

## Food Science and Technology Department

Impacting the world three times a day



### Dr. Andrew Benson Professor

**Education:**

B.S. Microbiology, Iowa State University  
Ph.D. Microbiology, University of Texas  
Post Doc. Molecular Biology, Princeton University

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**Teaching and/or Extension Activities:**

Food Microbiology, Advanced Food Microbiology, (908B Molecular Biology of FoodBorne Pathogens and 908B the Microarray Course)

[For more information, please click here.](#)

**Research Area:**

1. Genome evolution in pathogenic bacteria. Comparative genomics, phylogenetics, and molecular biology are used to identify important events in the genome of pathogenic bacteria and understand the effects of genes and pathways marked by these events.
2. Evolution and development of gut microflora. 16S rRNA fingerprinting and sequencing is being used to examine development of the highly complex gut microflora in mammalian model systems, with the ultimate goal of identifying host genes that affect gut flora development.

**Five Selected Publications:**

- Kim, J., J. Nietfeldt, and A.K. Benson. 1999. Octamer-based genome scanning distinguishes a unique subpopulation of *Escherichia coli* O157:H7 strains in cattle. *Proc. Natl. Acad. Sci. USA.* 96: 13288-13293.
- Kim, J., J. W. Nietfeldt, J. Ju, J. Wise, P. Desmarchelier, N. Fegan, and A.K. Benson. 2001. Ancestral divergence, genome diversification, and phylogeographic variation in subpopulations of sorbitol-negative, b-glucuronidase negative Enterohemorrhagic *Escherichia coli* O157. *J. Bacteriol.* 183: 6885-6897.
- Zhang, C., M. Zhang, J. Ju, J. Nietfeldt, J. Wise, P.M. Terry, M. Olson, S.D. Kachman, M. Wiedmann, M. Samadpour, and A.K. Benson. 2003. Genome diversification in phylogenetic lineages I and II of *Listeria monocytogenes*: Identification of segments unique to lineage II populations. *J. Bacteriol.* 185: 5573-5584.
- Zhang, C., J. Nietfeldt, M. Zhang, and A.K. Benson. 2005. Functional consequences of genome evolution in *Listeria monocytogenes*: the Imo0423 and Imo0422 genes encode sigma C and LstR, a lineage II-specific heat shock system. *J. Bacteriol.* 187: 7243-7253.
- Dempsey, M.P., J. Nietfeldt, J. Ravel, S. Hinrichs, R. Crawford, and A.K. Benson. 2006. Paired-end sequence mapping detects extensive genomic rearrangement and translocation during divergence of *Francisella tularensis* subsp. *tularensis* and *Francisella tularensis* subsp. *holartica* populations. *J. Bacteriol.* 188(16). 5904-5914.