

# Oral Programme

Tuesday, 6 November 2018			
17:00-19:00	<b>Registration</b>   Room: <i>Tramuntana Foyer</i>		
19:00	<b>Welcome drinks</b>   Room: <i>Tramuntana 1</i>		
Wednesday, 7 November 2018			
07:30-09:00	<b>Registration</b>   Room: <i>Tramuntana Foyer</i>		
09:00-10:00	<b>Opening session</b>		
Room	<i>Tramuntana 2</i>		
10:00-12:00	<b>Plenary session</b>		
10:00-10:30	<b>[PL01]</b> <b>Antibiotic resistant septicemic <i>E. coli</i></b> D. Biran, Y. Yair, E. Ron*, <i>Tel Aviv University, Israel</i>		
10:30-11:00	<b>Coffee break</b>   Room: <i>Tramuntana 1</i>		
11:00-11:30	<b>[PL16]</b> <b>Vector population genetics</b> T. De Meeûs, <i>IRD, France</i>		
11:30-12:00	<b>[PL03]</b> <b>Selection imposed by pathogens and archaic introgression have shaped the human immune system</b> L. Quintana-Murci, <i>Institut Pasteur, CNRS, France</i>		
12:00-13:30	<b>Poster session and lunch</b>   Room: <i>Tramuntana 1</i>		
13:30-14:50	<b>Symposium 1</b>		
	<b>Stream 1: Coronavirus Evolution</b>	<b>Stream 2: Helminthic Diseases Evolution</b>	<b>Stream 3: Host Factors in Transmissible Diseases</b>
Room	<i>Tramuntana 2</i>	<i>Tramuntana 3</i>	<i>Mestral 1&amp;2</i>
13:30-13:50	<b>[SYM1.01.01]</b> <b>Phylogeography of coronavirus in bats in the Western Indian Ocean</b> L. Joffrin* <sup>1</sup> , S.M. Goodman <sup>2,3</sup> , P. Mavingui <sup>1</sup> , C. Lebarbenchon <sup>1</sup> , <sup>1</sup> <i>Université de La Réunion, Reunion</i> , <sup>2</sup> <i>Association Vahatra, Madagascar</i> , <sup>3</sup> <i>Field Museum of Natural History, USA</i>	<b>[SYM1.02.01]</b> <b>Oxamniquine resistance alleles are widespread in Old World <i>Schistosoma mansoni</i> and predate drug deployment</b> F.D. Chevalier* <sup>1</sup> , W. Le Clec'h <sup>1</sup> , M. Guzman <sup>2</sup> , S.P. Holloway <sup>2</sup> , X. Cao <sup>2</sup> , A.B. Taylor <sup>2</sup> , A.M. Emery <sup>3</sup> , D. Rollinson <sup>3</sup> , S. Al Yafae <sup>4</sup> , H. Moné <sup>5</sup> , <sup>1</sup> <i>Texas Biomedical Research Institute, USA</i> , <sup>2</sup> <i>University of Texas Health, USA</i> , <sup>3</sup> <i>The Natural History Museum, UK</i> , <sup>4</sup> <i>Sultan Qaboos Hospital, Oman</i> , <sup>5</sup> <i>Interactions Hosts Pathogens Environments at the University of Perpignan, France</i>	<b>[SYM1.03.01]</b> <b>The diversity of mammalian hemoproteins and microbial heme scavengers is shaped by an arms race for iron piracy</b> D. Forni <sup>1</sup> , A. Mozzi <sup>1</sup> , M. Clerici <sup>2,3</sup> , R. Cagliani <sup>1</sup> , M. Sironi* <sup>1</sup> <sup>1</sup> <i>Scientific Institute IRCCS E. MEDEA, Italy</i> , <sup>2</sup> <i>University of Milan, Italy</i> , <sup>3</sup> <i>Don C. Gnocchi Foundation ONLUS, Italy</i>
13:50-14:10	<b>[SYM1.01.02]</b> <b>Phylogeographic and evolutionary insights into the circulation of MERS-CoV in dromedary camels</b> S.N. Seifert* <sup>1</sup> , M. Letko <sup>1</sup> , N. van Doremalen <sup>1</sup> , J.E. Schulz <sup>1</sup> , Z.S.K. Hijazeen <sup>2</sup> , E. Abu-Basha <sup>3</sup> , A.M. Al-Majali <sup>3</sup> , J.A. Richt <sup>4</sup> , V.J. Munster <sup>1</sup> , <sup>1</sup> <i>National Institutes of Health, USA</i> , <sup>2</sup> <i>Food and Agriculture Organization of the United Nations, Jordan</i> , <sup>3</sup> <i>Jordan University of Science and Technology, Jordan</i> , <sup>4</sup> <i>Kansas State University, USA</i>	<b>[SYM1.02.02]</b> <b>The zoonotic risk of <i>Ancylostoma ceylanicum</i> isolated from stray cats residing in Bangkok temples, Thailand</b> P. Phoosangwalthong, J. Wongwigkan, C. Kengradomkij, T. Inpankaew*, <i>Kasetsart University, Thailand</i>	<b>[SYM1.03.02]</b> <b>Natural and bioinformatically predicted tumor specific bacterial promoters</b> I.V. Deyneko* <sup>3</sup> , N. Kasnitz <sup>1</sup> , S. Weiss <sup>1,2</sup> , <sup>1</sup> <i>Helmholtz Centre for Infection Research, Germany</i> , <sup>2</sup> <i>Medical School Hannover, Germany</i> <sup>3</sup> <i>Timiryazev Institute of Plant Physiology Russian Academy of Sciences, Russia</i>

14:10-14:30	<p><b>[SYM1.01.03]</b>  <b>Phylogenetics of coronaviruses in wildlife and intra-colony evolution of the SARS-CoV sister-clade Betacoronavirus in bats in western Europe.</b>  M. Ar Guilh*<sup>1,2</sup>, E. Monchatre-Leroy<sup>3</sup>, S. Puechmaille<sup>4</sup>, L. Diancourt<sup>5</sup>, A. Kwasiborski<sup>5</sup>, M. Vandenbergert<sup>5</sup>, V. Caro<sup>5</sup>, J. Serra<sup>6</sup>, A. Vabret<sup>1,2</sup>, J-C. Manuguerra<sup>5</sup>, <sup>1</sup>Normandy University, France, <sup>2</sup>University Hospital of Caen, France, <sup>3</sup>Agence Nationale de Sécurité Sanitaire, France, <sup>4</sup>Greifswald University, Germany, <sup>5</sup>Institut Pasteur, France, <sup>6</sup>Universitat de Barcelona, Spain</p>	<p><b>[SYM1.02.03]</b>  <b>Genetic diversity of Fasciola hepatica in Portugal: 28S, Tubulin B3 and Cytochrome oxidase I</b>  N.P. Chinjengue*, M. Calado, S. D'Almeida, I.L. Mauricio, <i>Universidade Nova de Lisboa, Portugal</i></p>	<p><b>[SYM1.03.03]</b>  <b>Characterisation and somatic mosaicism of the human glycophorin DUP4 structural variant, and association with haemoglobin levels in a malaria-endemic village</b>  W. Algady*<sup>1</sup>, S. Gomes<sup>2</sup>, D. Carpenter<sup>1</sup>, P. Brajer<sup>1</sup>, A. Färnert<sup>3</sup>, I. Rooth<sup>4</sup>, M. Shaw<sup>5</sup>, F. Yang<sup>2</sup>, E. Hollox<sup>1</sup>, <sup>1</sup>University of Leicester, UK, <sup>2</sup>Wellcome Sanger Institute, UK, <sup>3</sup>Karolinska Institutet, Sweden, <sup>4</sup>National Institute for Medical Research, Tanzania, <sup>5</sup>University of Leeds, UK</p>
14:30-14:50	<p><b>[SYM1.01.04]</b>  <b>Phylogenetics and recombination patterns of Human coronavirus NL63 (HCoV-NL63): An insight using data from France 2004 – 2017</b>  M. Ar Guilh*<sup>1,3</sup>, N. Kin<sup>1,2</sup>, F. Miszczak<sup>3</sup>, A. Letrouit<sup>1,3</sup>, L. Diancourt<sup>4</sup>, V. Caro<sup>4</sup>, A. Vabret<sup>2,3</sup>, <sup>1</sup>Normandy University, France, <sup>2</sup>UNICAEN, GRAM, France, <sup>3</sup>University Hospital of Caen, France, <sup>4</sup>Institut Pasteur, France</p>		<p><b>[SYM1.03.04]</b>  <b>Infected horses from Iceland harbour a specific genetic variant of equine papillomavirus type 2</b>  S. Brandt*, C. Jindra, C. Kerscher, E.K. Hainisch, S. Sykora, <i>University of Veterinary Medicine, Austria</i></p>
14:50-15:20	<b>Coffee break</b>   Room: <i>Tramuntana 1</i>		
15:20-17:20	<b>Symposium 2</b>		
	<b>Stream 1: Bacterial Molecular Epidemiology and Evolution 1</b>	<b>Stream 2: Virus Molecular Epidemiology and Evolution 1</b>	<b>Stream 3: Modelling Approaches of Transmissible Diseases 1</b>
<b>Room</b>	<i>Tramuntana 2</i>	<i>Tramuntana 3</i>	<i>Mestral 1&amp;2</i>
15:20-15:40	<p><b>[SYM2.01.01]</b>  <b>Application of MALDI-TOF MS technology in rapid detection and differentiation of pathogenic microorganisms of public health importance</b>  I. Sulaiman*, N. Miranda, S. Simpson, <i>U.S. FDA, USA</i></p>	<p><b>[SYM2.02.01]</b>  <b>Hepatitis E virus genetic drift during persistent infection of HepaRG cells <i>in vitro</i></b>  V. Doceul<sup>1,2</sup>, S. Raileanu<sup>1,2</sup>, P. Lucas<sup>1</sup>, A. Leroux<sup>1</sup>, Y. Blanchard<sup>1</sup>, N. Pavio*<sup>1,2</sup>  <sup>1</sup>Anses, France, <sup>2</sup>INRA, France, <sup>3</sup>ENVA, France</p>	<p><b>[SYM2.03.01]</b>  <b>Multiple infections favour more virulent parasites</b>  M.T. Sofonea*, S. Alizon, Y. Michalakis, <i>CNRS, France</i></p>
15:40-16:00	<p><b>[SYM2.01.02]</b>  <b>Interaction of messengers-endogenous NO and H2S gasotransmitters in signaling and regulatory processes in bacterial cells</b>  S.V. Vasilieva, N.M. Emanuel <i>Institute of Biochemical Physics, Russian Academy of Sciences, Russia</i></p>	<p><b>[SYM2.02.02]</b>  <b>Evolutionary history and spread of JC polyomavirus</b>  D. Forni*, R. Cagliani, M. Sironi <i>Scientific Institute IRCCS E.MEDEA, Italy</i></p>	<p><b>[SYM2.03.02]</b>  <b>Characterizing the dynamics underlying global spread of emerging epidemics</b>  L. Wang<sup>2*</sup>, J.T. Wu<sup>1</sup>, <sup>1</sup>The University of Hong Kong, Hong Kong, <sup>2</sup>Institut Pasteur, France</p>

16:00-16:20	<p><b>[SYM2.01.03]</b>  <b>Influence of human disturbance on the prevalence of Lyme disease agents in ticks feeding on an avian host</b>  R.E. Rollins*<sup>1</sup>, N. Becker<sup>1</sup>, G. Margos<sup>2</sup>, V. Fingerle<sup>2</sup>, L. Chitimia-Dobler<sup>3</sup>, N. Dingemans<sup>1</sup>, <sup>1</sup>Ludwig-Maximilian-Universität München, Germany, <sup>2</sup>German National Reference Centre for Borrelia, Germany, <sup>3</sup>Bundeswehr Institute of Microbiology, Germany</p>	<p><b>[SYM2.02.03]</b>  <b>Ancestral gene resurrection of the papillomavirus oncogenes</b>  A. Willemsen*<sup>1</sup>, C. Cassan<sup>2</sup>, I.G. Bravo<sup>1</sup>, <sup>1</sup>Centre National de la Recherche Scientifique (CNRS) - MIVEGEC (UMR CNRS IRD UM), France, <sup>2</sup>Institut de Recherche pour le Développement (IRD) - MIVEGEC (UMR CNRS IRD UM), France</p>	<p><b>[SYM2.03.03]</b>  <b>The development and first application of comparative demography: A method to examine the evolutionary stability of parasitic and symbiotic relationships from genome sequences.</b>  L.B.B. Hecht<sup>1,2</sup>, P.C. Thompson<sup>1,2</sup>, B.M. Rosenthal*<sup>1</sup>, <sup>1</sup>Agricultural Research Service, USDA, USA, <sup>2</sup>Oak Ridge Institute for Science Education, USA</p>
16:20-16:40	<p><b>[SYM2.01.04]</b>  <b>Molecular detection of a novel Babesia sp. and pathogenic SFG rickettsiae in ticks collected from hedgehogs in Turkey: Haemaphysalis erinacei, a novel candidate vector for genus Babesia</b>  O. Orkun*, A. Cakmak, S. Nalbantoglu, Z. Karaer, Ankara University, Turkey</p>	<p><b>[SYM2.02.04]</b>  <b>Evolution of VP1 gene in non-polio enteroviruses</b>  Y.A. Vakulenko*<sup>1,2</sup>, A.N. Lukashev<sup>1</sup>, <sup>1</sup>Sechenov University, Russia, <sup>2</sup>Lomonosov Moscow State University, Russia</p>	<p><b>[SYM2.03.04]</b>  <b>ZooPhy and ZoDo: Bringing virus phylogeography to the public health epidemiologist</b>  M. Scotch*<sup>1</sup>, G. Gonzalez<sup>1</sup>, <sup>1</sup>Arizona State University, USA, <sup>2</sup>University of Pennsylvania, USA</p>
16:40-17:00	<p><b>[SYM2.01.05]</b>  <b>Whole genome sequence (WGS) analysis of Pseudomonas aeruginosa outbreaks in the Comunidad Valenciana (Spain)</b>  P. Ruiz-Hueso*<sup>1</sup>, N. Tormo<sup>2</sup>, M. Abreu-Di Berardino<sup>3</sup>, V. Dominguez<sup>4</sup>, V. Sánchez-Hellín<sup>3</sup>, C. Gimeno<sup>2</sup>, F. González-Candelas<sup>1,5</sup>, <sup>1</sup>FISABIO-Univ. Valencia, Spain, <sup>2</sup>Consorcio Hospital General Universitario de Valencia, Spain, <sup>3</sup>Hospital General de Elx, Spain, <sup>4</sup>Hospital Arnau de Vilanova, Spain, <sup>5</sup>CIBER in Epidemiology and Public Health, Spain</p>	<p><b>[SYM2.02.05]</b>  <b>Recombination in the rabies virus and other Lyssaviruses</b>  A.A. Deviatkin*, A.N. Lukashev, Sechenov, Russia</p>	<p><b>[SYM2.03.05]</b>  <b>One locus sequencing typing (OLST), a novel metagenomic approach to analyze intra-species abundance and diversity</b>  M.D. Fernández de Bobadilla*, S. Aracil, F. Baquero, T.M. Coque  Ramón y Cajal Health Research Institute (IRYCIS), Spain</p>
17:00-17:20	<p><b>[SYM2.01.06]</b>  <b>Recombination in the evolution of the syphilis-causing bacteria Treponema pallidum</b>  M. Pla-Díaz*<sup>1</sup>, V.J. Schuenemann<sup>1</sup>, L. Grillová<sup>1</sup>, L. Sánchez-Busó<sup>1</sup>, P. Bosshard<sup>1</sup>, D. Smajs<sup>1</sup>, H.C. Bagheri<sup>1</sup>, K. Nieselt<sup>1</sup>, N. Arora<sup>1</sup>, F. González-Candelas<sup>1</sup> et al  <sup>1</sup>University of Zurich, Switzerland, <sup>2</sup>Masaryk University, Czech Republic, <sup>3</sup>Wellcome Trust Sanger Institute, UK, <sup>4</sup>UT Health McGovern Medical School, USA, <sup>5</sup>University Hospital of Zurich, Switzerland, <sup>6</sup>University of Zurich, Switzerland, <sup>7</sup>University of Tübingen, Germany</p>	<p><b>[SYM2.02.06]</b>  <b>Avian contact transmission underlies early epidemic expansion of West Nile virus in the US</b>  M.A. Vaiente*, M. Scotch, Arizona State University, USA</p>	

Thursday, 8 November 2018			
08:30-12:00	<b>Plenary session</b>		
Room	Tramuntana 2		
08:30-09:00	<b>[PL04]</b> <b>Understanding pathogenesis of infectious disease through analyses of host genetic risk factors</b> J.M. Blackwell <sup>1</sup> , <sup>1</sup> University of Western Australia, Australia, <sup>2</sup> University of Cambridge, UK		
09:00-09:30	<b>[PL05]</b> <b>Computational approaches to microbiome characterization and infectious disease dynamics</b> K.A. Crandall, George Washington University, USA		
09:30-10:00	<b>[PL06]</b> <b>Unraveling the population structure of enterococcus faecalis: Host-associated differences in core and accessory genomes and adaptation to different environments</b> T. M. Coque, Ramón y Cajal Health Research Institute (IRYCIS), Spain		
10:00-10:30	<b>Coffee break</b>   Room: Tramuntana 1		
10:30-11:00	<b>[PL07]</b> <b>Molecular epidemiology and evolution in the human immunodeficiency virus</b> F. González-Candelas <sup>*1,2</sup> , J.A. Patiño Galindo <sup>1,2</sup> , B. Beamud <sup>1,2</sup> , M.A. Bracho <sup>1,3</sup> , <sup>1</sup> University of Valencia, Spain, <sup>2</sup> I2SysBio (CSIC-UV), Spain, <sup>3</sup> CIBER in Epidemiology and Public Health, Spain		
11:00-11:30	<b>[PL08]</b> <b>Viral phylodynamics: From ancient evolutionary histories to contemporary outbreaks</b> P. Lemey, KU Leuven, Belgium		
11:30-12:00	<b>[PL09]</b> <b>Massive human migration and spread of epidemic Mycobacterium tuberculosis strains</b> I. Mokrousov, St. Petersburg Pasteur Institute, Russia		
12:00-13:30	<b>Poster session and lunch</b>   Room: Tramuntana 1		
12:15-13:15	<b>Author workshop</b>   Room: Mestral 1&2		
13:30-15:30	<b>Symposium 3</b>		
	<b>Stream 1: Bacterial Molecular Epidemiology and Evolution 2</b>	<b>Stream 2: Diseases of Veterinary Relevance</b>	<b>Stream 3: Virus Molecular Epidemiology and Evolution 2</b>
Room	Tramuntana 2	Tramuntana 3	Mestral 1&2
13:30-13:50	<b>[SYM3.01.01]</b> <b>Molecular epidemiology of Salmonella enterica serovar enteritidis in Uruguay: Association of allelic variants with different epidemic ability of circulating lineages</b> B. D'Alessandro <sup>*1</sup> , L. Balestrazzi <sup>1</sup> , V. Perez Escanda <sup>1</sup> , A. Iriarte <sup>1</sup> , D. Pickard <sup>2</sup> , L. Yim <sup>1</sup> , J.A. Chabalgoity <sup>1</sup> , L. Betancor <sup>1</sup> , <sup>1</sup> UDELAR, Uruguay, <sup>2</sup> The Wellcome Trust Genome Campus, UK	<b>[SYM3.02.01]</b> <b>Small ruminant lentivirus isolation and characterization in piedmont</b> B. Colitti <sup>*1</sup> , E. Coradduzza <sup>2</sup> , M. Profiti <sup>1</sup> , M.T. Capucchio <sup>1</sup> , G. Puggioni <sup>2</sup> , L. Bertolotti <sup>1</sup> , S. Rosati <sup>1</sup> <sup>1</sup> University of Turin, Italy, <sup>2</sup> Istituto Zooprofilattico Sperimentale della Sardegna, Italy	<b>[SYM3.03.01]</b> <b>Dissemination of "Global Hepatitis Outbreak and Surveillance Technology"</b> S. Ramachandran <sup>*</sup> , Y. Khudyakov, Centers for Disease Control and Prevention (CDC), USA
13:50-14:10	<b>[SYM3.01.02]</b> <b>Comparative genomics analysis of translational frameshifting in aerobic cobalt chelatase genes</b> I.V. Antonov <sup>*1</sup> , M.A. Zamkova <sup>2</sup> , <sup>1</sup> Research Center of Biotechnology RAS, Russia, <sup>2</sup> Russian N.N. Blokhin Cancer Research Center, Russia	<b>[SYM3.02.02]</b> <b>Emergence of bluetongue serotypes 3 and 6 in Mediterranean Basin: So different and so closely related</b> N. Golender <sup>*1</sup> , A. Eldar <sup>1</sup> , Y. Khinich <sup>1</sup> , G. Kenigswald <sup>2</sup> , S. Varsano <sup>3</sup> , S. Ertracht <sup>4</sup> , I. Abramovitz <sup>2</sup> , I. Assis <sup>2</sup> , I. Shlamovitz <sup>2</sup> , E. Tiomkin <sup>2</sup> , <sup>1</sup> Kimron Veterinary Institute, Israel, <sup>2</sup> Hachaklait veterinary services, Israel, <sup>3</sup> Indi-Vet Ltd, Israel, <sup>4</sup> Dr. Amos Bareli LTD, Israel, <sup>5</sup> Lamikne veterinary services, Israel, <sup>6</sup> Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, Italy	<b>[SYM3.03.02]</b> <b>Population genetics in the surveillance of resistance mutations and outbreaks in hepatitis C virus (HCV)</b> N. García-González <sup>1</sup> , N. Caro-Pérez <sup>2,3</sup> , E. Perpiñan <sup>2,3</sup> , X. Forns <sup>2,3</sup> , S. Pérez del Pulgar <sup>2,3</sup> , F. González-Candelas <sup>*1,4</sup> , <sup>1</sup> FISABIO-CSISP / Univ. Valencia. Joint Research Unit Infection and Public Health, Spain, <sup>2</sup> Hosp. Clínic, IDIBAPS, Univ. Barcelona, Spain, <sup>3</sup> CIBEREHD, Spain, <sup>4</sup> CIBERESP, Spain

14:10-14:30	<p><b>[SYM3.01.03]</b>  <b>Silencing RACK1 inhibits <i>shigella flexneri</i> motility within HeLa cells</b>  K. Valenzuela*, J. Rhode, Z. Cheng  <i>Dalhousie University, Canada</i></p>	<p><b>[SYM3.02.03]</b>  <b>Outbreaks of Bluetongue serotype 8 during the last two decades: Appearance, dynamic of circulation and interaction with local Bluetongue strains, leading to their reassortments</b>  N. Golender*, A. Eldar<sup>1</sup>, Y. Khinich<sup>1</sup>, S. Zientara<sup>2</sup>, V. Bumbarov<sup>1</sup>, <sup>1</sup><i>Kimron Veterinary Institute, Israel</i>, <sup>2</sup><i>ANSES, France</i></p>	<p><b>[SYM3.03.03]</b>  <b>Detection and identification of viral RNA in biological samples using next-generation sequencing</b>  K. Khafizov*<sup>1,2</sup>, A.A. Ayginin<sup>1,2</sup>, A.D. Matsvay<sup>1,2</sup>, E.V. Pimkina<sup>1</sup>, A.S. Speranskaya<sup>1,3</sup>, I.V. Artyushin<sup>3</sup>, M.V. Safonova<sup>1</sup>, V.G. Dedkov<sup>1,4</sup>, G.A. Shipulin<sup>1</sup>  <sup>1</sup><i>Central Research Institute of Epidemiology, Russia</i>, <sup>2</sup><i>Moscow Institute of Physics and Technology, Russia</i>, <sup>3</sup><i>Moscow State University, Russia</i>, <sup>4</sup><i>Saint-Petersburg Pasteur Institute, Russia</i></p>
14:30-14:50	<p><b>[SYM3.01.04]</b>  <b>Whole-genome sequencing as a tool to investigate an animal listeriosis outbreak in Slovenia in 2013</b>  B. Papic*, M. Pate, D. Kusar  <i>University of Ljubljana, Slovenia</i></p>	<p><b>[SYM3.02.04]</b>  <b>Microevolution of <i>Listeria monocytogenes</i> in the dairy farm environment</b>  H. Castro*, H. Korkeala, M. Lindström, <i>University of Helsinki, Finland</i></p>	<p><b>[SYM3.03.04]</b>  <b>Combining phylogenetic and network approaches to identify HIV-1 transmission links in San Mateo County, California</b>  S. C. Dalaj<sup>1,2</sup>, D. Maletich Junqueira*<sup>3,4</sup>, E. Wilkinson<sup>3,4</sup>, R. Mehra<sup>5</sup>, V. Levy<sup>1,6</sup>, T. de Oliveira<sup>3,4</sup>, D. Katzenstein<sup>1</sup>, <sup>1</sup><i>Stanford University School of Medicine, USA</i>, <sup>2</sup><i>University of California, USA</i>, <sup>3</sup><i>KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), South Africa</i>, <sup>4</sup><i>University of KwaZulu-Natal, South Africa</i>, <sup>5</sup><i>Johns Hopkins Hospital, USA</i>, <sup>6</sup><i>San Mateo Medical Center, USA</i></p>
14:50-15:10	<p><b>[SYM3.01.05]</b>  <b>Concordance of SNP and gene typing workflows in defining epidemic clusters - The example of a <i>salmonella enteritidis</i> outbreak investigation</b>  C. Coipan*<sup>1</sup>, T. Dallman<sup>2</sup>, D. Brown<sup>3</sup>, H. Hartman<sup>2</sup>, M. van der Voort<sup>4</sup>, R. van den Berg<sup>4</sup>, D. Palm<sup>5</sup>, S. Kotila<sup>5</sup>, T. van Wijk<sup>1</sup>, E. Franz<sup>1</sup>, <sup>1</sup><i>Dutch Institute for Public Health (RIVM), The Netherlands</i>, <sup>2</sup><i>Public Health England (PHE), UK</i>, <sup>3</sup><i>Scottish Microbiology Reference Laboratory (SMiRL), UK</i>, <sup>4</sup><i>Dutch Food and Consumer Product Safety Authority (NVWA), The Netherlands</i>, <sup>5</sup><i>European Centre for Disease Control (ECDC), Sweden</i></p>	<p><b>[SYM3.02.05]</b>  <b>Novel pestivirus isolated from an aborted lamb foetus in Italy</b>  E. Sozzi<sup>1</sup>, A. Lavazza<sup>1</sup>, A. Gaffuri<sup>1</sup>, F.C. Bencetti<sup>2</sup>, A. Prosperi<sup>1</sup>, D. Lelli<sup>1</sup>, C. Chiapponi<sup>1</sup>, L. Baioni<sup>1</sup>, A. Moreno*<sup>1</sup>  <sup>1</sup><i>Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Italy</i>, <sup>2</sup><i>Veterinary Practitioner, Italy</i></p>	<p><b>[SYM3.03.05]</b>  <b>The effect of interventions on the transmission and spread of HIV in South Africa: A phylodynamic analysis</b>  E. Wilkinson*<sup>1,2</sup>, D.M. Junqueira<sup>1</sup>, R. Lessells<sup>1</sup>, S. Engelbrecht<sup>3</sup>, G. van Zyl<sup>3</sup>, T. de Oliveira<sup>1</sup>, M. Salemi<sup>1</sup>, <sup>1</sup><i>University of KwaZulu-Natal, South Africa</i>, <sup>2</sup><i>University of Florida, USA</i>, <sup>3</sup><i>University of Stellenbosch, South Africa</i></p>

15:10-15:30	<p><b>[SYM3.01.06]</b>  <b>Molecular epidemiology and antimicrobial resistance by WGS of <i>Neisseria gonorrhoeae</i> in Spain</b>  C. Francés-Cuesta*<sup>1</sup>, A. Fabregat-Bolufer<sup>2</sup>, J. Serra-Pladevall<sup>3</sup>, B. Romero-Hernández<sup>4</sup>, B. Menéndez<sup>5</sup>, T. Pumarola<sup>3</sup>, J.C. Galán-Montemayor<sup>4,6</sup>, J. Colomina<sup>7</sup>, F. González-Candelas<sup>1,6</sup>, <sup>1</sup>FISABIO-CSISP / Univ. Valencia. Joint Research Unit Infection and Public Health, Spain, <sup>2</sup>Hosp. La Ribera, Spain, <sup>3</sup>Hosp. Vall d'Hebrón, Spain, <sup>4</sup>Hosp. Ramón y Cajal, Spain, <sup>5</sup>Clínica Sandoval, Spain, <sup>6</sup>CIBER Epidemiología Salud Pública, Spain, <sup>7</sup>Hosp. Clínico Univ., Spain</p>	<p><b>[SYM3.02.06]</b>  <b>BVDV2 viral compartmentalization in pi infected calf</b>  B. Colitti*, M.T. Capucchio, C. Nogarol, L. Bertolotti, S. Rosati  University of Turin, Italy</p>	<p><b>[SYM3.03.06]</b>  <b>Astroviruses diversity and ecology in South African bats</b>  W. Preiser<sup>1</sup>, N.L. Ithete<sup>1</sup>, S. Schultz-Cherry<sup>2</sup>, K. Barnard*<sup>1</sup>  <sup>1</sup>Stellenbosch University, South Africa, <sup>2</sup>St. Jude Children's Research Hospital, USA</p>
15:30-16:00	Coffee break   Room: Tramuntana 1		
16:00-18:00	Symposium 4		
	<b>Stream 1: Vectors of Transmissible Diseases: Molluscs And Insects</b>	<b>Stream 2: Mycobacterium Tuberculosis Evolution</b>	<b>Stream 3: Infectious Agents Pathogenicity and Resistance 1</b>
Room	Tramuntana 2	Tramuntana 3	Mestral 1 & 2
16:00-16:20	<p><b>[SYM4.01.01]</b>  <b>Genetic differentiation of <i>glossina pallidipes</i> tsetse flies in Kenya</b>  W.A. Okeyo*<sup>1,2</sup>, R. Bateta<sup>2</sup>, N.P. Saarman<sup>4</sup>, K. Dion<sup>4</sup>, M. Mengual<sup>4</sup>, P.O. Mireji<sup>2</sup>, C. Ouma<sup>1</sup>, S. Okoth<sup>2</sup>, G. Murilla<sup>2,3</sup>, S. Aksoy<sup>3</sup>, <sup>1</sup>Maseno University, Kenya, <sup>2</sup>KALRO, Kenya, <sup>3</sup>Yale School of Public Health, USA, <sup>4</sup>Yale University, USA, <sup>5</sup>Kenya Medical Research Institute, Kenya</p>	<p><b>[SYM4.02.01]</b>  <b>Genomic determinants of sympatric speciation of the <i>mycobacterium tuberculosis</i> complex across evolutionary timescales.</b>  A. Chiner-Oms*<sup>1</sup>, L. Sánchez-Busó<sup>2</sup>, J. Corander<sup>3,4</sup>, S. Gagneux<sup>5,6</sup>, S. Harris<sup>2</sup>, D. Young<sup>7</sup>, F. González-Candelas<sup>1,8</sup>, I. Comas<sup>8,9</sup>, <sup>1</sup>Universidad de Valencia, Spain, <sup>2</sup>Wellcome Trust Sanger Institute, UK, <sup>3</sup>University of Oslo, Norway, <sup>4</sup>University of Helsinki, Finland, <sup>5</sup>Swiss Tropical and Public Health Institute, Switzerland, <sup>6</sup>University of Basel, Switzerland, <sup>7</sup>The Francis Crick Institute, UK, <sup>8</sup>CIBER en Epidemiología y Salud Pública, Spain, <sup>9</sup>Instituto de Biomedicina de Valencia (IBV_CSIC), Spain</p>	<p><b>[SYM4.03.01]</b>  <b>Core genome MLST versus single nucleotide polymorphism phylogenetic analysis for extended-spectrum beta-lactamase producing <i>Klebsiella pneumoniae</i> isolated from Oran, Algeria.</b>  A. Zemmour*<sup>1</sup>, M. Maatallah<sup>4</sup>, R. Abi-ayad<sup>2,3</sup>, N. Saidi-ouahrani<sup>1</sup>, B. Rahmani<sup>1</sup>, A. Camporeale<sup>4</sup>, G.C. Giske<sup>4</sup>  <sup>1</sup>University of Sciences &amp; Technology of Oran, Algeria, <sup>2</sup>University Hospital Establishment of Oran, Algeria, <sup>3</sup>Medical Faculty of Oran, Algeria, <sup>4</sup>Karolinska Institute, Sweden</p>

16:20-16:40	<p><b>[SYM4.01.02]</b>  <b>The blood microbiome of Biomphalaria snails: The missing link in snail-schistosome interactions?</b>  W. Le Clech<sup>h*</sup>, M. McDew-White, R. Diaz, T. Anderson, F. Chevalier, <i>Texas Biomedical Research Institute, USA</i></p>	<p><b>[SYM4.02.02]</b>  <b>24-locus MIRU-VNTR profiles of drug-resistant mycobacterium tuberculosis strains isolated from Northeastern Thailand</b>  K. Rueangsak<sup>1</sup>, C. Wilailuckana<sup>1</sup>, P. Pinlaor<sup>1</sup>, S. Tanuchit<sup>2</sup>, K. Faksri<sup>1</sup>, W. Namwat<sup>1</sup>, A. Sangka<sup>1</sup>, <sup>1</sup><i>Khon Kaen University, Thailand,</i> <sup>2</sup><i>Health Intervention and Technology Assessment Program (HITAP), Ministry of Public Health, Thailand</i></p>	<p><b>[SYM4.03.02]</b>  <b>Targeting candida glabrata biofilm using quorum quenching molecules</b>  P. Gupta*, P.K. Meena, K.M. Poluri, V. Pruthi  <i>Indian Institute of Technology Roorkee, India</i></p>
16:40-17:00	<p><b>[SYM4.01.03]</b>  <b>Detection of non-patent infection with schistosoma haematobium in populations of Bulinus sp. as risk factor for urinary schistosomiasis in the province of Zambezia, Mozambique</b>  L.B. Constantino, C. Alfredo, P. Ferreira, S. Belo, M. Calado, I.L. Mauricio*, <i>Instituto de Higiene e Medicina Tropical, Portugal</i></p>	<p><b>[SYM4.02.03]</b>  <b>DNA sequencing complements variable number of tandem repeats typing methods for mycobacterium tuberculosis Bayesian phylogeny inference</b>  A. Dhawan<sup>1</sup>, H. Korthals Altes<sup>*1</sup>, D. van Soolingen<sup>1</sup>, M. Bootsma<sup>2</sup>, D. Klinkenberg<sup>1</sup>, <sup>1</sup><i>National Institute for Public Health and the Environment, The Netherlands,</i> <sup>2</sup><i>Utrecht University, The Netherlands</i></p>	<p><b>[SYM4.03.03]</b>  <b>Antimicrobial resistance of neisseria gonorrhoeae isolates in Russian Federation, 2015 to 2017.</b>  B. Shaskolskiy<sup>*1</sup>, A. Leinsoo<sup>1</sup>, I. Kandinov<sup>1</sup>, E. Dementieva<sup>1</sup>, D. Deryabin<sup>2</sup>, A. Kubanov<sup>2</sup>, D. Gryadunov<sup>1</sup>  <sup>1</sup><i>Russian Academy of Sciences (EIMB), Russia,</i> <sup>2</sup><i>Russian Ministry of Health, Russia</i></p>
17:00-17:20	<p><b>[SYM4.01.04]</b>  <b>New tools to detect and discriminate causes of homozygous excess and linkage disequilibrium in vectors</b>  T. De Meeûs<sup>*1</sup>, O. Manangwa<sup>2</sup>, S. Ravel<sup>1</sup>, L. Beati<sup>3</sup>, <sup>1</sup><i>IRD, France,</i> <sup>2</sup><i>Vector and Vector Borne Disease Research Institute, Tanzania,</i> <sup>3</sup><i>Georgia Southern University, USA</i></p>	<p><b>[SYM4.02.04]</b>  <b>Classification of mixed mycobacterium tuberculosis infections from WGS data</b>  C. Anyansi<sup>1,2</sup>, B. Walker<sup>2</sup>, T. Straub<sup>2</sup>, A. Manson<sup>2</sup>, A. Earl<sup>2</sup>, T. Abeel<sup>*1,2</sup>, <sup>1</sup><i>Delft University of Technology, The Netherlands,</i> <sup>2</sup><i>Broad Institute of MIT and Harvard, USA</i></p>	<p><b>[SYM4.03.04]</b>  <b>Modulation of the NFκB pathway by methylthioadenosine treatment in PBMCs from HTLV-1 patients</b>  A. Posadas*, M. Talledo,  <i>Universidad Peruana Cayetano Heredia, Peru</i></p>
17:20-17:40	<p><b>[SYM4.01.05]</b>  <b>Bacteria communities from the gut of glossina palpalis palpalis flies sampled in Human African trypanosomiasis foci in Cameroon, and relevance to their involvement in the flies' vector competence</b>  F. Jacob<sup>1</sup>, T.T. Melachio<sup>2</sup>, G.R. Njitichouang<sup>2</sup>, F. Njiokou<sup>2</sup>, G. Gimonneau<sup>1</sup>, L. Abate<sup>3</sup>, J. Reveillaud<sup>4,5</sup>, A. Geiger<sup>*6,7</sup>, <sup>1</sup><i>IRD, INTERTRYP, France,</i> <sup>2</sup><i>University of Yaounde, Cameroon,</i> <sup>3</sup><i>IRD, MIVEGEC, France,</i> <sup>4</sup><i>INRA, France,</i> <sup>5</sup><i>CIRAD, France,</i> <sup>6</sup><i>IRD, Cameroon,</i> <sup>7</sup><i>Center for Research on Filariasis and other Tropical Diseases, Cameroon</i></p>		

17:40-18:00	[SYM4.01.06] <b>Malaria vector population genetics to inform bednet effectiveness trials and deployment schedules</b> L. Yakob London School of Hygiene & Tropical Medicine, UK		
19:30-22:00	<b>Conference dinner</b>   Can Laury Restaurant		
<b>Friday, 9 November 2018</b>			
09:00-12:00	<b>Plenary session</b>		
<b>Room</b>	Tramuntana 2		
09:00-09:30	[PL10] <b>Dynamics and evolution of dengue virus populations within their mosquito vector</b> L. Lambrechts <sup>1</sup> , <sup>1</sup> Institut Pasteur, France, <sup>2</sup> CNRS, France		
09:30-10:00	[PL11] <b>Neisseria genomics: Current status and future perspectives</b> O.B. Harrison*, M. Varga, H.B. Bratcher, K.A. Jolley, M.C.J. Maiden, University of Oxford, UK		
10:00-10:30	<b>Coffee break</b>   Room: Tramuntana 1		
10:30-11:00	[PL12] <b>Recent insights into the evolutionary history of arenaviruses</b> D. Forni, C. Pontremoli, R. Cagliani, M. Sironi*, Bioinformatic Unit of the Scientific Institute IRCCS E. Medea, Italy		
11:00-11:30	[PL15] <b>Tuberculosis molecular evolution: The quest of the Grail?</b> C. Sola, Institute for Integrative Biology of the Cell (I2BC), CEA, CNRS, France		
11:30-12:00	[PL14] <b>The role of founder effects in speciation of parasitic protozoa: A unique Leishmania model in the Peruvian Andes</b> F. Van den Broeck* <sup>1</sup> , J. Cotton <sup>2</sup> , J-C Dujardin <sup>1</sup> , et al, <sup>1</sup> Institute of Tropical Medicine, Belgium, <sup>2</sup> Wellcome Sanger Institute, UK		
12:00-13:00	<b>Lunch</b>   Room: Noray Restaurant Marquee		
13:00-14:40	<b>Symposium 5</b>		
	<b>Stream 1: Trypanosomatid Molecular Epidemiology and Evolution</b>	<b>Stream 2: WGS in Tuberculosis: Recent Progress and User-Friendly Approaches</b>	<b>Stream 3: Wildlife Transmissible Diseases</b>
<b>Room</b>	Tramuntana 2	Tramuntana 3	Mestral 1&2
13:00-13:20	[SYM5.01.01] <b>Very high prevalence of rodent-borne trypanosoma lewisi in Cotonou, Benin: A new threat for human health?</b> P. Truc* <sup>1</sup> , C. Tatar <sup>2</sup> , G. Houemenou <sup>3</sup> , S. Badou <sup>3</sup> , H.J. Dossou <sup>3,4</sup> , J. Etougbétché <sup>3</sup> , A. Cœur d'acier <sup>2</sup> , P. Gauthier <sup>2</sup> , G. Dobigny <sup>1,3</sup> , <sup>1</sup> Institut de Recherche pour le Développement, France, <sup>2</sup> Institut National de Recherche Agronomique, France, <sup>3</sup> Ecole Polytechnique d'Abomey-Calavi, Benin, <sup>4</sup> Université d'Abomey-Calavi, Benin	[SYM5.02.01] <b>Genomics of mycobacterium tuberculosis to investigate the ecology and evolution of the M. tuberculosis complex</b> M. Coscolla* <sup>1</sup> , D. Brites <sup>2</sup> , F. Menardo <sup>2</sup> , C. Loiseau <sup>2</sup> , S. Borrell <sup>2</sup> , S. Gagneux <sup>2</sup> , I. Darko Otchere <sup>3</sup> , A. Asante-Poku <sup>3</sup> , D. Yeboah-Manu <sup>3</sup> , M. Conor <sup>4</sup> et al <sup>1</sup> University of Valencia, Spain, <sup>2</sup> Swiss Tropical and Public Health Institute, Switzerland, <sup>3</sup> University of Ghana, Ghana, <sup>4</sup> Institute of Tropical Medicine, Belgium	[SYM5.03.01] <b>Prevalence and molecular characterization of giardia duodenalis infection from stray cats residing in Bangkok temples, Thailand</b> P. Phoosangwalthong, J. Wongwigkan, C. Kengradomkij, K. Kamyngkird, W. Chimnoi, T. Inpankaew*, Kasetsart University, Thailand



<p>13:20-13:40</p>	<p><b>[SYM5.01.02]</b>  <b>Is <i>Trypanosoma cruzi</i> genetic variability an essential parameter to be considered during drug development?</b>  A. Vela*<sup>1,2</sup>, B. Oury<sup>1</sup>, C. Barnabé<sup>1</sup>, E. Davioud-Charvet<sup>3</sup>, J. Costales<sup>2</sup>, S.F. Brenière<sup>1,2</sup>, <sup>1</sup>Université de Montpellier, France, <sup>2</sup>Pontifical Catholic University of Ecuador, Ecuador, <sup>3</sup>Polymers and Materials (ECPM), France</p>	<p><b>[SYM5.02.02]</b>  <b>Next-Generation sequencing approaches and implementation considerations for diagnosis and surveillance of drug-resistant tuberculosis</b>  A.M. Cabibbe*, D.M. Cirillo, <i>IRCCS San Raffaele Scientific Institute, Italy</i></p>	<p><b>[SYM5.03.02]</b>  <b>Specific capture and whole-genome sequencing of dolphin morbillivirus from the Mediterranean Sea</b>  F. Cerutti*, F. Giorda, A. Pautasso, C. Grattarola, W. Mignone, M. Goria, L. Masoero, P.L. Acutis, C. Casalone, S. Peletto  <i>Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Italy</i></p>
<p>13:40-14:00</p>	<p><b>[SYM5.01.03]</b>  <b>Comparative proteomics of <i>Trypanosoma cruzi</i> strains</b>  A. Herreros*<sup>1</sup>, F. Callejas-Hernández<sup>1</sup>, N. Gironès<sup>1,2</sup>, M. Fresno<sup>1,2</sup>  <sup>1</sup>Centro de Biología Molecular Severo Ochoa (UAM-CSIC), Spain, <sup>2</sup>Instituto Sanitario de Investigación Princesa, Spain</p>	<p><b>[SYM5.02.03]</b>  <b>Short-cuts for optimizing transnational tuberculosis transmission based on whole genome sequencing data</b>  E. Abascal<sup>1,2</sup>, L. Pérez-Lago<sup>1,2</sup>, A.M. Cabibbe<sup>3</sup>, J. Agapito<sup>4</sup>, C. Sola<sup>5</sup>, A. Goodridge<sup>6</sup>, V. Ritacco<sup>7,8</sup>, D.M. Cirillo<sup>3</sup>, E. Gotuzzo<sup>4</sup>, D. García de Viedma*<sup>1,2,3</sup>, <sup>1</sup>Instituto de Investigación Sanitaria Gregorio Marañón, Spain, <sup>2</sup>Hospital General Universitario Gregorio Marañón, Spain, <sup>3</sup>IRCCS San Raffaele Scientific Institute, Italy, <sup>4</sup>Universidad Peruana Cayetano Heredia, Peru, <sup>5</sup>Sud, Université Paris, France, <sup>6</sup>Ciudad del Saber, Panama, <sup>7</sup>CONICET, Argentina, <sup>8</sup>CIBERES, CIBER Enfermedades Respiratorias, Argentina, <sup>9</sup>CIBER Enfermedades Respiratorias, CIBERES, Spain</p>	<p><b>[SYM5.03.03]</b>  <b>The evolution of endogenous viruses in bats and their potential contribution to the immune response</b>  E.C. Skirmuntt*, A. Katourakis, <i>University of Oxford, UK</i></p>
<p>14:00-14:20</p>	<p><b>[SYM5.01.04]</b>  <b>Role of domestic and wild mammals in the epidemiology of chagas disease in the Sierra Nevada of Santa Marta</b>  M.T. Mojica-Ortiz*, J.C. Dib, <i>Centro de Investigación en Medicina Tropical - CIMET, Universidad del Magdalena, Colombia</i></p>	<p><b>[SYM5.02.04]</b>  <b>TB genomic diversity and spatial genetics made easier: scientific and methodological issues in multi-scaling methods and analysis for epidemiological and evolutionary genetics of tuberculosis.</b>  G. Refrégier<sup>1</sup>, B. Klotoe<sup>1</sup>, R. Debry<sup>1</sup>, A. Pinto<sup>1</sup>, A. Le Meur<sup>1</sup>, D. Haj Slimene<sup>1,2</sup>, H. Mardassi<sup>2</sup>, D. Garcia de Viedma<sup>3,5</sup>, C. Sola*<sup>1</sup>, <sup>1</sup>Institut of Integrative Cell Biology, Gif-sur-Yvette, France, <sup>2</sup>Institut Pasteur of Tunisia, Tunisia, <sup>3</sup>Instituto de Investigación Sanitaria Gregorio Marañón, Spain, <sup>4</sup>Hospital General Universitario Gregorio Marañón, Spain, <sup>5</sup>CIBER Enfermedades Respiratorias, CIBERES, Spain</p>	<p><b>[SYM5.03.04]</b>  <b>Bartonella unearched - prevalence &amp; diversity in subterranean mahali mole-rats (<i>Cryptomys hottentotus mahali</i>) from Gauteng Province, South Africa</b>  D.J. Kleynhans*<sup>1</sup>, D. Hart<sup>1</sup>, J. Rossouw<sup>2</sup>, N.C. Bennett<sup>1</sup>, A.D.S. Bastos<sup>1</sup>, <sup>1</sup>University of Pretoria, South Africa, <sup>2</sup>National Institute for Communicable Diseases, South Africa</p>

14:20-14:40	<b>[SYM5.01.05]</b> <b>Evolution of RNA viruses in trypanosomatids: leishmaniaviruses are no longer confined to leishmania</b> V. Yurchenko*, D. Grybchuk, D. Macedo, A. Kostygov <i>University of Ostrava, Czech Republic</i>		
14:40-15:10	<b>Coffee break</b>   Room: <i>Tramuntana 1</i>		
15:10-16:10	<b>Symposium 6</b>		
	<b>Stream 1: Parasitic Protozoa Molecular Epidemiology and Evolution</b>	<b>Stream 2: Modelling Approaches of Transmissible Diseases 2</b>	<b>Stream 3: Infectious Agents Pathogenicity and Resistance 2</b>
<b>Room</b>	<i>Tramuntana 2</i>	<i>Tramuntana 3</i>	<i>Mestral 1&amp;2</i>
15:10-15:30	<b>[SYM6.01.01]</b> <b>Plasmodium vivax-like genome sequences shed new insights into plasmodium vivax biology and evolution.</b> V. Rougeron <sup>1</sup> , G. Gilabert <sup>1</sup> , T. D. Otto <sup>2,3</sup> , F. Prugnolle <sup>1</sup> , <sup>1</sup> Université de Montpellier-CNRS-IRD, France, <sup>2</sup> Wellcome Trust Sanger Institute, UK, <sup>3</sup> University of Glasgow, UK	<b>[SYM6.02.01]</b> <b>Enzyme immunoassays for screening clostridium difficile: A meta-analysis</b> J.P. Martins <sup>1,2</sup> , R. Santos <sup>1,2</sup> , M. Felgueiras <sup>1,2</sup> , <sup>1</sup> Polytechnic Institute of Leiria, Portugal, <sup>2</sup> CEAUL - Center of Statistics and Applications, Portugal	<b>[SYM6.03.01]</b> <b>Short-term evolution of antimicrobial resistant strains of klebsiella pneumoniae in Comunidad Valenciana (Spain)</b> N. García-González <sup>1</sup> , S. Sabater <sup>2</sup> , B. Gomila <sup>2</sup> , C. Gimeno <sup>3</sup> , B. Fuster <sup>3</sup> , C. Salvador <sup>3</sup> , N. Tormo <sup>3</sup> , R. Moreno <sup>2</sup> , F. González-Candela <sup>1,4</sup> , <sup>1</sup> FISABIO-CSISP / Univ. Valencia. Joint Research Unit Infection and Public Health, Spain, <sup>2</sup> HGUC - H.Gen.Univ. Castello, Spain, <sup>3</sup> CHGUV - H.Gen.Univ. Valencia, Spain, <sup>4</sup> CIBER Epidemiologia Salud Publica, Spain
15:30-15:50	<b>[SYM6.01.02]</b> <b>PCR detection and phylogenetic analysis of haemoprotozoan parasites in livestock in Myanmar by using selected target genes</b> K. Katakura <sup>1</sup> , S. Bawm <sup>1,2</sup> , H.M. Chel <sup>1,2</sup> , M.J. Thu <sup>1,2</sup> , L.L. Htun <sup>2</sup> , Y. Imasato <sup>1</sup> , R. Nakao <sup>1</sup> , <sup>1</sup> Hokkaido University, Japan, <sup>2</sup> University of Veterinary Science, Myanmar	<b>[SYM6.02.02]</b> <b>Combining GoogleTrends and viral genetic data for public health surveillance: The case of influenza A/H3N2 in Arizona</b> M.A. Vaiente*, M. Scotch, <i>Arizona State University, USA</i>	<b>[SYM6.03.02]</b> <b>The oxidative stress induced by a new photosensitizer activate response element of MDR K. pneumoniae related to higher virulence of health associated infections strains</b> C. Nuñez, I. Gonzalez, M. Valenzuela, C. Palavecino*, <i>Universidad central de Chile, Chile</i>
15:50-16:10	<b>[SYM6.01.03]</b> <b>A possible role of invasive commensal rodents in shaping current Toxoplasma gondii population structure in Senegal</b> L. Galal <sup>1</sup> , A. Sarr <sup>1</sup> , T. Cuny <sup>1</sup> , C. Brouat <sup>2</sup> , M-L. Dardé <sup>1,3</sup> , M. Sembène <sup>4</sup> , D. Ajzenberg <sup>1,3</sup> , A. Mercier <sup>1,3</sup> , <sup>1</sup> INSERM, Université de Limoges, France, <sup>2</sup> Univ. Montpellier, France, <sup>3</sup> CHU Limoges, France, <sup>4</sup> Campus de Bel-Air, France	<b>[SYM6.02.03]</b> <b>Appearance of positive frequency-dependent alleles triggers an evolutionary force selecting for silence</b> I. Hashem, V. De Buck, J. Van Impe* <i>KU Leuven, Belgium</i>	<b>[SYM6.03.03]</b> <b>Tracking epidemic carbapenemase-producing bacteria in hospital: More complete is the sampling, more complex is the jigsaw</b> S. Baranovsky <sup>1,2</sup> , S. Romano-Bertrand <sup>1,2</sup> , P. Licznar-Fajardo <sup>1,2</sup> , L. Téot <sup>3</sup> , D. Grau <sup>1,2</sup> , S. Parer <sup>1,2</sup> , E. Jumas-Bilak <sup>1</sup> <sup>2</sup> HydroSciences, France, <sup>3</sup> CHRU Montpellier, France, <sup>4</sup> CHU Montpellier, France
16:10-16:45	<b>Closing ceremony &amp; awards</b>		