



BISMis-2014

Edinburgh, Scotland
Defining Microbial Diversity in the Genomic Era

Welcome from the Chairs

Dear Delegate,

On behalf of the international organising committee, we welcome you to Edinburgh for **BISMis-2014**. Following on from the highly successful inaugural meeting of Bergey's International Society for Microbial Systematics (BISMis) in Beijing we have organised BISMis-2014. The theme of the meeting will be "*Defining Microbial Diversity in the Genomic Era*". As more and more complete and draft genome sequences as well as environmental sequences become available and the cost of obtaining these falls rapidly the microbial systematics community needs to discuss how this information can be used in routine identification, the description of new taxa, and in the delineation of higher level taxa. The meeting will bring together experts and interested parties to present and discuss their ideas and concepts. This meeting represents the only international meeting dedicated solely to those working in microbial systematics at which they can gather, present and discuss their findings.

We thank you for coming to this event in Edinburgh.

Fred A. Rainey and Brian Austin
Chairs of the Organizing Committee

INTERNATIONAL ORGANIZING COMMITTEE

Jongsik Chun	Seoul National University, Korea
Milton S. da Costa	University of Coimbra, Portugal
Svetlana N. Dedysh	Winogradsky Institute of Microbiology, Moscow
Mike Goodfellow	University of Newcastle, UK
Paul Lawson	University of Oklahoma, USA
Iain Sutcliffe	Northumbria University, UK
Martha Trujillo	Universidad de Salamanca, Spain
Antonio Ventosa	University of Sevilla, Spain
William Wade	Queen Mary University of London, UK
William Whitman	University of Georgia, USA
Lixin Zhang	Institute of Microbiology, Beijing, China

General information

Location

The conference will take place in the Apex International Hotel located at 31-35 Grassmarket, Edinburgh.

Registration desk

The conference registration desk, which will be located in the Metro Restaurant of the Apex International Hotel, will open at 16.00 – 18.00 h on Monday April 7th, and then from 08.30 h on Tuesday April 8th. The desk will remain open throughout the conference. Your contacts will be Fred Rainey and Brian Austin.

Badges

For security reasons, please ensure that you wear your name badge in the conference hotel.

Oral presentations

Speakers should ensure that they submit their PowerPoint presentations to the technician an hour before the start of the session. Presenters should introduce themselves to the session chair, at least 15 minutes before the start of the session. It is important to stick to your time.

Messages

Messages will be displayed on the message board.

Catering

Refreshments will be served in Gallery Bar; lunch will be taken in the Metro Restaurant.

Oral Programme	
Monday April 7, 2014	
16.00 – 18.00	Registration Desk Opens
18.00 – 18.15	Welcome F.A. Rainey, <i>University of Alaska, Anchorage, USA</i> B. Austin, <i>University of Stirling, Scotland, UK</i>
18.15 – 19.00	Keynote: The genomic encyclopedia of <i>Bacteria</i> and <i>Archaea</i> project and its use for microbial taxonomy H.-P. Klenk, <i>German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany</i>
19.00 – 21.00	Welcome mixer
Tuesday April 8, 2014	
08.30 – 09.00	Refreshments and registration
09.00–09.45	Keynote: The state of microbial taxonomy today W.B. Whitman, <i>University of Georgia, USA</i>
09.45	Session 1 – Use of genomic sequences in microbial taxonomy Chair: Jongsik Chun
09.45 – 10.30	Keynote: Gene-by-gene approaches to characterising genomic variation in bacterial populations M.C.J. Maiden, <i>University of Oxford, United Kingdom</i>
10.30 – 10.45	Refreshments [and posters]
10.45 – 11.15	Genetic boundaries to delineate bacteria into natural clusters L. Tang, Y.-P. Liu, G.-R. Liu and S.-L. Liu*, <i>Harbin Medical University, China</i>
11.15 – 11.45	Average nucleotide identity calculations with taxonomic purposes: case studies at CECT D.R. Arahal*, T. Lucena, M.A. Ruvira, M.C. Macián, R. Aznar, and M.J. Pujalte, <i>University of Valencia, Spain</i>
11.45 – 12.15	Genome sequence-based taxonomy: I will know it when I see it M. Krichevsky, <i>Bionomics International, USA</i>
12.15 – 13.30	Lunch [and posters]
13.30 – 14.15	Keynote: Taxono-genomics: an example of genomic data incorporation in bacterial taxonomy equation P.E. Fournier, <i>Aix-Marseille University, France</i>
14.15 14.45	Whole genome analyses support the taxonomic separation of “<i>Rhodococcus equi</i>” from other rhodococci V. Sangal*, A.L. Jones, M. Goodfellow, I.C. Sutcliffe, and P.A. Hoskisson, <i>Northumbria University, United Kingdom</i>
14.45 – 15.15	Whole genome sequence analysis of <i>Kosakonia radicincitans</i>, a bacterial strain associated with bacterial wilt diseased banana plant N.S.M. Suhaimi*, K.-P. Yap, N. Ajam, and K.-L. Thong, <i>University of Malaya, Malaysia</i>
15.15 – 15.30	Refreshments [and posters]
15.30 – 16.00	Microbial genomic taxonomy A.P.B. Moreira*, G. Amaral, M. Campeao, G. Dias, C. Thompson, and F. Thompson, <i>Federal University of Rio de Janeiro, Brazil</i>
16.00-16.30	Phylo- and comparative genomics of the <i>Pantoea</i> core genome M. Du Plessis, E.T. Steenkamp, M.P.A. Coetzee, T.A. Coutinho, and S.N. Venter*, <i>University of Pretoria, South Africa</i>
16.30 – 16.45	Molecular-genetic markers in determination of taxonomic position Cyanobacteria from Subsection III N.V. Velichko and M.S. Emeljanova, <i>Saint-Petersburg State University, Russia</i>
16.45 – 17.00	Chairman’s session review and discussion Jongsik Chun

	Wednesday April 9, 2014
08.30 – 09.00	Refreshments [and posters]
09.00	Session 2 – Chemotaxonomy <i>in vitro</i> vs. <i>in silico</i> Chair: Iain Sutcliffe
09.00 – 09.45	Keynote: The ups and downs of chemotaxonomic analysis for bacterial systematics M.S. da Costa, <i>University of Coimbra, Portugal</i>
09.45 – 10.15	The dumping ground <i>Arthrobacter</i>: phylogeny and chemotaxonomy H.-J. Busse, <i>Veterinary Medicine University of Vienna, Austria</i>
10.15 – 10.45	Refreshments [and posters]
10.45 – 11.30	Keynote: <i>In silico</i>: Reconciling computer conjectures with facts G. Olsen, <i>University of Illinois, USA</i>
11.30 – 12.00	MLSA and polar lipid profile applied to species delineation in the genus <i>Halorubrum</i> R.R. de la Haba*, P. Corral, C. Sánchez-Porro, A. Makkay, R.T. Papke and A. Ventosa, <i>University of Sevilla, Spain, University of Connecticut, Storrs, USA</i>
12.00 – 12.15	Chairman's session review and discussion Iain Sutcliffe
12.15 – 13.30	Lunch [and posters]
13.30 – 14.30	BISMis Business Meeting <i>All members welcome</i>
14.30	Session 3 – Microbial Systematics in the Classroom Chair: Fred A. Rainey
14.30 – 15.15	Keynote: Microbial systematics in the classroom. Stewardship of taxonomy for the 21st century Paul Lawson, <i>University of Oklahoma, USA</i>
15.15 – 15.30	Refreshments [and posters]
15.30 – 16.00	Shaping the future of taxonomy through learning, teaching and assessment A.L. Jones, <i>Northumbria University, United Kingdom</i>
16.00 – 16.30	The microbial diversity assessment club for learning systematics in the classroom K. Jangid*, S. Pawar, N. Marathe, and Y. Shouche, <i>University of Pune Campus, India</i>
16.30 – 17.00	Open discussion on teaching microbial systematics Speakers and delegates

	Thursday April 10, 2014
08.30 – 09.00	Refreshments [and posters]
09.00	Session 4 – Lessons for systematics from metagenomic studies Chair: Paul Lawson
09.00 – 09.45	Keynote: How many species are out there? Balances after almost 40 years of use of 16S rRNA gene sequence in prokaryote systematics R. Rosselló-Móra* and P. Yarza, <i>Institut Mediterrani d'Estudis Avancats, Mallorca, Spain</i>
09.45 – 10.15	"Microbial dark matter" genomes from geothermal springs: progress report and taxonomic perspective B.P. Hedlund*, S.K. Murugapiran, and J.A. Dodsworth, <i>University of Nevada, Las Vegas, USA</i>
10.15 – 10.45	Refreshments [and posters]
10.45 – 11.15	Metagenomic studies on hypersaline habitats and their impact on the systematics of halophiles A. Ventosa*, M.J. León, A.B. Fernández, B. Vera-Gargallo, and C. Sánchez-Porro, <i>University of Sevilla, Spain</i>
11.15	Session 5 – New approaches and new taxa Chair: Martha Trujillo
11.15 – 11.45	EzGenome: a genome database for accurate taxonomic identification of prokaryotes based on genome sequences S. Park and J. Chun*, <i>Seoul National University, Republic of Korea</i>
11.45 – 12.15	CVTree3: an effective genome-based and alignment-free phylogenetic tool with interactive tree display and taxonomic comparison G.H. Zuo* and B.L. Hao, <i>Fudan University, China</i>
12.15 – 13.30	Lunch [and posters]
13.30 – 14.00	Three-dimensional graph analysis of prokaryotic and eukaryotic groups and mathematical model of evolution of life E. Pikuta*, A. Lewis, D. Newland, P. Glaze, S. Kline, and R. Merritt, <i>Athens State University, Athens, Alabama, USA</i>
14.00 – 14.30	MALDI-TOF MS, a transformative analytical tool for the characterisation and authentication of microorganisms H. McGregor*, J.E. Russell, A. Deheer-Graham, R. Culak, T. Gaulton, H.N. Shah, <i>NCTC, Public Health England, United Kingdom</i>
14.30 – 15.00	Problems of describing bacteria from rarely cultured phyla S. Dedysh, <i>Russian Academy of Sciences, Moscow, Russia</i>
15.00 – 15.15	Refreshments [and posters]
15.15 – 15.45	Is there still any room for improvement on the systematics of genera of the family <i>Micromonosporaceae</i>? L.A. Maldonado*, E.T. Quintana, E.O. López-Villegas, and W. Lara, <i>Universidad Nacional Autónoma de México, México, Instituto Politécnico Nacional, México</i>
15.45 – 16.15	A new polyphasic approach for the characterization of the fish pathogen <i>Francisella noatunensis</i>: a baseline for a proposal of minimal standards within the genus <i>Francisella</i> J.G. Ramírez-Paredes*, S. Duodu, E. Soto, C. Öhrman, K.D. Thompson, A. Adams, R.H. Richards, P. Larsson, and D.J. Colquhoun, <i>University of Stirling, Scotland, United Kingdom, Norwegian Veterinary Institute, Norway, Ross University, West Indies, Swedish Defense Research Agency, Sweden</i>
16.15 – 16.45	Novel streptomycetes related to the <i>Streptomyces acidiscabies</i> subclade A. Alejo-Viderique, L.A. Maldonado, R. Felix-Gastelum, G. Herrera-Rodriguez, E. Burgueno-Tapia, and E.T. Quintana*, <i>Instituto Politécnico Nacional, México, Universidad Nacional Autónoma de México, México, Universidad de Occidente, México, Edificio AARFS, México</i>
16.45 – 17.00	BIMiS President, overview and closing remarks Brian Austin

	Posters
P01	<p>A novel thermophilic anaerobic saccharolytic bacterium isolated from an anaerobic batch digester treating animal manure and rice straw</p> <p>S. Ma*, Y. Huang, and Y. Deng, <i>Ministry of Agriculture, China</i></p>
P02	<p><i>Ferruginibacter profunda</i> sp. nov., Novel members of the family <i>Chitinophagaceae</i>, isolated from deep freshwater sediment of a reservoir</p> <p>L. Jin*, H.-G. Lee, C.-Y. Ahn, and H.-M. Oh, <i>Korea Research Institute of Bioscience & Biotechnology, Republic of Korea</i></p>
P03	<p>Actinobacterial diversity in high altitude Atacama desert soils and regoliths and its biotechnological potential</p> <p>H. Idris*, A.T. Bull, M.E. Rateb, M. Jaspars, and M. Goodfellow, <i>Newcastle University, University of Kent, University of Aberdeen, United Kingdom</i></p>
P04	<p>Taxonomoic diversity of acidophilic actinobacteria as a roadmap to drug discovery</p> <p>P. Golinska*, H. Dahm, and M. Goodfellow, <i>Nicolaus Copernicus University, Poland and Newcastle University, United Kingdom</i></p>
P05	<p>Molecular diversity of bacteria isolated from groundnut (<i>Arachis hypogaea</i>) rhizosphere and nodules from rainfed Pothwar, Pakistan</p> <p>R. Khalid*, R. Hayat, U. Amara, and S. Ali, <i>PMAS-Arid Agriculture University, Pakistan</i></p>
P06	<p>The gut microbiota of pollinators: an unknown and unexplored treasure chest of biodiversity</p> <p>J. Praet*, I. Meeus, G. Smaghhe, and P. Vandamme, <i>Ghent University, Belgium</i></p>
P07	<p>A new thermophilic species of the genus <i>Rubrobacter</i>, <i>R. chenensis</i> from a geothermal spring in Alaska</p> <p>M. Johnson, L. Albuquerque, M.S. da Costa and F.A. Rainey*, <i>University of Alaska, Anchorage, USA and University of Coimbra, Coimbra, Portugal</i></p>
P08	<p>Relationship of whole genome sequence similarity to DNA hybridization in prokaryotes</p> <p>L. Xun, Y. Huang and W. B. Whitman*, <i>University of Georgia, Athens, USA, Nanjing Forestry University, Nanjing, China</i></p>