



# GENOMES 2008 Functional Genomics of Microorganisms

April 8-11, 2008  
Institut Pasteur, Paris, France

## SCIENTIFIC PROGRAM

### Tuesday April 8<sup>th</sup>, 2008

1.30 pm - 5.30 pm	<b>Registration</b>
2.00 pm - 5.00 pm	Workshop "Systems Biology for beginners" organized by <b>Philippe GLASER</b> and <b>Benno SCHWIKOWSKI</b> , Institut Pasteur, Paris, France
5.30 pm - 6.00 pm	<b>Welcome addresses</b>  <b>Bernard DUJON</b> , Senior Executive-Vice President for Scientific Affairs, Institut Pasteur, Paris, France  <b>Carmen BUCHRIESER</b> , Institut Pasteur, Paris, France
6.00 pm	<b>Opening lectures</b>  Chair: <b>Jörg HACKER</b> , Robert Koch-Institut, Berlin, Germany  <b>Martin J. BLASER</b> , New York University School of Medicine, New York, USA The extensive and changing conversations between <i>Helicobacter pylori</i> and human cells  <b>Pascale COSSART</b> , Institut Pasteur, France <i>Listeria monocytogenes</i> : RNA lessons from the genome
7.30 pm	Welcome Reception at Institut Pasteur

### Wednesday April 9<sup>th</sup>, 2008

8.30 am - 10.25 am	<b>Session 1: Host - Microorganism Interactions: a) Pathogens</b>  Chair: <b>Tony PUGSLEY</b> , Institut Pasteur, Paris, France
8.30 am - 8.55 am	<b>S1-1: Dirk BUMANN</b> , University of Hannover, Germany Systems Biology of <i>Salmonella</i> infection
8.55 am - 9.20 am	<b>S1-2: Ulla BONAS</b> , Martin-Luther University, Halle, Germany New insights into how the phytopathogen <i>Xanthomonas</i> manipulates the host
9.20 am - 9.45 am	<b>S1-3: Andrew CAMILLI</b> , Tufts University, Boston, USA Genetic analysis of the transmissible state of <i>Vibrio cholerae</i>
9.45 am - 10.05 am	<b>S1-4: Thomas F. MEYER</b> , Max Planck Institute for Infection Biology, Berlin, Germany Systematic dissection of host cell function during infection
10.05 am - 10.25 am	<b>S1-5: Sigrid DE KEERSMAECKER</b> , Ctre of Microbial & Plant Genetics, Leuven, Belgium Towards systems biology, the <i>Salmonella typhimurium</i> luxS/AI-2 related pathway as a case study
10.25 am - 11.00 am	Coffee break

<p><b>11.00 am - 12.35 pm</b></p> <p><b>11.00 am - 11.25 am</b></p> <p><b>11.25 am - 11.50 am</b></p> <p><b>11.50 am - 12.15 pm</b></p> <p><b>12.15 pm - 12.35 pm</b></p>	<p><b>Session 1: Host - Microorganism Interactions: a) Pathogens</b></p> <p>Chair: <b>Birgitta HENRIQUES NORMARK</b>, Karolinska Institute Stockholm, Stockholm, Sweden</p> <p><b>S1-6: Eliora Z. RON</b>, University of Tel Aviv, Tel Aviv, Israel Systemic <i>E. coli</i> infections – what can we predict from genomics?</p> <p><b>S1-7: Stephen LORY</b>, Harvard University, Boston, USA Insights into the evolution of virulence in <i>Pseudomonas aeruginosa</i>: covering all bases</p> <p><b>S1-8: Roland BROSCH</b>, Institut Pasteur, Paris, France The tubercle bacilli: Molecular determinants of pathogenicity and attenuation</p> <p><b>S1-9: Christoph DEHIO</b>, University of Basel, Basel, Switzerland Comparative and functional genomic analysis of <i>Bartonella</i> identifies type IV secretion systems as host adaptability factors</p>		
<p>12.35 pm - 2.00 pm</p>	<p><i>Lunch at Institut Pasteur</i></p>		
<p><b>2.00 pm - 3.30 pm</b></p>	<table border="1"> <tr> <td data-bbox="507 734 694 1124"> <p>Poster session</p> </td> <td data-bbox="702 734 1396 1124"> <p><b>Company presentations</b></p> <p><b>2.00 pm-2.30 pm: Applied Biosystems</b> Paolo Vatta - Comparative Whole Genome Sequencing using SOLiD™ System</p> <p><b>2.30 pm-3.00 pm: Cogenics</b> Marcel de Leeuw - Putting Next Generation sequencing of microbial genomes to work</p> <p><b>3.00 pm-3.30 pm: Roche Diagnostics</b> Andreas Tauch - Ultrafast pyrosequencing of the human pathogens <i>Corynebacterium urealyticum</i> and <i>Corynebacterium</i></p> </td> </tr> </table>	<p>Poster session</p>	<p><b>Company presentations</b></p> <p><b>2.00 pm-2.30 pm: Applied Biosystems</b> Paolo Vatta - Comparative Whole Genome Sequencing using SOLiD™ System</p> <p><b>2.30 pm-3.00 pm: Cogenics</b> Marcel de Leeuw - Putting Next Generation sequencing of microbial genomes to work</p> <p><b>3.00 pm-3.30 pm: Roche Diagnostics</b> Andreas Tauch - Ultrafast pyrosequencing of the human pathogens <i>Corynebacterium urealyticum</i> and <i>Corynebacterium</i></p>
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<p><b>3.30 pm - 5.05 pm</b></p> <p><b>3.30 pm - 3.55 pm</b></p> <p><b>3.55 pm - 4.20 pm</b></p> <p><b>4.20 pm - 4.45 pm</b></p> <p><b>4.45 pm - 5.05 pm</b></p>	<p><b>Session 2: Host - Microorganism Interactions: b) Symbionts, Commensals</b></p> <p>Chair: <b>Peter ŠEBO</b>, Czech Academy of Science, Prague, Czech Republic</p> <p><b>S2-1: Oded BEJA</b>, Tel Aviv University, Tel Aviv, Israel Metagenomics of viral 'photosynthesis'</p> <p><b>S2-2: Dusko EHRLICH</b>, INRA, Jouy en Josas, France Metagenomics of the human digestive tract – insights into commensal bacteria</p> <p><b>S2-3: Richard FFRENCH-CONSTANT</b>, University of Bath, United Kingdom Rapid virulence annotation of bacterial genomes: Lessons from the insect pathogen <i>Photorhabdus</i></p> <p><b>S2-4: Sascha STOLL</b>, University of Würzburg, Würzburg, Germany The transcriptome of the endosymbiont <i>Blochmannia floridanus</i> in the different life stages of its holometabolous host</p>		
<p>5.05 pm - 5.35 pm</p>	<p><i>Coffee break</i></p>		
<p><b>5.35 pm - 6.50 pm</b></p> <p><b>5.35 pm - 6.00 pm</b></p> <p><b>6.00 pm - 6.25 pm</b></p>	<p><b>Session 3: Host Genomics and Vaccines</b></p> <p>Chair: <b>Agnès ULLMANN</b>, Institut Pasteur, Paris, France</p> <p><b>S3-1: Catharina SVANBORG</b>, University of Lund, Lund, Sweden Innate immune response genetics and susceptibility to urinary tract infection</p> <p><b>S3-2: Philippe SANSONETTI</b>, Institut Pasteur, Paris, France How <i>Shigella</i> hijacks host-cell gene transcription and signalling pathways to modulate the innate immune response</p>		
<p>6.30 pm - 8.00 pm</p>	<p>Wine and Cheese Party</p>		

<p><b>8.30 am - 10.05 am</b></p> <p>8.30 am - 8.55 am</p> <p>8.55 am - 9.20 am</p> <p>9.20 am - 9.45 am</p> <p>9.45 am - 10.05 am</p>	<p align="center"><b>Session 4: New Technologies – What are the Results</b></p> <p align="center">Chair: <b>Antoine DANCHIN</b>, Institut Pasteur, Paris, France</p> <p><b>S4-1: Michael HECKER</b>, University of Greifswald, Greifswald, Germany Towards the entire proteome of gram-positive bacteria</p> <p><b>S4-2: Amos BAIROCH</b>, Swiss Institute of Bioinformatics, Geneva, Switzerland UniProtKB and microbial proteomes: status and future developments</p> <p><b>S4-3: Julian PARKHILL</b>, Sanger Center, Cambridge, United Kingdom Variation detection in highly monomorphic bacteria using new sequencing technologies</p> <p><b>S4-4: Trent NORTHEN</b>, The Scripps Research Institute, La Jolla, USA High throughput mass spectrometry based metabolomic and enzymatic assays for functional genomics</p>
<p>10.05 am - 10.40 am</p>	<p><i>Coffee break</i></p>
<p><b>10.40 am - 12.15 pm</b></p> <p>10.40 am - 11.05 am</p> <p>11.05 am - 11.30 am</p> <p>11.30 am - 11.55 am</p> <p>11.55 pm - 12.20 pm</p> <p>12.20 pm - 12.40 pm</p>	<p align="center"><b>Session 5: Functional Genomics</b></p> <p align="center">Chair: <b>Brendan WREN</b>, London, United Kingdom</p> <p><b>S5-1: Susan GOTTESMAN</b>, Nat. Cancer Inst., Bethesda, USA Small RNAs and <i>E. coli</i> regulatory circuits</p> <p><b>S5-2: Peer BORK</b>, EMBL, Heidelberg, Germany Predicting biological function at different scales</p> <p><b>S5-3: Tracy PALMER</b>, University of Dundee, Dundee, United Kingdom Functional genomic analysis of protein secretion in <i>Streptomyces</i> species</p> <p><b>S3-3: Mariagrazia PIZZA</b>, Novartis Vaccines, Siena, Italy Microbial genomes as basis of vaccine discovery: the Meningococcus B challenge</p> <p><b>S5-4: Athanasios TYPAS</b>, University of California at San Francisco, San Francisco, USA The first high-throughput system for quantitatively assessing genetic interactions in bacteria</p>
<p>12.40 pm - 2.00 pm</p>	<p><i>Lunch at Institut Pasteur</i></p>
<p>2.00 pm - 3.30 pm</p>	<p>Poster session</p>
<p><b>3.30 pm - 4.45 pm</b></p> <p>3.30 pm - 3.55 pm</p> <p>3.55 pm - 4.20 pm</p> <p>4.20 pm - 4.45 pm</p>	<p align="center"><b>Session 6 : Microbial Metagenomics</b></p> <p align="center">Chair: <b>Didier MAZEL</b>, Institut Pasteur, Paris, France</p> <p><b>S6-1: Jean WEISSENBACH</b>, Genoscope, Paris, France Mining metagenomes</p> <p><b>S6-2: Victor DE LORENZO</b>, Centro Nacional de Biotecnología, Madrid, Spain Debugging and reconstructing regulatory networks of <i>Pseudomonas putida</i> for environmental release</p> <p><b>S6-3: George WEINSTOCK</b>, Baylor College, Huston, USA Approaching the Human Microbiome</p>
<p>4.45 pm - 5.10 pm</p>	<p><i>Coffee break</i></p>
<p><b>5.10 pm - 6.20 pm</b></p> <p>5.10 pm - 5.35 pm</p> <p>5.35 pm - 6.00 pm</p> <p>6.00 pm - 6.20 pm</p>	<p align="center"><b>Session 6 : Microbial Metagenomics</b></p> <p align="center">Chair: <b>Hilde DE REUSE</b>, Institut Pasteur, Paris, France</p> <p><b>S6-4: Karl O. STETTER</b>, University of Regensburg, Regensburg Germany The hyperthermophilic Archaea</p> <p><b>S6-5: Virginia ARMBRUST</b>, University of Washington, USA Life in the sea: new insights from diatom genomes</p> <p><b>S6-6: Lena TASSE</b>, INSA Toulouse, Toulouse, France Screening of the human intestinal microbiota for the discovery of new enzymes specific for fiber degradation</p>
<p>8.00 pm</p>	<p>Congress dinner</p>

<p><b>8.30 am - 10.05 am</b></p> <p><b>8.30 am - 8.55 am</b></p> <p><b>8.55 am - 9.20 am</b></p> <p><b>9.20 am - 9.45 am</b></p> <p><b>9.45 am - 10.05 am</b></p>	<p style="text-align: center;"><b>Session 7: Computational, Structural Genomics and Systems Biology</b></p> <p style="text-align: center;">Chair: <b>Benno SCHWIKOWSKI</b>, Institut Pasteur, Paris, France</p> <p><b>S7-1: Russel L. FINLEY JR</b>, Wayne State University, Detroit, USA Generating protein interaction maps for pathogens using yeast two-hybrid</p> <p><b>S7-2: Jörg STELLING</b>, ETH Zürich, Switzerland Systems analysis of signal transduction pathways</p> <p><b>S7-3: Fiona BRINKMAN</b>, Simon Fraser University, Burnaby, Canada Insights into the evolution of pathogens using improved bioinformatics approaches</p> <p><b>S7-4: Alexei SAVCHENKO</b>, University of Toronto, Toronto, Canada Genomewide structural and biochemical annotation of uncharacterised proteins from pathogenic bacteria</p>
<p>10.05 am - 10.35 am</p>	<p><i>Coffee break</i></p>
<p><b>10.35 am - 12.30 pm</b></p> <p><b>10.35 am - 11.00 am</b></p> <p><b>11.00 am - 11.25 am</b></p> <p><b>11.25 am - 11.50 am</b></p> <p><b>11.50 am - 12.30 pm</b></p>	<p style="text-align: center;"><b>Session 8: Comparative Genomics and Evolution</b></p> <p style="text-align: center;">Chair: <b>Agnès LABIGNE</b>, Institut Pasteur, Paris, France</p> <p><b>S8-1: Erick DENAMUR</b>, Medical Faculty Xavier Bichat, Paris, France Population phylogenomics of the <i>Escherichia coli</i> species</p> <p><b>S8-2: Carmen BUCHRIESER</b>, Institut Pasteur, Paris, France Comparative genomics of <i>Legionella pneumophila</i> and <i>Legionella longbeachae</i>, two human pathogens that coevolved with protozoa</p> <p><b>S8-3: Tim STINEAR</b>, Monash University, Victoria, Australia Insight into tuberculosis and Buruli ulcer from the complete genome sequence of <i>Mycobacterium marinum</i></p> <p><b>Pathogenomics PhD award</b></p> <p><b>Marie BOUVIER</b>, Max Planck Institute for Infection Biology, Berlin, Germany Single strand recombination in integrons</p> <p><b>Sascha THEWES</b>, Freie Universität Berlin, Berlin, Germany Molecular investigation of invasive properties of <i>Candida albicans</i></p> <p><b>Cristina D. RODRIGUES</b>, Instituto de Medicina Molecular, Lisboa, Portugal Revealing Host Factors Important for Hepatocyte Infection by <i>Plasmodium falciparum</i></p>
<p>12.30 pm - 2.00 pm</p>	<p><i>Lunch at the Institut Pasteur</i></p>
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<p>4.40 pm</p>	<p><b>Poster competition award</b></p>
<p><b>4.45 pm - 5.05 pm</b></p>	<p><b>Closing Lecture</b> <b>Frank KUNST</b>, Genoscope, Evry, France</p>

