



MEEGID XII

12th International Conference on Molecular Epidemiology
and Evolutionary Genetics of Infectious Diseases

11-13 December 2014
The Royal River Hotel,
Bangkok

Wednesday, 10 December 2014

Room	Phanurangsi Foyer
17:00-19:00	Registration
Room	Phanurangsi A & B
19:00-20:00	Welcome Drinks Reception
Thursday, 11 December 2014	
09:00-09:05	Welcome
Room	Phanurangsi C
09:05-09:45	Opening Remarks
Plenary Session	
Room	Phanurangsi C
Chair	M. Tibayrenc, Institut de recherche pour le développement, France
09:45-10:15	PL01: Genomic epidemiology of bacterial pathogens S. Brisse, Institut Pasteur, France
Chair	S. Brisse, Institut Pasteur, France
10:15 -10:45	PL02: Exploring the evolution and epidemiology of parasitic helminths in the -omics age R.B. Gasser, The University of Melbourne, Australia
Room	Phanurangsi A & B
10:45-11:15	Coffee Break
Room	Phanurangsi C
Chair	J. Heitman, Duke University, USA
11:15-11:45	PL03: Ebola viruses: from the wild to humans Prof. Jean-Claude Piffaretti, Interlifesciences, Massagno, Switzerland; President of the Federation of European Microbiological Societies
Chair	Prof. Jean-Claude Piffaretti, Interlifesciences, Massagno, Switzerland; President of the Federation of European Microbiological Societies
11:45-12:15	PL04: Unisexual reproduction and the evolution of eukaryotic microbial pathogens J. Heitman, Duke University, USA
Room	Phanurangsi A & B
12:15-13:30	Lunch & poster session 1

<i>Rooms</i>	<i>Phanurangsi C</i>	<i>Bongkotrat A</i>	<i>Bongkotrat B</i>	<i>Busabongkot A</i>
13:30-15:30	Symposium 1-Modelling	Symposium 2-Molecular epidemiology parasitic protozoa 1	Symposium 3-Host parameters 1	Symposium 4-In silico approaches
Chairs	R. Duboz, CIRAD, France, A. Stern, Tel Aviv University, Israel	A. Das, Birla Institute Of Technology and Science, India	J-P. Hugot, UMR-CNRS 7205, MNHN, France D.H. Rubin, Vanderbilt University, USA; VA TVHS, USA	J.F. Pothier, ZHAW Zurich University of Applied Sciences, Switzerland P. Munk, Technical University of Denmark, Denmark
	13:30-14:00 [O01.1] Temporal modeling of Crimean-Congo hemorrhagic fever in Iran E. Mostafavi* ^{1,5} , A.A. Haghdoost ² , A. Doost Irani ^{1,3} , S. Bokaei ⁴ , S. Chinikar ¹ , ¹ Pasteur Institute of Iran, Iran, ² Kerman University of Medical Sciences, Iran, ³ Tehran University of Medical Sciences, Iran, ⁴ University of Tehran, Iran, ⁵ Research Centre for Emerging and Reemerging Infectious Diseases (Akanlu), Iran	13:30-14:00 [O02.1] Molecular detection of vector-borne haemoparasites in wild rodent species in South Africa M.C. Oosthuizen* ¹ , M. Troskie ¹ , I. Vorster ¹ , R. Jansen ² , B.L. Penzhorn ¹ , S. Matthee ³ , ¹ University of Pretoria, South Africa, ² Tshwane University of Technology, South Africa, ³ Stellenbosch University, South Africa	13:30-13:54 [O03.1] Genetic variability of Talpa europea and Nova hantavirus (NVAV) in France J-P. Hugot* ¹ , C. Feliu ² , A. Ribas ² , J. Dormion ³ , S.H. Gu ⁴ , V. Nicolas ¹ , ¹ UMR-CNRS 7205, MNHN, France, ² UNIV-BARCELONA, Spain, ³ TAUP'GREEN FRANCE BP 19 92201 Neuilly sur Seine, France, ⁴ University of Hawaii, USA	13:30-14:00 [O04.1] Withdrawn
	14:00-14:30 [O01.2] Japanese encephalitis in a peri-urban pig slaughterhouse of Cambodia : A deterministic meta-population model to quantify the risk of transmission to humans M. Yakovlevff ^{1,2} , J. Cappelle ^{1,2} , V. Chevalier ¹ , R. Duboz* ¹ , ¹ CIRAD, France, ² Institut Pasteur, Cambodia	14:00-14:30 [O02.2] Making sense out of antisense in clinical isolates of the Plasmodium spp. A. Das* ¹ , P.A. Boopathi ¹ , A.K. Boopathi ¹ et al, ¹ Birla Institute Of Technology and Science, India, ² Sardar Patel Medical College, India, ³ Genotypic Technology Pvt. Ltd., India, ⁴ University of Health Sciences, India	13:54-14:18 [O03.2] Systems biology-based host-virus pathogen gene interaction network analysis F. Cheng ¹ , J. Murray ² , J. Sheng ¹ , Z. Zhao ¹ , D.H. Rubin* ^{3,1} , ¹ Vanderbilt University, USA, ² Zirus, USA, ³ VA TVHS, USA	14:00-14:30 [O04.2] Sequence-based analysis reveals plasmid-borne ESBL genes encoding resistance to critically important antimicrobials most often linked with other resistance genes in swine and pork E. coli isolates P.Munk*, Y. Agersø, Technical University of Denmark, Denmark
	14:30-15:00 [O01.3] To be or not to be diverse: Dilemmas of a virus A. Stern* ¹ , S. Bianco ² , M. Te Yeh ³ , C. Wright ³ , K. Butcher ³ , R. Nielsen ⁴ , R. Andino ³ , ¹ Tel Aviv University, Israel,	14:30-15:00 [O02.3] Diversity of Cryptosporidium from rodents in Thailand A. Masakul ¹ , N. Thapraphom ¹ , K. Chaisiri ² , A. Anamika Karnchanabanthoeng ¹ , M.	14:18-14:42 [O03.3] Association of the HLA-B*52 allele with non-progression to AIDS in Brazilian HIV-1-infected individuals S.L.M. Teixeira* ¹ , N.B.R. De Sa ¹ , D.P. Campos ² , A.B. Coelho ² , M.L.	14:30-15:00 [O04.3] The Salmonella In Silico typing resource (SISTR), a platform for rapid analysis and interpretation of Salmonella draft genome sequence data

	<p>²IBM Research - Almaden, USA, ³UCSF, USA, ⁴UC Berkeley, USA</p>	<p>Desquesnes^{3,1}, S. Morand⁴, S. Herder^{5,1}, A. Binot^{6,1}, S. Jittapalpong^{*1}, ¹Kasetsart University, Thailand, ²Mahidol University, Thailand, ³Centre de Coopération Internationale en Recherche Agronomique pour le Développement; Cirad-Bios, UMR-InterTryp, France, ⁴CNRS-CIRAD AGIRs, Centre d'Infectiologie Christophe Mérieux du Laos, France, ⁵IRD - UMR177-Intertryp, France, ⁶CIRAD-UPR AGIRs, France</p>	<p>Guimaraes¹, T.C.N.F. Leite¹, V.G. Dos Santos², M.G. Morgado¹, ¹IOC/FIOCRUZ, Brazil, ²INI/FIOCRUZ, Brazil</p>	<p>P. Kruczkiewicz¹, C. Yoshida¹, E. Linghor¹, D. Barker^{1,2}, C.R. Laing¹, V.P.J. Gannon¹, J.H.E. Nash¹, E.N. Taboada^{*1}, ¹Public Health Agency of Canada, Canada, ²University of Lethbridge, Canada</p>
<p>15:00-15:30 [O01.4] On the risk of severe dengue during secondary infection: Mathematical modeling coupled with a systematic review K. Mizumoto^{*1}, K. Ejima², T. Yamamoto³, H. Nishiura¹, ¹The University of Tokyo, Japan, ²The University of Alabama, USA, ³Nagasaki University, Japan</p>	<p>15:00-15:30 [O02.4] Molecular identification of Cryptosporidium parvum from roaming Long-tailed macaque (<i>Macaca fascicularis</i>) in Lopburi province, Thailand W. Srichareern^{*1,2}, S. Saengow¹, P. Simking^{1,2}, B. Yimming¹, A. Panthawong¹, K. Saeng-chuto¹, J. Supanam³, S. Morand⁴, S. Jittapalpong¹, ¹Kasetsart University, Thailand, ²Center of Excellence on Agricultural Biotechnology: (AG-BIO/PERDO-CHE), Thailand, ³Private Animal Clinic, Thailand, ⁴CNRS-CIRAD AGIRs, Centre d'Infectiologie</p>	<p>14:42-15:06 [O03.4] Adaptation of pandemic H1N1 influenza viruses in experimental model of mammals E.A. Prokopeva^{*1,2}, A.V. Gluschenko², S.G. Sayfutdinova¹, M.V. Sivay², S.V. Alkhovskiy³, A.M. Schetinin³, M.Y. Shchelkanov³, L.V. Shestopalova¹, A.M. Shestopalov^{2,1}, ¹Novosibirsk State University, Russia, ²Research Center of Clinical and Experimental Medicine, Siberian Division of the Russian Academy of Medical Sciences, Russia, ³D. I. Ivanovsky Inst. of Virology, Russian Academy of Medical Sciences, Russia</p>	<p>15:00-15:30 [O04.4] MALDI-TOF MS for microorganism identification: From pattern recognition towards marker based approaches J.F. Pothier^{*1}, V. Pflüger², D. Ziegler², G. Vogel², B. Duffy¹, ¹ZHAW Zurich University of Applied Sciences, Switzerland, ²Mabritec AG, Switzerland</p>	

		<i>Christophe Mérieux du Laos, France</i>	15:06-15:30 [O03.5] Association study between Japanese encephalitis vaccine immunity and single nucleotide polymorphisms (SNPs) of TNF-α, IL-2, IL-4 and IL-10 genes X.W. Xu [*] , J. Zhou, Y. Li, Y. Zhang, J.K. Yu, L. Shi, Y.F. Yao, M.B. Sun, <i>Institute of Medical Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, China</i>	
Plenary Session				
<i>Room</i>	<i>Phanurangsi C</i>			
Chair	N. Mideo, University of Toronto, Canada			
15:30-16:00	PL05: The greatest experiment in evolution: Viral biocontrol of rabbits E.C. Holmes, <i>The University of Sydney, Australia</i>			
<i>Room</i>	<i>Phanurangsi A & B</i>			
16:00-16.30	Coffee Break			
<i>Room</i>	<i>Phanurangsi C</i>			
Chair	E.C. Holmes, The University of Sydney, Australia			
16.30-17:00	PL06: New tools for detecting drug resistance in malaria infections N. Mideo, <i>University of Toronto, Canada</i>			
<i>Rooms</i>	<i>Phanurangsi C</i>	<i>Bongkotrat A</i>	<i>Bongkotrat B</i>	<i>Busabongkot A</i>
17:00-19:00	Symposium 5-Modern epidemiological approaches	Symposium 6-Phylogeny virus 1	Symposium 7-Mycobacterial diseases 1	Symposium 8-Population genetics/evolution vectors
Chairs	E.N. Taboada, V.P.J. Gannon, Public Health Agency of Canada, Canada B.A. Wilcox, Tufts University, USA	T. Stadler, ETH Zürich, Switzerland K. Tohma, Tohoku University, Japan	T. Wirth, EPHE, Paris, France; Natural History Museum, France	T. De Meeûs, IRD, Burkina Faso, France S.J. Jacquet, Cirad, France; INRA, France
	17:00-17:30 [O05.1] Detection of tick-borne infections in birds in West Siberia I.G. Korobitsyn ^{*1} , N.S. Moskvitina ¹ , O.Y. Tyuten'kov ¹ , S.I. Gashkov ¹ , Y.V.	17:00-17:30 [O06.1] A unified framework for phylodynamic inference of epidemic spread T. Stadler ^{*1} , A. Drummond ² , D.	17:00-17:30 [O07.1] Mycobacterium tuberculosis Beijing lineage: Origin, spread and selection signatures T. Wirth ^{*1,2} , M. Merker ³ , P. Supply ^{4,5} , S.	17:00-17:24 [O08.1] Ecotype evolution in <i>Glossina palpalis</i> subspecies, major vectors of sleeping sickness T. De Meeûs ^{*1,3} , J. Bouyer ^{2,4} , S. Ravel ³ ,

	<p>Kononova², S.S. Moskvitin¹, V.N. Romanenko¹, T.P. Mikryukova², E.V. Protopopova², M.Y. Kartashov² et al, ¹<i>Tomsk State University, Russia</i>, ²<i>State Research Center for Virology and Biotechnology "Vector", Russia</i></p>	<p>Kühnert¹, S. Bonhoeffer¹, ¹<i>ETH Zürich, Switzerland</i>, ²<i>University of Auckland, New Zealand</i></p>	<p>Niemann³, ¹<i>EPHE, Paris, France</i>, ²<i>Natural History Museum, France</i>, ³<i>Research Center Borstel, Germany</i>, ⁴<i>INSERM, Lille, France</i>, ⁵<i>CNRS-UMR 8204, Lille, France</i></p>	<p>P. Solano^{1,3}, ¹<i>IRD, Burkina Faso</i>, ²<i>CIRAD, Senegal</i>, ³<i>IRD, France</i>, ⁴<i>CIRAD, France</i></p>
<p>17:30-18:00 [O05.2] SuperPhy: Molecular epidemiology and predictive genomics for bacterial pathogens M.D. Whiteside, C.R. Laing, A. Manji, P. Kruczkiewicz, E.N. Taboada*, V.P.J. Gannon, <i>Public Health Agency of Canada, Canada</i></p>	<p>17:30-18:00 [O06.2] Pattern of HRSV epidemics in Iran: Molecular epidemiology of the G protein over seven years E. Faghihloo, J. Yavarian *, T. Mokhtari Azad, <i>School of Public Health, Tehran University of Medical Sciences, Iran</i></p>	<p>17:30-18:00 [O07.2] The N-Terminal Region Of M. tuberculosis PPE Protein RvXXXX Induces Strong B Cell Response In Active TB Patients P.R. Abraham*, G. Suman Lata², S. Mukhopadhyay¹, ¹<i>Center for DNA Fingerprinting and Diagnostics, India</i>, ²<i>Mahavir Hospital and Research Centre, India</i></p>	<p>17:24-17:48 [O08.2] Detecting isolation by distance with different genetic distances, with and without null alleles of insect vectors (tsetse flies) M. Séré*, S. Thévenon², A.M.G. Belem³, T. De Meeûs^{1,2}, ¹<i>Centre International de Recherche-Développement sur l'Élevage en zone Subhumide (CIRDES), 01 BP 454 Bobo-Dioulasso 01, Burkina Faso</i>, ²<i>Interactions hôtes - vecteurs - parasites dans les infections par des trypanosomatidae - (INTERTRYP), UMR IRD/CIRAD 177, France</i>, ³<i>Université Polytechnique de Bobo-Dioulasso, 01 BP 1091 Bobo-Dioulasso 01, Burkina Faso</i></p>	
<p>18:00-18:30 [O05.3] Ecology, evolution and genetics in education and infectious disease research in Southeast Asia P. Saenna¹, H. Nguyen-Viet², J. Steele³, I. Mendenhall⁴, B.A. Wilcox *^{5,3}, ¹<i>Khon Kaen University, Thailand</i>, ²<i>Hanoi School of Public Health, VietNam</i>, ³<i>Tufts University, USA</i>, ⁴<i>Duke-NUS, Singapore</i>, ⁵<i>Mahidol University, Thailand</i></p>	<p>18:00-18:30 [O06.3] Recently observed island-to-island transmission of rabies in Romblon, the Philippines K. Tohma*, M. Saito¹, C.S. Demetria², D.L. Manalo², B.P. Quiambao², T. Kamigaki¹, H. Oshitani¹, ¹<i>Tohoku University, Japan</i>, ²<i>Research Institute for Tropical Medicine, The Philippines</i></p>	<p>18:00-18:30 [O07.3] MixTB: An optimization-based method for classifying complex TB infections L. Chindelevitch*^{1,2}, C. Colijn³, P. Moodley⁴, D. Wilson^{4,5}, T. Cohen^{1,2}, ¹<i>Brigham and Women's Hospital, USA</i>, ²<i>Harvard School of Public Health, USA</i>, ³<i>Imperial College, UK</i>, ⁴<i>University of KwaZulu-Natal, South Africa</i>, ⁵<i>Edendale Hospital, South Africa</i></p>	<p>17:48-18:12 [O08.3] Phylogeography of <i>Culicoides imicola</i> (Diptera: Ceratopogonidae), biting midge vector species of <i>Orbivirus</i>: expansion and colonization? S.J. Jacquet*^{1,2}, K.H. Huber^{2,1}, J.B. Bouyer^{1,3}, C.C. Chevillon⁴, T.B. Balenghien^{1,2}, C.G. Garros^{1,2}, ¹<i>Cirad, France</i>, ²<i>INRA, France</i>, ³<i>ISRA, Senegal</i>, ⁴<i>IRD, France</i></p>	

	<p>18:30-19:00 [O05.4] Liver fluke infection and associated diseases in southeast asia: An eco-evolutionary perspective P. Echaubard^{*1,2}, C. Richter^{3,4}, B. Wilcox^{5,6}, ¹Laurentian University, Canada, ²Khon Kaen University, Thailand, ³Kunming Institute of Botany, China, ⁴Graduate University of Chinese Academy of Sciences, China, ⁵Mahidol University, Thailand, ⁶Tufts University, USA</p>	<p>18:30-19:00 [O06.4] Tick-borne Encephalitis virus in Ixodes ticks and wild birds in the Russia V.B. Loktev^{*1,4}, T.P. Mikryukova¹, E.V. Protopopova¹, Y.V. Kononova¹, V.N. Romanenko², E.V. Chaousov¹, V.A. Ternovoi¹, I.G. Korobitsyn², I.V. Korabel'nikov³, N.S. Moskvitina², ¹State Research Center for Virology and Biotechnology Vector, Russia, ²Tomsk State University, Russia, ³Desinfection of Rospotrebnadzor, Russia, ⁴Institute of Cytology and Genetics, Russia</p>	<p>18:30-19:00 [O07.4] Thioethers - active against Mycobacterium tuberculosis M.I. Konaklieva^{*1}, R. Kuskovsky¹, K. Arora², H.I. Boshoff², C.E. Barry III², ¹American University, USA, ²Tuberculosis Research Section, LCID, NIAID, NIH, USA</p>	<p>18:12-18:36 [O08.4] Anopheles darlingi microgeographic population structure M. Campos*, D.P. Alonso, P.E.M. Ribolla, Sao Paulo State University, Brazil</p> <p>18:36-19:00 [O08.5] Molecular phylogenetics of anopheline (Anophelinae: Culicidae) mosquitoes from the oriental and afrotropical zoogeographic zones K. Munawar*, A. Saleh, E.I. Khater, King Saud University, Saudi Arabia</p>
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Friday, 12 December 2014

Plenary Session

Room	Phanurangsi C			
Chair	M. Tibayrenc, Institut de recherche pour le développement, France			
08:45-09:15	<p>PL07: Human nature: Genes to culture F.J. Ayala, University of California, USA</p>			
Chair	F.J. Ayala, University of California, USA			
09:15-09:45	<p>PL08: Molecular epidemiology of Group A rotaviruses: Implications for vaccine introduction into countries of South East Asia M.D. Bowen, Centers for Disease Control and Prevention, USA</p>			
Room	Phanurangsi A & B			
09:45-10:15	Coffee Break			
Rooms	Phanurangsi C	Bongkotrat A	Bongkotrat B	Busabongkot A
10:15-12:15	Symposium 9-Molecular epidemiology parasitic protozoa 2	Symposium 10-Coevolution	Symposium 11-Molecular epidemiology virus 1	Symposium 12- Molecular epidemiology bacteria 1
Chairs	<p>G.L.A. Harrison, Infection and Immunity Division, Walter and Eliza Hall Institute, Australia L. González-Cerón, Instituto Nacional de Salud Pública, Mexico</p>	P. Surasombatpana, Prince of Songkla University, Thailand	<p>K. Chumakov, Food and Drug Administration, USA J. Yavarian, Tehran University of Medical Sciences, Iran</p>	<p>S.E.G. Greiman, University of North Dakota, USA M.C. Dela Cruz, Cavite State University, The Philippines</p>
	<p>10:15-10:45 [O09.1] First case of cryptic speciation in avian Plasmodium parasites, with remarks on</p>	<p>10:15-10:45 [O10.1] Co-evolution of the parasitic fungi Pneumocystis and their Muridae</p>	<p>10:15-10:45 [O11.1] Adamantane and neuraminidase resistant influenza A/H3N2 isolated in</p>	<p>10:15-10:35 [O12.1] Molecular epidemiology of Vibrio cholerae associated with flood in</p>

	<p>molecular characterization, virulence and sporogony V. Palinauskas*, R. Žiegyte, M. Ilgunas, T. Iezhova, R. Bernotiene, G. Valkiunas, <i>Nature Research Centre, Lithuania</i></p>	<p>rodent hosts in Southeast Asia A. Latinne*^{1,2}, F. Bezé³, S. Morand^{4,5}, M. Chabé⁶, ¹<i>University of Liege, Belgium</i>, ²<i>Université Montpellier 2, France</i>, ³<i>Dunkerque Hospital, France</i>, ⁴<i>CIRAD, France</i>, ⁵<i>CNRS-CIRAD, People's Democratic Republic of Lao</i>, ⁶<i>Institut Pasteur de Lille, France</i></p>	<p>Iran from 2005 to 2013 J. Yavarian*, T. Mokhtari Azad, N.Z. Shafiei Jandaghi, <i>Tehran University of Medical Sciences, Iran</i></p>	<p>Brahmaputra river, Assam, India P. Kumar*¹, S.K. Bhuyan¹, M.G. Vairale², N. Arya¹, V. Veer², L. Singh³, P.K. Yadava¹, ¹<i>Jawaharlal Nehru University, India</i>, ²<i>Defence Research Laboratory, India</i>, ³<i>DRDO, India</i></p>
	<p>10:45-11:15 [O09.2] Rewriting the evolutionary history of Plasmodium falciparum with whole mitochondrial genome sequence analyses S. Tyagi, A. Das*, <i>National Institute of Malaria Research, India</i></p>	<p>10:45-11:15 [O10.2] Diversity of chigger mites (Acari: Trombiculidae) and their microbiomes across stratified habitats in Thailand K. Chaisiri*¹, A.C. Gill¹, A. Stekolnikov², A.C. Darby¹, S. Morand³, J.W. McGarry¹, B.L. Makepeace¹, ¹<i>University of Liverpool, UK</i>, ²<i>Russian Academy of Sciences, Russia</i>, ³<i>Centre d'Infectiologie Christophe Mérieux du Laos, People's Democratic Republic of Lao</i></p>	<p>10:45-11:15 [O11.2] Withdrawn</p>	<p>10:35-10:55 [O12.2] Molecular prospecting for an elusive pathogen: The detection, molecular phylogeny, and host associations of Neorickettsia S.E.G. Greiman*, J.A.V. Vaughan, V.V.T. Tkach, <i>University of North Dakota, USA</i></p>
	<p>11:15-11:45 [O09.3] Molecular epidemiology of Plasmodium vivax in Nicaragua L. González-Cerón*¹, A. Montoya², F. Santillán¹, J.C. Corzo-Gómez¹, M.T. Ovilla-Muñoz¹, R. Cerritos³, R. Avendaño¹, M.A. Sandoval¹, J. Martínez-Barnetche¹, ¹<i>Instituto Nacional de Salud Pública, Mexico</i>, ²<i>CNDR-Ministerio de Salud, Nicaragua</i>, ³<i>Universidad Nacional Autónoma de México, Mexico</i></p>	<p>11:15-11:45 [O10.3] Inhibitory effects of organic acids produced by Clostridium ramosum on enterohaemorrhagic Escherichia coli O157:H7 Y.K. Koyanagi*¹, R.S. Suzuki¹, M.M. Masuda¹, H.I. Isogai¹, T.A. Ando¹, H.Y. Yoneyama¹, E.I. Isogai¹, ¹<i>Tohoku University, Japan</i>, ¹<i>Sapporo Medical University, Japan</i></p>	<p>11:15-11:45 [O11.3] Deep sequencing for metagenomics-based molecular epidemiology V. Furtak¹, M. Roivainen², O. Mirochnichenko¹, M. Laassri¹, B. Bidzhieva¹, T. Zagorodnyaya¹, C. Chizhikov¹, K. Chumakov*¹, ¹<i>Food and Drug Administration, USA</i>, ²<i>National Institute for Health and Welfare, Finland</i></p>	<p>10:55-11:15 [O12.3] Epidemiology and evolution of the genetic variability of Anaplasma marginale in South Africa A.M. Mutshembele^{1,2}, A. Cabezas-Cruz^{3,4}, M.S. Mtshali*^{1,2}, O.M.M. Thekiso², R.C. Galindo⁴, J. de la Fuente⁵, ¹<i>National Zoological Gardens of South Africa, South Africa</i>, ²<i>University of the Free State, South Africa</i>, ³<i>Instituto de Investigación en Recursos Cinegéticos IRES-CSIC-UCLM-JCCM, Spain</i>, ⁴<i>Université Lille Nord de France, France</i>, ⁵<i>Oklahoma State University, USA</i></p>

	<p>11:45-12:15 [O09.4] The population genomic structure of Plasmodium falciparum in Papua new guinea G.L.A. Harrison*¹, N. Tessier², L. Tavul³, M. Manske⁴, O. Miotto^{5,6}, I. Betuela³, P. Siba³, I. Mueller¹, M. Bahlo², A. Barry¹ et al, ¹Infection and Immunity Division, Walter and Eliza Hall Institute, Australia, ²Bioinformatics Division, Walter and Eliza Hall Institute, Australia, ³Papua New Guinea Institute of Medical Research, Papua New Guinea, ⁴Wellcome Trust Sanger Institute, UK, ⁵University of Oxford, UK, ⁶Mahidol University, Thailand</p>	<p>11:45-12:15 [O10.4] Role of saliva in Dengue virus transmission P. Surasombatpana*², D. Misse¹, R. Hamel¹, S. Patramool¹, S. Thongrungrat⁴, M. Debizot⁶, P. Delaunay³, F. Thomas¹, N. Luplertlop⁴, H. Yssel¹ et al, ¹Laboratoire MIVEGEC, UMR CNRS 5290/IRD 224/UM1, France, ²Prince of Songkla University, Thailand, ³Hôpital de l'Archet, CHU de Nice-Université de Nice-Sophia Antipolis/Inserm U1065, France, ⁴Mahidol University, Thailand, ⁵Inserm, U844, France, ⁶CNRS-UMR 5236/UM1/UM2, France</p>	<p>11:45-12:15 [O11.4] Hepatitis C virus genotype diversity among general population in Yunnan Province, southwestern China Y.F. Yao¹, Y.S. Shen², D.F. Cao¹, S.Q. Zhang³, Y.L. Li², L. Shi¹, M.B. Sun¹, L. Shi*¹, ¹Chinese Academy of Medical Sciences & Peking Union Medical College, China, ²The First People's Hospital in Yunnan Province & The Affiliated Hospital of Kunming Science and Technology University, China, ³The Third People's Hospital of Kunming, China</p>	<p>11:15-11:35 [O12.4] Molecular identification of Nocardia spp. collected from patients with symptom Tuberculosis S. Zaker Bostanabad, <i>Islamic Azad University, Iran</i></p>
				<p>11:35-11:55 [O12.5] Occurrence and characterization of verotoxigenic escherichia coli O157:H7 in healthy cattle (Bos taurus L.) in Luzon, Philippines M.C. Dela Cruz*, J.C Santos, <i>Cavite State University, The Philippines</i></p>
				<p>11:55-12:15 [O12.6] A model for assessing the concordance between genetic and epidemiological similarity of microbial isolates B. Hetman*^{1,2}, S.K. Mutschall¹, V.P.J. Gannon¹, J. Thomas², E.N. Taboada¹, ¹Public Health Agency of Canada, Canada, ²University of Lethbridge, Canada</p>
<i>Room</i>	<i>Phanurangsi A & B</i>			
12:15-13:45	Lunch & Poster Session 2			
<i>Rooms</i>	<i>Phanurangsi C</i>	<i>Bongkotrat A</i>	<i>Bongkotrat B</i>	<i>Busabongkot A</i>
13:45-15:45	Symposium 13-Molecular epidemiology bacteria 2	Symposium 14-Drug/antibiotic resistance 1	Symposium 15-Phylogeny virus 2	Symposium 16- Host parameters 2
Chairs	R.S. Kaas , <i>Technical University of Denmark, Denmark</i>	O.L. Franco , <i>Universidade Católica de Brasília, Brazil; Universidade de</i>	M. Calzolari , <i>Istituto Zooprofilattico Sperimentale della Lombardia e</i>	H.A.F. Stephens , <i>Mahidol University, Thailand; University College London,</i>

		<p><i>Brasília, Brazil</i> E. Talundzic, <i>Center for Disease Control and Prevention, USA; Atlanta Research and Education Foundation, USA</i></p>	<p><i>dell'Emilia Romagna, Italy</i> I.A. Sobolev, <i>State Research Center of Clinical and Experimental Medicine, Russia</i></p>	<p><i>UK</i> Y. Li, <i>Institute of Medical Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, China</i></p>
<p>13:45-14:09 [O13.1] Whole-genome MLST: Effect of sequence data quality on strain typeability and optimization of parameters for improved analysis D. Barker*^{1,2}, P. Kruczkiewicz¹, S. Mutschall¹, C.R. Laing¹, V.P.J. Gannon¹, J. Thomas², E.N. Taboada¹, ¹<i>Public Health Agency of Canada, Canada</i>, ²<i>University of Lethbridge, Canada</i></p>	<p>13:45-14:09 [O14.1] The utilization of multi-omics tools to shed some light on resistance and infectivity processes in two bacterial models K.C. Almeida^{1,2}, A.E.A.D. Barbosa¹, A.M. Murad³, G. Fernandes¹, C. Farias Jr⁴, S.C. Dias¹, O.L. Franco*^{1,2}, ¹<i>Universidade Católica de Brasília, Brazil</i>, ²<i>Universidade de Brasília, Brazil</i>, ³<i>EMBRAPA Recursos Genéticos e Biotecnologia, Brazil</i>, ⁴<i>Núcleo de Bacteriologia, Laboratório Central de Saúde Pública Distrito Federal, Brazil</i></p>	<p>13:45-14:15 [O15.1] A group of flaviviruses detected only in insects M. Calzolari*¹, L. Zé-Zé², A. Vazquez³, M.P. Sánchez Seco³, F. Amaro², M. Dottori¹, ¹<i>Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Italy</i>, ²<i>National Institute of Health, Portugal</i>, ³<i>Institute of Health "Carlos III," Spain</i></p>	<p>13:45-14:15 [O16.1] The association study between inactivated Japanese encephalitis vaccine immunity and HLA class II genes and its haplotypes M.B. Sun, Y.F. Yao, H.J. Yang, X.W. Xu, Y. Li, L. Shi, J.K. Y., L. Shi* ,<i>Institute of Medical Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, China</i></p>	
<p>14:09-14:33 [O13.2] Identification of a cellular receptor for Clostridium difficile toxin B M.E. LaFrance¹, M.A. Farrow¹, J. Sheng¹, D.H. Rubin*^{2,1}, D.B. Lacy¹, ¹<i>Vanderbilt University, USA</i>, ²<i>VA TVHS, USA</i></p>	<p>14:09-14:33 [O14.2] Modulations in cell-membrane composition confer pediocin resistance in Enterococcus faecalis Rashmi Kumariya* , Anita Kumari Garsa, S. K. Sood and Y. S. Rajput, <i>National Dairy Research Institute, India</i></p>	<p>14:15-14:45 [O15.2] Investigation of the influenza A/H3N2 virus circulated in the human population in Siberia, 2008-2013 I.A. Sobolev*¹, O.G. Kurskaya¹, T.N. Ilyicheva², A.G. Durymanov², A.M. Shestopalov¹, ¹<i>State Research Center of Clinical and Experimental Medicine, Russia</i>, ²<i>State Research Center of Virology and Biotechnology "Vector", Russia</i></p>	<p>14:15-14:45 [O16.2] Lipoprotein lipase and PPAR alpha gene polymorphisms, increased very-low-density lipoprotein levels, and decreased high-density lipoprotein levels as risk markers for the development of visceral leishmaniasis by Leishmania infantum M.D.T. Carvalho¹, D.P. Alonso*², C.M.V. Vendrame¹, D.L. Costa³, C.H.N. Costa³, G.L. Werneck^{4,5}, P.E.M. Ribolla², H. Goto¹, ¹<i>Universidade de Sao Paulo, Brazil</i>, ²<i>Universidade Estadual Paulista, Brazil</i>, ³<i>Universidade Federal do Piaui, Brazil</i>, ⁴<i>Universidade do Estado do Rio de Janeiro, Brazil</i>, ⁵<i>Universidade Federal do Rio de Janeiro, Brazil</i></p>	

<p>14:33-14:57 [O13.3] Genomic characterization of pathogenic Leptospire by variable-number Tandem-repeat method P. khaki*, M. Abdollahpour Alitappeh, S. Moradi Bidhendi, M. Esmaelizad, K. Tadayon, R. Ghaderi, A. Zarei, <i>Razi Vaccine & Serum Research Institute, Iran</i></p>	<p>14:33-14:57 [O14.3] The detection of oseltamivir-resistant influenza A/H3N2 viruses using a Real-time RT-PCR assay and comparison the results with direct sequencing J. Yavarian*, T. Mokhtari Azad, M.H. Karbalaie Niya, <i>School of Public Health, Tehran University of Medical Sciences, Iran</i></p>	<p>14:45-15:15 [O15.3] Molecular epidemiology of FMD in the Republic of Kazakhstan 2011-2013 M. Orynbayev*, K. Sultankulova, V. Strochkov, A. Kerimbayev, G. Musayeva, Z. Omarova, A. Sansyzbay, <i>Research Institute for Biological Safety Problems, Kazakhstan</i></p>	<p>14:45-15:15 [O16.3] HLA class I supertype associations with dengue in Bangkok S. Vejbaeysa¹, H.A.F. Stephens^{*1,2}, ¹<i>Mahidol University, Thailand,</i> ²<i>University College London, UK</i></p>
<p>14:57-15:21 [O13.4] Molecular epidemiology of human clinical <i>Campylobacter jejuni</i> isolates in the urban area of Brussels, Belgium L. Mekkaoui^{1,2}, D. Martiny^{1,2}, C. Ragimbeau³, L. Vlaes², M-J. Stouten², O. Vandenberg^{1,2}, M. Hallin^{*1,2}, ¹<i>Université Libre de Bruxelles, Belgium,</i> ²<i>Saint-Pierre University Hospital, Belgium,</i> ³<i>National Health Laboratory, Luxembourg</i></p>	<p>14:57-15:21 [O14.4] Detection of Panton-valentine leukocidin gene by polymerase chain reaction in Methicillin-resistant <i>Staphylococcus aureus</i> isolates from tertiary care hospital N. Nagalakshmi*, G. Sreejith, I. Bairy, G. Shenoy, <i>Manipal University, India</i></p>	<p>15:15-15:45 [O15.4] Detection and molecular characterization of noro, astro and adenoviruses circulating in children under five years of age in several regions of Angola C. Tavares¹, A. Esteves², C. Mendes¹, J. Nordgren³, J. Piedade², F. Fortes⁴, P.R. Dimbu⁴, N. Saraiva⁴, C. Istrate^{*1}, ¹<i>Universidade Nova de Lisboa, Portugal,</i> ²<i>Unidade de Parasitologia e Microbiologia Médicas, Portugal,</i> ³<i>Linköping University, Sweden,</i> ⁴<i>Departamento do Controlo de Doenças da Direção Nacional de Saúde Pública, Angola</i></p>	<p>15:15-15:45 [O16.4] Association study of TAP1 and TAP2 polymorphisms with hepatitis C virus chronic infection in Han population in Yunnan province of China Y. Li*, X.W. Xu, J. Zhou, J.K. Yu, Y.F. Yao, M.B. Sun, L. Shi, <i>Chinese Academy of Medical Sciences & Peking Union Medical College, China</i></p>
<p>15:21-15:45 [O13.5] Largest <i>Vibrio cholera</i> outbreak in Cameroon history studied using whole genome sequencing R.S. Kaas^{*1}, M.C. Fonkoua², A. Ngandjio², F.M. Aarestrup¹, R. Hendriksen¹, ¹<i>Technical University of Denmark, Denmark,</i> ²<i>Centre pasteur du Cameroun, Cameroon</i></p>	<p>15:21-15:45 [O14.5] Selection and spread of artemisinin resistant alleles in thailand prior to the malaria containment campaign E. Talundzic^{*1,2}, S. Akinyi², K. Congpuong^{3,4}, L. Morton¹, I. Goldman¹, S.P. Kachur¹, C. Wongsrichanalai⁵, W. Satimai³, J.S. Barnwell¹, V. Udhayakumar¹ et al, ¹<i>Center for Disease Control and Prevention, USA,</i> ²<i>Atlanta Research and Education Foundation, USA,</i> ³<i>Bureau of Vector Borne Diseases, Ministry of Public Health, Thailand,</i> ⁴<i>Bansomdej-chaopraya Rajabhat</i></p>		

		University, Thailand, ⁵ Independent Scholar, Thailand		
Plenary Session				
<i>Room</i>	<i>Phanurangsi C</i>			
Chair	RM. Pitchappan, Chettinad Academy of Research & Education, India			
15:45-16:15	PL09: Molecular epidemiology of giardia and cryptosporidium infections RC A. Thompson, Murdoch University, Australia			
Chair	RC A. Thompson, Murdoch University, Australia			
16:15-16:45	PL10: Human genomic diversities & disease susceptibility in India RM. Pitchappan, Chettinad Academy of Research & Education, India			
<i>Room</i>	<i>Phanurangsi A & B</i>			
16:45-17:15	Coffee Break			
<i>Rooms</i>	<i>Phanurangsi C</i>	<i>Bongkotrat A</i>	<i>Bongkotrat B</i>	<i>Busabongkot A</i>
17:15-19:15	Symposium 17-Drug/antibiotic resistance 2	Symposium 18-Molecular epidemiology Salmonella	Symposium 19-Molecular epidemiology Virus 2	Symposium 20-Mycobacterial diseases 2
Chairs	T. Chookajorn, Mahidol University, Thailand V. Chaumeau, Université Montpellier 1, France; Centre hospitalo-universitaire de Montpellier, France	R. Ghaderi, Razi Vaccine & Serum Research Institute, Karaj, Iran E. Litrup, Statens Serum Institute, Denmark	A. Lacroix, Réseau international des Instituts Pasteur, Cambodia	U.G. Gurjav, The University of Sydney, Australia; Institute of Clinical Pathology and Medical Research – Pathology West, Australia C.A. Ahlstrom, University of Calgary, Canada
	17:15-17:39 [O17.1] Global health crisis in the making: How malaria parasites improve robustness to become drug resistance	17:15-17:45 [O18.1] Salmonella Typhimurium core genome typing and its public health significance for phylogeny inference	17:15-17:39 [O19.1] Evolution of the influenza A H1N1 HA1 receptor-binding site M.E. Cueno*, K. Ochiai, Nihon	17:15-17:45 [O20.1] Genetic diversity of the mycobacterium tuberculosis Beijing family based on multiple genotyping

	T. Chookajorn, <i>Mahidol University, Thailand</i>	and epidemiological investigation S.F. Fu*, S.O. Octavia, M.T. Tanaka, R.L. Lan, <i>UNSW, Australia</i>	<i>University School of Dentistry, Japan</i>	profiles in eastern Asian areas Y. Liu, Y. Zhang, B. Xu, Q. Zhao, W.B. Wang*, <i>Fudan University, China</i>
	17:39-18:03 [O17.2] Moved to Symposium 12: Molecular epidemiology bacteria 1	17:45-18:15 [O18.2] Iranian clonal population of Salmonella enterica serovar Enteritidis, recovered by multi-locus sequence typing (MLST) method R. Ghaderi*, K. Tadayon, P. Khaki, S. Moradi Bidhendi, L. Djozebayat, S.R. Banihashemi, M. Sekhavati, A. Zarei, N. Mosavari, <i>Razi Vaccine & Serum Research Institute, Karaj, Iran</i>	17:39-18:03 [O19.2] Detection of coronaviruses in bats in Cambodia and Laos A. Lacroix*, V. Duong ¹ , V. Hul ¹ , S. San ^{1,2} , K. Omaliss ^{1,2} , R. Frutos ^{1,3} , W. Theppangna ^{1,5} , Z. Greateorex ^{1,6} , L. Keatts ^{1,4} , P. Buchy ¹ et al, ¹ <i>Réseau international des Instituts Pasteur, Cambodia</i> , ² <i>Ministry of Agriculture Forestry and Fisheries, Cambodia</i> , ³ <i>Université Montpellier 2, France</i> , ⁴ <i>Wildlife Conservation Society, Cambodia</i> , ⁵ <i>National Animal Health Laboratory, Ministry of Agriculture Forestry and Fisheries, People's Democratic Republic of Lao</i> , ⁶ <i>Wildlife Conservation Society, People's Democratic Republic of Lao</i>	17:45-18:15 [O20.2] Mycobacterium tuberculosis reactivation in New South Wales, Australia U.G. Gurjav* ^{1,2} , P.J. Jelfs ^{2,3} , G.H.C. Hill-Cawthorne ¹ , B.M. Marais ¹ , V.S. Sintchenko ^{1,3} , ¹ <i>The University of Sydney, Australia</i> , ² <i>Institute of Clinical Pathology and Medical Research – Pathology West, Australia</i> , ³ <i>Centre for Infectious Diseases and Microbiology – Public Health, Australia</i>
	18:03-18:27 [O17.3] Genomic epidemiology of Klebsiella pneumoniae in Italy provides novel insights into the origin of resistance to carbapenem antibiotics F. Comandatore* ^{1,2} , S. Gaiarsa ^{1,3} , P. Gaibani ⁴ , M. Corbella ³ , C. Dalla Valle ³ , S. Epis ¹ , E. Scaltriti ⁵ , E. Carretto ⁶ , C. Farina ⁷ , M. Labonia ⁸ et al, ¹ <i>Università degli studi di Milano, Italy</i> , ² <i>Università degli Studi di Pavia, Italy</i> , ³ <i>Fondazione IRCCS Policlinico San Matteo (Pavia), Italy</i> , ⁴ <i>St. Orsola University Hospital (Bologna), Italy</i> , ⁵ <i>Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna,</i>	18:15-18:45 [O18.3] Global genomic epidemiology and evolutionary genetics of Salmonella Typhimurium DT104 P. Leekitcharoenphon*, R.S. Hendriksen, F.M. Aarestrup, <i>Technical University of Denmark, Denmark</i>	18:03-18:27 [O19.3] siRNA Silencing: mRNA expression knockdown of Potato Leaf Roll Virus-Capsid Protein gene Co-transfection with mammalian (CHO-k) cell line in-vivo M.B. Hossain* ¹ , I.A. Nasir ¹ , T. Husnain ¹ , ¹ <i>Sher-e-Bangla Agricultural University, Bangladesh</i> , ² <i>University of the Punjab, Pakistan</i> , ³ <i>University of the Punjab, Pakistan</i>	18:15-18:45 [O20.3] The epidemiology and phylogenomics of Mycobacterium avium subsp. paratuberculosis on a global, national, and provincial level C.A. Ahlstrom* ¹ , H.W. Barkema ¹ , K. Stevenson ² , R.N. Zadoks ^{2,3} , R. Biek ³ , R.R. Kao ³ , H. Trewby ³ , J. De Buck ¹ , ¹ <i>University of Calgary, Canada</i> , ² <i>Moredun Research Institute, UK</i> , ³ <i>University of Glasgow, UK</i>

	Italy, ⁶ IRCCS Arcispedale S. Maria Nuova (Reggio Emilia), Italy, ⁷ AO Papa Giovanni XXIII (Bergamo), Italy, ⁸ IRCCS Casa Sollievo della Sofferenza (San Giovanni Rotondo), Italy, ⁹ The Greater Romagna Area-Hub Laboratory (Pievesestina), Italy			
	<p>18:27-18:51 [O17.4] Dynamic of malaria transmission along the Thai-Myanmar border in a context of Targeted Chemo elimination V. Chaumeau*^{1,2}, N. Kwansomboon⁴, C. Montazeau¹, B. Fustec^{3,4}, C. Andolina^{5,6}, D. Cerqueira¹, T. Chareonviriyaphap⁴, F. Nosten^{5,6}, V. Corbel^{3,4}, ¹Université Montpellier 1, France, ²Centre hospitalo-universitaire de Montpellier, France, ³Maladies Infectieuses et Vecteurs, Ecologie, Génétique, Evolution et Contrôle, Institut de Recherche pour le Développement, France, ⁴Kasetsart University, Thailand, ⁵Maidol-Oxford Research Unit, Thailand, ⁶Shoklo Malaria Research Unit, Thailand</p>	<p>18:45-19:15 [O18.4] Impact of prophages on the evolution of the salmonella infantis population E. Litrup*¹, P. Gyomai¹, K. Kiil¹, Z. Zhou², G. Soerensen³, D. Guttman⁴, M. Torpdahl¹, M. Achtman², E.M. Nielsen¹, ¹Statens Serum Institute, Denmark, ²University of Warwick, UK, ³National Food Institute, Denmark, ⁴University of Toronto, Canada</p>	<p>18:27-18:51 [O19.4] Population genetic analysis of pathogen sequences to infer prevalence of poliovirus infection L.M. Li*, N.C. Grassly, C. Fraser, Imperial College London, UK</p>	<p>18:45-19:15 [O20.4] Understanding impacts of pathogen genetics and host management on the phylodynamics of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> C.A. Ahlstrom*¹, H.W. Barkema¹, J.D. Wasmuth¹, C. Colijn², J. De Buck¹, ¹University of Calgary, Canada, ²Imperial College London, UK</p>
	<p>18:51-19:15 [O17.5] Attempts to control Trypanosoma lewisi in rats using intramuscular injection of veterinary trypanocidal drugs M. Desquesnes*^{1,2}, S. Herder^{2,3}, S. Yangtarra², S. Jittapalapong², ¹CIRAD-Bios, France, ²Kasetsart University, Thailand, ³IRD, France</p>		<p>18:51-19:15 [O19.5] Dengue virus serotypes and genotypes circulating in Indonesia for the last 13 years H. Harapan^{1,2}, A.M. Setiawan*^{2,3}, ¹Syah Kuala University, Indonesia, ²The University of Western Australia, Australia, ³Maulana Malik Ibrahim Islamic State University, Indonesia</p>	
19:45-22:30	Gala Dinner – Riverboat Cruise (Optional – tickets can be purchased)			

Saturday, 13 December 2014

Plenary Session

Room	Phanurangsi C			
Chair	A.F. Read, <i>The Pennsylvania State University, USA; Fogarty International Center, NIH, USA</i>			
09:00-09:30	PL11: Molecular epidemiology of chikungunya virus infection Y. Poovorawan*, P. Linsuwanon, S. Vongpunsawad, <i>Chulalongkorn University, Thailand</i>			
Chair	Y. Poovorawan, <i>Chulalongkorn University, Thailand</i>			
09:30-10:00	PL12: Vaccination and the emergence of virulent viruses. Evolutionary lessons from a poultry disease A.F. Read* ^{1,2} , S.J. Baigent ³ , C. Powers ³ , L.B. Kgosana ³ , L. Blackwell ³ , L.P. Smith ³ , D.A. Kennedy ^{1,2} , S. Walkden-Brown ⁴ , V. Nair ³ , ¹ <i>The Pennsylvania State University, USA</i> , ² <i>Fogarty International Center, NIH, USA</i> , ³ <i>Pirbright Institute, UK</i> , ⁴ <i>University of New England, Australia</i>			
Room	Phanurangsi A & B			
10:00-10:30	Coffee Break			
Room	Phanurangsi C	Bongkotrat A	Bongkotrat B	Busabongkot A
10:30-12:30	Symposium 21-Clonality vs recombination	Symposium 22-Diseases of veterinary relevance	Symposium 23-Molecular epidemiology helminths	Symposium 24-Molecular epidemiology bacteria 3
Chairs	M. Tibayrenc, <i>Institut de recherche pour le développement, France</i> K. Yahara, <i>University of Tokyo, Japan</i>	G. Kaewmongkol, <i>Kasetsart University Thailand</i> T. Forde, <i>University of Calgary, Canada</i>	A. Ito, <i>Asahikawa Medical University, Japan</i> J-P. Hugot, <i>UMR-CNRS 7205, MNHN, France</i>	L. Zhang, <i>Michigan State University, USA</i> E.C. Coipan, <i>National Institute for Public Health and Environment (RIVM), The Netherlands; Wageningen University, The Netherlands</i>
	10:30-10:54 [O21.1] Phylogenetic analysis of a circulating hepatitis C virus recombinant 1b/1a strain isolated in a French hospital centre V. Morel* ^{1,2} , F. Ghoubra ³ , L. Izquierdo ^{1,2} , E. Martin ^{1,2} , C. Grillo de Oliveira ¹ , C. Francois ^{1,2} , E. Brochot ^{1,2} , F. Helle ¹ , G. Duverlie ^{1,2} , S. Castelain ^{1,2} , ¹ <i>Jules Verne University of Picardie, France</i> , ² <i>Amiens University Hospital, France</i> , ³ <i>Pasteur Institute of Tunis, Tunisia</i>	10:30-10:50 [O22.1] Identification of uncultured-bacteria detected from abscesses of pet animals by broad range nested 16S rRNA PCR G. Kaewmongkol* ¹ , S. Kaewmongkol ¹ , T. Duangurai ¹ , K. Sutasha ¹ , L. Areevijittrakul ¹ , T. Sirinarumit ¹ , S. Jittapalapong ¹ , S. Fenwick ² , ¹ <i>Kasetsart University Bangkok, Thailand</i> , ² <i>Murdoch University, Australia</i>	10:30-11:00 [O23.1] Recent advances and perspectives in molecular epidemiology of Taenia solium cysticercosis A. Ito*, T. Yanagida, M. Nakao, Y. Sako, M. Okamoto, <i>Asahikawa Medical University, Japan</i>	10:30-11:00 [O24.1] Molecular and phenotypic characterization of Photobacterium damsela, a pathogen of the grey mullet Mugil cephalus A. Abedian amiri* ^{1,2} , F. Naseri ¹ , M. Heidarzadeh ¹ , R. Zahedi ¹ , P. Arabzadeh ¹ , ¹ <i>Islamic Azad University, Iran</i> , ² <i>Veterinary Office of Chabahar, Iran</i> , ³ <i>Sistan and Baluchestan Veterinary, Iran</i>
	10:54-11:18 [O21.2] Chromosome painting <i>in silico</i> in a	10:50-11:10 [O22.2] Molecular epidemiology of viral	11:00-11:30 [O23.2] Dinosaurs had they pinworms ?	11:00-11:30 [O24.2] <i>E. coli</i> diversity and transmission of

	<p>bacterial species reveals fine population structure K. Yahara*¹, Y. Furuta¹, K. Oshima¹, M. Yoshida¹, T. Azuma¹, M. Hattori¹, I. Uchiyama¹, I. Kobayashi¹, ¹University of Tokyo, Japan, ²Max Planck Institute for Evolutionary Anthropology, Germany, ³National Institute for Basic Biology, Japan, ⁴Kobe University, Japan</p>	<p>infections of domestic animals S. Vilcek*¹, A. Jackova¹, M. Vlasakova¹, I. Sliz¹, W. Rossmanith², ¹University of Veterinary Medicine and Pharmacy, Slovakia, ²Office of the Government of Lower Austria, Dept. of Veterinary Affairs, Austria</p>	<p>(Origin of pinworm parasites: From mammalian reptiles to humans) J-P. Hugot*¹, S.L. Gardner², V. Borba³, P. Araujo⁴, D. Leles⁴, A. Da-Rosa⁵, L. Dutra³, L.F. Ferreira³, A. Araujo¹, ¹Museum National d'Histoire Naturelle, OSEB, UMR 7205 CNRS, France, ²University of Nebraska State Museum and School of Biological Sciences, University of Nebraska – Lincoln, USA, ³Escola Nacional de Saúde Pública Sergio Arouca, Fundação Oswaldo Cruz, Rua Leopoldo Bulhões 1480, Brazil, ⁴Universidade Federal Fluminense, Brazil, ⁵Universidade Federal de Santa Maria, Brazil</p>	<p>pathogens in Northwestern Ecuador: Spatial trends across a landscape L. Zhang*¹, K. Levy², G. Trueba³, W. Cevallos⁴, J.N. Eisenberg⁵, ¹Michigan State University, USA, ²Emory University, USA, ³Universidad San Francisco de Quito, Ecuador, ⁴Universidad Central del Ecuador, Ecuador, ⁵University of Michigan, USA</p>
<p>11:18-11:42 [O21.3] Withdrawn</p>	<p>11:10-11:30 [O22.3] Distribution pattern of virulence genes in Pasteurella multocida strains associated with porcine and bovine diseases in Thailand T. E-kobon*¹, P. Thongkamkoon², A. Thamchaipenet¹, N. Hussarangsi², P. Anuntasomboon¹, R. Leeaan¹, S. Pannoi¹, ¹Kasetsart University, Thailand, ²National Institute of Animal Health, Ministry of Agriculture & Cooperatives, Thailand</p>	<p>11:30-12:00 [O23.3] The high prevalence of human intestinal fluke, Haplorchis taichui among the thiarid snails and cyprinoid fishes in Bo Kluea district, Nan province, Thailand D. Boonmekam*¹, S. Namchote¹, W. Nak-ai², D. Krailas¹, ¹Silpakorn University, Thailand, ²Ministry of Public Health, Thailand</p>	<p>11:30-12:00 [O24.3] MRSA colonizing the anterior nares of hospitalized patients; are they originating from the hospital or in the community? S. Govindan*, A. Yong, M. Godinho, S. Raj, K.K. Gan, A. Dhillon, Manipal University, India</p>	
<p>11:42-12:06 [O21.4] The predominant clonal evolution (PCE) concept of microbial pathogens M. Tibayrenc*¹, F.J. Ayala¹, ¹Institut de recherche pour le développement, France, ²University of California Irvine, USA</p>	<p>11:30-11:50 [O22.4] Phylogenomic analyses suggest a recently emerged strain of Erysipelothrix rhusiopathiae is associated with muskox die-offs in the Canadian Arctic T. Forde*¹, K. Orsel¹, R. Biek², J. De Buck¹, H. Trewby², F. van der Meer¹, R. Zadoks², S. Kutz^{1,3}, ¹University of</p>	<p>12:00-12:30 [O23.4] Phylogenetic relationships and taxonomy of cestodes of Laonastes aenigmamus J-P. Hugot*¹, H. Henttonen², B. Douangboup³, V. Haukialmi², ¹Hugot UMR-CNRS 7205, France, ²University Of Helsinki, Finland, ³Nafri Nongviengkham, People's</p>	<p>12:00-12:30 [O24.4] Geodemographic analysis of Borrelia burgdorferi sensu lato using the 5S-23S rDNA spacer region E.C. Coipan*^{1,2}, M. Fonville¹, E. Tijsses-Klasen¹, J.W.B. van der Giessen¹, W. Takken², H. Sprong^{1,2}, K. Takumi¹, ¹National Institute for Public Health and Environment (RIVM), The</p>	

		Calgary, Canada, ² University of Glasgow, UK, ³ Canadian Wildlife Health Cooperative, Canada	Democratic Republic of Lao	Netherlands, ² Wageningen University, The Netherlands
	12:06-12:30 [O21.5] Use of PCR-RFLP HSP70 sequence targeting to identify putative hybrids of Leishmania sp. isolated from patients with cutaneous leishmaniasis in the Amazon region of Brazil A.C.S. Lima* ¹ , R.A. Zampieri ² , T.Y. Tomokane ¹ , C.M.C. Gomes ¹ , L.M. Floeter-Winter ² , F.T. Silveira ^{1,3} , C.E.P. Corbett ¹ , ¹ Medical School of University of São Paulo, Brazil, ² Biosciences Institute of University of São Paulo, Brazil, ³ Evandro Chagas Institute, Brazil	11:50-12:10 [O22.5] Heterogeneity of genes encoding the structural proteins of avian infectious bronchitis virus S.H. Abro* ^{1,3} , S. Zohari ^{1,2} , L. Renström ² , D. Jansson ² , F. Otman ² , K. Ullman ² , S. Belák ^{1,2} , C. Baule ² , ¹ Swedish University of Agricultural Sciences, Sweden, ² National Veterinary Institute, Sweden, ³ Sindh Agriculture University Tandojam, Pakistan		
		12:10-12:30 [O22.6] An innovative broad-range molecular screening of avian respiratory pathogens on a high throughput PCR microfluidic platform G. Croville*, A. Senet, C. Foret, M.F. Ducatez, J-L. Guérin, <i>Université de Toulouse, INP, ENVT and INRA, France</i>		
Room	Phanurangsi A & B			
12:45-14:00	Lunch			
13:00-14:00	Author Workshop			
Plenary Session				
Room	Phanurangsi C			
Chair	M. Tibayrenc , <i>Institut de recherche pour le développement, France</i>			
14:00-14:30	PL13: Worldwide population structure and molecular evolution of the Leishmania donovani complex G. Schoenian, <i>Charité University Medicine Berlin, Germany</i>			
Chair	C. Walton , <i>University of Manchester, UK</i>			
14:30-15:00	PL14: From antiquity to present - dengue, a constantly evolving story N. Vasilakis, <i>UTMB, USA</i>			
Room	Phanurangsi A & B			
15:00-15:30	Coffee break			
Room	Phanurangsi C			

Chair	N. Vasilakis, <i>UTMB, USA</i>
15:30-16:00	PL15: Population genetics and population genomics of Anopheles mosquitoes in SE Asia C. Walton, <i>University of Manchester, UK</i>
16:00-16:30	Closing Remarks & Awards