



## SMRT® SEQUENCING PROGRAM PRESENTATIONS

### Friday, June 2

Session 119 - Hot Topics in Invasive  
*Staphylococcus aureus* Infections  
3:30 - 3:45 p.m. - Room #267

#### **Comparative Genomics of Colonizing and Infectious *S. aureus* Isolates from Single Hosts**

D. R. Altman et al. Icahn Sch. of Med. at Mount Sinai, NY

Session 114 - Clinical Application of Genomics of Relevant Health Care Associated MDR Bacteria

5:00 - 5:15 p.m. - Room #265

#### **Continuous Surveillance by Whole Genome Sequencing Identifies Genomic Characteristics of Highly Transmissible MRSA**

M. J. Sullivan et al. Icahn Sch. of Med. at Mount Sinai, NY

### Saturday, June 3

Session 274 - Long Reads: Transforming Microbiology

3:15 - 3:45 p.m. - Room #267

#### **Resolving the Complexity of Human Skin Metagenomes Using Single-Molecule Sequencing**

J. Oh et al. The Jackson Lab., Farmington

4:00 - 4:30 p.m. - Room #267

#### **The Long and the Short of it: Metagenomic Binning, Assembly, and Discovery with Long Read Sequencing Platforms**

L. Wilbanks et al. Univ. of California, Santa Barbara, Santa Barbara

3:45 - 4:00 p.m. - Room #267

#### **Population Structure Analysis of *Mycoplasma pneumoniae* Using Whole Genome Sequencing**

M. H. Diaz et al. Center for Disease Control, Atlanta

4:30 - 4:45 p.m. - Room #267

#### **2000 Genomes and Counting: An Update on NCTC3000, a Type Culture Reference Genome Project**

S. Alexander et al. Publ. Hlth. England, London, United Kingdom

### Sunday, June 4

Session 432 - Marine Microbial Activities and Interactions

3:45 - 4:00 p.m. - Room #238

#### **Outstanding Abstract Award: Viral Predation Drives the Diversification of Natural Microbial Populations**

F. A. Hussain et al. Massachusetts Inst. of Technology, Cambridge



**MICROBIOLOGY AND  
INFECTIOUS DISEASE**

## Live Poster Talks – Exhibit Hall D, Exhibit and Poster Hall

Time	Title	Author
<b>Friday, June 2</b>		
1:25 - 1:35 p.m.	<b>EES: The Rapid <i>In Vivo</i> Evolution of <i>Pseudomonas aeruginosa</i> in Ventilator-Associated Pneumonia Patients Leads to Attenuated Virulence</b>	Y. Ding et al. Nanyang Technological Univ., Singapore
2:25 - 2:35 p.m.	<b>AAID: Outstanding Abstract Award - Using Whole-Genome Sequencing to Elucidate the Epidemiology of <i>Candida auris</i> - A Globally Emerging, Multidrug-Resistant Yeast</b>	N. A. Chow et al. Centers for Disease Control and Prevention, Atlanta
6:20 - 6:25 p.m.	<b>AAID: Whole Genome Sequence Based Identification of a ST-5 Sub-Cluster of Linezolid-Resistant <i>Staphylococcus epidermidis</i> Causing Invasive Disease in Cancer Patients</b>	X. Li et al. UT MD Anderson Cancer Ctr., Houston
<b>Saturday, June 3</b>		
12:25 - 12:35 p.m.	<b>AES: A Novel Putative Propane Monooxygenase Initiating Metabolism of 1,4-Dioxane</b>	Y. He et al. Rice Univ., Houston
<b>Sunday, June 4</b>		
5:40 - 5:45 p.m.	<b>AES: The Curious Case of Spontaneous Antibiotic Resistance in <i>Liberibacter crescens</i></b>	E. W. Triplett et al. Univ. of Florida, Gainesville
5:45 - 5:50 p.m.	<b>EES: The Genomics of Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) O91:H21</b>	K. L. Galindo et al. California State Univ., Northridge (CSUN), Northridge

## Poster Presentations – Exhibit and Poster Hall

Time	#	Title	Author	
<b>Friday, June 2</b>	12:45 - 2:45 p.m.	73	<b>BlaTEM-1 Mediated Resistance to Piperacillin/Tazobactam in a Clinical Isolate of <i>Escherichia coli</i></b>	L. M. Schechter et al. bioMerieux, Inc.
		99	<b>Emergence of NDM Beta-Lactamases on Diverse Mobilizable Vectors Carried by Extremely Drug Resistant <i>Enterobacteriaceae</i> Isolated from Domestic and International Patients in the Boston Area</b>	N. Pecora et al. Brigham and Women's Hosp., Boston
		147	<b>Hospital-Wide Whole Genome Sequencing of Emerging Antibiotic Resistant Enterococcus</b>	K. Chacko et al. Icahn Sch. of MSed. at Mount Sinai, New York
		582	<b>Sequence Analysis of a Historic Collection of Commercial Acetone-Butanol-Ethanol Clostridia</b>	S. D. Brown et al. Oak Ridge Natl. Lab., Oak Ridge
		590	<b>The Genomics of Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) O91:H21</b>	K. L. Galindo et al. California State Univ., Northridge (CSUN), Northridge
		620	<b>Identification of Antifungal Compound of <i>Burkholderia cepacia</i> JBK9 and Confirmation of Its Potential Agriculturally Useful Activities by Complete Genome Sequencing and Annotation</b>	M-C. Kim, Male et al. Kyungpook Natl. Univ., Daegu, Korea, Republic of
		642	<b>The Curious Case of Spontaneous Antibiotic Resistance in <i>Liberibacter crescens</i></b>	E. W. Triplett et al. Univ. of Florida, Gainesville
		670	<b>A Novel Putative Propane Monooxygenase Initiating Metabolism of 1,4-Dioxane</b>	Y. He et al. Rice Univ., Houston
		702	<b>Complete Genome Sequencing of <i>Salmonella enterica</i> Serovar Virchow FORC_038 Isolated from Raw Chicken Meat in South Korea</b>	J. Song et al. Seoul Natl. Univ., Seoul
		709	<b>Analysis of Full Genome of <i>Escherichia coli</i> Forc_043 Isolated from a Korean Patient Revealed its Similarity to the <i>E. coli</i> HUSEC2011</b>	H. Na et al. Seoul Natl. Univ., Seoul
		758	<b>An Integrated Bioinformatics Pipeline and Database for Microbial Genome Sequencing</b>	M. Julius et al. Walter Reed Army Inst. of Res., Silver Spring
<b>Saturday, June 3</b>	12:15 - 2:15 p.m.	AAID LB5	<b>Whole-Genome Sequence and Assembly Analysis to Identify Unique Molecular Biomarkers for Multi-Resistant <i>Pseudomonas aeruginosa</i></b>	S. Shaikh et al. Florida Intl. Univ., Miami
		67	<b>Whole Genome Sequence Based Identification of a ST-5 Sub-Cluster of Linezolid-Resistant <i>Staphylococcus epidermidis</i> Causing Invasive Disease in Cancer Patients</b>	X. Li et al. UT MD Anderson Cancer Ctr., Houston
		98	<b>A Nosocomial Outbreak of Extensively Drug Resistant (XDR) <i>Acinetobacter baumannii</i> Isolates Containing <i>bla</i><sub>OXA-237</sub> Encoded on a Plasmid</b>	A. M. Hujer et al. VAMC and CWRU, Cleveland
		136	<b>Conjugal Transfer, Whole Genome Sequencing and Plasmid Analysis of Three <i>mcr-1</i> Bearing <i>Escherichia coli</i> Isolated from U.S. Patients</b>	W. Zhu et al. Centers for Disease Control and Prevention, Atlanta
		138	<b>Whole Sequences of <i>mcr-1</i>-Harboring Plasmids from <i>Escherichia coli</i> Isolates from Livestock in South Korea</b>	J. Y. Lee et al. Sungkyunkwan Univ., Suwon, Korea

Time	#	Title	Author	
Saturday, June 3, continued	12:15 - 2:15 p.m., continued	219	<b>Outstanding Abstract Award: Using Whole-Genome Sequencing to Elucidate the Epidemiology of <i>Candida auris</i> - A Globally Emerging, Multidrug-Resistant Yeast</b>	N. A. Chow et al. Centers for Disease Control and Prevention, Atlanta
		503	<b>Multiplexing Strategies for Microbial Whole Genome Sequencing Using the Sequel System</b>	C. Lambert et al. PacBio, Menlo Park
		566	<b>The Rapid <i>In Vivo</i> Evolution of <i>Pseudomonas aeruginosa</i> in Ventilator-Associated Pneumonia Patients Leads to Attenuated Virulence</b>	Y. Ding et al. Nanyang Technological Univ., Singapore
		571	<b>Phylogenomic Analysis of Atypical Non-Shiga Toxin-Producing <i>Escherichia coli</i> O157:H7</b>	A. Allué Guardia et al. Univ. of Texas at San Antonio, South Texas Ctr. for Emerging Infectious Diseases (STCEID), San Antonio
		577	<b>Complete Genome Analysis of <i>Bacillus cereus</i> FORC_013 Isolated from Fried Eel</b>	H. Kim et al. Seoul Natl. Univ., Seoul, Republic of Korea
		633	<b>Updated Genome Sequence and Genome Wide Functional Annotation of Benzalkonium Chloride-Resistant <i>Burkholderia contaminans</i> LMG 23361T</b>	J. Y. Jung et al. Natl. Ctr. for Toxicological Res., U.S. Food and Drug Admin., Jefferson
		665	<b>Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Thomson Strain MFDS1004026 Isolated from Korean Food-Borne Outbreak</b>	W. Lee et al. Food Microbiol. Div., Ministry of Food and Drug Safety, Cheongju-si, Republic of Korea
		893	<b>Phenotypic and Pan-Genomic Characterisation of <i>Salmonella enterica</i> Serovar Uganda, an Uncommon Food-Borne Pathogen</b>	D. Hurley et al. Univ. Coll. Dublin, Dublin
		AAID LB23	<b>Establishment of a Metabolism-Induced <i>In Vitro</i> <i>Plasmodium berghei</i> Liver Stage Assay for Prodrug Screening</b>	B. A. Vesely et al. WRAR, Silver Spring
Sunday, June 4	12:15 - 2:15 p.m.	168	<b>Drug Resistance Elements from a Multidrug-Resistant <i>Staphylococcus cohnii</i> Subsp. <i>urealyticus</i> Determined by Whole Genome Sequencing</b>	Y-T. Lin et al. Natl. Taiwan Univ., Taipei
		169	<b>Adenine Methylation and Antimicrobial Resistance</b>	D. Johnson et al. Leeds Beckett Univ., Leeds
		179	<b>Acquisition of <i>msr(E)</i> by <i>P. aeruginosa</i> Abolishes Anti-Quorum Sensing Effect of Azithromycin</b>	Y. Ding et al. Nanyang Technological Univ., Singapore
		687	<b>Full-Length cDNA Sequencing of Prokaryotic Transcriptome and Metatranscriptome Samples</b>	M. Boitano et al. PacBio, Menlo Park
		779	<b>Unraveling HT-58-2, a Cyanobacterial Holobiont that Produces the Efflux Pump Inhibitor Tolyporphin</b>	R-A. Hughes et al. North Carolina State Univ., Raleigh
		792	<b>Generalized Strategy Enabling High-Throughput Genetics in Diverse Bacteria</b>	H. H. M. R. Liu, Lawrence Berkeley Natl. Lab., Berkeley
		793	<b>Rapid Inactivation of Bacteria by Denator T1 Heat Stabilization Technology is Compatible with Isolation of High-Molecular Weight DNA for Downstream Genomics Applications</b>	V. N. Loparev et al. Centers for Disease Control, Atlanta
		805	<b>Single-Strand Specific, Plasmid Borne DNA Methyltransferases M.BceJIII and M.EcoGIX Regulate Plasmid and Single-Stranded Phage Replication</b>	A. Fomenkov et al. New England Biolabs, Ipswich
		869	<b>Closed Genomes and Phenotypes of Seven <i>Histophilus somni</i> Isolates from Beef Calves with Bovine Respiratory Disease Complex</b>	G. P. Harhay et al. USDA-ARS Meat Animal Res. Ctr. (USMARC), Clay Center
		CPHM LB4	<b>Methodological Improvements On Urine Sample Analysis: Towards Comprehensive Understanding Of Urinary Microbiome</b>	L. Peixe et al. Univ. of Porto, Porto

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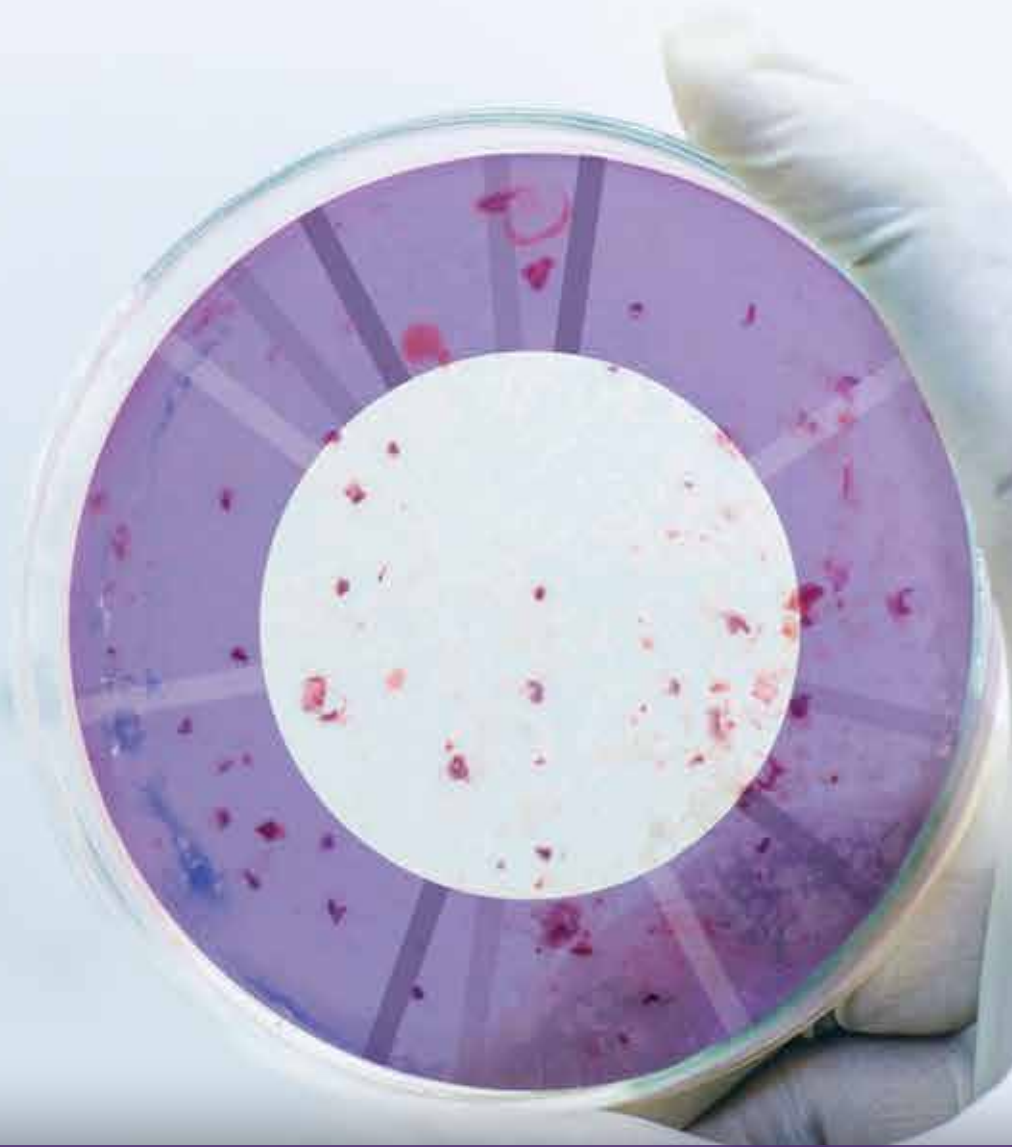
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