David T. Pride, MD PhD

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Education and Honors:

1992-1996	Wake Forest University Undergraduate
1992-1996	Dean's List at Wake Forest University
1994-1996	Tri-Beta Biological Honor Society
1995	Fogarty Fellowship for International Study
1995-1996	Mortar Board Honor Society
1996	B.S. in Biology, Magna cum Laude, Wake Forest University
1996-2001	Vanderbilt University MSTP program
1998-2001	Microbes and Defense Society
2000	UNCF-Merck Graduate Research Fellowship
2000	Gates Millennium Scholarship
2001	PhD, Vanderbilt University Department of Microbiology and Immunology
2001-2003	New York University MSTP program
2003	MD, New York University School of Medicine
2006-2010	Postdoctoral Research Fellow, Stanford University School of Medicine
2007	UNCF-Merck Postdoctoral Research Fellowship
2007	Harold Amos Medical Faculty Development Fellowship
2008	Burroughs Wellcome Foundation Career Award for Medical Scientists
2009	ITI Young Investigator Innovation Award
2010-present	Assistant Professor of Pathology and Medicine, University of California, San
	Diego
	Director of Molecular Microbiology, UCSD Clinical Laboratories
	Associate Director of Microbiology, UCSD Clinical Laboratories
2015-present	Doris Duke Clinical Scientist Development Fellowship

Medical License History:

2006-present Board Certified Internal Medicine 2008-present Board Certified Infectious Disease

2014-present Board Certified American Board of Medical Microbiology

Hospitalist – Santa Clara Valley Medical Center – 2006 to 2011

Clinical Experience:

Resident – Internal Medicine – Massachusetts General Hospital – 2003 to 2005 Fellow – Infectious Diseases – Stanford University Hospital – 2005 to 2007 Hospitalist – Mills Peninsula Hospital – 2007 to 2009 Hospitalist – VA Medical Center Palo Alto – 2007 to 2010

Research Experience:

1992-1996	Research Assistant in the laboratory of Dr. Rosanna J. Spolski in the Wake Forest University Department of Biology.
1993-1996	Research Assistant in the laboratory of Dr. Catherine Harris in the Wake Forest University Department of Sociology.
1994	Research Assistant in the laboratory of Dr. Robert J. Christy at the University of Texas San Antonio Institute of Biotechnology.
1995	Research Assistant in the laboratory of Dr. Luz Angela Labrada at the Center for the International Study of Epidemiology and Disease in Medicine (CIDEIM) in Cali, Colombia.
1998-2001	Graduate Student in the laboratory of Dr. Martin Blaser in the Department of Microbiology and Immunology at Vanderbilt University.
2002-2006	Independent research at New York University and Massachusetts General Hospital.
2006-2010	Postdoctoral Research Fellow in the laboratory of Dr. David Relman at Stanford University.

Volunteer Service

1995	Wake Forest University representative at the North American Conference on
	Minorities in Math, Science, and Engineering (NACME)
1995-1996	Alpha Phi Alpha Fraternity Community Service Chairman
1995-1996	Volunteer work at hospice in Winston-Salem, NC
1998-2000	Teaching assistant for medical microbiology course
1998-2001	Vanderbilt University representative at the Minority Access to Research
	Conference (MARC).
2006-2009	Volunteering medical services at Santa Clara Valley PACE clinic

Oral Presentations

<u>CRISPR_10 Meeting 2009</u> – Session Convener and invited speaker – Comparisons of streptococcal CRISPRs and viromes in human saliva reveal bacterial adaptations specific to human oral viruses.

<u>Infection, Immunity and Transplantation Annual Meeting 2010</u> – Invited Speaker – Comparisons of CRISPRs and viromes in human saliva reveal bacterial adaptations specific to salivary bacteriophage.

<u>SD Microbiology Group – 2011</u> – Invited Speaker – Analysis of streptococcal CRISPRs in human saliva reveals substantial sequence diversity within and between subjects.

<u>BCRS Seminar Series – 2011</u> – Invited Speaker – Insights into the role of viral communities in the human oral cavity.

<u>CRISPR_12 Meeting 2012</u> – Invited Speaker – Comparisons of CRISPR content between saliva and skin: viral exposures may not be body site specific.

<u>Pathology Research Lecture Series – 2012</u> – Invited Speaker – Association between living environment, ecological niche, and human viral ecology.

<u>American Society for Microbiology – Annual Meeting 2013</u> – Invited Speaker – Association between living environment and human oral viral ecology.

<u>Exploring Host Microbiome Interactions – 2014</u> – Invited Speaker – Effects of bacteria on oral viruses and implications for spread.

<u>International Society for Microbial Ecology – Annual Meeting 2014</u> – Human oral viruses are personal, persistent, and gender consistent.

<u>Infectious Diseases Grand Rounds UCSD 2014</u> – Invited Speaker– Mass spectrometry for the identification of bacteria and fungi

<u>Microbiome Connections to the environment, health and disease</u> – Invited Speaker 2014 – The oral Virome.

<u>International Human Microbiome Congress – Annual Meeting 2015</u> – Invited Speaker - Roles of viruses in the human microbiome.

<u>Pathology Lecture Series, UC Irvine 2015</u> - Invited Speaker - Roles of viruses in the human microbiome.

ICAAC 2015 - Invited Speaker - Roles of viruses in the human microbiome.

Publications

Pride, D.T., R.J. Meinersmann, and M.J. Blaser. 2001. Allelic variation within *Helicobacter pylori babA* and *babB*. Infect. Immun. 69: 1160-1171. PMID 11160014.

Ando, T., R.M. Peek, **D. Pride**, S.M. Levine, T. Takata, Y.C. Lee, K. Kusugami, A. van der Ende, E.J. Kuipers, J.G. Kusters, and M.J. Blaser. 2002. Polymorphisms of *Helicobacter pylori* HP0638 reflect geographic origin and correlate with *cagA* status. J Clin Microbiol. 40: 239-46. PMID 11773122.

Pride, D.T., and M. J. Blaser. 2002. Concerted evolution between duplicated genetic elements in *Helicobacter pylori*. J. Mol. Biol. 316: 627-640. PMID 11866522.

- Ghose, C., G. Perez-Perez, M.C. Dominguez, **D.T. Pride**, and M.J. Blaser. 2002. Amerindians harbor *Helicobacter pylori* strains with East Asian genotypes: evidence for ancient *Helicobacter pylori* origin in humans. Proc Nat Acad Sci. 99: 15107-15111. PMID 12417749.
- Drake, W.P., Z. Pei, **D.T. Pride,** R.D. Collins, T.L. Cover, and M.J. Blaser. 2002. Molecular analysis of sarcoidosis and control tissues for *Mycobacteria* DNA. Emerging Infectious Diseases. 8: 1334-1341. PMID 12453366.
- **Pride, D.T.**, and M.J. Blaser. 2002. Identification of recently acquired genetic elements in *Helicobacter pylori* using oligonucleotide difference analysis. Genome Letters. 1: 2-15.
- **Pride, D.T.**, R.J. Meinersmann, T. Wassenaar, and M.J. Blaser. 2003. Evolutionary implications of tetranucleotide frequencies in prokaryotes. Genome Research. 13: 145-158. PMID 12566393.
- Tu, Z., D.W. Ussery, **D.T. Pride**, and M.J. Blaser. 2003. Genomic characteristics of the *C. fetus sap* Island. Genome Letters. 2: 34-40.
- Pei, Z., L. Yang, R.M. Peek, S.M. Levine, **D.T. Pride**, and M.J. Blaser. 2005. Bacterial biota in reflux esophagitis and Barrett's Esophagus. World Journal of Gastroenterology. 11: 7277-7283. PMID 16437628.
- **Pride, D.T.**, T. Wassenaar, C. Ghose, and M. J. Blaser. 2006. Evidence of host-virus co-evolution in tetranucleotide usage patterns of bacteriophages and eukaryotic viruses. BMC Genomics. 7: 8. PMID 16417644.
- Allen, S.S., W. Evans, J. Carlisle, R. Hajizadeh, M. Nadaf, B.E. Shepherd, **D.T. Pride**, J.E. Johnson, and W.P. Drake. 2008. Superoxide dismutase A antigens derived from molecular analysis of sarcoidosis granulomas elicit systemic Th-1 immune responses. Respiratory Research. 9:36. PMID 18439270.
- **Pride, D.T.**, and T. Schoenfeld. 2008. Genome signature analysis of thermal virus metagenomes reveals Archaea and thermophilic signatures. BMC Genomics. 9: 420. PMID 18798991.
- Willner, D., M. Furlan, R. Schmeider, J. Grasis, **D.T. Pride**, D.A. Relman, F.E. Angly, T. McDole, R.P. Mariella, F. Rohwer, and M. Haynes. 2010. Metagenomic detection of phage-encoded platelet binding factors in the human oral cavity. Proc Nat Acad Sci. 20547834.
- **Pride, D.T.**, Sun C.L., Salzman J., Rao N., Loomer P., Armitage G.C., Banfield J.F., Relman D.A. 2011. Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. Genome Res. 21: 126-136. PMID 21149389
- **Pride, D.T.**, Salzman J., Haynes M., Rohwer F., Davis-Long C., White R.A. III, Loomer P., Armitage G.C., Relman D.A. 2012. Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. ISME J. 6: 915-926. PMID 22158393

- **Pride, D.T.**, Salzman J., and Relman D.A. 2012. Comparisons of clustered regularly interspaced short palindromic repeats and viromes in human saliva reveal bacterial adaptations to salivary viruses. Environ Microbiol. 14: 2564-2576. PMID 22583485
- Robles-Sikisaka, R., Ly M., Boehm T., Naidu M., Salzman J., and **Pride D.T.** 2013. Association between living environment and human oral viral ecology. ISME J. PMID 23598790.
- Abeles, S.R., Robles-Sikisaka, R., Ly, M., Lum, A.G., Salzman, J., Boehm, T.K., and **Pride, D.T.** 2014. Human oral viruses are personal, persistent, and gender consistent. ISME J. PMID 24646696.
- Ly, M., Abeles, S.R., Boehm, T.K., Robles-Sikisaka, R., Naidu, M., Santiago-Rodriguez, T., and **Pride, D.T.** 2014. Altered oral viral ecology in association with periodontal disease. mBio. 5(3): e01133-14. PMID 24846382.
- Robles-Sikisaka, R., Naidu, M., Ly, M., Salzman, J., Abeles, S.R., Boehm, T.K., and **Pride, D.T.** 2014. Conservation of streptococcal CRISPRs on human skin and saliva. BMC Microbiology. 14: 146. PMID 24903519.
- Naidu, M., Robles-Sikisaka, R., Abeles S.R., Boehm T.K., and **Pride D.T.** 2014. Characterization of bacteriophage communities and CRISPR profiles from dental plaque. BMC Microbiol. 14:175. PMID 24981669. <u>Highly Accessed.</u>
- Abeles, S.R, and **Pride D.T.** 2014. Molecular bases and role of viruses in the human microbiome. J. Mol. Biol. PMID 25020228.
- Santiago-Rodriguez, T.M., Ly M., Bonilla N., and **Pride D.T.** 2015. The human urine virome in association with urinary tract infections. Front Microbiol. 6:14. PMID 25667584.
- Edlund, A., Santiago-Rodriguez T.M., Boehm T.K., and **Pride D.T.** 2015. Bacteriophage and their potential roles in the human oral cavity. J Oral Microbiol. 7: 27423. PMID 25861745.
- Santiago-Rodriguez, T.M. Naidu M., Jones M.B., Ly M., and **Pride D.T.** 2015. Identification of staphylococcal phage with reduced transcription in human blood through transcriptome sequencing. Front Microbiol. PMID 26074882.
- Lum, A.G., Santiago-Rodriguez T.M., Naidu M., Boehm T.K., and **Pride D.T.** 2015. Global transcription of CRISPR loci in the human oral cavity. BMC Genomics. 16: 401. PMID 25994215.
- Santiago-Rodriguez, T.M., Naidu M., Abeles S.R., Boehm T.K., Ly M., and **Pride D.T.** 2015. Transcriptome analysis of bacteriophage communities in periodontal health and disease. BMC Genomics. 16: 549. PMID 26215258.
- Abeles, S.R., Ly M., Santiago-Rodriguez T.M., and **Pride D.T.** 2015. Effects of long term antibiotic therapy on human oral and fecal viromes. PLOS One. 10:

e0134941. PMID 26309137.

Jones, M.B, Highlander S.K., Anderson E.L., Li W., Dayrit M., Klitgord N., Fabani M.M., Seguritan V., Green J., **Pride D.T.**, Yooseph S., Biggs W. Nelson K.E., and Venter J.C. Library preparation methodology can influence genomic and functional predictions in human microbiome research. Proc Natl Acad Sci USA. 112: 14024. PMID 26512100.

Santiago-Rodriguez, T.M., Ly M., Daigneault M.C., Brown I.H., McDonald J.A., Bonilla N., Allen-Vercoe E., and **Pride D.T.** 2015. Chemostat culture systems support diverse bacteriophage communities from human feces. Microbiome. 3: 58. PMID 26512100.

Hwang, J.H., Lyes M., Sladewski K., Enany S., McEachern E., Mathew D.P, Das S., Moshensky A., Bapat S., **Pride D.T.**, Ongkeko W.M., Crotty-Alexander L.E. 2016. Electronic cigarette inhalation alters innate immunity and airway cytokines while increasing the virulence of colonizing bacteria. J Mol Med. PMID 26804311.

Ghose C., Eugenis I., Sun X., Edwards A.N. McBride S.M., **Pride D.T.**, Kelly C.P. Ho D.D. 2016. Immunogenecity and protective efficacy of recombinant Clostridium difficile flagellar protein FliC. Emerg Microbes Infect. 5: e8. PMID 26839147.

Software

Pride DT. 2001. Swaap 1.0.3: A tool for analyzing substitutions and similarity in multiple alignments. Distributed by the author, Department of Microbiology and Immunology, Vanderbilt University School of Medicine in Nashville, TN.

Pride DT. 2001. Swaap PH 1.0.2: A tool for analyzing nucleotide usage patterns in coding and noncoding portions of microbial genomes. Distributed by the author, Department of Microbiology and Immunology, Vanderbilt University School of Medicine in Nashville, TN.

Pride DT. 2008. Swaap Genome Search: A tool for phylogenetic classification of metagenome fragments from prokaryotes and bacteriophages. Distributed by the author, Department of Medicine, Division of Infectious Diseases, Stanford University School of Medicine, Stanford, CA.

Pride DT. 2008. Swaap Gene: A tool for one step phylogenetic reproduction. Distributed by the author, Department of Medicine, Division of Infectious Diseases, Stanford University School of Medicine, Stanford, CA.

Ongoing Research Support

Burroughs Wellcome Fund CAMS Award Pride (PI) 03/01/09-08/01/16

Title: Bacteriophage communities in oral health and disease

The objective of this proposal is to develop techniques to evaluate the members of double stranded DNA bacteriophage communities from the oral cavity of human subjects with oral

health and disease.

Role: PI

Doris Duke Foundation CDSA Award Pride (PI) 07/01/15-06/30/18

Title: Human viral communities as vehicles for the spread of antibiotic resistance in the community.

The objective of this proposal is to develop techniques to decipher the role of human bacteriophage communities in the transmission of antibiotic resistance among human subjects in close contact.

Role: PI

Previous Research Support

UNCF-Merck Postdoctoral Research Fellowship Pride (PI) 08/01/07-09/01/09

Title: None

The objective of this proposal is to provide support for the creation of new algorithms for improving the phylogenetics of prokaryotes based on patterns of oligonucleotide usage.

Role: PI

ITI Young Investigator Innovation Award Pride (PI) 01/01/09-8/31/09

Title: Pyrosequencing analysis of human bacteriophage communities in health and disease The objective of this proposal is to develop Roche/454 Pyrosequencing techniques to evaluate bacteriophage communities in the human oral cavity.

Role: PI

Harold Amos Medical Faculty Development Award Pride (PI) 01/01/08-04/31/12 Title: The phylogenetics of nucleotide usage patterns: origin of metagenome DNA fragments and unknown bacteriophages revealed.

The objective of this proposal is to generate new methodology for understanding the origin and host prokaryotes of bacteriophages isolated from metagenome data.

Role: PI

1K08AI08502 Pride (PI) 08/19/11 – 07/31/14

NIH/NIAID

Title: Microbiome analysis of human oral bacteriophage communities

The objective of this proposal is identify and compare bacteriophages and their bacterial hosts in human saliva.

Role: PI