



Programme

Tuesday 14 November 2023

17:00 - 19:00	Registration and Welcome Reception Congress Foyer
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Wednesday 15 November 2023

09:00 - 10:15	Welcome and Plenary Session 1 Room: Congress Saal 1&2 Chairs: Manuela Sironi, Fernando Gonzalez-Candelas	
09:00-09:15	Opening remarks Manuela Sironi, Fernando Gonzalez-Candelas	
09:15 - 09:45	[PL.01] Ecology and evolution of multidrug-resistant <i>Mycobacterium tuberculosis</i> <u>Sebastien Gagneux</u> <i>Swiss Tropical and Public Health Institute, Switzerland</i>	
09:45 - 10:15	[PL.02] The Evolutionary Paradox of Host-Virus Interactions <u>Tzachi Hagai</u> <i>Tel Aviv University, Israel</i>	
10:15 - 10:45	Refreshment Break Congress Foyer	
10:45 - 11:45	Plenary Session 1 (Cont.) Room: Congress Saal 1&2 Chairs: Manuela Sironi, Fernando Gonzalez-Candelas	
10:45 - 11:15	[PL.03] An ancient DNA perspective on human herpesvirus evolution <u>Charlotte Houldcroft</u> <i>University of Cambridge Department of Genetics, UK</i>	
11:15 - 11:45	[PL.04] Coronaviruses Are Abundant and Genetically Diverse in West and Central African Bats, including Viruses Closely Related to Human Coronaviruses <u>Audrey Lacroix</u> , <i>TransVIHMI, University of Montpellier, INSERM, Institut de Recherche pour le Développement, Montpellier, France</i>	
11:45 - 12:30	Lunch Hotel Restaurant	
12:30 - 13:30	Poster session 1 Room: Rotterdam	
13:30 - 14:50	Symposium 1 - Genetics and Genomics- Viruses Room: Congress Saal 1 Chair: Tzachi Hagai	Symposium 2 - Genetics and Genomics-bacteria Room: Congress Saal 2 Chair: Charlotte Houldcroft
13:30 - 13:50	[O1.1] Emergence of Chikungunya Virus in a Hyperendemic Dengue Region: Viral Phylogenetic Analysis <u>Simone Kashima</u> <i>Blood Center of Ribeirão Preto, Brazil</i>	[O2.1] Genomic Characterization and Population Structure of Clinical <i>Listeria monocytogenes</i> in New York, USA, Spanning Over Two Decades <u>Odion Ikhimiukor</u> <i>University at Albany Department of Biological Sciences, USA</i>
13:50 - 14:10	[O1.2] Temporal and coevolutionary analyses reveal the events driving the emergence and circulation of human mamastroviruses <u>Lester Perez</u> , <i>Abbott Laboratories, USA</i>	[O2.2] High genomic diversity of multidrug-resistant <i>Helicobacter pylori</i> in Malaysia <u>Asif Sukri</u> <i>Department of Biological Sciences and Biotechnology, Universiti Kebangsaan Malaysia, Malaysia</i>
14:10 - 14:30	[O1.3] HPAI H5 of clade 2.3.4.4b in Europe and beyond – why trends of virus evolution are more difficult to predict <u>Alice Fusaro</u> , <i>European Reference Laboratory (EURL) for Avian Influenza and Newcastle Disease, Istituto Zooprofilattico Sperimentale delle Venezie, Italy</i>	[O2.3] Two novel Bartonella (sub)species isolated from edible dormice (<i>Glis glis</i>): Hints of cultivation stress-induced genomic changes <u>Oldřich Bartoš</u> <i>Military Health Institute, Military Medical Agency, Prague, Czech Republic</i>

14:30 - 14:50	[O1.4] Hesperetin blocks interaction of poxvirus mRNA with eIF4E without producing drug-resistant mutants. <u>Assim Verma</u> ^{1,2} ¹ Guru Jambheshwar University of Science & Technology Department of Physics, India. ² National Centre for Veterinary Type Cultures, India	[O2.4] Temporal shifts in the population structure and genome content of Staphylococcus aureus bacteremia sampled over two decades <u>Cheryl Andam</u> University at Albany, USA
14:50 - 15:20	Refreshment break Congress Foyer	
15:20 - 17:20	Symposium 3 - Genetics and Genomics- Viruses Room: Congress Saal 1 Chair: Martine Peeters	Symposium 4 - Genetics and Genomics- Bacteria and Protozoa Room: Congress Saal 2 Chair: Niyaz Ahmed
15:20 - 15:40	[O3.1] Long-term evolutionary dynamics and variant switching of Dengue virus 3 lineages during two successive outbreaks in a hyperendemic environment <u>Hapuarachchige Chanditha Hapuarachchi</u> , Environmental Health Institute, National Environment Agency, Singapore	[O4.1] Ten years later: genomes evolution of ST228 SCCmec-I MRSA after a major nosocomial outbreak <u>Florian Mauffrey</u> , Infection Prevention and Control Unit, Lausanne University Hospital, University of Lausanne, Switzerland
15:40 - 16:00	[O3.2] Codon usage and genome composition of poxviruses <u>Cristian Molteni</u> , Eugenio Medea Scientific Institute for Research Hospitalization and Health Care, Italy	[O4.2] Distinctive mobilome of <i>Neisseria meningitidis</i> from South America <u>Michel Abanto</u> , Universidad de La Frontera, Chile
16:00 - 16:20	[O3.3] Prevalence and Risk Factors for Virologic Failure when using Ganciclovir/Valganciclovir for Cytomegalovirus therapy in Solid Organ Transplant Recipients <u>Julio Mendez</u> , Mayo Clinic in Florida, USA	[O4.3] A study molecular-genetic characteristics of drug-resistant strains of tuberculosis mycobacteria spreading in the Republic of Azerbaijan <u>Gulzar Aliyeva</u> , Scientific Research Institute of Lung Diseases, Azerbaijan
16:20 - 16:40	[O3.4] Norovirus prevalence and genotypes in children with acute gastroenteritis attending emergency rooms in Lima, Peru. <u>Alejandra Ingunza</u> , Instituto de Investigación Nutricional, Peru	[O4.4] Lineage-specific evolutionary histories and selective forces shape the landscape of <i>Mycobacterium tuberculosis</i> diversity in East Asia <u>Matthew Silcocks</u> , The Peter Doherty Institute for Infection and Immunity, Australia
16:40 - 17:00	[O3.5] Human Papillomavirus (HPV) 52 genotype detection and phylogenetic analysis among women referred to colposcopy for cervical dysplasia <u>Marianna Martinelli</u> , University of Milano-Bicocca, Italy	[O4.5] The adaptive landscape of <i>M. tuberculosis</i> dominant lineage 2 <u>Thierry Wirth</u> ^{1,2} , ¹ EPHE, PSL University, Paris, France. ² The Institute of Systematics, Evolution, Biodiversity, France
17:00 - 17:20	[O3.6] The principles of SARS-CoV-2 inter-variant competition are exemplified in the pre-Omicron era of the Colombian epidemic <u>Gregory Orf</u> , Abbott Laboratories, USA	[O4.6] The diversity of Babesia spp. in free-living deer and free-roaming cats from Poland <u>Anna Bajer</u> , Department of Eco-epidemiology of Parasitic Diseases, University of Warsaw, Poland
Thursday 16 November 2023		
09:00 - 10:00	Plenary Session 2 Room: Congress Saal 1&2	
09:00 - 09:30	[PL.05] Evolution on the very fast lane: bacterial genomes as playgrounds for mobile elements <u>Eduardo Rocha</u> Institut Pasteur, France	
09:30 - 10:00	[PL.06] Determinants of plant RNA virus evolution at different scales: from cells to ecosystems <u>Santiago Elena</u> CSIC, Spain. Santa Fe Institute, USA	
10:00 - 10:30	Refreshment break Congress Foyer	
10:30 - 12:00	Plenary session 2 (Cont.) Room: Congress Saal 1&2	
10:30 - 11:00	[PL.07] Genomics of virulence and fitness in Gram negative bacteria in different settings <u>Niyaz Ahmed</u> Department of Biotechnology and Bioinformatics, University of Hyderabad, India	
11:00 - 11:30	[PL.08] Molecular archeology of RNA viruses <u>Sebastien Calvignac-Spencer</u> Helmholtz Institute for One Health, University of Greifswald, Germany	

11:30 - 12:00	[PL.09] How to understand the holobiont response to the Anthropocene at the end of the world? <u>Valeria Souza</u> ^{1,2} , ¹ National Autonomous University of Mexico, Mexico ² CEQUA, Chile	
12:00 - 13:00	Lunch Hotel Restaurant	
12:30 - 13:30	Poster Session 2 Room: Rotterdam	
13:30 - 14:50	Symposium 5 - One Health approaches to infectious diseases Room: Congress Saal 1 Chair: Tung Phan	Symposium 6 - Genetics and Genomics-bacteria Room: Congress Saal 2 Chair: Eduardo Rocha
13:30 - 13:50		[O6.1] Molecular epidemiological analysis of <i>Salmonella</i> Schwarzengrund isolated in Japan <u>Shunsuke Ikeuchi</u> , Tokyo University of Agriculture and Technology, Japan
13:50 - 14:10	[O5.2] Interspecies transmission of G4P[6] rotavirus A between pigs and humans revealed by synchronized spatiotemporal approach in Croatia <u>Valentina Kunić</u> , ¹ Croatian Veterinary Institute, Croatia	[O6.2] Genomic overview, population structure and international context of non-epidemic <i>Vibrio cholerae</i> in Canada <u>Taylor Wells</u> ^{1,2} , ¹ National Microbiology Laboratory, Public Health Agency of Canada, Canada ² Rady Faculty of Health Sciences, University of Manitoba, Canada
14:30 - 14:10	[O5.3] One Health approach during outbreaks of avian influenza in wild birds in northern Senegal, 2022 and 2023 <u>Nicolas D. Diouf</u> , Gaston Berger University, Senegal	[O6.3] Bacteria associated with Chronic Infections: An Unsuccessful Microbial Path to Host Symbiosis <u>Xuan Qin</u> Oregon Health Science University, USA
14:30 - 14:50	[O5.4] One Health Approaches for Infectious Diseases: A Focus on Tuberculosis in Brazil <u>Maykon Jhuly Martins de Paiva</u> ^{1,2} , University of Gurupi, GURUPI, Brazil ² University of Brasilia, Brazil	[O6.4] Role of <i>jhp0947</i> as one of the potential markers of <i>Helicobacter pylori</i>-related disease outcome in India <u>Sangita Paul</u> , ICMR-National Institute of Cholera and Enteric Diseases, India
14:50 - 15:20	Meet the Editors Session & Refreshment break Congress Foyer	
15:20 - 17:20	Symposium 7 - Genetics and genomics of pathogens and vectors Room: Congress Saal 1 Chair: Valeria Souza	Symposium 8 - Genetics and genomics-fungi, helminths, and protozoa Room: Congress Saal 2 Chair: Santiago Elena
15:20 - 15:40	[O7.1] Population genetic variation in <i>Ixodes scapularis</i> is linked to differences in host parasitism behavior <u>Jory Brinkerhoff</u> , University of Richmond, USA	[O8.1] The importance of the genomic analysis of host and pathogens for malaria control and elimination <u>Ronise Silva</u> ^{1,2} , ¹ Global Health and Tropical Medicine, GHTM, IHMT, Universidade Nova de Lisboa, Portugal ² Bandim Health Project, Guinea-Bissau
15:40 - 16:00	[O7.2] Population genomics of <i>Plasmodium ovale</i> in sub-Saharan Africa <u>Kelly Carey-Ewend</u> , The University of North Carolina at Chapel Hill, USA	[O8.2] Genomic analysis of a large <i>Candida auris</i> outbreak in a tertiary hospital of Comunitat Valenciana (Spain) <u>Fernando González-Candelas</u> ^{1,3,4} ¹ University of Valencia, Spain, ³ Foundation for the Promotion of the Research in Healthcare and Biomedicine, Spain ⁴ Center for Biomedical Research in Epidemiology and Public Health Network, Spain
16:00 - 16:20	[O7.3] A new reference genome for the human hookworm <i>necator americanus</i> <u>Vladislav Ilik</u> ^{1,2} , ¹ Department of Botany and Zoology, Masaryk University, Czech Republic ² Institute of Vertebrate Biology Czech Academy of Sciences, Czech Republic	[O8.3] Global Prevalence Estimates of <i>Toxascaris leonina</i> Infection in Dogs and Cats <u>Ali Mirzapour</u> , Innovative Medical Research center, Mashhad Branch, Islamic Azad University, Iran
16:20 - 16:40	[O7.4] Genome-wide association study of an African snail vector of schistosomiasis identifies genes associated with resistance to infection by <i>Schistosoma mansoni</i> <u>Michelle Steinauer</u> , University of Health Sciences, USA	[O8.4] Haplotypes of <i>Dirofilaria repens</i> and <i>Dirofilaria immitis</i> from 16 countries: a comparison of the genetic diversity between the two zoonotic nematodes <u>Mustafa Alsarraf</u> , University of Warsaw, Department of Eco-Epidemiology of Parasitic Diseases, Poland

16:40 - 17:00	[O7.5] A century of evolution in Australian arboviruses co-circulating in mosquito populations <u>Carla S P Vieira</u> ^{1,2} , ¹ QIMR Berghofer Medical Research Institute Mosquito Control Laboratory, Australia ² Queensland University of Technology School of Biomedical Sciences, Australia	[O8.5] <i>Plasmodium falciparum</i> population structure in southwestern Africa, using whole genome sequence data: Initial genome-wide sequence data from Angola. <u>Wilson Tavares</u> , GHTM, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Portugal
17:00 - 17:20	[O7.6] Low prevalence of lenacapavir resistance associated mutations in a large set of HIV-1 subtype C sequences from people living with HIV in Botswana <u>Una Roven</u> ^{1,3} , ¹ Botswana-Harvard AIDS Institute Partnership, Gaborone, Botswana. ³ Harvard University, USA	[O8.6] Genetic complexity influence on <i>in vitro</i> phenotypes and antimalarial susceptibility of <i>P. falciparum</i> asexual and gametocyte clinical isolates <u>Nicola Greyling</u> , ¹ University of Pretoria Faculty of Natural and Agricultural Sciences, South Africa
17:20 - 18:20	Author Workshop Congress Saal 1	
19:00 - 21:30	Conference Dinner Cruise (ticketed)	
Friday 17 November 2023		
09:00 - 10:00	Plenary session 3 Congress Saal 1&2	
09:00 - 09:30	[PL.10] Pathogen Genomics: An ancient DNA perspective <u>Verena Schuenemann</u> University of Basel, Basel, Switzerland. University of Zurich, Switzerland	
09:30 - 10:00	[PL.11] Genomic Surveillance and Characterization of Microbial Threats Facilitates Early Detection and Containment of Disease Outbreaks in West Africa. <u>Christian Happi</u> , Redeemer's University, Ede, Nigeria	
10:00 - 10:30	Refreshment break Congress Foyer	
10:30 - 12:00	Plenary session 3 (Cont.) Congress Saal 1&2	
10:30 - 11:00	[PL.12] Deciphering the horizontal traffic rules of aminoglycoside resistance genes. <u>Stéphanie bedhomme</u> , Center for Functional and Evolutionary Ecology, CNRS, France	
11:00 - 11:30	[PL.13] Coronacoaster: clinical laboratory's experience navigating diagnostics for SARS-CoV-2 infections <u>Tung Phan</u> University of Pittsburgh Department of Pathology, USA This will be an online presentation	
11:30 - 12:00	[PL.14] Zika DNA Vaccine Induces Virus-Specific Protection and Cross-Protection Against Dengue Virus <u>Ran Wang</u> Beijing Children's Hospital, Capital Medical University, China	
12:00 - 13:00	Lunch Hotel Restaurant	
13:00 - 15:00	Symposium 9 - Host genetics and mathematical modelling Room: Congress Saal 1 Chair: Christian Happi	Symposium 10 - Genetics and Genomics- Viruses Room: Congress Saal 2 Chair: Ran Wang
13:00 – 13:20	[O9.1] Infection by SARS-CoV-2 with alternate frequencies of mRNA vaccine boosting for immuno-typical and immunocompromised individuals <u>Hayley Hassler</u> ^{1,2} , ¹ Yale University School of Public Health, USA. ² Georgia Institute of Technology, USA	[O10.1] Target capture sequencing for the first Nigerian genotype I ASFV genome <u>Adeniyi Charles Adeola</u> ^{1,2} , ¹ State Key Laboratory of Genetic Resources and Evolution, China. ² Sino-Africa Joint Research Center, Chinese Academy of Sciences, China
13:20 - 13:40	[O9.2] Genomic analysis of measles virus: uncovering molecular evolutionary dynamics and factors driving resurgence <u>Nefert Candace Dossou</u> , Univ Caen Normandie, Univ Rouen Normandie, INSERM, DYNAMICURE UMR 1311, France.	[O10.2] SARS-CoV-2 and batCoV RaTG13 ORF3c accessory proteins differentially impair mitochondrial respiratory metabolism, oxidative stress, and autophagic flux <u>Alessandra Mozzi</u> , Medea Scientific Institute for Research Hospitalization and Health Care, Italy. University of Milan-Bicocca Department of Biotechnology and Biosciences, Milano

13:40 - 14:00	<p>[O9.3] Systems level analysis of probiotic-pathogen-host crosstalk in a Caco2 gut epithelial model <u>Claire Shaw</u>, Bart Weimer <i>University of California Davis School of Veterinary Medicine, USA</i></p>	<p>[O10.3] Genomic surveillance of dengue virus in a Brazilian endemic area <u>Debora La-Roque</u>, <i>University of Sao Paulo Faculty of Medicine of Ribeirao Preto, Brazil</i></p>
14:00 - 14:20	<p>[O9.4] Adaptive and innate immune responses during TB infection: CD4+ T-lymphocyte - neutrophil interactions depend upon the MHC-II alleles and result in different expression levels of S100A genes <u>Alexander Apt</u>, <i>Central Research TB Institute Central Tuberculosis Research Institute, Russia</i></p>	<p>[O10.4] The impact of pre-existing immunity on the emergence of within host immune-escape mutations in Omicron lineages <u>Muna Nizar</u>, <i>Qatar University Biomedical Research Center, Qatar</i></p>
14:20 - 14:40	<p>[O9.5] Longitudinal study of the bovine cervical-vaginal bacterial microbiota throughout pregnancy using 16S ribosomal gene sequences <u>Lucía Calleros</u> <i>University of the Republic Faculty of Sciences, Montevideo, Uruguay</i></p>	<p>[O10.5] Purifying selection decreases the potential for Bangui orthobunyavirus outbreaks in humans <u>Gregory Orf</u>, <i>Abbott Laboratories, USA</i></p>
14:40 - 15:00	<p>[O9.6] PIM, inferring recombination and horizontal gene transfer by phylogenetic incongruence <u>Fernando González-Candelas</u>^{1,3,4} ¹<i>University of Valencia, Spain</i> ³<i>Foundation for the Promotion of the Research in Healthcare and Biomedicine, Spain.</i> ⁴<i>Center for Biomedical Research in Epidemiology and Public Health Network (CIBERESP), Spain</i></p>	<p>[O10.6] Evolutionary Trade-offs and Public Health Implications of SARS-CoV-2 Circulation in Animal Hosts: Insights from White-Tailed Deer and Comparative Replication Kinetics <u>Suresh Kuchipudi</u>, <i>University of Pittsburgh Graduate School of Public Health, USA</i></p>
15:00 - 15:15	<p>Closing remarks Congress Saal 1</p>	