

## Oral Program

### Tuesday, 30 October 2012

17:00-19:00 Registration - St. Charles Room

19:00-20:00 Welcome Drinks Reception – Hosted by J. Edgar & Louise S. Monroe Library, 3<sup>rd</sup> Floor

### Wednesday, 31 October 2012

9:00-9:05 Welcome from Prof. Marc K. Manganaro, Provost and Vice President for Academic Affairs at Loyola University New Orleans – Roussell Hall

9:05-9:45 Opening Remarks – Roussell Hall

#### Plenary Session Roussell Hall

9:45-10:15 **[PL1] Whence *Plasmodium falciparum*? A new understanding of its evolutionary origin**  
F.J. Ayala, *University of California, Irvine, USA*

10:15 -10:45 **[PL2] The evolution of new signal transduction pathways involved in fungal pathogenesis**  
D.R. Soll, *University of Iowa, USA*

10:45-11:30 **Coffee Break - St. Charles Room**

11:30-12:00 **[PL3] Molecular epidemiologist's view of *M. tuberculosis* pathogenesis**  
B.N. Kreiswirth, *University of Medicine and Dentistry of New Jersey, USA*

12:00-12:30 **[PL4] The population genetics concept of clonality: Biomedical implications for pathogenic viruses, bacteria, fungi, and parasitic protozoa**  
M. Tibayrenc<sup>\*1</sup>, F.J. Ayala<sup>2</sup>, <sup>1</sup>*Institut de Recherche pour le Développement (IRD), USA*, <sup>2</sup>*University of California, Irvine, USA*

12:30-14:00 **Lunch – St. Charles Room**

**Life Technologies Workshop (13:00-14:00) - Audubon**

	<b>Symposium 1 Roussell Hall</b>	<b>Symposium 2 Audubon</b>	<b>Symposium 3 Multimedia 1</b>	<b>Symposium 4 Multimedia 2</b>
Theme	HIV molecular epidemiology & phylogenetics	Clonal vs Sexual Evolution in pathogens	Pathogens of Veterinary Relevance	Epidemiology of Transmissible Diseases
Session Chair	Philippe Lemey & Loubna Tazi	Rodrigo Baptista & Michel Tibayrenc	Susan Payne & Sébastien Calvignac-Spencer	Marina Ascunce & Algimantas Paulauskas
14:00-14:20	<b>[S1.1] Reconstruction of an HIV transmission history in a Bayesian coalescent framework</b> B. Vrancken <sup>*1</sup> , A. Rambaut <sup>2</sup> , G. Baele <sup>1</sup> , A-M. Vandamme <sup>1,3</sup> , K. van Laethem <sup>1</sup> , E. van Wijngaerden <sup>4</sup> , A. Drummond <sup>5</sup> , M. Suchard <sup>6,7</sup> , P. Lemey <sup>1</sup> , <sup>1</sup> <i>KU Leuven, Belgium</i> , <sup>2</sup> <i>University of Edinburgh, UK</i> , <sup>3</sup> <i>Universidade Nova de Lisboa, Portugal</i> , <sup>4</sup> <i>University Hospitals Leuven, Belgium</i> , <sup>5</sup> <i>University of Auckland, New Zealand</i> , <sup>6</sup> <i>David Geffen School of Medicine at UCLA, USA</i> , <sup>7</sup> <i>UCLA School of Public Health, USA</i>	<b>[S2.1] Genome-wide survey of homologous recombination and diversifying selection in <i>H. pylori</i>, a highly sexual bacterial species</b> K. Yahara <sup>*1</sup> , M. Kawai <sup>1,2</sup> , Y. Furuta <sup>1</sup> , J. Bujnicki <sup>4,5</sup> , I. Uchiyama <sup>2</sup> , I. Kobayashi <sup>1</sup> , <sup>1</sup> <i>University of Tokyo, Japan</i> , <sup>2</sup> <i>National Institute for Basic Biology, Japan</i> , <sup>3</sup> <i>Kobe University, Japan</i> , <sup>4</sup> <i>International Institute of Molecular and Cell Biology, Poland</i> , <sup>5</sup> <i>Adam Mickiewicz University, Poland</i>	<b>[S3.1] Detection and phylogenetic analysis of canine coronavirus in dogs</b> L.D. Pinto <sup>1</sup> , I.N. Barros <sup>*2</sup> , R.F. Budaszewski <sup>1</sup> , J.R. Antunes <sup>1</sup> , O.F.O. Granados <sup>1</sup> , P.E. Brandão <sup>2</sup> , C.W. Canal <sup>1</sup> , <sup>1</sup> <i>Universidade Federal do Rio Grande do Sul, Brazil</i> , <sup>2</sup> <i>Universidade de São Paulo, Brazil</i>	<b>[S4.1] The MHC determinants of AIDS-related Kaposi's sarcoma</b> A.K. Boehme <sup>*</sup> , K.M. Ogwaro, H. Weiner, S. Shrestha, R.A. Kaslow, B. Aissani, <i>University of Alabama at Birmingham, USA</i>
14:20-14:40	<b>[S1.2] HIV-1 evolution in monozygotic twins</b> L. Tazi <sup>*1</sup> , H. Imamichi <sup>2,3</sup> , M. Pérez-Losada <sup>4</sup> , D. Posada <sup>5</sup> , H.C. Lane <sup>3</sup> , K.A. Crandall <sup>6</sup> , <sup>1</sup> <i>Kansas State University, USA</i> , <sup>2</sup> <i>Frederick National Laboratory for Cancer Research, USA</i> , <sup>3</sup> <i>National Institutes of Health, USA</i> , <sup>4</sup> <i>Universidade</i>	<b>[S2.2] Gross incongruence between nuclear and mitochondrial genomes suggest widespread genetic exchange and the origins of domestic <i>Trypanosoma cruzi</i></b> J.D. Ramirez <sup>*1</sup> , F. Guhl <sup>1</sup> , L. Messenger <sup>2</sup> , M. Lewis <sup>2</sup> , M. Montilla <sup>3</sup> , Z.M. Cucunuba <sup>3</sup> , <sup>1</sup> <i>Universidad de los Andes,</i>	<b>[S3.2] The role of vaccination in induction of mucosal disease in persistent BVDV infection</b> A. Chernick <sup>*</sup> , F.J.U.M. van der Meer, <i>University of Calgary, Canada</i>	<b>[S4.2] Investigation of genetic diversity of <i>Ixodes ricinus</i> ticks</b> A. Paulauskas <sup>*1</sup> , E. Galdikaite <sup>1</sup> , A. Slettan <sup>2</sup> , J. Radzijeuskaja <sup>1</sup> , L. Korslund <sup>2</sup> , A. Banaityte <sup>1</sup> , <sup>1</sup> <i>Vytautas Magnus University, Lithuania</i> , <sup>2</sup> <i>University of Agder, Norway</i>

	<i>do Porto, Portugal,<sup>5</sup>University of Vigo, Spain,<sup>6</sup>George Washington University, USA</i>	<i>Colombia,<sup>2</sup>London School of Hygiene and Tropical Medicine, UK,<sup>3</sup>Instituto Nacional de Salud, Colombia</i>				
14:40-15:00	<b>[S1.3] Determinants of HIV genetic clustering in Michigan: Implications for surveillance and control</b> L. Zhong <sup>*1</sup> , E.O. Romero-Severson <sup>1</sup> , E.M. Volz <sup>1</sup> , M.G. Brandt <sup>1</sup> , E.D. Mokotoff <sup>1</sup> , J.S. Koopman <sup>1</sup> , <sup>1</sup> University of Michigan, USA, <sup>2</sup> Michigan Department of Community Health, USA	<b>[S2.3] Population genetic evidence suggests recurrent transitions to asexuality in a microsporidian parasite</b> K.L. Haag <sup>*1</sup> , E. Sheik-Jabbari <sup>1</sup> , F. Ben-Ami <sup>2</sup> , D. Ebert <sup>1</sup> , <sup>1</sup> University of Basel, Switzerland, <sup>2</sup> Tel Aviv University, Israel	<b>[S3.3] Dynamics of bovine viral diarrhea virus in three generations of persistently infected cattle</b> N. Dow <sup>*</sup> , F.J.U.M. van der Meer, <i>University of Calgary, Canada</i>	<b>[S4.3] Molecular characterization of Brazilian canine coronavirus strains</b> I.N. Barros <sup>*1,3</sup> , L.D. Pinto <sup>2</sup> , R.B.S. Kuroda <sup>1</sup> , S.O.S. Silva <sup>1,3</sup> , C.W. Canal <sup>2</sup> , P.E. Brandao <sup>1,3</sup> , <sup>1</sup> University of São Paulo, Brazil, <sup>2</sup> University of Rio Grande do Sul, Brazil, <sup>3</sup> Coronavirus Research Group, Brazil		
15:00-15:20	<b>[S1.4] Recombination affects origin estimates: Rethinking the HIV-1 subtype B global pandemic</b> C.M. Hepp <sup>*</sup> , M.S. Rosenberg, <i>Arizona State University, USA</i>	<b>[S2.4] Role of recombination in genetic diversity of banana bunchy top virus population</b> F. Sundus <sup>1</sup> , M. Farukh <sup>1</sup> , M. Ali <sup>1</sup> , M. Imran <sup>1</sup> , S.M.S. Naqvi <sup>2</sup> , M.Z. Hyder <sup>*1,3</sup> , <sup>1</sup> COMSATS Institute of Information Technology, Pakistan, <sup>2</sup> PMAS Arid Agriculture University Rawalpindi, Pakistan, <sup>3</sup> Health Services Academy, Pakistan	<b>[S3.4] Avian bornaviruses and their distribution in North American waterfowl: Emerging pathogens?</b> S. Payne <sup>*1</sup> , J. Guo <sup>1</sup> , J. Baroch <sup>2</sup> , I. Tizard <sup>1</sup> , <sup>1</sup> Texas A&M University, USA, <sup>2</sup> U.S. Department of Agriculture, USA	<b>[S4.4] Microsatellite diversity of human lice (<i>Pediculus humanus</i>) reveals continental differences among worldwide populations</b> M. Ascunce <sup>*1</sup> , M. Toups <sup>1</sup> , G. Kassu <sup>1</sup> , J. Fane <sup>1</sup> , K. Scholl <sup>1</sup> , A. Toloza <sup>2</sup> , <sup>1</sup> University of Florida, USA, <sup>2</sup> Centro de Investigaciones de Plagas e Insecticidas, Argentina, <sup>3</sup> Universidad Nacional Autónoma de México, Mexico		
15:20-15:40	<b>[S1.5] Antiviral drug resistance development in HIV-1 in the gastrointestinal tract and peripheral blood lymphocytes of a patient treated with Azidothymidine (AZT) followed by Didanosine (DDI)</b> F.J.U.M. van der Meer <sup>*1</sup> , M.J. Gill <sup>1</sup> , D.L. Church <sup>2</sup> , G. van Marle <sup>1</sup> , <sup>1</sup> University of Calgary, Canada, <sup>2</sup> Calgary Laboratory Services, Canada	<b>[S2.5] Evidence of significant recombination among <i>Trypanosoma cruzi</i> II strains from minas gerais</b> R.P. Baptista <sup>*</sup> , D.A. D'Ávila, M. Segatto, E. Chiari, A.M. Macedo, C.R. Machado, <i>Universidade Federal de Minas Gerais, Brazil</i>	<b>[S3.5] Polyomavirus transmission between sympatric wild chimpanzees (<i>Pan troglodytes troglodytes</i>) and gorillas (<i>Gorilla gorilla gorilla</i>)</b> N.F. Madinda <sup>1,2</sup> , C. Boesch <sup>2</sup> , M. Robbins <sup>2</sup> , F.H. Leendertz <sup>1</sup> , S. Calvignac-Spencer <sup>*1</sup> , <sup>1</sup> Robert Koch-Institute, Germany, <sup>2</sup> Max Planck-Institute for Evolutionary Anthropology, Germany			
15:40-17:00	<b>Poster Session 1 &amp; Coffee Break – St. Charles Room</b>					
<b>Plenary Session Russell Hall</b>						
17:00-17:30	<b>[PL5] The macro- and micro-evolution of <i>Mycobacterium tuberculosis</i></b> S. Gagneux, <i>Swiss Tropical and Public Health Institute, Switzerland</i>					
	<b>Symposium 5 Russell Hall</b>	<b>Symposium 6 Audubon</b>	<b>Symposium 7 Multimedia 1</b>	<b>Symposium 8 Multimedia 2</b>	<b>Symposium 9 Octavia 1</b>	
<b>Theme</b>	<b>Arbovirus evolution</b>	<b>Coevolution 1</b>	<b>Omics approaches</b>	<b>Antibiotic/drug resistance</b>	<b>Mathematical modeling/phylogeny 1</b>	
<b>Session Chair</b>	Ruian Ke & Jorge L. Munoz-Jordan	Majoline T. Tchioffo & Iñaki Comas	Octavio Franco & Betsy Foxman	Ghassan M. Matar & Raquel Muniz-Salazar	Philippe Lemey & Pejman Naraghi-Arani	
17:40-18:00	<b>[S5.1] Long term endurance of dengue virus serotype 2 and transient emergence of dengue virus serotype 3 in Puerto Rico: 1986-2010</b> J.L. Munoz-Jordan, G.A. Santiago <sup>*</sup> , <i>Centers for Disease Control and Prevention, USA</i>	<b>[S6.1] Parallel population expansions of the tuberculosis bacilli and anatomically modern humans</b> I. Comas <sup>*1,8</sup> , Q. Gao <sup>4</sup> , S. Niemann <sup>6</sup> , J. Parkhill <sup>5</sup> , D. Young <sup>7</sup> , S. Gagneux <sup>2,3</sup> , <sup>1</sup> Centre for Public Health Research	<b>[S7.1] Deciphering the proteome and transcriptome of magainin-resistant <i>Escherichia coli</i> strains</b> S. Maria-Neto, A.E.A.D. Barbosa, O.N. Silva, S.C. Dias, B.S. Magalhães, O.L. Franco <sup>*</sup> , <i>Universidade Católica</i>	<b>[S8.1] Increased prevalence of carbapenem resistance in Extended Spectrum-β-Lactamases (ESBLs) producing <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> in Lebanon due to bla<sub>OXA-48</sub>, bla<sub>NDM-1</sub> carbapenemase</b>	<b>[S9.1] Combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection</b> P. Lemey <sup>*1</sup> , V.N. Minin <sup>2</sup> , F. Bielejec <sup>1</sup> , S.L. Kosakovsky Pond <sup>3</sup> , M.A. Suchard <sup>4,5</sup> , <sup>1</sup> KU Leuven, Belgium, <sup>2</sup> University of	

		(CSISP), Spain, <sup>2</sup> Swiss Tropical and Public Health Institute, Switzerland, <sup>3</sup> University of Basel, Switzerland, <sup>4</sup> Fudan University, China, <sup>5</sup> Wellcome Trust Sanger Institute, UK, <sup>6</sup> Research Center Borstel, Germany, <sup>7</sup> National Institute for Medical Research, UK, <sup>8</sup> CIBER Epidemiology and Public Health, Spain	de Brasilia, Brazil	and ESBLs encoding genes G.M. Matar, American University of Beirut, Lebanon	Washington, USA, <sup>3</sup> UC San Diego Department of Medicine, USA, <sup>4</sup> David Geffen School of Medicine at UCLA, USA, <sup>5</sup> UCLA School of Public Health, USA
18:00-18:20	<b>[S5.2] Phylodynamic analysis of the emergence and epidemiological impact of transmissible defective dengue viruses</b> R. Ke <sup>*1</sup> , J. Aaskov <sup>2</sup> , E.C. Holmes <sup>3,4</sup> , J.O. Lloyd-Smith <sup>1,4</sup> , <sup>1</sup> University of California, Los Angeles, USA, <sup>2</sup> Queensland University of Technology, Australia, <sup>3</sup> The Pennsylvania State University, USA, <sup>4</sup> National Institutes of Health, USA	<b>[S6.2] Contribution of interactions between M-related proteins and human IgG to host specificity and virulence of <i>Streptococcus pyogenes</i></b> H.S. Courtney <sup>*1,2</sup> , Y. Li <sup>1</sup> , <sup>1</sup> Veterans Affairs Medical Center, USA, <sup>2</sup> University of Tennessee Health Science Center, USA	<b>[S7.2] Exploring the effect of dentition, dental decay and familiarity on oral health using metabolomics</b> U. Srinivasan <sup>1</sup> , A. Wen <sup>1</sup> , C. Marrs <sup>1</sup> , L. Zhang <sup>1</sup> , R. Weyant <sup>2</sup> , D. McNeil <sup>3</sup> , M. Marazita <sup>2</sup> , R. Crout <sup>3</sup> , B. Foxman <sup>*1</sup> , <sup>1</sup> University of Michigan, USA, <sup>2</sup> University of Pittsburgh, USA, <sup>3</sup> West Virginia University, USA	<b>[S8.2] Isoniazid and Rifampin resistance in <i>Mycobacterium tuberculosis</i> clinical isolates from Baja California, Mexico</b> R. Muniz-Salazar <sup>*1</sup> , R. Laniado-Laborin <sup>2</sup> , A.C. Vargas-Ojeda <sup>1</sup> , R. Zenteno-Cuevas <sup>3</sup> , N.L. Victoria-Cota <sup>1</sup> , P. Radilla-Chávez <sup>1</sup> , <sup>1</sup> Universidad Autónoma de Baja California, Mexico, <sup>2</sup> Hospital General de Tijuana, ISESALUD, Mexico, <sup>3</sup> Universidad Veracruzana, Mexico	<b>[S9.2] GeneSV- a novel approach to study sequence-structure variabilities in genome sequences</b> A. Zemla <sup>1</sup> , T. Kostova <sup>1</sup> , D.W.C. Beasley <sup>2</sup> , S.C. Weaver <sup>2</sup> , N. Vasilakis <sup>2</sup> , P. Naraghi-Arani <sup>*1</sup> , <sup>1</sup> Lawrence Livermore National Laboratory, USA, <sup>2</sup> University of Texas Medical Branch, USA
18:20-18:40	<b>[S5.3] The evolution and potential role in host adaptation of 3'UTR in CHIKV</b> R. Chen <sup>*</sup> , E. Wang, K.A. Tsetsarkin, S.C. Weaver, University of Texas Medical Branch, USA	<b>[S6.3] Bacteria diversity in the midgut of wild mosquito vector <i>Anopheles gambiae</i>: A step toward finding suitable bacteria that mediate refractoriness to <i>Plasmodium falciparum</i></b> M.T. Tchioffo <sup>*1,2</sup> , A. Boissière <sup>1</sup> , L. Abate <sup>1</sup> , P.H. Awono-Ambene <sup>2</sup> , B. Antoine <sup>3</sup> , I. Morlais <sup>1,2</sup> , <sup>1</sup> IRD-MIVEGEC, France, <sup>2</sup> LRP-OCEAC, Cameroon, <sup>3</sup> Centre Hospitalier Universitaire de Toulouse, France	<b>[S7.3] Non-protein coding mammalian genes associated with virus infection: Broad effects on virus replication</b> J. Murray <sup>1</sup> , J. Sheng <sup>2</sup> , T.W. Hodge <sup>1</sup> , D.H. Rubin <sup>*2,3</sup> , <sup>1</sup> Zirus, USA, <sup>2</sup> Vanderbilt University, USA, <sup>3</sup> VA Tennessee Valley Healthcare System, USA		<b>[S9.3] Bioinformatics methods for reconstruction of infectious bronchitis virus quasispecies from next generation sequencing data</b> I. Mandouiu <sup>1</sup> , R. O'Neill <sup>1</sup> , M. Khan <sup>1</sup> , A. Zelikovsky <sup>2</sup> , B. Tork <sup>*2</sup> , N. Mancuso <sup>2</sup> , <sup>1</sup> University of Connecticut, USA, <sup>2</sup> Georgia State University, USA
<b>Thursday, 1 November 2012</b>					
<b>Plenary Session</b> <b>Roussell Hall</b>					
9:00-9:30	<b>[PL6] Comparative genomics of the monkey malaria clade</b> J.M. Carlton, New York University, USA				
9:30-10:00	<b>[PL7] Landscape genetics and estimation of the effective population size (<math>N_e</math>) as genetic epidemiological tools to monitor metazoan parasite population and transmission dynamics</b> C.D. Criscione, Texas A&M University, USA				
10:00-10:45	<b>Coffee Break – St. Charles Room</b>				

	Symposium 10 Roussell Hall	Symposium 11 Audubon	Symposium 12 Multimedia 1
Theme	Influenza	Bacteria Molecular Epidemiology 1	Bacteria Molecular Epidemiology 2
Session Chair	Martha Nelson & Hsiang-Yu Yuan	Peter Timms & Kathryn Holt	Don H Rubin & Ali Khalid
10:45-11:05	<p><b>[S10.1] Transmission tree reconstruction using genetic data yields evidence of wind-mediated spread of avian influenza</b> R.J.F. Ypma<sup>1,2</sup>, M. Jonges<sup>1</sup>, A. Bataille<sup>3,4</sup>, A. Stegeman<sup>3</sup>, G. Koch<sup>4</sup>, M. Koopmans<sup>1,5</sup>, M. van Boven<sup>1</sup>, W.M. van Ballegooijen<sup>1</sup>, J. Wallinga<sup>1</sup>, <sup>1</sup>National Institute of Public Health and the Environment, The Netherlands, <sup>2</sup>University Medical Centre Utrecht, The Netherlands, <sup>3</sup>Utrecht University, The Netherlands, <sup>4</sup>Central Veterinary Institute, The Netherlands, <sup>5</sup>Erasmus Medical Center, The Netherlands</p>	<p><b>[S11.1] Genetic diversity and relationships between <i>Chlamydia pecorum</i> strains from koalas and domestic livestock</b> A. Polkinghorne, P. Timms*, Queensland University of Technology, Australia</p>	<p><b>[S12.1] The detection of <i>cagA</i> gene expression in the clinical isolates of <i>Helicobacter pylori</i> from a tertiary care hospital of Pakistan</b> A. Khalid<sup>1</sup>, F. Rasheed<sup>2,3</sup>, J. Usman<sup>4</sup>, <sup>1</sup>Najran University Hospital, Saudi Arabia, <sup>2</sup>Nuclear Medicine, Oncology and Radiotherapy Institute (NORI), Pakistan, <sup>3</sup>Pakistan Institute of Nuclear Science and Technology, Pakistan, <sup>4</sup>National University of Sciences and Technology, Pakistan</p>
11:05-11:25	<p><b>[S10.2] The evolution of novel reassortant A/H3N2 influenza viruses in North American swine and humans, 2009-2012</b> M.I. Nelson<sup>1</sup>, A.L. Vincent<sup>3</sup>, P. Kitikoon<sup>1</sup>, E.C. Holmes<sup>4,1</sup>, M.R. Gramer<sup>2</sup>, <sup>1</sup>National Institutes of Health, USA, <sup>2</sup>University of Minnesota, USA, <sup>3</sup>United States Department of Agriculture, USA, <sup>4</sup>Pennsylvania State University, USA</p>	<p><b>[S11.2] A powerful fast molecular method based on CRISPR polymorphisms for <i>Salmonella Typhimurium</i> characterization</b> A. Brisabois<sup>1</sup>, S.C. Pfister<sup>1</sup>, M. Marault<sup>1</sup>, S. Roussel<sup>1</sup>, S. Le Hello<sup>2</sup>, F.X. Weill<sup>2</sup>, <sup>1</sup>ANSES, France, <sup>2</sup>Institut Pasteur, France</p>	<p><b>[S12.2] Oligomerization of <i>Clostridium perfringens</i> epsilon toxin is dependent upon caveolins 1 and 2</b> C.M. Fennessey<sup>1</sup>, J. Sheng<sup>1</sup>, D.H. Rubin<sup>1,2</sup>, M.S. McClain<sup>1</sup>, <sup>1</sup>Vanderbilt University, USA, <sup>2</sup>VA Tennessee Valley Healthcare System, USA</p>
11:25-11:45	<p><b>[S10.3] The evolutionary dynamics of receptor binding avidity in influenza A: A mathematical model for a new antigenic drift hypothesis</b> H.Y. Yuan<sup>1</sup>, K. Koelle<sup>1,2</sup>, <sup>1</sup>Duke University, USA, <sup>2</sup>National Institutes of Health, USA</p>	<p><b>[S11.3] Evaluation of WGS for epidemiological typing of <i>Salmonella typhimurium</i> highly successful outbreak strains</b> P. Leekitcharoenphon<sup>1</sup>, E.M. Nielsen<sup>1</sup>, F.M. Aarestrup<sup>1</sup>, <sup>1</sup>Technical University of Denmark, Denmark, <sup>2</sup>Statens Serum Institut, Denmark</p>	<p><b>[S12.3] Diversity and evolution of <i>Dichelobacter nodosus</i>, the causative agent of footrot in sheep</b> E.M. Smith<sup>1</sup>, C.L. Russell<sup>2</sup>, L.A. Calvo-Bado<sup>1</sup>, L.E. Green<sup>1</sup>, E.M.H. Wellington<sup>1</sup>, G.F. Medley<sup>1</sup>, R. Gronono-Thomas<sup>2</sup>, <sup>1</sup>University of Warwick, UK, <sup>2</sup>University of Bristol, UK</p>
11:45-12:05	<p><b>[S10.4] Phylogeography of influenza A in human and avian species in the southwest United States</b> M. Scotch<sup>1</sup>, K. Pablonia<sup>2</sup>, T. Anderson<sup>2</sup>, J. Baroch<sup>3</sup>, D. Kohler<sup>3</sup>, T.J. DeLiberto<sup>3</sup>, M. Espy<sup>4</sup>, B. Pritt<sup>4</sup>, M.T. Seville<sup>4</sup>, <sup>1</sup>Arizona State University, USA, <sup>2</sup>Colorado State University, USA, <sup>3</sup>U.S. Department of Agriculture, USA, <sup>4</sup>Mayo Clinic, USA</p>	<p><b>[S11.4] The pressures of urban life: Adaptive evolution of <i>Shigella sonnei</i> in urban Vietnam</b> K.E. Holt<sup>1</sup>, S. Baker<sup>2</sup>, <sup>1</sup>University of Melbourne, Australia, <sup>2</sup>Hospital for Tropical Diseases, Vietnam</p>	<p><b>[S12.4] A dynamic whole-genome database for comparative analyses, molecular epidemiology and phenotypic summary of bacterial pathogens</b> C.R. Laing<sup>1,2</sup>, J.E. Thomas<sup>2</sup>, V.P.J. Gannon<sup>1</sup>, <sup>1</sup>Public Health Agency of Canada, Canada, <sup>2</sup>University of Lethbridge, Canada</p>
12:05-12:25	<p><b>[S10.5] The emergence of a highly pathogenic avian influenza virus - an evolutionary approach</b> A. Fusaro<sup>1</sup>, I. Monne<sup>1</sup>, M.I. Nelson<sup>2</sup>, A. Moreno<sup>3</sup>, L. Bonfanti<sup>1</sup>, G. Cattoli<sup>1</sup>, <sup>1</sup>Istituto Zooprofilattico Sperimentale delle Venezie, Italy, <sup>2</sup>National Institutes of Health, USA, <sup>3</sup>Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna, Italy</p>	<p><b>[S11.5] Genus wide, sequence informed design of an evolutionary informative bacterial MLST scheme</b> M.E. Hall<sup>1</sup>, S. Reuter<sup>2</sup>, T. Connor<sup>2</sup>, N. Thomson<sup>2</sup>, A. McNally<sup>1</sup>, <sup>1</sup>Nottingham Trent University, UK, <sup>2</sup>Wellcome Trust Sanger Institute, UK</p>	<p><b>[S12.5] Understanding uropathogenic <i>Escherichia coli</i> transmission and pathogenicity via next-generation sequencing</b> Y.Y. Lo*, L. Zhang, S. Zollner, B. Foxman, University of Michigan, USA</p>
12:25-12:45	<p><b>[S10.6] Evolution of influenza A virus non-structural (NS) genes</b> G.L. Lu*, J.X. Xu, University of Nebraska at Omaha, USA</p>	<p><b>[S11.6] Extended range of zoonotic leprosy in the Americas</b> R. Sharma*, M. Pena, R.W. Truman, Louisiana State University, USA</p>	<p><b>[S12.6] Novel MLST scheme for genetic characterization of worldwide <i>Leptospira</i> sp strains collections</b> K. Caimi<sup>1</sup>, V. Varni<sup>1</sup>, J.J. Lauthier<sup>2</sup>, N. Tomasini<sup>2</sup>, R. Hartskeerl<sup>3</sup>, P. Ruybal<sup>1</sup>, <sup>1</sup>INTA Castelar, Argentina, <sup>2</sup>National University of Salta, Argentina, <sup>3</sup>Royal Tropical Institute, The Netherlands</p>
12:45-14:15	Poster Session 2 & Lunch – St. Charles Room		

Plenary Session Russell Hall				
14:15-14:45	<b>[PL8] Molecular epidemiology: Comparing and contrasting the evolution and epidemiology of HIV-1 to HTLV, HCV, HBV and other viruses</b> B.T. Foley, <i>Los Alamos National Laboratory, USA</i>			
14:45-15:15	<b>[PL9] Genomic epidemiology of bacterial pathogens – perils and potential</b> W.P. Hanage, <i>Harvard School of Public Health, USA</i>			
	Symposium 13 Russell Hall	Symposium 14 Audubon	Symposium 15 Multimedia 1	Symposium 16 Multimedia 2
Theme	Host Genetics	Coevolution 2	Coevolution 3	Pathogen Molecular Diagnosis
Session Chair	Ana Paula Arez & Stefan Rothenburg	Naomi Forrester & Sumathi Ramachandran	Andre J Nahmias & Pavel Skums	Dhany Saputra & Sayani Tewari
15:25-15:45	<b>[S13.1] Pyruvate kinase deficiency and malaria protection in humans: A population genetics study</b> P. Machado <sup>1</sup> , L. Manco <sup>2</sup> , C. Gomes <sup>1</sup> , C. Mendes <sup>1</sup> , N. Fernandes <sup>3</sup> , G. Salomé <sup>3</sup> , S. Chibute <sup>3</sup> , L. Ribeiro <sup>4</sup> , J. Miranda <sup>5</sup> , J. Cano <sup>6</sup> , J. Pinto <sup>1</sup> , L. Gusmão <sup>7</sup> , A. Amorim <sup>7,8</sup> , V.E. do Rosário <sup>1</sup> , A.P. Arez <sup>*1</sup> , <sup>1</sup> Universidade Nova de Lisboa, Portugal, <sup>2</sup> Universidade de Coimbra, Portugal, <sup>3</sup> Universidade Eduardo Mondlane, Mozambique, <sup>4</sup> Centro Hospitalar de Coimbra, Portugal, <sup>5</sup> Hospital Pediátrico David Bernardino, Angola, <sup>6</sup> Instituto de Salud Carlos III, Spain, <sup>7</sup> Instituto de Patologia e Imunologia Molecular da Universidade do Porto, Portugal, <sup>8</sup> University of Porto, Portugal	<b>[S14.1] Varying severity of bottlenecks in experimental infections of VEEV IE in <i>Culex taeniopus</i> mosquitoes</b> N.L. Forrester*, M. Guerbois, R.L. Seymour, H. Spratt, S.C. Weaver, <i>University of Texas Medical Branch, USA</i>	<b>[S15.1] Is congenital transmission of <i>Trypanosoma cruzi</i> associated with parasite genotypes?</b> Y. Carlier <sup>1,2</sup> , <sup>1</sup> Université Libre de Bruxelles, Belgium, <sup>2</sup> Tulane University, USA	<b>[S16.1] Comparison of whole blood and PBMC-s for PCR to detect CMV infection in AIDS</b> S. Tewari*, A. Chakravarti, <i>Maulana Azad Medical College, India</i>
15:45-16:05	<b>[S13.2] Host-specific inhibition of the antiviral protein kinase PKR by myxoma and rabbit fibroma viruses</b> C. Peng <sup>1</sup> , S. Bassett <sup>1</sup> , S. Li <sup>2</sup> , G. McFadden <sup>2</sup> , T.E. Dever <sup>3</sup> , S. Rothenburg <sup>*1</sup> , <sup>1</sup> Kansas State University, USA, <sup>2</sup> University of Florida, USA, <sup>3</sup> National Institute of Child Health and Human Development (NICHD), USA	<b>[S14.2] Differential expansion of viral lineages in acute hepatitis B cases in the United States</b> S. Ramachandran*, G. Xia, M. Purdy, D. Campo, Z. Dimitrova, Y. Khudyakov, <i>Centers for Disease Control and Prevention, USA</i>	<b>[S15.2] Evolution-Development (EVO-DEVO) interactions involving infection and immune responses during human gestation</b> A.J. Nahmias, <i>Emory University, USA</i>	<b>[S16.2] Reads2Type: Rapid microbial taxonomy identification</b> D. Saputra*, T. Sicheritz-Pontén, O. Lund, <i>Technical University of Denmark, Denmark</i>
16:05-16:25	<b>[S13.3] The human gene connectome: A map of short cuts for morbid allele discovery</b> Y. Itan <sup>*1</sup> , S-Y. Zhang <sup>1,2</sup> , G. Vogt <sup>1,2</sup> , A. Abhyankar <sup>1</sup> , L. Quintana-Murci <sup>3</sup> , L. Abel <sup>1,2</sup> , J-L. Casanova <sup>1,2</sup> , <sup>1</sup> The Rockefeller University, USA, <sup>2</sup> Paris Descartes University, France, <sup>3</sup> Institut Pasteur, France, <sup>4</sup> Necker Hospital for Sick Children, France	<b>[S14.3] A novel approach to identify host susceptibility genes in virally-induced cancer: Application to HIV-related Kaposi's sarcoma</b> B. Aissani*, K. Zhang, H. Wiener, J. Wu, A.K. Boehme, K.M. Ogwaro, S. Shrestha, R.A. Kaslow, <i>University of Alabama at Birmingham, USA</i>	<b>[S15.3] Modeling intra-host adaptation of Hepatitis C virus</b> P. Skums*, D.S. Campo, Y. Khudyakov, <i>Centers for Disease Control and Prevention, USA</i>	<b>[S16.3] Early diagnosis of Chagas disease reactivation and <i>Trypanosoma cruzi</i> genotyping by PCR analyses directly in tissues of patients submitted to heart transplantation</b> M. Segatto*, S.A. Andrade, C. Gelape, E. Chiari, G. Brasileiro-Filho, A.M. Macedo, <i>Universidade Federal de Minas Gerais, Brazil</i>
16:25-17:10	Coffee Break – St. Charles Room			

	Symposium 17 Russell Hall	Symposium 18 Audubon	Symposium 19 Multimedia 1
<b>Theme</b>	<b>Apicomplexa molecular epidemiology and evolution</b>	<b>Chagas Vectors/Homage to François Noireau</b>	<b>Helminth Molecular epidemiology and evolution</b>
<b>Session Chair</b>	Pramod Kumar & Irshad M. Sulaiman	Patricia Dorn & Claudia Herrera	Benjamin Rosenthal & James Wasmuth
17:10-17:30	<b>[S17.1] Multilocus genetic characterization of human-pathogenic <i>Cyclospora cayentanensis</i> parasites from three endemic regions</b> I.M. Sulaiman <sup>1</sup> , Y. Ortega <sup>2</sup> , S. Simpson <sup>1</sup> , K. Kerdahi <sup>1</sup> , <sup>1</sup> U.S. Food and Drug Administration, USA, <sup>2</sup> University of Georgia, USA	<b>[S18.1] Phylogenetic relationships of Central and North American <i>Triatoma</i> inferred from DNA and morphology</b> P. Dorn <sup>1</sup> , N. de la Rúa <sup>2</sup> , M. Menes <sup>3</sup> , D.M. Bustamante <sup>3</sup> , C. Monroy <sup>3</sup> , C.W. Kilpatrick <sup>2</sup> , L. Stevens <sup>2</sup> , <sup>1</sup> Loyola University New Orleans, USA, <sup>2</sup> University of Vermont, USA, <sup>3</sup> Universidad de San Carlos, Guatemala	<b>[S19.1] Transmission history and dynamics of <i>Trichinella</i> species inferred from population genetic variation</b> B.M. Rosenthal, Agricultural Research Service, USDA, USA
17:30-17:50	<b>[S17.2] Global population structure of the malaria vaccine candidate, <i>Plasmodium vivax</i> apical membrane antigen 1 (pvAMA1)</b> A. Arnott <sup>1</sup> , I. Mueller <sup>2,3</sup> , P. Siba <sup>4</sup> , J.C. Reeder <sup>1,5</sup> , A.E. Barry <sup>3,6</sup> , <sup>1</sup> Burnet Institute, Australia, <sup>2</sup> Barcelona Centre for International Health Research, Spain, <sup>3</sup> Walter and Eliza Hall Institute of Medical Research, Australia, <sup>4</sup> Papua New Guinea Institute for Medical Research, Papua New Guinea, <sup>5</sup> Monash University, Australia, <sup>6</sup> University of Melbourne, Australia	<b>[S18.2] "Getting rid of uninvited guests &amp; picky eaters": Chagas bug feeding and habitat preference in Bolivia</b> D.E. Lucero <sup>1</sup> , W. Ribera <sup>2</sup> , J.C.C. Pizarro <sup>2</sup> , L. Stevens <sup>1</sup> , <sup>1</sup> University of Vermont, USA, <sup>2</sup> Universidad San Francisco Xavier de Chuquisaca, Bolivia	<b>[S19.2] The natural history of the beta-tubulin gene family in nematodes has consequences for anthelmintic efficacy</b> J.D. Wasmuth <sup>1</sup> , G.I. Saunders <sup>2</sup> , J.S. Gilleard <sup>1,2</sup> , <sup>1</sup> University of Calgary, Canada, <sup>2</sup> University of Glasgow, UK
17:50-18:10	<b>[S17.3] Molecular epidemiology of <i>Plasmodium falciparum</i> clonal populations in Peru</b> V. Udhayakumar*, S. Griffing, Centers for Disease Control and Prevention, USA	<b>[S18.3] Relevance of <i>Triatoma dimidiata</i> ITS-2 genotypes for <i>Trypanosoma cruzi</i> transmission in the Yucatán Peninsula, Mexico</b> M. Herrera-Aguilar, M. Dzul-Canul, S. Perez-Carrillo, M.J. Ramirez-Sierra, E. Dumonteil*, Universidad Autonoma de Yucatan, Mexico	<b>[S19.3] A genetic approach to identify ivermectin resistance conferring loci using serial backcrossing in the parasitic nematode <i>Haemonchus contortus</i></b> A. Rezansoff <sup>1</sup> , E. Redman <sup>1</sup> , N. Sargison <sup>2</sup> , J. Gilleard <sup>1</sup> , <sup>1</sup> University of Calgary, Canada, <sup>2</sup> Moredun Research Institute, UK, <sup>3</sup> University of Glasgow, UK
18:10-18:30	<b>[S17.4] Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia</b> S. Takala-Harrison <sup>1</sup> , T.G. Clark <sup>2</sup> , C.G. Jacob <sup>1</sup> , M.P. Cummings <sup>3</sup> , O. Miotto <sup>4,5</sup> , C.V. Plowe <sup>1</sup> , <sup>1</sup> University of Maryland School of Medicine, USA, <sup>2</sup> London School of Tropical Medicine, UK, <sup>3</sup> University of Maryland, USA, <sup>4</sup> Oxford University, UK, <sup>5</sup> Mahidol University, Thailand	<b>[S18.4] Phylogeography of <i>Triatoma dimidiata</i> (Latreille, 1811) inferred from the mitochondrial cytochrome b and nuclear its-2 genes</b> N. de la Rúa <sup>1</sup> , L. Stevens <sup>1</sup> , C. Monroy <sup>3</sup> , B. Richards <sup>2</sup> , J. Suarez <sup>2</sup> , P. Dorn <sup>2</sup> , <sup>1</sup> University of Vermont, USA, <sup>2</sup> Loyola University New Orleans, USA, <sup>3</sup> Universidad de San Carlos, Guatemala	<b>[S19.4] Could bioinformatics and molecular modeling be useful against schistosomiasis?</b> I.V.C. Evangelista, A.G. Taranto, F.M. Oliveira, D.O. Lopes, M. Comar*, Universidade Federal de São João del Rey, Brazil
19:30	Gala Dinner - Palace Café (Optional – tickets can be purchased)		
<b>Friday, 2 November 2012</b>			
<b>Plenary Session</b> Russell Hall			
9:00-9:30	<b>[PL10] Bioinformatic approaches to DNA sequence analysis: Evolution and phylogenetics of pathogens</b> K.A. Crandall <sup>1</sup> , E. Castro <sup>2</sup> , M. Bendall <sup>2</sup> , <sup>1</sup> George Washington University, USA, <sup>2</sup> Brigham Young University, USA		
9:30-10:00	<b>[PL11] "All animals are equal but some animals are more equal than others" - exploring the genetics of susceptibility to infectious disease</b> M-A. Shaw, University of Leeds, UK		
10:00-10:45	Coffee Break – St. Charles Room		

	Symposium 20 Russell Hall	Symposium 21 Audubon	Symposium 22 Multimedia 1	Symposium 23 Multimedia 2
<b>Theme</b>	<b><i>Mycobacterium</i> sp. genetics and molecular typing</b>	<b>Mathematical modeling/phylogeny 2</b>	<b><i>Staphylococcus</i> genetics and molecular epidemiology</b>	<b>Kinetoplastidae molecular epidemiology and evolution</b>
<b>Session Chair</b>	Christina Ahlstrom & Kristin Bennett	Rolf Ypma & Min Roh	Tijbbe Donker & Edward Smith	Juan-David Ramírez González & Michel Tibayrenc
10:45-11:05	<p><b>[S20.1] Genetic diversity of Beijing family strains of <i>Mycobacterium tuberculosis</i> in Peru compared with that of strains from East Asia</b> T. Iwamoto<sup>*1</sup>, L. Grandjean<sup>2,3</sup>, K. Arikawa<sup>1</sup>, N. Nakanishi<sup>1</sup>, J. Coronel<sup>4</sup>, L. Caviedes<sup>4</sup>, P. Sheen<sup>4</sup>, T. Wada<sup>5</sup>, C. Taype<sup>6</sup>, M.A. Shaw<sup>6</sup>, D.A.J. Moore<sup>3,4</sup>, R.H. Gilman<sup>4,7</sup>, <sup>1</sup><i>Kobe Institute of Health, Japan</i>, <sup>2</sup><i>Imperial College, UK</i>, <sup>3</sup><i>London School of Hygiene and Tropical Medicine, UK</i>, <sup>4</sup><i>Universidad Peruana Cayetano Heredia, Peru</i>, <sup>5</sup><i>Osaka City Institute of Public Health and Environmental Sciences, Japan</i>, <sup>6</sup><i>University of Leeds, UK</i>, <sup>7</sup><i>Johns Hopkins Bloomberg School of Public Health, USA</i></p>	<p><b>[S21.1] Efficient estimation of stochastic rare event probabilities in epidemiological systems</b> M.K. Roh<sup>*</sup>, P. Eckhoff, <i>Intellectual Ventures Lab, USA</i></p>	<p><b>[S22.1] Analysis of diversity of <i>Staphylococcus aureus</i> strains associated with food poisoning outbreaks in France</b> S. Roussel<sup>*1</sup>, B. Pichon<sup>2</sup>, B. Felix<sup>1</sup>, N. Vingadassalon<sup>1</sup>, A.M. Kearns<sup>2</sup>, J-A. Hennekinne<sup>1</sup>, A. Brisabois<sup>1</sup>, <sup>1</sup><i>ANSES, France</i>, <sup>2</sup><i>Laboratory of HealthCare Associated Infection (LHCAI), UK</i></p>	<p><b>[S23.1] Multilocus PCR-RFLP profiling in <i>Trypanosoma cruzi</i> I highlights an intraspecific genetic variation pattern</b> J.D. Ramirez<sup>*1</sup>, M.C. Duque<sup>1</sup>, M. Montilla<sup>2</sup>, Z.M. Cucunuba<sup>2</sup>, F. Guhl<sup>1</sup>, <sup>1</sup><i>Universidad de los Andes, Colombia</i>, <sup>2</sup><i>Instituto Nacional de Salud (INS), Colombia</i></p>
11:05-11:25	<p><b>[S20.2] Genotyping of <i>Mycobacterium tuberculosis</i> strains isolated in Baja California, Mexico by MIRU-VNTR method</b> R. Muniz-Salazar<sup>*1</sup>, R. Laniado-Laborin<sup>2</sup>, A.C. Vargas-Ojeda<sup>1</sup>, N.L. Victoria-Cota<sup>1</sup>, A.A. Arreola-Cruz<sup>1</sup>, D.S. Salas-Vargas<sup>1</sup>, <sup>1</sup><i>Universidad Autonoma de Baja California, Mexico</i>, <sup>2</sup><i>Hospital General de Tijuana, ISESALUD, Mexico</i></p>	<p><b>[S21.2] Bayesian framework to identify the determinants of viral cross-species transmission and host shifts</b> N.R. Faria<sup>*1</sup>, M.A. Suchard<sup>2,3</sup>, A. Rambaut<sup>4,5</sup>, D.G. Streicker<sup>6</sup>, P. Lemey<sup>1</sup>, <sup>1</sup><i>KU Leuven, Belgium</i>, <sup>2</sup><i>David Geffen School of Medicine at UCLA, USA</i>, <sup>3</sup><i>UCLA School of Public Health, USA</i>, <sup>4</sup><i>University of Edinburgh, UK</i>, <sup>5</sup><i>National Institutes of Health, USA</i>, <sup>6</sup><i>University of Georgia, USA</i></p>	<p><b>[S22.2] Observing the spread of MRSA through a national patient referral network</b> T. Donker<sup>*1,2</sup>, J. Wallinga<sup>1</sup>, H. Grundmann<sup>1,2</sup>, <sup>1</sup><i>National Institute for Public Health and the Environment, The Netherlands</i>, <sup>2</sup><i>University Medical Center Groningen, The Netherlands</i></p>	<p><b>[S23.2] <i>Trypanosoma cruzi</i> protein expression: A path toward understanding molecular dialogue</b> J. Telleria<sup>*</sup>, M. Tibayrenc, <i>IRD, France</i></p>
11:25-11:45	<p><b>[S20.3] TB-Vis: Visualizing TB patient-pathogen relationships</b> K.P. Bennett, <i>Rensselaer Polytechnic Institute, USA</i></p>	<p><b>[S21.3] The evolution of sexually-transmitted infectious (STI) agents in humans and other mammals</b> A.J. Nahmias<sup>*1</sup>, D. Danielsson<sup>2</sup>, M. Unemo<sup>2</sup>, <sup>1</sup><i>Emory University, USA</i>, <sup>2</sup><i>Örebro University, Sweden</i></p>	<p><b>[S22.3] Diversity of ovine associated <i>Staphylococcus aureus</i></b> E.M. Smith<sup>*</sup>, P.F. Needs, L.E. Green, <i>University of Warwick, UK</i></p>	<p><b>[S23.3] In the race of the mitochondrial eve of The <i>T. cruzi</i></b> I.F. Valle, R.P. Baptista, G.R. Franco, C.R. Machado, S.D.J. Pena, A.M. Macedo<sup>*</sup>, <i>Universidade Federal de Minas Gerais, Brazil</i></p>
11:45-12:05	<p><b>[S20.4] Transmission dynamics of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in Canadian dairy herds using MALDI-TOF mass spectrometry</b> C. Ahlstrom<sup>*</sup>, H.W. Barkema, J. De Buck, <i>University of Calgary, Canada</i></p>	<p><b>[S21.4] Who infected whom - finding the transmission trees in which phylogenetic trees are rooted</b> R.J.F. Ypma<sup>*1,2</sup>, W.M. van Ballegooijen<sup>1</sup>, <sup>1</sup><i>National Institute for Public Health and the Environment, The Netherlands</i>, <sup>2</sup><i>University Medical Centre Utrecht, The Netherlands</i></p>	<p><b>[S22.4] Bayesian assignment of <i>Staphylococcus epidermidis</i> multilocus sequence types to populations with contrasting virulence-associated traits</b> J.C. Thomas<sup>*</sup>, L. Zhang, D.A. Robinson, <i>University of Mississippi Medical Center, USA</i></p>	<p><b>[S23.4] Extensive diversity of <i>Trypanosoma cruzi</i> discrete typing units circulating in <i>Triatoma dimidiata</i> from Southern Mexico</b> A. Ramos-Ligonio<sup>*2</sup>, J. Torres-Monteon<sup>2</sup>, M. Dzul-Canul<sup>1</sup>, S. Perez-Carrillo<sup>1</sup>, M.J. Ramirez-Sierra<sup>1</sup>, A. Lopez-Monteon<sup>2</sup>, E. Dumonteil<sup>1</sup>, <sup>1</sup><i>Universidad Autonoma de Yucatan, Mexico</i>, <sup>2</sup><i>Universidad Veracruzana, Mexico</i></p>

12:05-12:25			<p><b>[S22.5] Detection of enterotoxin genes in <i>Staphylococcus aureus</i> strains</b>  B. Felix*<sup>1</sup>, N. Vingadasalon<sup>1</sup>, B. Pichon<sup>2</sup>,  F. Dilasser<sup>1</sup>, A. Brisabois<sup>1</sup>, S. Roussel<sup>1</sup>, <sup>1</sup>Anses, France, <sup>2</sup>Health Protection Agency, UK</p>	<p><b>[S23.5] MLST approach for the description of genetic diversity of <i>Leishmania</i> spp. in Northern Argentina</b>  J.D. Marco<sup>1</sup>, P.A. Barroso<sup>1</sup>, F. Locatelli<sup>2</sup>,  K. Caimi<sup>3</sup>, M. Korenaga<sup>2</sup>, P. Ruybal*<sup>3</sup>, <sup>1</sup>Universidad Nacional de Salta, Argentina, <sup>2</sup>Kochi Medical School, Japan, <sup>3</sup>Instituto Nacional de Tecnología Agropecuaria, Argentina</p>
12:25-14:00	Lunch – St. Charles Room		Author Workshop (13:00-14:00), S. Agarwal – Jans, Elsevier - Audubon	
<b>Plenary Session</b> <b>Russell Hall</b>				
14:00-14:30	<p><b>[PL12] Meet the neighbors: Discovery of cryptic <i>escherichia</i> clades changes our understanding of <i>E. coli</i> evolution</b>  S.T. Walk, <i>University of Michigan Hospital and Health Systems, USA</i></p>			
14:30-15:00	<p><b>[PL13] Arbovirus emergence via adaptive evolution: Mechanisms and constraints</b>  S.C. Weaver, <i>University of Texas Medical Branch, USA</i></p>			
15:00-15:30	<p><b>[PL14] Population genetics, evolution and epidemiological role of main mosquito vector species</b>  F. Simard*, C. Paupy, J-P. Dujardin, D. Fontenille, <i>Institut de Recherche pour le Développement (IRD), France</i></p>			
15:30-16:00	<b>Closing Remarks &amp; Awards</b>			