

Shana R. Leopold

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EDUCATION

Ph.D. Molecular Microbiology and Microbial Pathogenesis,
Washington University School of Medicine, St. Louis, MO, June 2010

B.S. Biology, University of Massachusetts, Boston, MA, June 2000

RESEARCH EXPERIENCE

2014-Present **Associate Research Scientist**, The Jackson Laboratory for Genomic Medicine,
Dr. George Weinstock Group, Farmington, CT

Applications of genomic sequencing for the study of the human microbiome, as well as nosocomial and community acquired infectious diseases.

2010-2013 **Post-Doctoral Researcher**, Laboratory of Dr. H. Karch, Dr. A. Mellmann Group,
Institute of Hygiene, University Hospital Münster, Germany

Conducted a retrospective investigation of a methicillin-resistant *Staphylococcus aureus* (MRSA) cluster within the University Hospital using whole genome sequencing (WGS) and single nucleotide polymorphism (SNP) profiling. Showed that WGS typing can identify distinct clusters that appeared identical by all other typing methods (e.g., spa typing, PFGE, and optical mapping), and that WGS is a relevant tool for prospective surveillance and outbreak detection.

During the German *Escherichia coli* O104:H4 outbreak in 2011, worked as part of a team to rapidly sequence, phylogenetically analyze and characterize the strain. The core genome, which was essential in constructing the evolutionary history of this hybrid strain, was determined using a series of Perl scripts and BLAST. Assembled and analyzed Ion Torrent sequence data in collaboration with Life Technologies. Have also served as a consultant to colleagues on *E. coli* evolutionary relationships.

Developed a core genome definer using Perl scripts and BLAST, named MCNGenome. This tool facilitates a comparison of annotated genomes, as well as unannotated contigs. Full transparency is achieved with adjustable parameters and return of all data, including non-core ORFs, in categorized worksheets. This tool is useful for in-depth analysis of the bacterial core genome, and has been utilized in the aforementioned *S. aureus* and *E. coli* investigations. This technology is available as a free, web-based service (www.mcngenome.net).

- 2004-2010 **Ph.D. Thesis**, Laboratory of Dr. Phillip Tarr, Washington University School of Medicine, St. Louis, MO.
Created a precise reconstruction of the emergence of pathogenic *Escherichia coli* O157:H7 and O157:H⁻ by sequencing evolutionarily informative strains and characterizing genome-wide single nucleotide polymorphisms (SNPs) that have arisen as these groups descended from less virulent *E. coli* O55:H7. This technology was extended to further investigate the structure of the *E. coli* species as a whole using selected members of the *E. coli* reference (ECOR) collection and published strains representing the four major groups of *E. coli*.
- Investigated the clonal relatedness of *Enterococcus faecium* and *Enterococcus faecalis* isolated from patients with Crohn's Disease or Urinary Tract Infections using multi-locus variance analysis (MLVA) and multi-locus sequence typing (MLST).
- 2000-2004 **Associate Scientist**, Paratek Pharmaceuticals, Inc., Boston, MA.
Involved in the Anti-Inflammatory Program investigating the mechanism of action of tetracyclines on various inflammatory proteins and molecules in diseases such as Huntington's disease, ALS and Multiple Sclerosis
- Assisted in creating the Tuberculosis Antibiotic Resistance Efflux Program, which consisted of generating a library of known and suspected efflux genes (including experimental design, plasmid extraction and transfection of both *Mycobacterium smegmatis* and *Escherichia coli*) as well as collecting and maintaining screening data from an outside institution.

HONORS AND AWARDS

- 2007-2009 NIH Training Grant in Infectious Diseases/Mechanisms of Microbial Pathogenesis
- 2006-2007 Infectious Diseases Scholars Program, Washington University in St. Louis

SERVICE

- Young Scientist Program, Washington University, St. Louis, MO, **Teacher** (2006-2010)
Student-run outreach program designed to provide hands-on research experience to high school students.
- Feed St. Louis, Washington University, St. Louis, MO, **Volunteer/Deliverer** (2006-2010)
A student-run organization that transports surplus food from Washington University's Center Court to community homeless shelters.

PUBLICATIONS

Leopold SR, Goering RV, Witten A, Harmsen D, Mellmann A. Bacterial whole genome sequencing revisited: portable, scalable and standardized analysis for typing and detection of virulence and antibiotic resistance genes. *J Clin Microbiol.*, **52**(7):2365-70, 2014

Leopold SR, Dobrindt U, Karch H, Mellmann A, Genome Plasticity and the Emergence of New Pathogenic *E. coli* In: Pathogenic *Escherichia coli*: Molecular and Cellular Microbiology, S Morabito ed., Horizon Scientific Press, 2014

Zhang W, Nadirk J, Kossow A, Bielaszewska M, **Leopold** SR, Witten A, Fruth A, Karch H, Ammon A, Mellmann A. Phylogeny and Phenotypes of Clinical and Environmental Shiga Toxin-Producing *Escherichia coli* O174. *Environ Microbiol.*, **16**(4):963-76, 2014

Bletz S, Bielaszewska M, **Leopold** SR, Köck R, Witten A, Schuldes J, Zhang W, Karch H, Mellmann A. Evolution of enterohemorrhagic *Escherichia coli* O26 based on single-nucleotide polymorphisms. *Genome Biol Evol*, **5**(10):1807-16, 2013

Jenke C, **Leopold** SR, Weniger T, Rothgänger J, Harmsen D, Karch H, Mellmann A. Identification of intermediate in evolutionary model of enterohemorrhagic *Escherichia coli* O157. *Emerg Infect Dis*, **18**(4):582-8, 2012

Mellmann A*, Harmsen D*, Cummings CA*, Zentz EB, **Leopold** SR, Rico A, Prior K, Szczepanowski R, Ji Y, Zhang W, McLaughlin SF, Henkhaus JK, Leopold B, Bielaszewska M, Prager R, Brzoska PM, Moore RL, Guenther S, Rothberg JM, Karch H (*co-first authors). Prospective genomic characterization of the German enterohemorrhagic *Escherichia coli* O104:H4 outbreak by rapid next generation sequencing technology. *PloS One* **6**(7):e22751, 2011

Leopold SR, Sawyer SA, Whittam TS, Tarr PI. Obscured phylogeny and restricted recombination in the *Escherichia coli* genospecies. *BMC Evol Biol* Jun 27;11:183, 2011

Leopold SR, Tarr, PI, Thomas Whittam, Shiga Toxin-Producing *Escherichia coli*, and the Clinical Relevance of Clonality, In: Population Genetics of Bacteria: A Tribute to Thomas S. Whittam, ST Walk and PCH Feng ed., Amer Society for Microbiology, 257-272, 2011

Bekassy ZD, Toledo CC, Gustav L, Kistoffersson AC, **Leopold** SR, Perez MR, Karpman D. Intestinal damage in enterohemorrhagic *Escherichia coli* infection; the role of Shiga toxin, intimin and *E. coli* secreted proteins. *Pediatr Nephrol*, 26(11):2059-71, 2011

Leopold SR, Shaikh N, Tarr PI. Further evidence of constrained radiation in the evolution of pathogenic *Escherichia coli* O157:H7. *Infect Genet Evol*, **10**(8):1282-5, 2010

Leopold SR*, Magrini V*, Holt N, Shaikh N, Mardis ER, Cagno J, Ogura Y, Iguchi A, Hayashi T, Mellman A, Karch H, Besser TE, Sawyer SA, Whittam TS, Tarr PI (*co-first authors). A precise reconstruction of the emergence and constrained radiations of *Escherichia coli* O157 portrayed by backbone concatenomic analysis. *Proc. Natl. Acad. Sci. USA*, **106**:8713, 2009

PRESENTATIONS

Oral:

“Using WGS and MLST+ to Investigate a MRSA Cluster”; Shana R Leopold, presented at MLST+ Curator Meeting, ‘Rapid NGS for Public Health Microbiology’, Institute for Hygiene, University of Muenster, Germany, July 2013.

“Core Genome Determination of Microbial Pathogens”; Shana R Leopold, presented at FGMS Seminar of the DGHM Section ‘Microbial Systematics, Population Biology and Infection Epidemiology’, Institute for Hygiene and Microbiology, University of Würzburg, Germany, November 2011.

“Comparison of PFGE, Optical Mapping, & Spa Typing for the Cluster Detection of MRSA” Shana R Leopold, Dag Harmsen, Richard V. Goering, Alexander Mellmann, presented at the DGHM (Deutschen Gesellschaft für Hygiene und Microbiologie) Annual Meeting, Essen, Germany, September 2011.

“Optical Mapping: Whole Genome Analysis of Microorganisms”; Shana R Leopold, presented at the Institute for Hygiene Lunch Seminar, University Hospital Münster, Germany, April 2011.

“Chromosomal Segment Investigation - CSI: *E. coli* Phylogeny”; Shana R Leopold, presented at the Infectious Disease and Basic Microbiological Mechanisms Seminar, Washington University in St. Louis, December 2009.

“A Precise Reconstruction of Pathogen Emergence: A Genomic Analysis of the Evolution of the EHEC 1 Clade”; Shana R Leopold, Invited Guest, Special Seminar, Institute for Hygiene, University Hospital Münster, Germany, November 2009.

“Evolution of a Pathogen: The Emergence and Constrained Radiations of *Escherichia coli* O157”; Shana R Leopold, Invited Guest, Special Seminar, University of Virginia, Charlottesville, VA, June 2009.

“The Emergence and Constrained Radiations of *Escherichia coli* O157”; Shana R Leopold, presented at the Microbiology Department Retreat, Pere Marquette Park, Grafton Illinois, September 2008.

“Evolution of a Pathogen: Pan-chromosomal single nucleotide polymorphisms illuminate the emergence and radiations of *Escherichia coli* O157:H7”; Shana R Leopold; presented at the Infectious Disease and Basic Microbiological Mechanisms Seminar, Washington University in St. Louis, December 2007.

“The Phylogeny of a Pathogen: Systematic SNP analyses of *Escherichia coli* O157:H7”; Shana R Dew, Phillip Tarr; presented at the Diagnostic Microbiology Journal Club, Washington University in St. Louis, June 2007.

“SNP Discovery in *E. coli* O157:H7”; Shana R Dew, presented at the Infectious Disease and Basic Microbiological Mechanisms Seminar, Washington University in St. Louis, April 2007.

“Green photoresists based on DNA photodimerization”; John C. Warner, Alessandra Morelli, Shana R Dew, Lisa Lloyd-Kindstrand; presented at the 220th ACS National Meeting, Washington, D.C., August 2000.

Poster:

“Core Genome Determination of Zoonotic Pathogens Using Whole Genome Data in Combination with a New Web Application”; Shana R. Leopold, David J. Schmitz-Hübsch,

Dag Harmsen, Alexander Mellmann, DGHM (Deutschen Gesellschaft für Hygiene und Microbiologie) Annual Meeting, September 2011, Essen, Germany.

“MCGenome: a user-friendly core genome definer for whole genome data analysis”; Shana R. Leopold, David J. Schmitz-Hübsch, Dag Harmsen, Alexander Mellmann, American Society for Microbiology General Meeting, May 2011, New Orleans, LA.

“Phylogeny of *Escherichia coli*: Extended segment sequence analysis demonstrates an evolutionary history obscured by recombination”; Shana R Leopold, Thomas S Whittam, Phillip I. Tarr; American Society for Microbiology General Meeting, May 2010, San Diego, CA.

“Evolution of a pathogen: Pan-chromosomal single nucleotide polymorphisms illuminate the emergence and radiations of *Escherichia coli* O157:H7”; Shana R Leopold, Vince Magrini, Thomas Whittam, Elaine R Mardis, Nicholas J Holt, Nurmohammad Shaikh, Joseph Cagno, Yoshitoshi Ogura, Tetsuya Hayashi, Phillip I Tarr; National DNA Day Symposium, April 2009, Saint Louis, MO.

“Evolution of a pathogen: Pan-chromosomal single nucleotide polymorphisms illuminate the emergence and radiations of *Escherichia coli* O157:H7”; Shana R Leopold, Vince Magrini, Thomas Whittam, Elaine R Mardis, Nicholas J Holt, Nurmohammad Shaikh, Joseph Cagno, Yoshitoshi Ogura, Tetsuya Hayashi, Phillip I Tarr; U.S.-Japan Cholera & Other Bacterial Enteric Infections Joint Panel Meeting, December 2007, Austin, TX.

“Validating EHEC Strain Genotyping Using 454-Based Pyrosequencing”; Vince Magrini, Shana R Dew, Phillip Tarr, Elaine R Mardis; American Society For Microbiology General Meeting, May 2007, Toronto, ON, Canada

“Triple hydrogen bonding in DNA and analogs”; Shana R Dew and John C Warner; 6th Annual Conference on Undergraduate Research, Scholarly, Creative and Public Service Activities for Students at Massachusetts Public Colleges and Universities, April 2000, Federal Reserve Bank, Boston, MA.

“Triple hydrogen bonding in DNA and analogs”; Shana R Dew and John C Warner; 2nd Annual Northeast Student Chemistry Research Conference, April 2000, Boston, MA.