

## Oral presentations ICETAR 2015

Wednesday 24 June 2015	
12.00 – 14.00	Registration with light lunch
14.00 – 18.15	<b>Evolution of Antibiotic Resistance (I)</b> Chairs: Fernando Baquero, Rob Willems
14.00 – 14.15	Opening  Rob Willems, Willem van Schaik <i>University Medical Center Utrecht, The Netherlands</i>
14.15 – 15.00	Understanding and controlling the evolution of antibiotic resistance  Roy Kishony <i>Technion-Israel Institute of Technology, Israel and Harvard Medical School, USA</i>
15.00 – 15.45	Predicting the risk of resistance evolution—which parameters to measure?  Dan Andersson <i>Uppsala University, Sweden</i>
15.45 – 16.15	Coffee/tea-break
16.15 – 16.45	Understanding the diversification mechanisms triggered by low antibiotic concentrations  Didier Mazel <i>Institut Pasteur, France</i>
16.45 – 17.30	Why bacteriostatic drugs are effective  Bruce Levin <i>Emory University, USA</i>
17.30 – 18.15	The clinical impact of antibiotic resistance  Marc Bonten <i>University Medical Center Utrecht, The Netherlands</i>

<b>Thursday 25 June 2015</b>	
<b>8.30 – 10.00</b>	<b>Evolution of Antibiotic Resistance (II)</b> Chairs: Dan Andersson, Didier Mazel
8.30 – 9.00	Deep genetic epidemiology of antibiotic resistance Fernando Baquero, Teresa Coque <i>Ramón y Cajal University Hospital, Spain</i>
9.00 – 9.30	The effect of antibiotic resistance on bacterial physiology José Luis Martinez <i>Centro Nacional de Biotecnología, Spain</i>
9.30 – 10.00	Changes in the mammalian intestinal architecture during antibiotic-induced perturbation of the microbiota Rob Willems <i>University Medical Center Utrecht, The Netherlands</i>
10.00 – 10.15	Bacterial evolution of antibiotic hypersensitivity Viktoria Lazar <i>Institute of Biochemistry, Biological Research Centre, Hungary</i>
10.15 – 10.30	Chance and necessity in the evolution of an antibiotic resistance enzyme Arjan de Visser <i>Wageningen University, The Netherlands</i>
10.30 – 11.00	Coffee/tea break
11.00 – 17.00	<b>Mechanisms and Microbial Ecology of Antibiotic Resistance (I)</b> Chairs: Mark Woolhouse, José Luis Martinez
11.00 – 11.30	The intestinal microbiota: a playground for clinicians to control bacterial resistance Antoine Andremont <i>Assistance Publique-Hôpitaux de Paris, France</i>
11.30 – 12.00	Development of a product protecting the gut microbiota during antibiotic treatment Jean de Gunzburg <i>DaVolterra, France</i>
12.00 – 12.30	The human gut microbiome in response to antibiotics S. Dusko Ehrlich <i>INRA, France</i>
12.30 – 12.45	Novel broad-spectrum beta-lactamase therapy to protect the gut microbiome from antibiotics Sheila Connelly <i>Synthetic Biologics, Inc., USA</i>
12.45 – 15.00	Lunch and poster presentations
15.00 – 17.30	<b>Mechanisms and Microbial Ecology of Antibiotic Resistance (I)</b> Chairs: Bruno Gonzalez Zorn, Willem van Schaik
15.00 – 15.45	Clinically relevant resistance mediated by a multi-drug efflux pump in <i>Salmonella</i>

	Laura Piddock <i>University of Birmingham, United Kingdom</i>
15.45 – 16.15	Epidemiology and mechanisms of emerging polymyxin resistance in <i>Klebsiella</i>  Gian Maria Rossolini <i>University of Siena, Italy</i>
16.15 – 16.45	Tapping into the resistome by integrating high throughput cultivation and functional genomics  Hauke Smidt <i>Wageningen University, The Netherlands</i>
16.45 – 17.00	Development of a high-throughput method to study persister gene expression  Theresa Henry <i>University of Princeton, USA</i>
18.00	Canal tour and conference dinner

<b>Friday 26 June 2015</b>	
8.30 – 10.30	<b>Transfer and Dissemination of Antibiotic Resistance (I)</b> Chairs: Luca Guardabassi, Antoine Andremont
8.30 – 9.15	An update on enterobacterial transmissible plasmids in the era of massive sequencing  Fernando de la Cruz <i>University of Cantabria, Spain</i>
9.15 – 9.45	Reading the small print: ecology and evolution of small plasmids  Bruno Gonzalez Zorn <i>Universidad Complutense de Madrid, Spain</i>
9.45 – 10.00	Host specificity in the diversity and transfer of <i>Isa</i> resistance genes in Group B <i>Streptococcus</i>  Pierre-Emmanuel Douarre <i>Institut Pasteur, Paris</i>
10.00 – 10.15	Evolution and global competition dynamics of community-associated MRSA  Melissa Ward <i>University of Edinburgh, United Kingdom</i>
10.15 – 10.45	Coffee + tea break
10.45 – 11.15	Elucidating the dynamics and dissemination of antibiotic resistance genes  Morten Sommer <i>Technical University of Denmark, Denmark</i>
11.15 – 11.30	Reservoirs and interactions of antimicrobial resistance in different microbiomes  Fiona Walsh <i>Maynooth University, Ireland</i>
11.30 – 11.45	Exogenous alanine or/and glucose plus kanamycin kills antibiotic-resistant bacteria  Xuanxian Peng <i>Sun Yat-sen University, China</i>
11.45 – 12.00	Applying population genetic theory from experimental microbial evolution to costs of resistance  Zachary Ardern <i>University of Auckland, New Zealand</i>
12.00 – 12.15	Multidrug evolution hysteresis in <i>Pseudomonas aeruginosa</i>  Phillip Yen <i>University of Virginia, USA</i>
12.15 – 13.15	Lunch
13.15 – 15.30	<b>Transfer and Dissemination of Antibiotic Resistance (II)</b> Chairs: Gian Maria Rossolini, Fernando de la Cruz
13.15 – 13.45	Evidence for inter-relationships between antimicrobial resistance in humans, livestock and the wider environment

	<p style="text-align: right;">Mark Woolhouse <i>University of Edinburgh, United Kingdom</i></p>
13.45 – 14.15	<p>Hunting for carbapemenases in the soil microbiota</p> <p style="text-align: right;">Luca Guardabassi <i>University of Copenhagen, Denmark</i></p>
14.15 – 14.45	<p>Dissemination of cephalosporin resistance genes between <i>Escherichia coli</i> strains from farm animals and humans</p> <p style="text-align: right;">Willem van Schaik <i>University Medical Center Utrecht, The Netherlands</i></p>
14.45 – 15.00	<p>A research funder's perspective on the evolution and transfer of antibiotic resistance</p> <p style="text-align: right;">Arjon van Hengel <i>European Commission, DG Research &amp; Innovation</i></p>
15.00 – 15.10	Closing remarks

## Poster presentations ICETAR2015

Poster#	Presenting author	Affiliation	Title
1	Sebastian Aguilar	Institut Pasteur, Paris, France	High throughput approaches identify genes with transcriptional/fitness alterations during exposure to sub-MICs of antibiotics in <i>Vibrio cholerae</i>
2	Richard Anthony	Royal Tropical Institute, Amsterdam, The Netherlands	Multi drug resistant tuberculosis, mutational diversity, mutation rates, drug usage, and bacterial genotype, what limits the emergence of successful epidemic strains?
3	Marco D'Andrea	University of Siena, Siena and University of Florence, Florence, Italy	First report of a NMC-A producing <i>Enterobacter cloacae</i> in Italy: clues of XerC/XerD-like recombination system involved in chromosomal integration of the carbapenemase gene
4	Jennifer Bender	Robert Koch Institute	Is linezolid resistance of German <i>Enterococcus faecium</i> clinical isolates linked to the acquisition of a Cfr methyltransferase from <i>Clostridium difficile</i> ?
5	Cristina Bernabe-Balas	Universidad Complutense de Madrid. Madrid, Spain	Understanding the adaptation of plasmids to a new bacterial host
6	Antonio Cannatelli	University of Siena, Siena, Italy	In-vitro stepwise evolution of colistin resistance in <i>Klebsiella pneumoniae</i> producing KPC-type carbapenemase
7	Xinhai Chen	Sun Yat-sen University, Guangdong, China	Myo-inositol improves host to eliminate balofloxacin-resistant
8	María de Toro	Instituto de Biomedicina y Biotecnología de Cantabria, Santander, Spain.	Plasmid "curing" and conjugation improve PLACNET performance
9	Yanfang Feng	University of Amsterdam, Amsterdam, The	Dynamics of genetic mutations during the de novo development of antibiotic resistance

		Netherlands	
10	Val Fernandez	Hospital Universitario Ramón y Cajal and Instituto Ramón y Cajal de Investigación Sanitaria IRYCIS, Madrid, Spain	The Deep Resistome: Discovering the resistome of minority populations.
11	Val Fernandez	Hospital Universitario Ramón y Cajal and Instituto Ramón y Cajal de Investigación Sanitaria IRYCIS, Madrid, Spain	Identification and dynamics of the accessory genes in the <i>Escherichia coli</i> O25b-ST131 clonal group causing blood stream infections in a Spanish University Hospital
12	Ana Guzman	Department of Medical Microbiology, University Medical Center Utrecht	Genome-wide screening for genetic determinants involved in decreased susceptibility to the antiseptic chlorhexidine in <i>Enterococcus faecium</i>
13	Joost Hordijk	Utrecht University, Utrecht, The Netherlands	Potential equine related <i>Escherichia coli</i> carrying CTX-M-1 on an IncHI1 plasmid
14	Pavel Kudrin	University of Tartu, Tartu, Estonia	Stringent response–dependent and stringent response–independent antibiotic tolerance is induced by sub-MIC antibiotic treatment
15	Hui Li	Sun Yat-sen University, Guangdong, China	Network of membrane proteins regulating streptomycin resistance in <i>Escherichia coli</i>
16	Felipe Lira	Centro Nacional de Biotecnología, CSIC, Cantoblanco, Madrid, Spain	The accessory genome of <i>Stenotrophomonas maltophilia</i>
17	Oto Melter	Charles University, Prague and Motol	High Rate of Ribosomal Mutation Conferring Resistance to MLS <sub>B</sub> Antibiotics as a Result of Long-Term and Low-Dose Azithromycin Treatment

		University Hospital, Prague, Czech Republic	
18	Gabriel Moyano	Universidad Complutense de Madrid, Madrid, Spain	A video tracked mouse-hospital-model to study the genetic flux of antimicrobial resistance determinants
19	Christian Munck	Technical University of Denmark, Hørsholm, Denmark.	Stability of large conjugative plasmids in <i>E. coli</i>
20	Veronica Negro	Institut Pasteur, Paris, France	Induction of the SOS response by antibiotics that do not target DNA in <i>V. cholerae</i>
21	Chandan Pal	University of Gothenburg, Sweden	Large-scale analysis of resistance genes towards antibiotics, biocides and metals in bacterial genomes and plasmids uncovers their co-selection potential
22	Andreas Porse	Technical University of Denmark, Hørsholm, Denmark.	Stability of plasmids: A host dilemma
23	Eleonora Riccobono	University of Siena, Siena, Italy	Characterization of an IncI1 ST71 epidemic plasmid lineage responsible for the recent dissemination of CTX-M-65 extended-spectrum beta-lactamase in the Bolivian Chaco region
24	Etienne Ruppe	INRA, Jouy-en-Josas, France	Evolution and (no) transfer of antibiotic resistance in the human intestinal microbiota
25	Ewa Sadowy	National Medicines Institute, Warsaw, Poland	Resistance to vancomycin among <i>Enterococcus faecium</i> in Polish hospitals: diversity of <i>vanB</i> gene clusters
26	María Blanca Sánchez	Centro Nacional de Biotecnología. (CNB-CSIC), Madrid, Spain	Identification of new antibiotic resistance genes in <i>Klebsiella pneumoniae</i> kp52145
27	Alfonso Santos-Lopez	Universidad Complutense de Madrid. Madrid, Spain	Behavior of ColE1 plasmids during cohabitation
28	Sugiyono	The University of	Emerging antimicrobial resistance in staphylococcal infections associated with companion

	Saputra	Adelaide, Roseworthy, Australia; Indonesian Institute of Sciences, Cibinong, Indonesia	animals in Australia
29	Vanessa Schmidt	University of Liverpool, Liverpool, United Kingdom	Longitudinal study of antimicrobial resistance and characterisation of faecal <i>Escherichia coli</i> from healthy dogs in the UK
30	Heike Schmitt	Utrecht University, Utrecht, The Netherlands	Role of antibiotic use for tetracycline resistance and integron carriage in Dutch pig farms and farmers
31	Samanta Sennati	University of Siena, Siena, Italy	Intercontinental dissemination of pHN7A8-like plasmids responsible for multiresistance to expanded-spectrum cephalosporins and aminoglycosides in <i>Enterobacteriaceae</i>
32	Wanchat Sirisarn	University of Manchester, Manchester, United Kingdom	Isolation and characterization of a novel bacteriophage infecting <i>S. aureus</i>
33	Yubin Su	Sun Yat-sen University, Guangdong, China	Fructose restores susceptibility of multidrug-resistant <i>Edwardsiella tarda</i> to kanamycin
34	Ana P. Tedim	Hospital Universitario Ramón y Cajal (IRYCIS), Madrid, Spain	Comparative genomics of worldwide distributed <i>Enterococcus faecium</i> ST117 clone
35	Ana P. Tedim	Hospital Universitario Ramón y Cajal (IRYCIS), Madrid, Spain.	Fitness cost of plasmids carrying Tn <sub>1546</sub> - <i>vanA</i> in diverse <i>Enterococcus faecium</i> clonal contexts
36	Dorina Timofte	University of Liverpool, Liverpool, United Kingdom	Occurrence and hospital dissemination of CTX-M-15 extended spectrum beta-lactamase producing <i>Escherichia coli</i> clinical isolates from companion animals in the UK
37	Thomas Van Boeckel	Princeton University, Princeton, United	Global trends in antimicrobial use in food animals

		States of America	
38	Bram van Bunnik	University of Edinburgh, United Kingdom	Efficient national surveillance for health-care-associated infections
39	Dennis Versluis	Wageningen University, Wageningen, The Netherlands	High throughput recovery of previously uncultured bacterial genera contributing to the resistome in three Mediterranean sponges
40	Mark Zwart	University of Cologne, Cologne, Germany	Synonymous mutations in TEM-1 beta-lactamase increase resistance to a novel antibiotic
41	Monika Schniederjans	Helmholtz Centre for Infection Research, Braunschweig, Germany	Quantitative and qualitative transcriptional profiling of antibiotic resistance in <i>Pseudomonas aeruginosa</i>
42	Ákos Nyerges	Biological Research Centre of the Hungarian Academy of Sciences, Szeged, Hungary	pMAGE: a highly precise and portable genome engineering method for studying antibiotic resistance
43	Valeria Bortolaia	University of Copenhagen, Frederiksberg C, Denmark	CMY-2-encoding plasmids without frontiers
44	Heidi Kira Gumpert	University of Copenhagen, Frederiksberg C, Denmark	The mobilization pool of CTX-M-14 in <i>Escherichia coli</i> of animal and human origin in Denmark