

## PRELIMINARY PROGRAMME OVERVIEW

	September 1, 2010 Wednesday	September 2, 2010 Thursday	September 3, 2010 Friday	September 4, 2010 Saturday
8.30		<b>Session 1</b> <b>Population structures, classification and typing</b>	<b>Session 5</b> <b>Progress in the analysis of emergence and spread of major pathogens, the Gram-positives</b>	<b>Session 9</b> <b>Analysis and typing of plasmids and mobile genetic elements</b>
8.45		<u>M. Achtman</u> : Population genetics and genomics of Salmonella	<u>C. Donati</u> : Population genetics and evolution of the pan-genome of <i>S. pneumoniae</i>	<u>A. Carattoli</u> : Plasmids in Gram-negatives: molecular typing, epidemiology and antimicrobial resistance
9.00		<u>S. Niemann</u> : <i>Mycobacterium tuberculosis</i> population structure and multidrug resistance	<u>E. Kuijper</u> : New <i>Clostridium difficile</i> PCR ribotypes in Europe and its virulence factors	<u>L. Poirel</u> : Diversity of genetic elements at the origin of beta-lactamase genes acquisition and expression
9.15		<u>B. Spratt</u> : Molecular typing for exploring the spread of gonorrhoea	<u>R. Willems</u> : Population dynamics of <i>Enterococcus faecium</i>	
9.30				Short oral presentations selected from submitted abstracts
9.45		Short oral presentations selected from submitted abstracts	Short oral presentations selected from submitted abstracts	
10.00				<b>Workshops</b> <b>I: VNTR Typing: Tips, tricks, and applications</b> <u>Chairs</u> : R. Goering, L. Dijkshoorn <b>II: Next generation sequencing, bioinformatics and genotyping</b> <u>Chairs</u> : (to be nominated)
10.15		<b>Coffee Break</b>	<b>Coffee Break</b>	
10.30		<b>Session 2</b> <b>New developments in methods for typing and strain characterization</b>	<b>Session 6</b> <b>Molecular epidemiology of antibiotic resistance</b>	
10.45		<u>M. Holden</u> : Genome sequencing as a tool for high-resolution genotyping	<u>U. Nübel</u> : Reconstructing MRSA spread based on DNA variation	
11.00		P. Glaser: Genomics and host specific markers in Streptococcus or Staphylococcus	<u>R. Canton</u> : Dynamics of emergence and spread of ESBL and carbapenemases	
11.15		<u>B.A. Lindstedt</u> : High resolution MLVA-genotyping of enteropathogenic bacteria	<u>P. Courvalin</u> : Resistance gene flow induced by low concentrations of antibiotics	
11.30				
11.45		Short oral presentations selected from submitted abstracts	Short oral presentations selected from submitted abstracts	
12.00				
12.15				
12.30				
12.45				
13.00		13.00 – 15.00 <b>Lunch and Poster Session</b>	13.00 – 15.00 <b>Lunch and Poster Session</b>	
15.00		<b>Session 3</b> <b>Progress in the analysis of emergence and spread of major pathogens, the Gram-negatives</b>	<b>Session 7</b> <b>Role of typing networks for surveillance; I. General aspects</b>	
15.15		<u>H. Karch</u> : What defines a pathovar as an intestinal pathogen?	<u>A. Ammon</u> : Integration of molecular typing into surveillance at EU level	
15.30		<u>U. Dobrindt</u> : What defines <i>E. coli</i> as an extraintestinal pathogen?	<u>J. Wain</u> : The role of whole genome sequencing for epidemiology	
15.45			<u>M. Struelens</u> : Role of typing in surveillance of nosocomial pathogens	
16.00		Short oral presentations selected from submitted abstracts		
16.15			<b>Coffee Break</b>	
16.30		<b>Coffee Break</b>	<b>Session 8</b> <b>Role of typing networks for surveillance; II. Typing networks</b>	
16.45		<b>Session 4</b> <b>Zoonoses</b>	<u>A. Friedrich</u> : Regional, international and crossborder molecular typing networks: Experience from SeqNet.org	
17.00		<u>L. Wieler</u> : Nosocomial infections (NI) in veterinary medicine	<u>H. de Lencastre, A. Tomasz</u> : Evolution of molecular tools – to track epidemic clones of staphylococci and pneumococci and to decipher genetic steps in antibiotic resistance	
17.15		<u>J.A. Wagenaar</u> : One world, one health: Staphylococci in animals and humans	<u>U. Vogel</u> : European efforts to harmonize typing of meningococci	
17.30				
17.45				
18.00		Short oral presentations selected from submitted abstracts		
18.15			<b>Break</b>	
19.00	<b>Opening ceremony</b> <u>R. Burger</u> : Welcome address <u>J. Hacker</u> : Microevolution in bacterial pathogens <u>M. Hecker</u> : Impact of functional genomics for understanding ecology, adaptation and pathogenesis	19.00 <b>Concert</b>	<b>Expert lecture</b> <u>F. Baquero</u>	
20.30	<b>Welcome Reception</b>		20.00 <b>Conference Dinner</b>	