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ASM 2018

POSTER TALKS

Ezbiocloud: An Integrated Database of Nomenclature, Taxonomy, 16s rRNA, Genome and Microbiome for *Bacteria* and *Archaea*

Jongsik Chun, ChunLab, Inc.

Friday, June 8, 11:00 a.m. – 11:10 a.m.

Session 29: Bioinformatics and Computational Genomics
Exhibit and Poster Hall, MBP Hub, Learn

Chromosome Rearrangement, Gene Amplification, and Insertion Sequence Elements in the Genome Evolution of *Bordetella pertussis* and the Genus *Bordetella*

Michael Weigand, CDC

Saturday, June 9, 11:00 a.m. – 11:10 a.m.

Session 207: Evolutionary Histories of Microbial Genomes
Exhibit and Poster Hall, MBP Hub, Learn

RAPID FIRE PRESENTATION

Outstanding Abstract Award: Clonal Evolution and Genomic Diversification of *Bordetella Hinzii* in an Immunocompromised Host

Adrien Launay, NIH

Saturday, June 9, 1:45 p.m. – 1:50 p.m.

Session 291: Microbe, Know Thy Host
Lounge and Learn 4, Building B,
Level 4



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INFECTIOUS DISEASE**

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Poster Talks – All posters are on display in the Exhibit and Poster Hall

Day	Time	Title	Author	Session# / Presentation #
Friday, June 8	11:00 a.m. - 1:00 p.m.	Whole Genome DNA Methylation (Methylome) Analysis and Role of Dam DNA Methyltransferase in the Entomopathogenic Bacterium <i>Photobacterium luminescens</i>	Amaury Payelleville et al. Université de Montpellier, INRA, Montpellier, France	93 / FRI - 1018
		Confounding Roles of the Shiga Toxin Phage Sequence Type and Bacterial Host Genome in <i>Stx2a</i> Production	Anna Allué Guardia et al. Univ. of Texas at San Antonio, South Texas Ctr. for Emerging Infectious Diseases (STCEID), San Antonio, TX	95 / FRI - 1056
		NCTC3000 the World's Largest Collection of Bacterial Reference Genomes	Sarah Alexander et al. Publ. Hlth.England, London, United Kingdom	46 / FRI - 331
		Genome Sequence of the Threonine-Production <i>Escherichia coli</i> Strain ATCC 98082	Junjie Yang et al. Inst. of Plant Physiology and Ecology, Shanghai Inst.s for Biological Sci., Chinese Academy of Sci., Shanghai, China	46 / FRI - 354
		Comparative Phenotype Analysis and Genome Completion of <i>Streptomyces venezuelae</i> Strains	Woori Kim et al. Korea Advanced Inst. of Sci. and Technology(KAIST), Daejeon, Korea, Republic of	88 / FRI - 964
		Chromosomally Encoded mcr-5 in Colistin Resistant <i>Pseudomonas aeruginosa</i>	Patrick Mc Gann et al. Walter Reed Army Inst. of Res., Silver Spring, MD	48 / FRI - AAR LB5
		The Use of Whole Genome Sequencing Technology to Elucidate the Genomic Variation and Epidemiology of <i>Candida glabrata</i> in United States	Rory Welsh et al. CDC, Atlanta, GA	65 / FRI - CIV LB3
Saturday, June 9	11:00 a.m. - 1:00 p.m.	Identification of Secondary Metabolites Gene Clusters in the Class <i>Ktedonobacteria</i> with Actinomycetes-Like-Morphology	Shuhei Yabe et al. Tohoku Univ., Sendai, Japan	446 / FRI - 89
		Kraken with Kalamari: Contamination Detection	Lee Katz et al. CDC, Atlanta, GA	270 / SAT - 1080
		Outstanding Abstract Award: Clonal Evolution and Genomic Diversification of <i>Bordetella hinzii</i> in an Immunocompromised Host	Adrien Launay et al. NIH Clinical Ctr., Bethesda, MD	211 / SAT - 32
		Transfer of a Lsa(E)-Carrying Resistance Island in <i>Enterococcus faecalis</i> by a Coresident Conjugative Plasmid	X-D. Du Henan Agricultural Univ., Zhengzhou, China	232 / SAT - 539
		Deciphering the Mechanisms for Attenuation in a Rifampin-Resistant Mutant of <i>Flavobacterium columnare</i> Used as a Modified-Live Vaccine against Columnaris Disease	Wenlong Cai et al. Auburn Univ., Auburn, AL	243 / SAT - 762
		Genome and Transcriptome Analyses of <i>Staphylococcus aureus</i> Forc_062, a Food-Borne Pathogen Isolated from Human Blood	Anna Cho et al. Seoul Natl. Univ., Seoul, Korea, Republic of	258 / SAT - 926
		Discovery of Novel Anti-Tuberculosis Drugs from Sphagnum Bog Bacteria	M. Espinoza-Moraga et al. NIH, Bethesda, MD	226 / SAT - AAR LB17
		Spread of bla _{NDM} -carrying Plasmids among Clinical and Wastewater Isolates of <i>Enterobacteriaceae</i> in Myanmar	Yo Sugawara et al. Res. Inst. for Microbial Diseases, Osaka Univ., Suita, Japan	226 / SAT - AAR LB5
		Understanding the Emergence of Multidrug Resistant <i>Candida</i> : Using Whole-Genome Sequencing to Determine the Population Structure of <i>Candida haemulonii</i> and <i>Candida duobushaemulonii</i>	Lalitha Gade et al. CDC, Atlanta, GA	237 / SAT - CIV LB3
		Single Chromosomal Genome Assemblies on the Sequel System with Circulomics High Molecular Weight DNA Extraction for Microbes	Cheryl Heiner et al. PacBio, Menlo Park, CA	265 / SAT - MBP LB13
Sunday, June 10	12:45 p.m. - 2:45 p.m.	Genome Plasticity Affecting Virulence and Social Activities in <i>Burkholderia glumae</i>	Minhee Kang et al. Seoul Natl. Univ., Seoul, Korea	265 / SAT - MBP LB6
		Evaluation of Average Nucleotide Identity Using Mummer (Ani-M) and <i>Rpob</i> Gene Phylogeny for Identification of <i>Vibrionaceae</i> by Whole Genome Sequence Analysis	Monica Im et al. IHRC/CDC, Atlanta, GA	442 / SUN - 1015
		Ezbiocloud: An Integrated Database of Nomenclature, Taxonomy, 16s rRNA, Genome and Microbiome for <i>Bacteria</i> And <i>Archaea</i>	Jongsik Chun et al. ChunLab, Inc., Seoul, Korea	442 / SUN - 1022
		Recovering Whole Sequence of Class 1 Integrons in Environments by Constructing A Comprehensive Class 1 Integrase Database and Designing New PCR Primers	An Zhang et al. The Univ. of Hong Kong, Hong Kong	429 / SUN - 787
		Chromosome Rearrangement, Gene Amplification, and Insertion Sequence Elements in the Genome Evolution of <i>Bordetella pertussis</i> and the Genus <i>Bordetella</i>	Michael Weigand et al. CDC, Atlanta, GA	438 / SUN - 951
		Genome Analysis of A Multidrug-Resistant (Mdr) <i>Salmonella enterica</i> Serovar I 4,[5],12,i:- Isolate Associated with a 2015 Foodborne Outbreak from Pork	Bradley Bearson et al. USDA, ARS, Natl. Lab. for Agriculture and the Environment, Ames, IA	438 / SUN - 965
A Path Toward Genetic Manipulation of <i>Megasphaera elsdenii</i>	E. Anne Hatmaker et al. Oak Ridge Natl. Lab., Oak Ridge, TN	426 / SUN - AES LB3		

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