Publications Cont'd

Chris Smith, Christopher Smith, Hugh Robertson, Martin Helmkampf, Aleksey Zimin, Mark Yandell, Carson Holt, Hao Hu, Ehab Abouheif, Richard Benton, Elizabeth Cash, Vincent Croset, Cameron Currie, Eran Elhaik, Christine Elsik, Marie-Julie Favé, Vilaiwan Fernandes, Joshua Gibson, Dan Graur, Wulfila Gronenberg, **Kirk J. Grubbs**, Darren Hagen, Ana Sofia Ibarraran Viniegra, Brian Johnson, Reed Johnson, Abderrahman Khila, Jay Kim, Kaitlyn Mathis, Monica Muñoz-Torres, Marguerite Murphy, Julie Mustard, Rin Nakamura, Oliver Niehuis, Surabhi Nigam, Rick Overson, Jennifer Placek, Rajendhran Rajakumar, Justin Reese, Garret Suen, Shu Tao, Candice Torres, Neil Tsutsui, Lumi Viljakainen, Florian Wolschin, Jürgen Gadau. **Draft genome of red harvester ant *Pogonomyrmex barbatus*.** PNAS 2011; published ahead of print January 31, 2011, doi:10.1073/pnas.1007901108

Kirk J. Grubbs, Peter H.W. Biedermann, Garret Suen, Sandra M. Adams, Joseph A. Moeller, Jonathan L. Klassen, Lynne A. Goodwin, Tanja Woyke, A. Christine Munk, David Bruce, Chris Detter, Roxanne Tapia, Cliff S. Han and Cameron R. Currie. **The Complete Genome Sequence of *Streptomyces* cf. *griseus* (XylebKG-1), an Ambrosia Beetle-Associated Actinomycete.** J. Bact. 2011; Accepted

Kirk J. Grubbs, Jarrod J. Scott, Kevin J. Budsberg, Teri C. Balser and Cameron R. Currie. Characterization of hive component associated microbial communities in Honey Bee colonies. In Prep

Kirk J. Grubbs, Renee Kontnik, Cameron Currie and Jon Clardy. Hive associated streptomycete produces novel antibiotic that specifically inhibits foulbrood. In Prep

Kirk J. Grubbs, Frank Surup, Jon Clardy and Cameron Currie. *Xyleborinus saxesenii* and *Xyleborus affinis* associated actinomycetes produce cycloheximide. In Prep

Honor & Awards

6TH International Symbiosis Society Congress Poster Contest Winner (2009)

Georgia HOPE Scholarship (2004-2005)

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Kirk Grubbs

Program of the Thesis Defense Seminar for the
Degree of Doctor of Philosophy
in Cellular and Molecular Pathology

"Organization and Function of the Microbial Communities Associated with the European Honey Bee, *Apis mellifera*, and its Hive Structures"

Monday, August 12, 2013, 10 am
1520 Microbial Sciences Building

Research conducted in the lab of
Cameron R. Currie, PhD
Department of Bacteriology

Kirk Grubbs' Thesis Abstract

Organization and Function of the Microbial Communities Associated with the European Honey Bee, *Apis mellifera*, and its Hive Structures

Kirk Grubbs
Under the supervision of
Professor Cameron R. Currie, PhD
at the University of Wisconsin-Madison

Symbiosis has shaped all living organisms. This is the result of adaptation to and maintenance of interspecific interactions. By far, the microbes studied in association with other organisms have generally been parasitic in nature. It has not been until the last half century that bacterial and fungal symbionts have become recognized for the necessary and beneficial roles they fulfill in reference to multicellular hosts. In this relatively short time, the scientific field has made great strides in the understanding of evolutionary processes by focusing on the dynamics of not only parasitic but also commensal and mutualistic relationships. Perhaps best understood are those nutrition based mutualisms in which the associated microbial community digests and makes more bioavailable complex and recalcitrant diet materials for the host. Beyond this type of relationship, microbial associates are known to function in certain aspects of development, immunomodulation and defense. In this dissertation I explore the microbial communities associated with honey bees and their complex hive components, with special attention paid to defense based mutualisms in social insects. I begin by discussing some basic and necessary concepts in understanding the importance and scope of symbiosis. I then move on to discuss honey bees, their hives and what is known about the microbial communities associated with them. In the second chapter I make use of a lipid based analysis to explore hives as a whole and individual components. I show that the communities associated with hives are structured by component. Thus in order to accurately describe the hive microbiome, profiles must be organized by component type. In chapter three, I recognize the expanding prevalence in scientific literature concerning defense based mutualisms between Actinobacteria and insects. I further my exploration of honey hives by using culture based techniques to isolate Actinobacteria from colony components. A number of these isolates prove to have growth inhibitive properties towards common insect pathogens. One isolate of particular interest was found to produce a novel antibiotic compound, named Apinimycin, that specifically inhibited growth of the most common and devastating honey bee pathogen, American foulbrood (Paenibacillus larvae). In the fourth chapter, I expand my exploration of insects for Actinobacteria based defensive mutualisms to ambrosia beetles. Using techniques similar to those in the previous chapter, I consistently isolate one Actinobacterial morphotype from both ambrosia beetle species explored. All isolates have identical 16S rRNA gene sequences and a model isolate is shown to inhibit the growth of a putatively antagonistic fungus, but not the mutualistic fungus via production of cycloheximide. This chapter effectively expands the ambrosia beetle symbiosis in one species from a bipartite to a quadripartite system. In total, this work underscores the necessity of microbial associations. This is done by organizing the communities associated with honey bee hives and elucidating two unique defense based symbioses in which Actinobacteria are producing antibiotics to inhibit the growth parasitic symbionts.

Publications

Garret Suen, Clotilde Teiling, Lewyn Li, Carson Holt, Ehab Abouheif, Erich Bornberg-Bauer, Pascal Bouffard, Eric J. Caldera, Elizabeth Cash, Amy Cavanaugh, Olgert Denas, Eran Elhaik, Marie-Julie Favé, Jürgen Gadau, Joshua D. Gibson, Dan Graur, **Kirk J. Grubbs**, Darren E. Hagen, Timothy T. Harkins, Martin Helmkampf, Hao Hu, Brian R. Johnson, Jay Kim, Sarah E. Marsh, Joseph A. Moeller, Mónica C. Muñoz-Torres, Marguerite C. Murphy, Meredith C. Naughton, Surabhi Nigam, Rick Overson, Rajendhran Rajakumar, Justin T. Reese, Jarrod J. Scott, Chris R. Smith, Shu Tao, Neil D. Tsutsui, Lumi Viljakainen, Lothar Wissler, Mark D. Yandell, Fabian Zimmer, James Taylor, Steven C. Slater, Sandra W. Clifton, Wesley C. Warren, Christine G. Elsik, Christopher D. Smith, George M. Weinstock, Nicole M. Gerardo, and Cameron R. Currie. **The Genome Sequence of the Leaf-cutter Ant *Atta cephalotes* Reveals Insights into its Obligate Symbiotic Lifestyle.** PLoS Gen 2011; 7(2): e1002007.doi:10.1371/journal.pgen.1002007

Christopher D. Smith, Ehab Abouheif, Richard Benton, Elizabeth Cash, Vincent Croset, Cameron R. Currie, Eran Elhaik, Christine G. Elsik, Marie-Julie Fave, Vilaiwan Fernandes, Jürgen Gadau, Joshua D. Gibson, Dan Graur, **Kirk J. Grubbs**, Darren E. Hagen, Martin Helmkampf, Jo-Anne Holley, Carson Holt, Hao Hu, Ana Sofia Ibarraran Viniegra, Brian R. Johnson, Reed M. Johnson, Abderrahman Khila, Jay W. Kim, Joseph Laird, Kaitlyn A. Mathis, Joseph A. Moeller, Monica C. Munoz-Torres, Marguerite C. Murphy, Rin Nakamura, Surabhi Nigam, Rick Overson, Jennifer E. Placek, Rajendhran Rajakumar, Justin T. Reese, Hugh M. Robertson, Chris R. Smith, Andrew V. Suarez, Garret Suen, Elissa L. Suhr, Shu Taoh, Candice W. Torres, Ellen van Wilgenburg, Lumi Viljakainen, Kimberly K. O. Walden, Alexander L. Wild, Mark D. Yandell, James A. Yorke, Aleksey Zimin, Neil D. Tsutsui. **Draft Genome of the Globally Widespread and Invasive Argentine ant (*Linepithema humile*).** PNAS 2011; published ahead of print January 31, 2011, doi:10.1073/pnas.1008617108