

PROGRAM

THURSDAY, September 7—3:00 PM

SESSION 1

Chairperson: **D.M. Bird**, North Carolina State University, Raleigh
D.F. Smith, University of York, United Kingdom

Opperman, C.H., Bird, D.M., Center for the Biology of Nematode Parasitism (CBNP) Sequencing Group, North Carolina State University, Raleigh: The complete genome sequence of *M. hapla*, a clade IV tylenchid plant-parasitic nematode. 1

Daily, J.P.,^{1,5} Le Roch, K.G.,⁴ Ndiaye, D.,³ Zhou, Y.,⁴ Ndir, O.,³ Mboup, S.,³ Scandfeld, D.,⁶ Tamayo, P.,⁶ Mesirov, J.,⁶ Winzeler, E.A.,^{2,4} Wirth, D.F.,¹ ¹Dept. of Immunology and Infectious Disease, Harvard School of Public Health, ⁵Dept. of Medicine, Brigham and Women's Hospital, Boston, ⁶Eli and Edyth Broad Institute of MIT and Harvard, Cambridge, Massachusetts; ²Dept. of Cell Biology, Scripps Research Institute, La Jolla, ⁴Genomics Institute of the Novartis Research Foundation, San Diego, California; ³Faculty of Medicine and Pharmacy, Cheikh Anta Diop University, Dakar, Senegal: Analysis of in vivo derived *P. falciparum* transcriptome and host features. 2

Koumandou, V.L., Field, M.C., Dept. of Pathology, University of Cambridge, United Kingdom: Developmental regulation of the endocytic system in the parasite *T. brucei*. 3

Gilchrist, C.A.,¹ Houpt, E.,¹ Trapaidze, N.,² Fei, Z.,³ Crasta, O.,³ Sobral, B.,³ Asgharpour, A.,¹ Evans, C.,³ Martino-Catt, S.,³ Baba, D.J.,¹ Stroup, S.,¹ Hamano, S.,¹ Ehrenkaufer, G.,⁴ Okada, M.,⁵ Singh, U.,⁴ Nozaki, T.,⁵ Mann, B.J.,¹ Petri, W.A.,¹ ¹University of Virginia, Charlottesville, ³Virginia Bioinformatics Institute, Blacksburg; ²National Center for Disease Control of Georgia, Tbilisi; ⁴Stanford University School of Medicine, California; ⁵Gunma University Graduate School of Medicine, Japan: Microarray-mediated transcriptome comparison of *E. histolytica* trophozoites in vivo and in vitro. 4

- Smith, D.F.,¹ Peacock, C.,² Berriman, M.,² Harris, D.,² Seeger, K.,² Depledge, D.,¹ Oyola, S.,¹ Kaye, P.M.,¹ Hilley, J.,³ Mottram, J.C.,³
¹Immunology and Infection Unit, Dept. of Biology, University of York and Hull York Medical School, ²Wellcome Trust Sanger Institute, Hinxton, ³Wellcome Centre for Molecular Parasitology, Biomedical Research Centre, University of Glasgow, United Kingdom: Comparative functional genomics of *Leishmania* species. 5
- Connolly, B., Robinson, M., Greig, R., Cwiklinski, K., Institute of Medical Sciences, University of Aberdeen, United Kingdom: Proteins acting at the host-parasite interface in infections with the nematode *Trichinella*. 6
- Turner, M., Tait, A., MacLeod, A., Morrison, L., Tweedie, A., McLellan, S., Sweeney, L., Cooper, A., Div. of Infection and Immunology, WCMP, University of Glasgow, United Kingdom: Genetic analysis in trypanosome parasites. 7
- THURSDAY, September 7—7:30 PM
- SESSION 2**
- Chairperson:** **B. Wren**, London School of Hygiene and Tropical Medicine, United Kingdom
S. Andersson, Uppsala University, Sweden
- Wren, B.W., Champion, O.L., Howard, S., Stabler, R., Gaunt, M., Dept. of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, United Kingdom: Application of comparative phylogenomics to study the evolution and host adaptation of pathogens. 8
- Chakravarty, S.D.,¹ Zhu, G.,^{1,2} Tsai, M.C.,¹ Wang, J.,² Xu, J.,² Mohan, V.P.,² Chan, J.,^{1,2} Depts. of ¹Microbiology and Immunology, ²Medicine/Infectious Diseases, Albert Einstein College of Medicine, Bronx, New York: Neutralization of tumor necrosis factor leads to increased pulmonary inflammation in a chronic murine tuberculosis model. 9
- Banaiee, N., New York University Medical Center, New York: *M. tuberculosis* lipoprotein processing is essential for cell wall integrity and virulence in mice. 10

Andersson, S.G.E.,¹ Berglund, E.,¹ Brindefalk, B.,¹ Calteau, A.,¹ Cho, N.-H.,² Choi, M.-S.,² Darby, A.,¹ Frank, C.,¹ Fuxelius, H.-H.,¹ Kim, I.-S.,² Klasson, L.,¹ Lindroos, H.,¹ Sällström, B.,¹ Viklund, J.,¹ Vinnere-Pettersson, O.,¹ ¹Program of Molecular Evolution, Dept. of Evolution, Genomics and Systematics, Evolutionary Biology Center, Uppsala University, Sweden; ²Dept. of Microbiology and Immunology, Seoul National University College of Medicine, Korea: Genome evolution of vector-borne intracellular pathogens. 11

Skindersoe, M., Givskov, M., Centre for Biomedical Microbiology, BioCentrum-DTU, Technical University of Denmark, Lyngby: Host-pathogen interaction—Cross talk between components of the immune defense and *P. aeruginosa*. 12

Ma, W., Stavrinides, J., Guttman, D.S., Dept. of Botany, University of Toronto, Canada: *P. syringae* type II effectors reveal the mechanism of a coevolutionary arms race. 13

Wollert, T.,^{1,4} Pasche, B.,² Gruber, A.D.,³ Rochon, M.,⁴ van den Heuvel, J.,⁴ Heinz, D.W.,⁴ Lengeling, A.,² Schubert, W.-D.,¹ ¹Molecular Host-Pathogen Interactions, ⁴Div. of Structural Biology, ²Infection Genetics, Div. of Microbiology, German Research Centre for Biotechnology (GBF), Braunschweig, ³Dept. of Veterinary Pathology, Freie Universität, Berlin, Germany: Structure-based pathogen design—A new murine listeriosis model. 14

FRIDAY, September 8—9:00 AM

SESSION 3

Chairperson: **J.M. Musser**, The Methodist Hospital, Houston, Texas
P. Keim, Northern Arizona University, Flagstaff

Musser, J.M., Center for Molecular and Translational Human Infectious Diseases Research, Methodist Hospital Research Institute, Houston, Texas: Molecular events contributing to group A *Streptococcus* clone emergence. 15

- Beatson, S.,^{1,2} Tobe, T.,³ Taniguchi, H.,⁴ Abe, H.,³ Bailey, C.,¹ Fivian, A.,¹ Younis, R.,¹ Matthews, S.,¹ Marches, O.,⁵ Frankel, G.,⁵ Hayashi, T.,⁶ Pallen, M.,¹ ¹Medical School, University of Birmingham, ⁵Div. of Cell and Molecular Biology, Imperial College, London, United Kingdom; ²School of Molecular and Microbial Sciences, University of Queensland, Australia; ³Graduate School of Medicine, Osaka University, ⁴RIKEN, Hyogo, ⁶Frontier Science Research Center, University of Miyazaki, Japan: An extensive repertoire of type III secretion effectors in *E. coli* O157:H7 and the role of lambdoid bacteriophages in their dissemination. 16
- McCarthy, N.D.,¹ Colles, F.M.,¹ Dingle, K.E.,² Bagnall, M.C.,⁴ Manning, G.,⁴ Maiden, M.C.J.,¹ Falush, D.,³ ¹Dept. of Zoology, ²Nuffield Dept. of Clinical Sciences, ³Dept. of Statistics, University of Oxford, ⁴Veterinary Laboratories Agency, Surrey, United Kingdom: Population genetic approaches to assigning the source of human pathogens—Host associated genetic import in *C. jejuni*. 17
- Keim, P., Translational Genomics Research Institute, Dept. of Biological Sciences, Northern Arizona University, Flagstaff: Geographic-genetic patterns in three recent emerged pathogens—*B. anthracis*, *F. tularensis* and *Y. pestis*. 18
- Ridley, A.M.,¹ Bagnall, M.,¹ Newell, D.G.,¹ van der Wal, F.,² Wagenaar, J.,² Bang, D.D.,³ Krogfelt, K.,⁴ Gierczynski, R.,⁵ Echeita, A.,⁶ Bartelt, E.,⁷ Alter, T.,⁷ Owen, R.,⁸ Olsson-Engvall, E.,⁹ ¹Veterinary Laboratories Agency, Surrey, ⁸Health Protection Agency Centre for Infections, London, United Kingdom; ²Animal Sciences Group, Wageningen, The Netherlands; ³Danish Institute for Food and Veterinary Research, Aarhus, ⁴Statens Serum Institut, Copenhagen, Denmark; ⁵National Institute of Hygiene, Warsaw, Poland; ⁶Servicio de Bacteriología Centro Nacional de Microbiología, Madrid, Spain; ⁷Federal Institute for Risk Assessment, Berlin, Germany; ⁹National Veterinary Institute, Uppsala, Sweden: Identification of molecular markers of pathogenicity for *C. jejuni* in a well characterized international strain set. 19
- Talaat, A.M., Immel, S.K., Vu, E., Animal Health and Biomedical Sciences, University of Wisconsin-Madison: Global perspective on virulence of *M. paratuberculosis* isolates and their evolution. 20

Mohamed, J.A.,¹ Jiang, Z.-D.,² DuPont, H.L.,^{1,2} Belkind-Gerson, J.,³ Martinez-Sandoval, F.,⁴ Guo, D.,¹ Okhuysen, P.C.,^{1,2} ¹School of Medicine, ²School of Public Health, University of Texas, Houston; ³Instituto Nacional de Salud Publica, Cuernavaca, ⁴Universidad Autonoma de Guadalajara, Mexico: A single nucleotide polymorphism (SNP) in the exon15 region of the lactoferrin gene (LTFEx15) is associated with traveler's diarrhea (TD). 21

FRIDAY, September 8—2:00 PM

SESSION 4

Chairperson: **J. Berman**, University of Minnesota, Minneapolis
T. Palzkill, Baylor College of Medicine, Houston, Texas

Berman, J., Barkai, N., Bergmann, S., Ihmels, J., University of Minnesota, Minneapolis: Global analysis of transcription patterns in the human fungal pathogen *C. albicans*. 22

Lucas, S.J.,¹ Schröder, M.,² Bowie, A.,² Smith, G.L.,¹ Imperial College, London, United Kingdom; ²Trinity College, Dublin, Ireland: Vaccinia virus shapes the host immune response by inhibiting intracellular signaling pathways. 23

Philips, J.A.,¹ Wang, H.,¹ Rubin, E.J.,² Perrimon, N.P.,¹ ¹Dept. of Genetics, Harvard Medical School, ²Dept. of Immunology and Infectious Diseases, Harvard School of Public Health, Boston, Massachusetts: Genome-wide RNAi screen identifies role for ESCRT factors in mycobacterial phagosome maturation. 24

Houben, E.N.G., Walburger, A., Pieters, J., Biozentrum, University of Basel, Switzerland: Translational control of a virulence factor in mycobacteria. 25

Brinkman, M.,¹ Pettersson, J.,¹ Weinstock, G.,¹ Norris, S.J.,² Palzkill, T.,¹ ¹Baylor College of Medicine, ²University of Texas Health Science Center, Houston: Genome scale identification of *T. pallidum* antigens and fibronectin binding proteins. 26

- van Baarlen, P.,^{1,5} Troost, F.,^{1,2} Pavan, S.,³ Siezen, R.,^{1,4,5}
 Kleerebezem, M.,^{1,4} Wageningen Centre for Food Sciences,² Dept.
 of Internal Medicine and Gastroenterology, Maastricht University,
³TNO Nutrition and Food Research, Zeist,⁴ NIZO Food Research,
 Ede,⁵ CMBI, Radboud University, Nijmegen, The Netherlands:
 Comprehensive transcriptome dataset interpretation to disclose
 functional responses of the human intestinal mucosa to interactions
 with *L. plantarum*. 27
- MacLean, J.,¹ Li, K.,¹ Krishnan, K.,² Fang, R.,¹ Petrauskene, O.V.,¹
 Purkayastha, B.,¹ Manohar, C.F.,³ Furtado, M.R.,¹ Applied
 Biosystems, Foster City,² University of California, Davis,³ Lawrence
 Livermore National Laboratory, California: An integrated approach
 for analysis of the interferon (IFN) induced gene regulatory network. 28
- Woelk, C.H.,¹ Good, B.M.,⁴ Lozach, J.,² Ashbaugh, M.,³ Viriyakosol,
 S.,³ Kirkland, T.N.,³ Depts. of ¹Pathology,² Cellular and Molecular
 Medicine,³ Pathology and Medicine, University of California, San
 Diego;⁴ James Hogg iCAPTURE Centre for Cardiovascular and
 Pulmonary Research, St. Paul's Hospital, University of British
 Columbia, Vancouver, Canada: A reverse vaccinology approach to
 vaccine design for the pathogenic fungus *Coccidioides*. 29

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SESSION 5 POSTER SESSION

- Andersen, M.T.,¹ Ingmer, H.,¹ Mulholland, F.,² Jørgensen, K.,¹ Wells,
 J.,² Brøndsted, L.,¹ Dept. of Veterinary Pathobiology, Royal
 Veterinary and Agricultural University, Copenhagen, Denmark;
²Institute of Food Research, Norwich, United Kingdom: Conserved
 ATP-dependent proteases of *C. jejuni*—Contribution to stress
 tolerance and virulence. 30
- Ascenso, R.M.T., Afonso, R.M., Leite, R.B., Cancela, M.L., CCMAR,
 University of Algarve, Faro, Portugal: Identification of differentially
 expressed target genes involved in *Perkinsus*-host interaction—
 Comparison of two alternative SSH methods. 31
- Binnewies, T., Center for Biological Sequence Analysis, DTU, Lyngby,
 Denmark: Prediction of bacterial pathogenicity networks. 32

- Bojesen, A.M., Kristensen, B.M., Dept. of Veterinary Pathobiology, Royal Veterinary and Agricultural University, Copenhagen, Denmark: Identification of a *Gallibacterium* RTX toxin gene cluster responsible for bovine erythrocyte lysis. 33
- Borenshtein, D.,¹ Fry, R.C.,^{1,3} Groff, E.B.,^{1,2} Nambiar, P.R.,² Fox, J.G.,^{1,2} Schauer, D.B.,^{1,2} ¹Dept. of Biological Engineering, ²Div. of Comparative Medicine, ³Center for Environmental Health Sciences, Massachusetts Institute of Technology, Cambridge: Global transcriptome analysis of diarrhea as a cause of mortality in a mouse model of colitis. 34
- Bozdech, Z., Chaal, B., Preiser, P., Hu, G., School of Biological Sciences, Nanyang Technological University, Singapore: Microarray in plasmodium research. 35
- Brown, A., Kamara, M., Gartner, S., Dept. of Neurology, Johns Hopkins University School of Medicine, Baltimore, Maryland: Isolation of messages selectively expressed in HIV-infected primary human macrophages. 36
- de Buhr, M.F.,¹ Mähler, M.,¹ Hansen, W.,² Westendorf, A.M.,² Buer, J.,² Hedrich, H.J.,¹ Bleich, A.,¹ ¹Central Animal Facility and Institute for Animal Science, Hannover Medical School, ²German Research Centre for Biotechnology, Braunschweig, Germany: In search of modifier genes for experimental IBD—*Cd14* as a candidate. 37
- Falush, D., Dept. of Statistics, University of Oxford, United Kingdom: Bacterial microevolution. 38
- Fedynak, A., Hsiao, W., Brinkman, F.S.L., Dept. of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, Canada: Quantifying global trends in virulence and pathogen-specific genes. 39
- Gadsby, N., Carter, R., Institute of Immunity and Infection Research, University of Edinburgh, United Kingdom: Investigating the genetic basis for the difference in growth rate between two strains of the rodent malaria parasite *P.c.adami*. 40
- Gaunt, M.W., London School of Hygiene and Tropical Medicine, United Kingdom: Zoonose phylogenomics and *T. cruzi* evolution. 41
- Grinde, B., Gayorfar, M., Hoddevik, G., Dept. of Virology, Norwegian Institute of Public Health, Oslo: Modulation of gene expression in a human cell line caused by poliovirus, vacciniavirus, and interferon. 42

- Hain, T.,¹ Steinweg, C.,¹ Kuenne, C.T.,¹ Billion, A.,¹ Ghai, R.,¹ Subhra, S.,¹ Domann, E.,¹ Kärst, U.,² Goesmann, A.,³ Bekel, T.,³ Bartels, D.,³ Kaiser, O.,³ Meyer, F.,³ Pühler, A.,⁴ Weisshaar, B.,⁵ Wehland, J.,² Liang, C.,⁶ Dandekar, T.,⁶ Lampidis, R.,⁷ Kreft, J.,⁷ Goebel, W.,⁷ Chakraborty, T.,¹ ¹Institute for Medical Microbiology, Justus-Liebig-University, Giessen, ²Dept. of Cell Biology, Gesellschaft für Biotechnologische Forschung GmbH, Braunschweig, ³Bioinformatics Resource Facility, Centrum für Biotechnology, ⁴Lehrstuhl für Genetik, ⁵Lehrstuhl für Genomforschung, University of Bielefeld, ⁶Lehrstuhl für Bioinformatik, ⁷Lehrstuhl für Mikrobiologie, University of Würzburg, Germany: Whole genome sequence of *L. welshimeri* reveals common steps in genome reduction with *L. innocua* as compared to *L. monocytogenes*. 43
- Huang, M., Tan, Y.J.T., Tan, C.Y., Ong, C.T., Zheng, F.H., Qian, F., Wen, Z.L., Institute of Molecular and Cell Biology, Singapore: Molecular dissection of the hematopoietic and angiogenic activities in the bHLH domain of the transcription factor Scf/Tal-1 in zebrafish. 44
- Johnston, K., Shields, D., Clinical Bioinformatics, Conway Institute, University College Dublin, Ireland: Bacterial-host interaction motifs. 45
- Kim, Y.R., Rhee, J.H., National Research Laboratory of Molecular Microbial Pathogenesis and Clinical Vaccine R&D Center, Chonnam National University Medical School, Gwangju, Korea: A study on the pathomechanism of a *V. vulnificus* RTX toxin and development of a live attenuated vaccine. 46
- Lazarev, V.N., Shkarupeta, M.M., Kostryukova, E.S., Levitskii, S.A., Basovskii, Y.I., Govorun, V.M., Research Institute for Physico-Chemical Medicine, Ministry of Health and Social Development of Russian Federation, Moscow: Analysis of *C. trachomatis* Inc proteins cellular localization during expression of their genes in HeLa cell line. 47
- Pasini, E.,¹ Khan, S.,² Kirkegaard, M.,³ Lasonder, E.,⁴ Berry, A.,⁵ Berriman, M.,⁵ Zeeman, A.,¹ Janse, C.,² Mann, M.,³ Waters, A.,² Thomas, A.,¹ ¹Biomedical Primate Research Centre, Rijswijk, ²Dept. of Parasitology, Leiden University Medical Center, ⁴University of Nijmegen, The Netherlands, ³University of Southern Denmark, Odense; ⁵Wellcome Trust Sanger Institute, Hinxton, United Kingdom: Comparative analysis of three malaria host/parasite associations—In depth proteomes for both erythrocytes and merozoites of human, monkey and rodent origin. 48

Pattaradilokrat, S., Culleton, R., Cheesman, S., Carter, R., School of Biological Sciences, University of Edinburgh, United Kingdom: Identifying genetic determinants controlling growth-rate of malaria parasite.	49
Schiellerup, P., Locht, H., Krogfelt, K.A., Statens Serum Institut, Copenhagen, Denmark: HLA-B27 is not a marker for susceptibility and severity of reactive arthritis after <i>Campylobacter</i> and <i>E. coli</i> enteritis.	50
Shin, H., Mally, M., Kuhn, M., Paroz, C., Cornelis, G.R., Biozentrum, University of Basel, Switzerland: Escape from immune surveillance of <i>C. canimorsus</i> .	51
van Ulsen, P., ¹ Rutten, L., ² Tommassen, J., ¹ Depts. of ¹ Molecular Microbiology, ² Crystal and Structural Chemistry, Utrecht University, The Netherlands: Two partner secretion systems of <i>N. meningitidis</i> .	52
Vegge, C.S., Brøndsted, L., Ingmer, H., Dept. of Veterinary Pathobiology, Royal Veterinary and Agricultural University, Fredriksberg, Denmark: Exploring the chemotactic attraction of <i>C. jejuni</i> in chicken colonization.	53
Vohra, P.K., Thomas, C.F., Thoracic Diseases Research Unit, Div. of Pulmonary and Critical Care Medicine, Mayo Clinic College of Medicine, Rochester, Minnesota: Pneumocystis and host lung signal transduction gene alterations during infection.	54
Wang, L., ¹ Khadijah, S., ² Law, Y.C., ² Tay, F., ² Liu, D., ^{1,2} ¹ School of Biological Sciences, Nanyang Technological University, ² Institute of Molecular and Cell Biology, Singapore: Analysis of the relationship between host cell response and the susceptibility of cultured cells to a coronavirus by genomic approaches.	55
Xiao, H., Xu, L.H., Khadijah, S., Law, Y.C., Liu, D.X., Institute of Molecular and Cell Biology, Singapore: Interaction between coronavirus spike protein and the eukaryotic initiation factor 3.5 regulates the translation of virus-inducible genes.	56

SESSION 6

Chairperson: **A.A. James**, University of California, Irvine
M.J. Lehane, Liverpool School of Tropical Medicine,
 United Kingdom

Marinotti, O.,¹ Dissanayake, S.,¹ Calvo, E.,² Nguyen, Q.K.,³ Ribeiro, J.M.C.,² James, A.A.,^{1,4} Depts. of ¹Molecular Biology and Biochemistry, ²Biological Chemistry, ⁴Microbiology and Molecular Genetics, University of California, Irvine; ²Laboratory of Malaria and Vector Research, NIAID, National Institutes of Health, Rockville, Maryland: Analyzing gene expression profiles of the mosquito, *A. gambiae*. 57

Kleino, A.,¹ Valanne, S.,¹ Myllymäki, H.,¹ Rämetsä, M.,^{1,2} ¹Institute of Medical Technology, University of Tampere, ²Dept. of Pediatrics and Biocenter Oulu, University of Oulu, Finland: Inhibitor of apoptosis 2 regulates antimicrobial peptide release in *Drosophila*. 58

Tu, Z.,¹ Li, S.,¹ Saunders, R.,¹ Mao, C.,² ¹Dept. of Biochemistry, ²Virginia Bioinformatics Institute, Virginia Polytechnic Institute and State University, Blacksburg: Comparative and functional genomics approaches to mosquito biology and mosquito-pathogen interactions. 59

Valanne, S.,¹ Kleino, A.,¹ Kallio, J.,^{1,2} Ulvila, J.,³ Myllymäki, H.,¹ Kotipelto, T.,¹ Kataja, L.,¹ Rämetsä, M.,^{1,2,3} ¹Institute of Medical Technology, University of Tampere, ²Dept. of Pediatrics, Tampere University Hospital, ³Dept. of Pediatrics and Biocenter Oulu, University of Oulu, Finland: Genome-wide analysis of the *Drosophila* toll pathway. 60

Dillon, R.J.,¹ Ivens, A.C.,² Sant'Anna, M.R.V.,¹ Lehane, M.J.,¹ Bates, P.A.,¹ ¹Liverpool School of Tropical Medicine, ²Wellcome Trust Sanger Institute, Hinxton, United Kingdom: Analysis of expressed sequence tags from *L. longipalpis* sand flies and their use to study vector-parasite interactions. 61

Hannick, L.L., *A. aegypti* Genome Sequencing Consortium, The Institute for Genomic Research, Rockville, Maryland: Annotation of the *A. aegypti* genome. 62

Haines, L.R.,¹ Lehane, S.M.,¹ Pearson, T.W.,² Lehane, M.J.,¹
¹Liverpool School of Tropical Medicine, United Kingdom; ²Dept. of
Biochemistry, University of Victoria, Canada: Partial
characterization of a tsetse protein that influences vector
competence.

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SATURDAY, September 9—2:00 PM

SESSION 7

Chairperson: **D. Roos**, University of Pennsylvania, Philadelphia
M. Blaxter, University of Edinburgh, United Kingdom

Roos, D.S., Dept. of Biology and Penn Genomics Institute, University
of Pennsylvania, Philadelphia: Apicomplexa parasites and the
comparative genomics of eukaryotic pathogens.

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Saeij, J.P.J.,¹ Coller, S.,¹ Boyle, J.P.,¹ Jerome, M.E.,² White, M.W.,²
Boothroyd, J.C.,¹ ¹Dept. of Microbiology and Immunology, Stanford
University School of Medicine, California; ²Dept. of Veterinary
Molecular Biology, College of Agriculture, Montana State University,
Bozeman: A combination of host genomics and parasite genetics
reveals a secreted, polymorphic protein kinase that co-opts host
transcription in toxoplasmosis.

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Balu, B., Adams, J.H., Center for Global Health and Infectious
Diseases, Dept. of Biological Sciences, University of Notre Dame,
Indiana: Whole genome analysis of the human malaria parasite,
P. falciparum, using *piggyBac*-mediated insertional mutagenesis.

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Blaxter, M.,¹ Wasmuth, J.,³ Schmid, R.,² Hedley, A.,¹ Parkinson, J.,³
¹Institute for Evolutionary Biology, University of Edinburgh, ²Dept. of
Biochemistry, University of Leicester, United Kingdom; ³Hospital for
Sick Children, Toronto, Canada: Mining nematode EST databases
for novelty, or, is *C. elegans* a good model nematode?

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Viney, M.,¹ Thompson, F.,¹ Barker, G.,¹ Mitreva, M.,² McCarter, J.,²
¹School of Biological Sciences, University of Bristol, United
Kingdom; ²Genome Sequencing Center, Washington University
School of Medicine, St. Louis, Missouri: Genomic analysis of the
parasitic nematode *S. ratti*.

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Cheesman, S., Degnan, K., Pattaradilokrat, S., O'Mahoney, E., Carter, R., Institute of Immunology and Infection Research, School of Biological Sciences, University of Edinburgh, United Kingdom: Fine mapping of a region of chromosome 8 of *P.c.chabaudi* that confers strain-specific protective immunity against malaria. 69

Chen, Z.Q., Bahl, A., Bernal, A., Liu, Q., Nishi, M., Wu, B., Pereira, F., Roos, D., Depts. of Biology, Computer and Information Science, Penn Genomics Institute, University of Pennsylvania, Philadelphia: Defining the secretome—A gene model extender for apicomplexan parasites (and other species). 70

SATURDAY, September 9—6:00 PM

KEYNOTE SPEAKER

Fouchier, R.A.M., Dept. of Virology, Erasmus Medical Center, Rotterdam, The Netherlands: Phenotype and genotype evolution of influenza A virus. 71

SATURDAY, September 9—7:30 PM

CONFERENCE DINNER