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EDUCATION AND TRAINING

1996-1998 IRTA Fellow National Institute of Allergy and Infectious Disease Laboratory of Viral Disease
1996 Ph.D., Dept. of Biology, University of North Carolina at Chapel Hill
1990 BA/BA, Biology and Chemistry, Bucknell University

RESEARCH AND PROFESSIONAL EXPERIENCE

Sep 2012 – present, **Scientist**, Pacific Northwest National Laboratory, Biological Sciences Division. Use of 'omics data to investigate metabolic potential of environmental microbial communities and dependent/competitive interactions between populations.
May 2007 – Aug 2012, **Research Assistant Professor**, University of Southern California, Dana and David Dornsife College of Letter, Arts & Sciences, Department of Biological Sciences, Marine Environmental Biology Section. Use of genomic and metagenomic data to identify insertion sequences and their derivatives in cyanobacteria and investigate their role in generating variation within a population.
Oct 2004 – Apr 2007, **Bioinformatics Analyst Manager**, The Institute for Genomic Research, Microbial Annotation team. Lead a team of eight Bioinformatics Analysts. Developed analysis protocols for genome and metagenome data. Developed tools and pipelines for automated functional annotation and manual curation of genome data.
Oct 1998 – Sept 2004, **Bioinformatics Analyst**, The Institute for Genomic Research, Microbial Annotation team. Performed genomic analysis and functional annotation on microbial genome data.

SELECTED PUBLICATIONS

Heidelberg KB, Nelson WC, Holm JB, Eisenkolb N, Andrade K, Emerson JB. Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. *Front Microbiol.* 2013;4:115.
López-Lozano NE, Heidelberg KB, Nelson WC, García-Oliva F, Eguiarte LE, Souza V. (2013) Microbial secondary succession in soil microcosms of a desert oasis in the Cuatro Ciénegas Basin, Mexico. *PeerJ.* Mar 5;1:e47.
Nelson WC, Bhaya D, Heidelberg JF. (2012) Novel miniature transposable elements in thermophilic Synechococcus strains and their impact on an environmental population. *J Bacteriol.* 194(14):3636-42.
Koid A, Nelson WC, Mraz A, Heidelberg KB. (2012) Comparative analysis of eukaryotic marine microbial assemblages from 18S rRNA gene and gene transcript clone libraries by using different methods of extraction. *Appl Environ Microbiol.* 78(11):3958-65.
Tully BJ, Nelson WC, Heidelberg JF. (2011) Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. *Environ Microbiol.* 2011 Nov 3. [Epub ahead of print].
Biddle JF, Sylvan JB, Brazelton WJ, Tully BJ, Edwards KJ, Moyer CL, Heidelberg JF, Nelson WC. (2011) Prospects for the study of evolution in the deep biosphere. *Front Microbiol.* 2011;2:285.
Nelson WC, Bhaya D, Heidelberg JF. (2011) Analysis of Insertion Sequences in Thermophilic Cyanobacteria: Exploring the Mechanisms of Establishing, Maintaining, and Withstanding High Insertion Sequence Abundance. *Appl Environ Microbiol* 77(15).

- Singer E, Emerson D, Webb EA, Barco RA, Kuenen JG, Nelson WC, Chan CS, Comolli LR, Ferriera S, Johnson J, Heidelberg JF, Edwards KJ. (2011) *Mariprofundus ferrooxydans* PV-1 the first genome of a marine Fe(II) oxidizing Zetaproteobacterium. *PLoS One*. 6(9):e25386. Epub 2011 Sep 23.
- Singer E, Webb EA, Nelson WC, Heidelberg JF, Ivanova N, Pati A, Edwards KJ. (2011) Genomic Potential of *Marinobacter aquaeolei*, a biogeochemical “opportunotroph”. *Appl Environ Microbiol*. 77(8):2763-71.
- Morrison M, Daugherty SC, Nelson WC, Davidsen T, Nelson KE; The North American Consortium for Fibrolytic Ruminant Bacteria. (2010) The FibRumBa Database: A Resource for Biologists with Interests in Gastrointestinal Microbial Ecology, Plant Biomass Degradation, and Anaerobic Microbiology. *Microb Ecol*. 59(2):212-3.

SYNERGISTIC ACTIVITIES

- American Association for the Advancement of Science
- American Society of Microbiology