

Programme

Tuesday, 2 November 2021			
14:00-14:30	<p>Welcome and Opening session Chairs: Michel Tibayrenc, Manuela Sironi, Fernando Gonzalez-Candelas Session Chairs: Ananias Escalante, Patricia Dorn</p>		
14:30-15:00	<p>[PL.01] The Ecology of Zoonoses in the United States; a Focus on Vector-borne Disease Patricia Dorn, Loyola University, New Orleans, USA</p>		
15:00-15:30	<p>[PL.02] Genomic evolution of malaria parasites Ananias Escalante, Temple University, Philadelphia, USA</p>		
15:30-16:15	Break		
16:15-17:35	<table border="0" style="width: 100%;"> <tr> <td style="width: 50%; background-color: #e1f5fe;"> <p>O1. Bacterial Genetics and Evolution Chair: Alex Van Belkum</p> </td> <td style="width: 50%; background-color: #e1f5fe;"> <p>O2. Host Genetics and Infectious Diseases Chair: Cheryl Ann Winkler</p> </td> </tr> </table>	<p>O1. Bacterial Genetics and Evolution Chair: Alex Van Belkum</p>	<p>O2. Host Genetics and Infectious Diseases Chair: Cheryl Ann Winkler</p>
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MEEGID XV

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ONLINE
Live and On-demand
2-5 November
2021

Wednesday, 3 November 2021

09:00-10:00	Plenary 1 Chair: Marion Wassermann, Serge Morand	
09:00-09:30	[PL.03] Helminths - what their genes can tell us Marion Wassermann, <i>University of Hohenheim, Germany</i>	
09:30-10:00	[PL.04] The ecology of reservoirs: challenges for emerging zoonoses and neglected tropical diseases Serge Morand, <i>University of Montpellier, France</i>	
10:00-10:45	Break	
10:45-11:35	O3. Bacterial Genetics and Evolution Chair: Erick Denamur	O4. COVID-19 Chair: Katia Koelle
10:45-11:05	[O3.01] Evolution of a protein family involved in immune resistance in the Eurasian Lyme Disease agent <i>Borrelia bavariensis</i> Robert Rollins ¹ , Janna Wülbern ^{1,2} , Florian Röttgerding ³ , Tristan Nowak ⁴ , Sergey Kovalev ⁵ , Hiroki Kawabata ⁶ , Volker Fingerle ⁷ , Yi-Pin Lin ⁴ , Peter Kraiczky ³ , Noémie Becker ^{*1} , ¹ Ludwig-Maximilians Universität, Germany, ² Christian-Albrechts-Universität zu Kiel, Germany, ³ Goethe-Universität, Germany, ⁴ New York State Department of Health, USA, ⁵ Ural Federal University, Russia, ⁶ National Institute for Infectious Disease, Japan, ⁷ Bayerisches Landesamt für Gesundheit und Lebensmittelsicherheit, Germany	[O4.01] Untangling introductions and persistence in COVID-19 resurgence in Europe Philippe Lemey ¹ , Nick Ruktanonchai ² , Samuel Hong ¹ , Vittoria Colizza ³ , Marion Koopmans ⁴ , Adam Sadilek ⁵ , Andrew Tatem ² , Guy Baele ¹ , Marc Suchard ⁶ , Simon Dellicour ^{*7} , ¹ KU Leuven, Belgium, ² University of Southampton, UK, ³ Sorbonne Université, France, ⁴ Department of Viroscience, WHO, The Netherlands, ⁵ Google, United States Minor Outlying Islands, ⁶ University of California, Los Angeles, United States Minor Outlying Islands, ⁷ Université Libre de Bruxelles, Belgium
11:05-11:25	[O3.02] Emergence of <i>Escherichia coli</i> super clones with PBP3 insertions and clade defining ompC/F variations distinguishing ESBL, Non-ESBL and carbapenemase clones Naveen Kumar Devanga Ragupathi ^{*1,2} , Dhiviya Prabaa Muthurulandi Sethuvel ^{1,2} , Dhiviya Murugan ¹ , Karthick Vasudevan ¹ , Ramya Iyadurai ¹ , Balaji Veeraraghavan ^{1,3} , ¹ Christian Medical College, India, ² The University of Sheffield, UK, ³ Biofilms and Antimicrobial Resistance Consortium of ODA receiving countries (BARCOD), The University of Sheffield, UK	[O4.02] The substitution spectra of coronavirus genomes Diego Forni ^{*1} , Rachele Cagliani ¹ , Chiara Pontremoli ¹ , Mario Clerici ² , Manuela Sironi ¹ , ¹ Scientific Institute IRCCS E. MEDEA, Italy, ² University of Milan, Italy
11:25-11:45	[O3.03] <i>Staphylococcus haemolyticus</i> as a reservoir of AMR genes in the preterm infant gut microbiome Lisa Lamberte ^{*1} , Raymond Kiu ² , Robert Moran ¹ , Karolina Drodz ¹ , William Rowe ¹ , Lindsay Hall ^{2,3} , Willem van Schaik ¹ , ¹ University of Birmingham, UK, ² The Quadram Institute, UK, ³ Technical University of Munich, Germany	[O4.03] Potential variations in immune recognition of SARS-CoV2 epitopes across different ethnicities Namrata Pant [*] , Tungadri Bose, Nishal Kumar Pinna, Subhrajit Bhar, Anirban Dutta, Sharmila S. Mande, TCS Research, Tata Consultancy Services Limited, Pune, India
11:45-12:15	Break	
12:15-13:45	Plenary 2 Chairs: Erick Denamur, Katia Koelle	
12:15-12:45	[PL.05] Evolutionary history of pathogenic <i>Escherichia coli</i> Erick Denamur, <i>Université de Paris, France</i>	



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12:45-13:15	[PL.06] Population genomic structure of <i>Trypanosoma cruzi</i> Martin Llewellyn, <i>University of Glasgow, Scotland</i>	
13:15-13:45	[PL.07] SARS-CoV-2 phylodynamics, with and without phylogenies Katia Koelle, <i>Emory University, USA</i>	
13:45-14:30	Break	
14:30-15:50	O5. Parasite Evolution Chair: Martin Llewellyn	O6. Virus Evolution Chair: Martine Peeters
14:30-14:50	[O5.01] High diversity of lemur malaria parasites: Origin and diversification. M. Andreina Pacheco ^{*1} , Randall E Junge ² , Ananias A. Escalante ¹ , ¹ Temple University, USA, ² Columbus Zoo and Aquarium and The Wilds, Ohio, USA	[O6.01] Transmission of different RNA viruses, lentivirus and Influenza virus at the human-animal interface in natural habitat in India Nandi J.S ^{*1} , Rathore S. S ² , Mathur BRJ ³ , ¹ National Institute of Virology, India, ² Government Zoo, Jodhpur, Rajasthan, India, ³ Veterinary Services, Jodhpur, Rajasthan, India
14:50-15:10	[O5.02] Whole genome sequence comparative analyses of north African <i>Leishmania infantum</i> may reveal genetic and molecular determinants of the parasite tissue tropism. Ahmed S. Chakroun ^{*1} , Souheila Guerbouj ¹ , Philippe Leprohon ² , Emna Harigua ¹ , Akila Fathallah Mili ³ , Marc Ouellette ² , Ikram Guizani ¹ , ¹ Institut Pasteur de Tunis, Tunisia, ² Centre de Recherche du CHU de Québec, Canada, ³ Faculté de Médecine de Sousse, Tunisia	[O6.02] Natural oil blend formulation (NOBF) protects <i>Penaeus vannamei</i> Boone, 1931 from white spot syndrome virus (WSSV) and enhances the productivity in the culture ponds Rajeev Kumar Jha ^{1,2} , Haig Babikian ^{*1} , Yusef Babikyan ² , Ashutosh Dhramendra Deo ³ , Tigran Davtyan ⁴ , ¹ Rhea Natural Sciences, Indonesia, ² PT. Central Proteina Prima, Indonesia, ³ ICAR-Central Institute of Fisheries Education, India, ⁴ Analytical Laboratory Branch, Scientific Centre of Drug and Medical Technology Expertise, JSC, Yerevan, Armenia, Armenia
15:10-15:30	[O5.03] Sero-and Molecular Epidemiology of Camel Trypanosomosis in Northern Nigeria Shadrach Mamman ¹ , Dana'an Dakul ² , Jael Yohanna ² , Goni Dogo ² , Rine Reuben ^{*3} , ¹ Nigeria Institute of Trypanosomiasis and Onchocerciasis Research, Vom, Nigeria, ² University of Jos, Nigeria, ³ German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Germany	[O6.03] Impact and mitigation of reporting bias in discrete phylogeography inference: a simulation study applied to rabies in Morocco Maylis Layan ^{*1,2} , Simon Dellicour ^{3,4} , Nicola De Maio ⁵ , Hervé Bourhy ¹ , Guy Baele ⁴ , Simon Cauchemez ¹ , ¹ Institut Pasteur, France, ² Sorbonne Université, France, ³ Université Libre de Bruxelles, Belgium, ⁴ Rega Institute, KU leuven, Belgium, ⁵ European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, UK
15:30-15:50	[O5.04] Next Generation Sequencing (NGS) of the Mitochondrial Genome of <i>Cyclospora cayentanensis</i> from a Naturally Contaminated Blackberry Sample using Illumina AmpliSeq Technology Hediye Cinar ^{*1} , Laura Lalonde ² , Sonia Almeria ¹ , ¹ US Food and Drug Administration, USA, ² Canadian Food Inspection Agency Saskatoon Laboratory, Canada	[O6.04] A novel network method MMVC for analysis of WGS data unveils high-resolution linkages in poliovirus clusters: application to polio eradication Jiahui Tan ^{*1} , Yutong Zhao ¹ , Kun Zhao ² , Cara C. Burns ² , Dechao Tian ¹ , ¹ Sun Yat-sen University, China, ² Centers for Disease Control and Prevention, USA
15:50-16:15	Break	
16:15-17:15	Plenary 3 Chairs: Caitlin Pepperell, Cheryl Winkler	
16:15-16:45	[PL.08] Evolution of <i>Mycobacterium tuberculosis</i> Caitlin Pepperell, <i>University of Wisconsin-Madison, USA</i>	
16:45-17:15	[PL.09] APOL1: Evolution, epidemiology, and health disparities in African and the African Cheryl Winkler, <i>National Institutes for Health, USA</i>	

Thursday, 4 November 2021		
09:00-10:00	Plenary 4 Chairs: François Balloux, Zhengli Shi	
09:00-09:30	[PL.10] The changing landscape of SARS-CoV-2 genetic diversity François Balloux, University College London, UK	
09:30-10:00	[PL.11] Evolutionary Conservative of Receptor Usage of SARS-related Coronaviruses Zhengli Shi, Wuhan Institute of Virology, China	
10:00-10:45	Break	
10:45-12:25	O7. Evolution of <i>Mycobacterium tuberculosis</i> Chair: Zhenhua Yang	O8. Parasite Evolution Chair: Marion Wassermann
10:45-11:05	[O7.01] Description of a new ancestral sublineage of the <i>Mycobacterium tuberculosis</i> complex Lineage 2 in Japan Christophe Guyeux ¹ , Gaetan Senelle ¹ , Guislaine Refrégier ^{2,3} , Emmanuelle Cambau ^{4,5} , Christophe Sola ^{*2,6} , ¹ Univ. Bourgogne Franche-Comté (UBFC), France, ² Université Paris-Saclay, Saint-Aubin, France, ³ CNRS, AgroParisTech, France, ⁴ Université de Paris, France, ⁵ AP-HP, Laboratoire associé au Centre National de Référence Tuberculose, Paris, France, ⁶ Université de Paris, IAME, UMR1137, INSERM, Paris, France	[O8.01] Are cercarial emergence rhythms of the diurnal and nocturnal chronotypes of the parasite <i>Schistosoma mansoni</i> circadian ? Chrystelle Lasica ^{*1} , Gabriel Mouahid ¹ , Frédéric Chevalier ² , Winka Le Clec'h ² , Cristian Chaparro ¹ , Christoph Grunau ¹ , Boris A.E.S. Savassi ¹ , Salem Al Yafae ³ , Tim J Anderson ² , Hélène Moné ¹ , ¹ University of Montpellier, France, ² Texas Biomedical Research Institute, USA, ³ Dhofar Governorate, Oman
11:05-11:25	[O7.02] Use of whole genome sequencing to explore <i>Mycobacterium tuberculosis</i> complex circulating in a hotspot department in France Typhaine Billard-Pomares ^{*1,2} , Julie Marin ² , Pauline Quagliaro ³ , Frédéric Méchai ⁴ , Violaine Walewski ^{1,2} , Etienne Carbonnelle ^{1,2} , Samira Dziri ¹ , ¹ APHP, HUPSSD, Hôpital Avicenne, Service de Microbiologie clinique, France, ² INSERM UMR 1137-IAME, Université de Paris, Université Sorbonne Paris Nord, France, ³ APHP, HUPSSD, Hôpital Jean Verdier, Service de pédiatrie, France, ⁴ APHP, HUPSSD, Hôpital Avicenne, Service de Maladies infectieuses, France	[O8.02] The influence of snail host microbiome in trematode parasite resistance Ruben Schols ^{*1,2} , Tine Huyse ¹ , Ellen Decaestecker ³ , ¹ Royal Museum for Central Africa, Belgium, ² KU Leuven Kulak, Belgium, ³ Laboratory of Aquatic Biology, KU Leuven Kulak, Kortrijk,, Belgium
11:25-11:45	[O7.03] New emerging highly-drug resistant clusters of <i>Mycobacterium tuberculosis</i> Beijing genotype in Russia: phylogenomics and pathobiology Igor Mokrousov ^{*1} , Tatiana Vinogradova ² , Polina Khromova ³ , Marine Dogonadze ² , Natalia Zabolotnykh ² , Maria Badleeva ⁴ , Irina Yarusova ⁵ , Anna Vyazovaya ¹ , Oksana Pasechnik ⁶ , Svetlana Zhdanova ³ , ¹ St. Petersburg Pasteur Institute, Russia, ² St. Petersburg Research Institute of Phthisiopulmonology, Russia, ³ Scientific Centre of the Family Health and Human Reproduction Problems, Russia, ⁴ Buryat State University, Russia, ⁵ Clinical Anti-tuberculosis Dispensary, Omsk, Russia, ⁶ Omsk State Medical University, Russia	[O8.03] Molecular typing of <i>Strongyloides stercoralis</i> in Latin America, the clinical connection Silvia Analía Repetto ¹ , Juan Quarroz Braghini ¹ , Marikena Guadalupe Risso ¹ , Estela Inés Batalla ¹ , Daniel Ricardo Stecher ² , Mariela Fernanda Sierra ² , Juan Miguel Burgos ^{3,4} , Marcelo Víctor Radisic ⁵ , Stella Maris González Cappa ¹ , Paula Ruybal ^{*1} , ¹ Universidad de Buenos Aires, Argentina, ² Universidad de Buenos Aires, Argentina, ³ Universidad Nacional de San Martín, Argentina, ⁴ Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina, ⁵ División de Enfermedades Infecciosas, Instituto de Nefrología/Nephrology., Argentina
11:45-12:05	[O7.04] RDscan workflow for analyzing regions of difference (RDs) diversity of <i>Mycobacterium tuberculosis</i> complex	[O8.04] Epidemiology and distribution of <i>Giardia intestinalis</i> assemblages in humans in New South Wales, Australia



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	Dmitry Bespiatykh, Egor Shitikov*, <i>Federal Research and Clinical Center of Physical-Chemical Medicine of Federal Medical Biological Agency, Russia</i>	Patricia Zajaczkowski ^{*1} , Abela Mahimbo ² , Kate Alexander ³ , Rogan Lee ⁴ , Damien Stark ⁵ , Stephanie Fletcher-Lartey ⁶ , John T Ellis ⁷ , ¹ <i>University of Technology Sydney School of Life Sciences, Australia,</i> ² <i>University of Technology Sydney Faculty of Health, Australia,</i> ³ <i>South Western Sydney Local Health District Public Health Unit, Australia,</i> ⁴ <i>Centre for Infectious Diseases and Microbiology Lab Services (CIDLMS), Weastmeas Hospital, Australia,</i> ⁵ <i>SydPath, St Vincent's Hospital, Australia,</i> ⁶ <i>South Western Sydney Local Health District Public Health Unit, Australia,</i> ⁷ <i>University of Technology Sydney School of Life Sciences, Australia</i>
12:05-12:25	[07.05] Predominance of the <i>Mycobacterium tuberculosis</i> Beijing strain amongst children from a high TB burden township in South Africa Junaid Shaik ^{*1,2} , Prakash Jeena ¹ , Manormoney Pillay ¹ , ¹ <i>University of KwaZulu-Natal, South Africa,</i> ² <i>MANCOSA, South Africa</i>	[08.05] Completing the puzzle: the second version of the <i>Plasmodium gonderi</i> reference genome. Axl S. Cepeda ^{*1} , Zunping Luo ² , Steven A. Sullivan ³ , Jane M. Carlton ² , M. Andreina Pacheco ¹ , Ananias A. Escalante ¹ , ¹ <i>Temple University, USA,</i> ² <i>New York University, USA,</i> ³ <i>Center for Genomics and Systems Biology, New York University, New York, USA</i>
12:25-13:00	Break	
13:00-14:00	Plenary 5 Chairs: Zhenhua Yang, Martine Peeters	
13:00-13:30	[PL.12] The evolution of tuberculosis and HIV dual epidemic Zhenhua Yang, <i>University of Michigan, USA</i>	
13:30-14:00	[PL.13] COVID-19 epidemic and Coronaviruses in Africa Martine Peeters, <i>Institut de Recherche pour le Développement (IRD), Montpellier, France</i>	
14:00-14:45	Break	
14:45-15:45	O9. Virus Evolution Chair: Zhengli Shi	O10. Vector Biology and Evolution Chair: Patricia Dorn
14:45-15:05	[O9.01] Phylogeographic Analysis of a Densely Sampled Watermelon Mosaic Virus Outbreak in Southern France. Patrick Hoscheit*, Imane Boualaoui, Cécile Desbiez, <i>INRAE, France</i>	[O10.01] Out of Asia? Vector switches leading to the expansion of Eurasian borreliosis disease bacteria Robert E. Rollins ^{*1} , Kozue Sato ² , Minoru Nakao ³ , Ricardo J. Pereira ¹ , Sergey Kovalev ⁴ , Gabriele Margos ⁵ , Volker Fingerle ⁵ , Hiroki Kawabata ² , Noémie S. Becker ¹ , ¹ <i>LMU, Germany,</i> ² <i>National Institute for Infectious Disease, Japan,</i> ³ <i>Asahikawa Medical University, Japan,</i> ⁴ <i>Ural Federal University, Russia,</i> ⁵ <i>Bayerisches Landesamt für Gesundheit und Lebensmittelsicherheit, Germany</i>
15:05-15:25	[O9.02] PRRSV-2 genetic diversity in piglets born to sows during an outbreak Mariana Kikuti ^{*1} , Carles Vilalta ^{1,2} , Juan Sanhueza ^{1,3} , Nakin Pamornchainavakul ¹ , Jessica Kevill ¹ , Igor Paploski ¹ , Ross Kiehne ⁴ , Kimberly VanderWaal ¹ , Declan Schroeder ¹ , Cesar Corzo ¹ , ¹ <i>University of Minnesota, USA,</i> ² <i>Upnorth Analytics, Spain,</i> ³ <i>Universidad Católica de Temuco, Chile,</i> ⁴ <i>Swine Vet Center, USA</i>	[O10.02] Genome dynamics in <i>Rhodnius</i> species, vectors of Chagas disease Marie Merle ^{*1} , Jonathan Filée ¹ , Héloïse Bastide ¹ , Jader de Oliveira ^{2,3} , Carlos Eduardo Almeida ⁴ , João Aristeu da Rosa ³ , Florence Mougél ¹ , Myriam Harry ¹ , ¹ <i>Université Paris-Saclay, France,</i> ² <i>Universidade de São Paulo (USP), Brazil,</i> ³ <i>São Paulo State University (UNESP), Brazil,</i> ⁴ <i>University of Campinas – UNICAMP, São Paulo, Brazil/Universidade Federal da Bahia (UFBA) - Salvador, Brazil</i>
15:25-15:45	[O9.03] Diversity of Myxovirus resistance gene (Mx) and its relation with avian influenza infection in indigenous chicken Jahangir Alam ^{*1} , Joyanta Halder ^{1,2} , Md. Rezuhanul Islam ² , Nandini Sarkar ^{1,3} , Ishrat Jabeen ³ , M.M. Kamal Hossain ¹ , Rubaya Rubaya ¹ , Nusrat Jahan ¹ , Md. Abdul	[O10.03] Evidence of circulation of West Nile virus in <i>Culex pipiens</i> mosquitoes and horses in Morocco Najlaa Assaid ^{*1} , Laurence Mousson ² , Sara Moutailler ³ , Soukaina Arich ¹ , Khadija Akarid ⁴ , Maëlle Monier ³ , Cécile Beck ³ , Sylvie Lecollinet ⁵ , Anna-Bella Failloux ² , M'hammed Sarih ¹ , ¹ <i>Institut Pasteur du Maroc,</i>



MEEGID XV

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	Alim ¹ , Anjuman Ara Bhuyan ¹ , ¹ National Institute of Biotechnology, Bangladesh, ² Islamic University, Bangladesh, ³ North South University, Bangladesh	Morocco, ² Institut Pasteur, France, ³ Université Paris-Est, France, ⁴ University of Hassan II Casablanca (UH2C), Morocco, ⁵ UMR1161 Virologie, INRAE, ANSES, Ecole Nationale Vétérinaire d'Alfort, Université Paris-Est, Maisons-Alfort, France, France
15:45-16:00	Break	
16:00-17:00	Author Workshop	
Friday, 5 November 2021		
09:00-10:30	Plenary 6 and O11 COVID-19 Chairs: Manuela Sironi, Fernando Gonzalez-Candelas	
09:00-09:30	[PL.14] Predominant clonal evolution of pathogenic microorganisms at the macro- and microevolutionary levels Michel Tibayrenc, Institut de recherche pour le Développement, France	
09:30-09:50	[O11.01] Herd immunity against severe acute respiratory syndrome Coronavirus 2 infection in 10 communities, Qatar Andrew Jeremijenko ^{*1} , M. Alishaq, ani, A. Al Khal, E. Al Kuwari, A. Al-Mohammed, N.H.A. Al Molawi, H.M. Al Naomi, A.A. Butt, P. Coyle, R.A. El KahloA.-B. Abou-Samra, J.A.A.A. Al Ajmi, N.A.A. Al Ansari, Z. Al Kanaut, I. Gillani, A.H. Kaleeckal, N.A. Masoodi, A.G. Thomas, H. Nafady-Hego, A.N. Latif, R.H. Shaik, N.B.M. Younes ² , H.H. Ayoub, H.F. Abdul Rahim, H.M. Yassine ³ , H. Chemaitelly, L.J. Abu-Raddad ^{4,5} , Hanaa Nafady-Hego ⁶ , H.E. Al Romaihi, M.H. Al-Thani, R. Bertollini ⁷ , M.G. Al Kuwari ⁸ , ¹ teledr1@gmail.com, Australia, ² Hamad Medical Corporation, Qatar, ³ Qatar University Qatar, ⁴ Weill Cornell Medicine-Qatar of Cornell University, Qatar, ⁵ World Health Organization Collaborating Centre for Disease Epidemiology Analytics on HIV/AIDS, Sexually Transmitted Infections, Qatar, ⁶ Assiut University, Egypt, ⁷ Ministry of Public Health, Qatar, ⁸ Primary Health Care Corporation, Qatar	
09:50-10:10	[O11.02] Development and Implementation of a Rapid and Extraction-Free Saliva LAMP Test for Workplace Surveillance and Reporting Zhuru Li [*] , Barry Cohen, William Jack, Bradley Langhorst, Jacob Miller, Catherine Poole, Richard Roberts, Nathan Tanner, Yinhua Zhang, Clotilde Carlow, <i>New England Biolabs Inc, USA</i>	
10:10-10:30	[O11.03] Factors associated to SARS-COV-2 infection in Mexican pregnant women aged 18-49 years old Daniel López-Hernández [*] , <i>Family Medicine Clinic "División del Norte". ISSSTE., Mexico</i>	
10:30-11:00	Break	
11:00-12:15	Plenary 7, Closing Ceremony and Awards Chairs: Michel Tibayrenc, Manuela Sironi, Fernando Gonzalez-Candelas	
11:00-11:30	[PL.15] Genomics and Evolution of Antimicrobial Resistance: <i>Pseudomonas aeruginosa</i> as a Model Organism Alex van Belkum, Biomerieux, France	
11:30-12:00	[PL.16] From HIV to COVID: leveraging collaborations for developing countermeasures to emerging pathogens Robert Garry, Tulane University, New Orleans, USA	
12:00-12:15	Closing ceremony & Awards	