• **Name:** James Borneman, Ph.D.

• **Current Position:** Professor and Vice Chair, Department of Microbiology and Plant Pathology, University of California, Riverside

• **Country:** USA

• **Educational Background:**

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Northern Illinois University, DeKalb, IL	B.S.	1986	Biological Sciences
Northern Illinois University, DeKalb, IL	Ph.D.	1994	Biological Sciences
University of Wisconsin, Madison, WI	Postdoc	1997	Molecular Microbial Ecology

• **Professional Experiences:**

1997-2003 Assistant Professor, University of California, Riverside
2003-2008 Associate Professor, University of California, Riverside
2008-present Professor, University of California, Riverside

• **Professional Organizations:**

2000 & 2004 Secretary, Western Regional Project W-147 on Biological Control
2001 Panel Member, USDA NRI Competitive Grants Program
2001-03 Panel Member, University of California Integrated Pest Management Program
2001 & 2005 Chair, Western Regional Project W-147 on Biological Control
2003-2005 Associate Editor, Phytopathology
2003-2010 Director, Graduate Program in Microbiology, University of California, Riverside
2006-2014 Editorial Board, Applied and Environmental Microbiology
2011 Chair, Steering Committee that Created Undergraduate Microbiology Major, University of California, Riverside.
2011-present Chair, Steering Committee, Undergraduate Microbiology Major, University of California, Riverside.
2010-2014 Meeting Organizer and Host, Annual Western Regional Project on Biological Control
2012-present Vice Chair, Department of Microbiology and Plant Pathology.
2015-present Editorial Board, Journal of Clinical Microbiology.
2016-present Senior Editor, Phytobiomes.

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• Main Scientific Publications:

1. The publications that came from my student and postdoc years were from several different areas of science. In my Ph.D. studies, my research focused on developing strategies to express and utilize catalytic RNA in plants. Two highlights from this period included publication A, which was the first report showing that a ribozyme could be expressed in a plant and maintain its catalytic activity. The second (publication B) was a practical byproduct of this line of research, where I created a simple an inexpensive way to produce an RNA size ladder for gel electrophoresis by using in vitro transcription of a series of concatemerized ribozymes. In my postdoc years, which occurred near the beginning of the field of molecular microbial ecology, my first publication (publication C) presented the first thorough (at that time) description of bacteria in soil. In addition, in this paper, I also presented a new method that I developed that adapted the FastPrep DNA extraction system for use with environmental samples. This method initiated a transformation in DNA and RNA extraction from environmental samples, based on bead-beating and column-based purification, providing the simplest and fastest way to extract nucleic acids from all types of samples. Building on this, researchers from FastPrep started their own company, MoBio Laboratories, which has become the leader in DNA and RNA extraction kits. My second publication (publication D) demonstrated the affect of deforestation in the amazon rainforest on soil bacterial communities. It also presented a simple but effective new method to described bacterial communities, which is still used today, 18 years after it was published.

A. **Borneman, J.,** Tritz, R., Hampel, A., Altschuler, M. 1995. Detection of cleavage products from an in vivo transcribed cis-hairpin ribozyme in turnips using the CaMV plant virus. Gene. Vol. 159: p.137-142.
B. **Borneman, J.,** Altschuler, M. 1995. Simple method to produce RNA size markers using cis ribozymes. Biotechniques. p.404-406.
C. **Borneman, J.,** Skroch, P.W., Jansen, J.A., O'Sullivan, K.L., Palus, J.A., Rumjanek, N.G., Nienhuis, J., Triplett, E.W. 1996. Molecular microbial diversity of an agricultural soil in Wisconsin. Applied and Environmental Microbiology. Vol. 62: p.1935-1943.
D. **Borneman, J.,** Triplett, E.W. 1997. Molecular microbial diversity in eastern Amazonian soils: Evidence for unusual microorganisms and population shifts caused by deforestation. Applied and Environmental Microbiology. Vol. 63: p.2647-2653.

2. During my 18 years as a faculty at UC Riverside, I have developed, or been part of a team that developed, numerous molecular, statistical or algorithmic methods for molecular microbial ecology studies. A few highlights include a novel strategy to identify the active microorganisms in an environment (publication A). This method involved adding a thymidine analog (BrdU) to an environmental sample, performing an incubation step, extracting DNA from the sample, immunopurifying the BrdU-labeled DNA and then performing a community analysis on this captured DNA. I also developed a polony-based method that provided the first semi-highthroughput method to examine microbial communities without the population skew that is created by PCR amplification, which is inherent in all current high throughput methods such as Illumina sequencing (publication B). In addition, I collaborated with Marek Chrobak (Professor of Computer Science, UC Riverside) to create software for designing sequence-selective primers

and probes (publication D). This software provides the only automated tool enabling primer-template mismatches to be placed at the 3' end of the primers, which is a property that is crucial for sequence selectivity, especially for highly conserved sequences such as rRNA genes. Finally, I created the first Illumina-based sequencing method that enables – for the fist time – species and sometimes strain level resolution by analyzing the rRNA internal transcribed spacer region (publication D).

A. **Borneman, J.** 1999. Culture-independent identification of microorganisms that respond to specified stimuli. Applied and Environmental Microbiology 65:3398-3400.
B. Ruegger PM, Bent E, Li W, Jeske DR, Cui X, Braun J, Jiang T, **Borneman J**. 2012. Improving oligonucleotide fingerprinting of rRNA genes by implementation of polony microarray technology. Journal of Microbiological Methods 90:235-240.
C. Huang YT, Jiue-in Yang, M. Chrobak and **J. Borneman.** 2014. PRISE2: Software for designing sequence-selective PCR primers and probes. BMC Bioinformatics 15:317.
D. Ruegger PM, Clark RT, Weger JR, Braun J, **Borneman J.** 2014. Improved resolution of bacteria by high throughput sequence analysis of the rRNA internal transcribed spacer. J Microbiol Methods 105:82-7.

3. The major focus of my research program has been understand the role of microbes in various processes in soil and human health. These research projects typically follow a three-phased strategy. The first is to identify microorganisms that correlate with the phenotype of interest. The second is to causally test these microorganisms using Koch′s postulates like experimentation. The third is to translate these findings into practical strategies to reduce agricultural pests or improve human health. In our agricultural research, we successfully identified a key fungus, from a complex soil microbial community, which was able to inhibit a plant parasitic nematode when applied to various soil types (publication A). We have completed the first two phases of this project, and now we are in the process of translating our findings into a practical solution for farmers in the form of a new cropping decision model. More recently, we have applied a similar strategy to identify microorganisms involved in inflammatory bowel disease (IBD), HIV, cancer, diabetes and obesity. In this area, we have identified shifts in rectal microbial communities and metabolic pathways associated with HIV infection (publication B). We posit that these pathways may represent novel interventional targets for HIV therapy if normalizing the microbial composition or functional activity of the microbiota proves therapeutically useful. I have also collaborated with researchers at UCLA and Stanford to demonstrate that a susceptibility locus (Fut2) in Crohn′s disease patients leads to changes in the intestinal microbiome and microbe-associated energy metabolism (publication C). These alterations in humans were consistent with changes in the murine genetic counterpart. Since *Fut2*-/- mice exhibit intestinal inflammation, our research indicates that changes to this locus and the associated downstream alterations in the intestinal microbiome may play a causative role in Crohn′s disease. Finally, in a recent study, we performed an analysis of host associated, intestinal bacteria from two colonies of isogenic mice exhibiting different lymphoma latencies. This work identified a bacterium, *Lactobacillus johnsonii*, which was more abundant in the small intestine of the more cancer-resistant mice, and

which decreased systemic DNA damage when orally administered to the more cancer-prone mice. This work is presented in publication D. My lab performed the research that identified and isolated the bacterium that was able to reduce systemic genotoxicity in mice, and I am one of the two cocorresponding authors on this paper.

A. **Borneman J.,** Becker O. 2007. Identifying Microorganisms Involved in Specific Pathogen Suppression in Soil. Annual Review of Phytopathology 45:153-172.
B. McHardy IH, Li X, Tong M, Ruegger P, Jacobs J, **Borneman J**, Anton P, Braun J. 2013. HIV Infection is associated with compositional and functional shifts in the rectal mucosal microbiota. Microbiome. 1:26. PMID: 24451087.
C. Tong M, McHardy I, Ruegger P, Goudarzi M, Kashyap PC, Haritunians T, Li X, Graeber TG, Schwager E, Huttenhower C, Fornace AJ Jr, Sonnenburg JL, McGovern DP, **Borneman J**, Braun J. 2014. Reprograming of gut microbiome energy metabolism by the FUT2 Crohn's disease risk polymorphism. ISME J. doi: 10.1038/ismej.2014.64. PMID: 24781901.
D. Yamamoto ML, Maier I, Dang AT, Berry D, Liu J, Ruegger PM, Yang JI, Soto PA, Presley LL, Reliene R, Westbrook AM, Wei B, Loy A, Chang C, Braun J, **Borneman J**, Schiestl RH. 2013. Intestinal bacteria modify lymphoma incidence and latency by affecting systemic inflammatory state, oxidative stress, and leukocyte genotoxicity. Cancer Res. 73:4222-32. PMID: 23860718.

Complete List of Published Work:
https://www.ncbi.nlm.nih.gov/sites/myncbi/1lMHplJA16FQV/bibliography/40779248/public/?sort=date&direction=ascending

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