

Young Investigator Award Session C

Sunday, October 28, 2018, 10:00 am - 3:00 pm

Sheraton - Rhythms III (2nd Floor)

The Young Investigator Award is presented to outstanding young researchers during the Annual Meeting. This award encourages developing young scientists to pursue careers in various aspects of tropical disease research. Support these young scientists by attending their presentations during this session.

Presentation Number	Title	Author Block
	Judge	Sasisekhar Bennuru <i>National Institutes of Health, Bethesda, MD, United States</i>
	Judge	Nicholas A. Bergren <i>Colorado State University, Fort Collins, CO, United States</i>
	Judge	Nicole Gottdenker <i>Odum School of Ecology, University of Georgia, ATHENS, GA, United States</i>
	Judge	Prakash Srinivasan <i>Johns Hopkins School of Public Health, Baltimore, MD, United States</i>
16	Introducing <i>S. mansoni</i> AMP-activated Protein Kinase (AMPK): Developmental Regulation, Activity, and Role in Schistosome Energy Metabolism	Kassandra S. Hunter <i>Uniformed Services University, North Bethesda, MD, United States</i>
264	Selection of seven-mutation <i>Pfcr</i>-<i>Pfmdr</i>1 genotype after scaling seasonal malaria chemoprevention with sulphadoxine-pyrimethamine and amodiaquine in Mali	Hamma I. Maiga¹ , Amadou Bamadio ² , Aliou Traore ² , Nouhoum Diallo ² , Modibo Diarra ² , Issaka Sagara ² , Samba Coumare ² , Soma Bahanan ³ , Boubou Sangare ² , Hamidou Niangaly ² , Aboubecrine Haidara ² , Yeyia Dicko ² , Aly Tembely ² , Francois Daou ² , Djibril Traore ² , Michel Vaillant ⁴ , Alassane Dicko ² , Estrela Lasry ³ , Ogobara K. Doumbo ² , Abdoulaye A. Djimde ² <i>¹INRSP-Mali/MRTC, Bamako, Mali, ²MRTC, Bamako, Mali, ³MSF, Bamako, Mali, ⁴LIH, Luxembourg, Luxembourg</i>
350	Whole genome sequencing to measure complexity of infection and genetic diversity in	Sonia Agrawal¹ , Fang Huang ² , Biraj Shrestha ¹ , Matthew Adams ¹ , Sandra Ott ³ , Lisa Sadzewicz ³ , Hui Lui ⁴ , David Serre ³ , Shannon

	<i>Plasmodium vivax</i> clinical isolates from the China-Myanmar border	Takala-Harrison ¹ , Myaing Nyunt ⁵ , Joana Carneiro Da Silva ³ , Christopher Plowe ⁵ ¹ <i>Institute for Global Health, University of Maryland School of Medicine, Baltimore, Baltimore, MD, United States</i> , ² <i>National Institute of Parasitic Diseases, Chinese Centre for Disease Control and Prevention, Shanghai, China</i> , ³ <i>Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, Baltimore, MD, United States</i> , ⁴ <i>Yunnan Institute of Parasitic Diseases, Puer, China</i> , ⁵ <i>Global Health Institute, Duke University, Durham, NC, United States</i>
866	Genome-wide association study identifies genes underlying dengue virus susceptibility in wild-type <i>Aedes aegypti</i> fed on viremic human blood	Laura B. Dickson¹ , Albin Fontaine ¹ , Sarah H. Merklings ¹ , Benjamin R. Evans ² , Andrea Gloria-Soria ² , Mo Li ² , Xiaoqing Yu ² , Kuang-Yao Lee ² , Lauren B. Carrington ³ , Cameron P. Simmons ⁴ , Hongyu Zhao ² , Jeffrey R. Powell ² , Louis Lambrechts ¹ ¹ <i>Pasteur Institute, Paris, France</i> , ² <i>Yale University, New Haven, CT, United States</i> , ³ <i>Oxford University Clinical Research Unit, Ho Chi Minh City, Viet Nam</i> , ⁴ <i>Monash University, Monash, Australia</i>
878	Upgrade of a physical genome map for <i>Aedes aegypti</i>	Atashi Sharma¹ , Vladimir Timoshevskiy ² , Wu Yang ¹ , Igor Sharakhov ¹ , Zhijian (Jake) Tu ¹ , Maria Sharakhova ¹ ¹ <i>Virginia Tech, Blacksburg, VA, United States</i> , ² <i>University of Kentucky, Lexington, KY, United States</i>
927	Structural proteins prME dictate sexual transmission potential of ZIKV in an immunocompetent mouse model	Erin M. McDonald¹ , Nisha K. Duggal ² , Jana M. Ritter ³ , Aaron C. Brault ¹ ¹ <i>Division of Vector-Borne Diseases, Centers for Disease Control and Prevention, Fort Collins, CO, United States</i> , ² <i>Department of Biomedical Sciences & Pathobiology, Virginia-Maryland College of Veterinary Medicine, Blacksburg, VA, United States</i> , ³ <i>Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA, United States</i>

1053	Genome-wide differences in <i>P. falciparum</i> parasites in Malawian children and adults	Zalak Shah¹ , Kara Moser ¹ , Matthew Adams ¹ , Andrea Buchwald ¹ , Karl Seydel ² , Don Mathanga ³ , David Serre ¹ , Miriam K. Laufer ¹ , Joana C. Silva ¹ , Shannon Takala-Harrison ¹ <i>¹University of Maryland School of Medicine, Baltimore, MD, United States, ²Michigan State University College of Osteopathic Medicine, East Lansing, MI, United States, ³University of Malawi College of Medicine, Blantyre, Malawi</i>
1170	Minimal genetic diversity and spatial clustering of cholera cases in the Kathmandu Valley: Implications for a ring-vaccination strategy	Mellisa Roskosky , Mohammad Ali, Jyoti Acharya, Amanda Debes, Colin Stine, David Sack <i>Johns Hopkins University, Baltimore, MD, United States</i>
2018	Study of changes in the transcriptome of mouse bladder following bladder wall injection of <i>Schistosoma haematobium</i> eggs	Kenji Ishida , Evaristus Mbanefo, Loc Le, Michael Hsieh <i>Biomedical Research Institute, Rockville, MD, United States</i>
2051	Extreme diversity and population structure of <i>var</i> genes can explain why immunity to the blood stages of <i>Plasmodium falciparum</i> is non-sterilizing	Shazia Ruybal-Pesántez¹ , Kathryn E. Tiejde ¹ , Gerry Tonkin-Hill ² , Shai Pilosof ³ , Abraham R. Oduro ⁴ , Michael F. Duffy ¹ , Kwadwo A. Koram ⁵ , Mercedes Pascual ³ , Karen P. Day ¹ <i>¹University of Melbourne, Melbourne, Australia, ²Walter and Eliza Hall Institute, Melbourne, Australia, ³University of Chicago, Chicago, IL, United States, ⁴Navrongo Health Research Centre, Navrongo, Ghana, ⁵Noguchi Memorial Institute for Medical Research, Legon, Ghana</i>
2069	Transcriptome profiling unravels novel ligands required for <i>Plasmodium vivax</i> infections in <i>Saimiri</i> monkey - Implications on <i>Plasmodium vivax</i> infections in Africa	Karthigayan Gunalan¹ , Juliana M. Sa ¹ , Roberto R. de Moraes Barros ¹ , Kishore Kanakabandi ² , Sarah L. Anzick ² , Ramoncito L. Caleon ¹ , J. Patrick Mershon ¹ , Craig Martens ² , Thomas E. Wellems ¹ , Louis H. Miller ¹ <i>¹National Institutes of Health, Rockville, MD, United States, ²National Institutes of Health, Hamilton, MT, United States</i>
2081	Characterization of Genetic Variation Between Host-specific <i>Theileria parva</i> Populations	Nicholas C. Palmateer¹ , Claudia A. Daubenberger ² , Richard P. Bishop ³ , Joana C. Silva ¹

		<i>¹Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD, United States, ²Swiss Tropical and Public Health Institute and University of Basel, Basel, Switzerland, ³Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, United States</i>
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