KEITH H. TURNER

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Citizenship: USA

The University of Texas at Austin Section of Molecular Genetics and Microbiology 1 University Station, A5000 Austin, TX 78712-0162

Education

Harvard University, Program in Biological and Biomedical Sciences

Ph.D., Microbiology (May 2012)

Dissertation: Bistability in Pseudomonas aeruginosa

University of Iowa

B.S., Microbiology with Honors, Computer Science (May 2006)

Research Experience

The University of Texas at Austin

Postdoctoral Fellow (2012-present)

Advisor: Marvin Whiteley

Project: Fitness determinants of P. aeruginosa for growth in disease conditions

- Investigating the genetic requirements for *P. aeruginosa* growth in CF lung secretions
- Map the conditionally essential genome for burn wound infection and systemic invasion

Project: Mapping all synthetic genetic interactions in a bacterium using second-generation sequencing

Harvard University

Ph.D. Student (2006-2012)

Advisor: Simon L. Dove

Project: An epigenetic switch that controls virulence gene expression in P. aeruginosa

- Characterized the bistable BexR regulon in *P. aeruginosa*
- Determined a requirement for positive feedback in bistable expression of bexR and the bexR regulon Project: Control of cupA fimbrial gene expression in P. aeruginosa by the LysR-type transcription regulator MexT
- Discovered a role for PrrA, an unannotated sRNA encoded downstream of the MexT-regulated mexEFoprN antibiotic efflux pump genes, in bistable cupA gene expression
- Generated evidence suggesting that PrrA negatively regulates the H-NS-like protein MvaU Project: Inducible protein degradation in P. aeruginosa
- Adapted a targeted protein depletion system for use in P. aeruginosa and demonstrated its utility in determining the co-essentiality of the H-NS-like proteins MvaT and MvaU

University of Iowa

Research Assistant (2002-2006)

Advisor: Michael A. Apicella

Project: Biochemistry of sialic acid transport in Haemophilus influenzae

Purified the sialic acid transport protein SiaP and characterized its sugar-binding biochemistry

Technical Skills

- Bacterial Genetics (genetic screens and directed mutagenesis in P. aeruginosa)
- Molecular biology (DNA manipulation, Western and Southern blot analysis, β-Galactosidase assays)
- Chromatin immunoprecipitation and gPCR
- RNA purification and real-time gRT-PCR
- Light and quantitative fluorescence microscopy of live and fixed bacterial cells
- Affymetrix GeneChips sample preparation and analysis (GeneSpring GX10)
- Numerical simulation of dynamic systems (Matlab)
- Computer programming (Java, C++, Perl)

Teaching Experience

Harvard University

Teaching Assistant, Graduate Principles of Genetics (Fall 2007, 2008)

Course Director: Fred Winston

Duties: Conducted weekly discussion sections, wrote and graded homework and exam questions

Awards and Honors

Presidential Scholar, University of Iowa (2002-2006)

National Merit Scholar, University of Iowa (2002-2006)

Kathleen K. Beninga Microbiology Scholar, University of Iowa (2004-2005)

Research Experience for Undergraduates Fellow, University of Iowa (2003-2004)

Peer-Reviewed Publications

<u>Turner, K.H.</u>, McManus, H.R., McFarland, K., and Dove, S.L. (2012). A transcription activator extends its regulatory reach to control an H-NS family member via a novel sRNA in *Pseudomonas aeruginosa*. In preparation.

Basset, A., <u>Turner, K.H.</u>, Boush, E., Sayeed, S., Dove, S.L., and Malley, R. (2012). An epigenetic switch mediates bistable expression of the type I pilus genes in *Streptococcus pneumoniae*. J Bacteriol. 194(5): 1088-91.

Basset, A., <u>Turner, K.H.</u>, Boush, E., Sayeed, S., Dove, S.L., and Malley, R. (2011). Expression of the type I pneumococcal pilus is bistable and negatively regulated by the structural component RrgA. Infect. Immun. 79(8): 2914-83.

<u>Turner, K.H.</u>, Vallet-Gely, I., and Dove, S.L. (2009). Epigenetic control of virulence gene expression in *Pseudomonas aeruginosa* by a LysR-type transcription activator. PLoS Genet. 5(12): e1000779.

Castang, S., McManus, H.R., <u>Turner, K.H.</u>, and Dove, S.L. (2008). H-NS family proteins function coordinately in an opportunistic pathogen. Proc. Natl. Acad. Sci. U.S.A. 105(48): 18947-18952.

Johnston, J.W., Coussens, N.P., Allen, S., Houtman, J.C., <u>Turner, K.H.</u>, Zaleski, A., Ramaswamy, S., Gibson, B.W., and Apicella, M.A. (2008). Characterization of the N-acetyl-neuraminic acid-binding site of the extracytoplasmic solute receptor (SiaP) of nontypeable *Haemophilus influenzae* strain 2019. J Biol. Chem. 283(2): 855-865.

References

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