	<p><b>[S5.B.03] Genetic structure, transmission dynamics and bottleneck events of <i>Plasmodium vivax</i> population in the Peruvian Amazon</b>  C. Delgado-Ratto*, D. Gamboa<sup>2</sup>, V. Soto-Calle<sup>2</sup>, P. Van den Eede<sup>3</sup>, E. Torres<sup>2</sup>, L. Sánchez-Martínez<sup>2</sup>, J. Contreras-Mancilla<sup>2</sup>, A. Rosanas-Urgell<sup>3</sup>, H.R. Ferrucci<sup>4</sup>, A. Llanos-Cuentas<sup>2</sup>, A. Erhart<sup>3</sup>, J.-P. Van Geertruyden<sup>1</sup>, U. D'Alessandro<sup>5,6</sup>, <sup>1</sup><i>University of Antwerp, Belgium</i>, <sup>2</sup><i>Universidad Peruana Cayetano Heredia, Peru</i>, <sup>3</sup><i>Institute of Tropical Medicine, Belgium</i>, <sup>4</sup><i>Ministry of Health of Peru, Peru</i>, <sup>5</sup><i>Medical Research Council Unit, Gambia</i>, <sup>6</sup><i>London School of Hygiene and Tropical Medicine, UK</i></p>	<p><b>[S5.C.03] Detecting antimicrobial resistance in enteropathogenic <i>E. coli</i></b>  D.J. Ingle*<sup>1</sup>, K.L. Kotloff<sup>2</sup>, M.M. Levine<sup>2</sup>, K.E. Holt<sup>1</sup>, R.M. Robins-Browne<sup>1,3</sup>, <sup>1</sup><i>University of Melbourne, Australia</i>, <sup>2</sup><i>Center for Vaccine Development, University of Maryland School of Medicine, USA</i>, <sup>3</sup><i>Murdoch Childrens Research Institute, Royal Children's Hospital, Australia</i></p>
14:00-14:20	<p><b>[S5.A.04] The predominant clonal evolution model applied to the population genetics of bacteria and viruses</b>  M. Tibayrenc, <i>IRD Center, France</i></p>	<p><b>[S5.B.04] Looking at the "real" parasites: Contrasting <i>P. falciparum</i> clag3 genes expression patterns between culture and human conditions</b>  S. Mira-Martinez*<sup>1,2</sup>, E. van Schuppen<sup>5</sup>, A.A. Ngwa<sup>3</sup>, M. Affara<sup>3</sup>, E. Bottieau<sup>1</sup>, M. Van Esbroeck<sup>1</sup>, E. Vlieghe<sup>1</sup>, P. Guetens<sup>1</sup>, G.P. Gómez-Pérez<sup>2</sup>, J. Muñoz<sup>2</sup>, P.L. Alonso<sup>2</sup>, U. D'Alessandro<sup>2</sup>, A. Cortés<sup>2,4</sup>, A. Rosanas-Urgell<sup>1</sup>, <sup>1</sup><i>Institute of Tropical Medicine, Belgium</i>, <sup>2</sup><i>Barcelona Institute for Global Health, Spain</i>, <sup>3</sup><i>Medical Research Council Unit, Gambia</i>, <sup>4</sup><i>Catalan Institution for Research and Advanced Studies (ICREA), Spain</i>, <sup>5</sup><i>Radboud University, The Netherlands</i></p>	<p><b>[S5.C.04] Phenotypic versus genotypic drug susceptibility testing for <i>Mycobacterium tuberculosis</i></b>  P. Lempens*<sup>1</sup>, C. Sola<sup>2</sup>, M. Gomgnimbou<sup>3</sup>, F. Coll<sup>1</sup>, M. Diels<sup>1</sup>, A. Pain<sup>5</sup>, R. Mc Nerney<sup>4,6</sup>, T.G. Clark<sup>4</sup>, C.J. Meehan<sup>1</sup>, L. Rigouts<sup>1,7</sup>, <sup>1</sup><i>Institute of Tropical Medicine, Belgium</i>, <sup>2</sup><i>Université Paris-Saclay, France</i>, <sup>3</sup><i>Centre Muraz, Burkina Faso</i>, <sup>4</sup><i>London School of Hygiene &amp; Tropical Medicine, UK</i>, <sup>5</sup><i>King Abdullah University of Science and Technology, Saudi Arabia</i>, <sup>6</sup><i>University of Cape Town, South Africa</i>, <sup>7</sup><i>University of Antwerp, Belgium</i></p>
14:20-14:40	<p><b>[S5.A.05] Genetic diversity of human T-lymphotropic virus 1 in Peru</b>  J. Rosado<sup>1</sup>, F. Falconi<sup>1</sup>, C. Ocampo<sup>1</sup>, C. Alvarez*<sup>1,2</sup>, G. López<sup>1</sup>, K. Verdonck<sup>1,3</sup>, E. Gotuzzo<sup>1</sup>, M. Talledo<sup>1,4</sup>, <sup>1</sup><i>Universidad Peruana Cayetano Heredia, Peru</i>, <sup>2</sup><i>KU Leuven - University of Leuven, Belgium</i>, <sup>3</sup><i>Institute of Tropical Medicine, Belgium</i>, <sup>4</sup><i>University of Antwerp, Belgium</i></p>	<p><b>[S5.B.05] Identification of protective epitopes within <i>Plasmodium falciparum</i> antigens using reverse immunodynamics</b>  A.S. Walker*<sup>1</sup>, K.J. Spensley<sup>1</sup>, P. Wikramaratna<sup>1</sup>, B.S. Penman<sup>1</sup>, J. Lourenço<sup>1</sup>, A.L. Smith<sup>1</sup>, O.G. Pybus<sup>1</sup>, L. Jean<sup>1</sup>, S. Gupta<sup>1</sup>, <sup>1</sup><i>University of Oxford, UK</i>, <sup>2</sup><i>University of Edinburgh, UK</i></p>	<p><b>[S5.C.05] Is <i>E. coli</i> ST131 a universal marker of antibiotic resistance and virulence?</b>  M.D. Ismail, S. Hatt, B. Salzman, A. Rickard, B. Foxman*, <i>University of Michigan, USA</i></p>
14:40-15:00	<p><b>[S5.A.06] Phylogenetic analyses of the canine distemper virus in Chile</b>  C. Verdugo*<sup>1</sup>, M. Salazar<sup>3</sup>, M. Sepulveda<sup>2</sup>, <sup>1</sup><i>Universidad Austral de Chile, Chile</i>, <sup>2</sup><i>Pontificia Universidad Católica de Chile, Chile</i>, <sup>3</sup><i>Bioscan S.A., Chile</i></p>		
15:00-15:30	<b>Coffee break   Karibu</b>		

15:30-17:30 Symposium 6			
Room	Auditorium Rochus	Aula PG Janssens	Forum 2&3
	<b>Taxonomy and Evolution of <i>Leishmania</i> parasites</b> <i>Chairs : Jean-Claude Dujardin and Elisa Cupolillo</i>	<b>Ecology and Evolution of Bacteria 2</b> <i>Chairs : Igor Mokrousov and Shima M. Abdulgader</i>	<b>Cancer and transmissible diseases</b> <i>Chairs : Michel Tibayrenc and Ignacio Bravo</i>
15:30-15:50	<b>[S6.A.01] The controversial taxonomy of <i>Leishmania</i> parasites: Applying col barcode in a taxonomically challenging group</b> M.C. Boité, G.C. da Graça, R.R. Cuadrat, G.E.M. Ferreira, C.P.B. Filgueiras, R. Porrozzì, E. Cupolillo*, <i>Fundação Oswaldo Cruz, Brazil</i>	<b>[S6.B.01] Longitudinal assessment of <i>Staphylococcus aureus</i> nasopharyngeal carriage patterns during infancy in a South African birth cohort</b> S.M. Abdulgader*, L. Robberts <sup>1</sup> , S. Lubbe <sup>1</sup> , H. Zar <sup>1</sup> , M. Nicol <sup>1,2</sup> , <sup>1</sup> University of Cape Town, South Africa, <sup>2</sup> National Health Laboratory Service, South Africa	<b>[S6.C.01] An eco-immunological approach for cancer: A new role for infectious diseases?</b> C. Jacqueline* <sup>1,2</sup> , F. Renaud <sup>1,2</sup> , F. Thomas <sup>1,2</sup> , B. Roche <sup>1,3</sup> , <sup>1</sup> Institut de Recherche pour le Développement, France, <sup>2</sup> Centre National de la Recherche Scientifique, France, <sup>3</sup> UPMC UMMISCO, France
15:50-16:10	<b>[S6.A.02] MLMT to unravel mixed infections and the selection of <i>L. infantum</i> clones in a study of canine visceral leishmaniasis</b> A.S. Cavalcanti, G.E.M. Ferreira, M.C. Boité, E. Cupolillo*, R. Porrozzì, <i>Fundação Oswaldo Cruz, Brazil</i>	<b>[S6.B.02] Molecular epidemiology of <i>Staphylococcus aureus</i> identified in healthy South African infants</b> S.M. Abdulgader*, L. Robberts <sup>1</sup> , H. Zar <sup>1</sup> , M. Nicol <sup>1,2</sup> , <sup>1</sup> University of Cape Town, South Africa, <sup>2</sup> National Health Laboratory Service, South Africa	<b>[S6.C.02] Ancient origins, dispersal and diversity of HPV16, the most oncogenic human papillomavirus</b> I.G. Bravo* <sup>1,2</sup> , V.N. Pimenoff <sup>2,3</sup> , S. Nicolás-Párraga <sup>2,3</sup> , <sup>1</sup> National Center for Scientific Research (CNRS), France, <sup>2</sup> Catalan Institute of Oncology (ICO), Spain, <sup>3</sup> Bellvitge Institute of Biomedical Research, Spain
16:10-16:30	<b>[S6.A.03] Spatial distribution of <i>Leishmania donovani</i> genotypes circulating in Nepal</b> K. Rai <sup>1</sup> , N. Bhattarai <sup>1</sup> , B. Khanal <sup>1</sup> , S. Rijal <sup>1</sup> , M. Boelaert <sup>2</sup> , P. Karki <sup>1</sup> , M. Vanaerschot <sup>4</sup> , G. Gebru <sup>5</sup> , H. Imamura <sup>2</sup> , J.C. Dujardin <sup>2,3</sup> , G. Van der Auwera* <sup>2</sup> , <sup>1</sup> B.P. Koirala Institute of Health Sciences, Nepal, <sup>2</sup> Institute of Tropical Medicine, Belgium, <sup>3</sup> University of Antwerp, Belgium, <sup>4</sup> Columbia University College of Physicians and Surgeons, USA, <sup>5</sup> Aksum University, Ethiopia	<b>[S6.B.03] The microbiome associated with buruli ulcer lesions</b> C. Van Leuvenhaege <sup>1</sup> , K. Vandelannoote <sup>1</sup> , D. Affolabi <sup>2</sup> , F. Portaels <sup>1</sup> , G. Sopoh <sup>3</sup> , B.C. de Jong <sup>1</sup> , M. Eddyani <sup>1</sup> , C.J. Meehan* <sup>1</sup> , <sup>1</sup> Institute of Tropical Medicine, Belgium, <sup>2</sup> Laboratoire de Référence de Mycobactéries, Benin, <sup>3</sup> Institut Régionale de Santé Publique, Benin	<b>[S6.C.03] High association of <i>Cryptosporidium</i> infection with digestive cancer in humans</b> G. Certad* <sup>1,2</sup> , M. Osman <sup>1,3</sup> , S. Benamrouz <sup>1,4</sup> , F. Gantois <sup>1,4</sup> , <sup>1</sup> Institut Pasteur de Lille, France, <sup>2</sup> Université Catholique de Lille, France, <sup>3</sup> Laboratoire de Microbiologie Santé et Environnement, Lebanon, <sup>4</sup> Université Lille Nord de France, France
16:30-16:50	<b>[S6.A.04] Speciation, divergence and genome structure in New World <i>Leishmania</i> populations along the Andes</b> F. Van den Broeck* <sup>1</sup> , H. Imamura <sup>1</sup> , J. Arevalo <sup>2</sup> , V. Adau <sup>2</sup> , M. Jara <sup>1,2</sup> , L. Garcia <sup>3</sup> , M.J. Sanders <sup>4</sup> , M. Berriman <sup>4</sup> , J.A. Cotton <sup>4</sup> , J.C. Dujardin <sup>1</sup> , <sup>1</sup> Institute of Tropical Medicine, Belgium, <sup>2</sup> Instituto de Medicina Tropical A. von Humboldt, Peru, <sup>3</sup> CUMETROP, Bolivia, <sup>4</sup> Wellcome Trust Sanger Institute, UK	<b>[S6.B.04] A comparative study of different methods for phylogenetic analyses of <i>Vibrio cholerae</i> O1 epidemic strains</b> P. Kumar* <sup>1,2</sup> , P. Yadav <sup>1</sup> , M. Jain <sup>3</sup> , D.G. Deshmukh <sup>4</sup> , A.K. Goel <sup>5</sup> , P.K. Yadava <sup>1</sup> , <sup>1</sup> Jawaharlal Nehru University, India, <sup>2</sup> National Centre for Disease Control, India, <sup>3</sup> Jiwaji University, India, <sup>4</sup> SVN Government Medical College, India, <sup>5</sup> Defence Research and Development Establishment, India	<b>[S6.C.04] Genome wide identification of virulence factors of the carcinogenic protist <i>Cryptosporidium parvum</i></b> M. Chabé* <sup>1</sup> , S. Caboche <sup>1</sup> , C. Audebert <sup>2</sup> , S. Merlin <sup>2</sup> , K. Guyot <sup>1</sup> , N. Gantois <sup>1</sup> , C. Creusy <sup>3</sup> , E. Viscogliosi <sup>1</sup> , S. Benamrouz <sup>1</sup> , G. Certad <sup>1</sup> , <sup>1</sup> Institut Pasteur de Lille, France, <sup>2</sup> Genes Diffusion, France, <sup>3</sup> GHICL, France

16:50-17:10	<p><b>[S6.A.05] A systems biology compendium for <i>Leishmania donovani</i></b>  B. Cuypers*<sup>1,2</sup>, P. Meysman<sup>2</sup>, M. Vanaerschot<sup>1</sup>, M. Berg<sup>1</sup>, M.A. Domagalska<sup>1</sup>, K. Laukens<sup>2</sup>, J-C. Dujardin<sup>1,2</sup>, <sup>1</sup><i>Institute Of Tropical Medicine, Belgium</i>, <sup>2</sup><i>University Of Antwerp, Belgium</i>, <sup>3</sup><i>Columbia University Medical Center, USA</i></p>	<p><b>[S6.B.05] Multilocus sequence typing reveals association of <i>Borrelia burgdorferi</i> s.l. sequence types with clinical manifestations of Lyme borreliosis</b>  E.C. Coipan*<sup>1</sup>, S. Jahfari<sup>1</sup>, M. Fonville<sup>1</sup>, G.A. Oei<sup>2</sup>, L. Spanjaard<sup>2</sup>, K. Takumi<sup>1</sup>, J.W.R. Hovius<sup>2</sup>, H. Sprong<sup>1</sup>, <sup>1</sup><i>National Institute for Public Health and Environment (RIVM), The Netherlands</i>, <sup>2</sup><i>Academic Medical Center of University of Amsterdam, The Netherlands</i></p>	<p><b>[S6.C.05] Bacterial infections associated with cancer: Whole-proteome microarrays for antigenic target identification</b>  K. Hufnagel*, S. Lueong, M. Willhauck-Fleckenstein, B. Miao, A. Michel, J. Butt, M. Pawlita, J.D. Hoheisel, T. Waterboer, <i>German Cancer Research Center (DKFZ), Germany</i></p>
17:10-17:30	<p><b>[S6.A.06] Genomic analysis of intra-specific hybrids and ancestor-like donors among natural Ethiopian isolates of <i>Leishmania donovani</i>, and the experimental production of abundant, viable <i>L. donovani</i> hybrids in two sand fly species</b>  M. Yeo*<sup>1</sup>, J.A. Cotton<sup>1,2</sup>, J. Sadlova<sup>1,3</sup>, C. Durrant<sup>1,2</sup>, M. Sanders<sup>1,2</sup>, M. Berriman<sup>1,2</sup>, A. Hailu<sup>1,4</sup>, T. Gelanew<sup>1,5</sup>, M.A. Miles<sup>1</sup>, <sup>1</sup><i>LSHTM, UK</i>, <sup>2</sup><i>Sanger Institute, UK</i>, <sup>3</sup><i>Charles University, Czech Republic</i>, <sup>4</sup><i>Addis Abba University, Ethiopia</i>, <sup>5</sup><i>CDC, Puerto Rico</i></p>	<p><b>[S6.B.06] Occurrence of <i>Chlamydomydia psittaci</i> in domestic and wild birds and its zoonotic potential</b>  N. Ghoneim*, K. Abdel-Moein, N. Kamal, <i>Cairo University, Egypt</i></p>	
17:30-18:00	Closing ceremony & Awards   <i>Aula PG Janssens</i>		