NATIONAL CENTER FOR AGRICULTURAL UTILIZATION RESEARCH

Microbial Genomics & Bioprocessing Research

Todd J. Ward

Research Geneticist

Ph.D. Genetics, Texas A&M University
B.S. Biology, University of Cincinnati

Microbial Genomics and Bioprocessing Research Unit
National Center for Agricultural Utilization Research
United States Department of Agriculture
Peoria, IL 61604-3999

Tel: (309)-681-6394
Fax: (309)-681-6672
E-mail: wardtj@ncaur.usda.gov

Research

Research in my lab is focused on molecular evolution and population genetics of microbial pathogens. The approach is largely computational and aimed at understanding adaptation and diversification of microbial pathogens and their virulence factors.

Population genetics and molecular evolution of foodborne bacterial pathogens
Listeria monocytogenes is responsible for one-quarter of foodborne disease-related deaths linked to known pathogens and is the leading cause of food recalls in the U.S. Current research in my laboratory is focused on developing a comparative evolutionary framework for understanding diversification and ecological adaptation of *L. monocytogenes*. We have used a combination of multigene phylogenetic analyses, ecological surveys, and analyses of demographic history to understand the evolution and current phylogenetic distribution of phenotypic, ecological and genetic variation within this species. As a result, we have demonstrated that lineage-specific differences in frequency of association with human listeriosis likely reflect ecological adaptations to the food processing environment, and not differences in virulence or host range as had been previously suggested. This work has also identified that the epidemic-associated lineage (lineage 1) has been exposed to a series of population bottlenecks that did not impact variation in the other *L. monocytogenes* lineages, indicating that these lineages have limited demographic exchangeability and suggesting that these lineages may actually represent different species. Current work is focused on characterizing the nature of selective constraint across the genome and identifying examples of lineage-specific adaptive evolution through a combination of comparative genomic and molecular evolutionary approaches. Information on genetic diversity and population structure developed from these projects is also being applied to enhance outbreak detection and epidemiological investigation.

Evolution of mycotoxigenic plant pathogens
Mycotoxigenic plant pathogens in the *Fusarium graminearum* species complex cause billion dollar yearly losses to agriculture as a result of reduced yields and price discounts. These pathogens also represent a serious threat to food safety due to contamination of cereal grains with trichothecene mycotoxins that are potent inhibitors of eukaryotic protein synthesis and powerful modulators of vertebrate immune function. Previous and ongoing research in our lab has been focused on understanding the evolution and adaptive significance of differences in trichothecene metabolite profiles (chemotypes) produced by *Fusarium*. Our previous phylogenetic and molecular evolutionary analyses demonstrated that trichothecene chemotypes are strain-specific but have a polyphyletic distribution within the B-trichothecene lineage of *Fusarium* due to balancing selection acting on chemotype differences that originated in the ancestor of all B-trichothecene species. This selection is focused on interacting polymorphisms located at both ends of a trichothecene biosynthetic gene cluster, resulting in the maintenance of disequilibrium between the ends of the cluster which include genes responsible for chemotype-specific steps in trichothecene biosynthesis. We are currently investigating the phylogenetic, geographic, and host distributions of trichothecene chemotypes globally in order to elucidate the basis for the observed balancing selection, and provide the evolutionary information and molecular tools needed for global monitoring and disease control efforts.

Selected Publications

M. K. Borucki, J. Reynolds, D. R. Call, **T. J. Ward**, B. Page and J. Kadushin. Suspension microarray with dendrimer signal amplification allows direct and high throughput subtyping of *Listeria monocytogenes* from genomic DNA. *Journal of Clinical Microbiology* (in press).

A. P. Rooney and **T. J. Ward**. 2005. Evolution of a large ribosomal RNA multigene family in filamentous fungi: Birth and death of a concerted evolution paradigm. *Proceedings of the National Academy of Sciences of the USA* 102:5084-5089.

T. J. Ward, L. Gorski, M. K. Borucki, R. E. Mandrell, J. Hutchins and K. Pupedis. 2004. Intraspecific phylogeny and lineage group identification based on the *prfA* virulence gene cluster of *Listeria monocytogenes*. *Journal of Bacteriology* 186:4994-5002.

K. O'Donnell, **T. J. Ward**, D. M. Geiser, H. C. Kistler and T. Aoki. 2004. Genealogical concordance between the mating type locus and seven other nuclear genes supports formal recognition of nine phylogenetically distinct species within the *Fusarium graminearum* clade. *Fungal Genetics and Biology* 41:600-623.

M. Kimura, T. Tokai, K. O'Donnell, **T. J. Ward**, M. Fujimura, H. Hamamoto, T. Shibata and I. Yamaguchi. 2003. The trichothecene biosynthesis gene cluster of *Fusarium graminearum* F15 contains a limited number of essential pathway genes and expressed nonessential genes. *Federation of European Biochemical Societies Letters* 539:105-110.

T. J. Ward, J. P. Bielawski, H. C. Kistler, E. Sullivan and K. O'Donnell. 2002. Ancestral polymorphism and adaptive evolution in the trichothecene mycotoxin gene cluster of phytopathogenic *Fusarium*. *Proceedings of the National Academy of Sciences, USA* 99:9278-9283.

K. O'Donnell, F. M. Lutzoni, **T. J. Ward** and G. L. Benny. 2001. Evolutionary relationships among mucoralean fungi (Zygomycota): Evidence for family polyphyly on a large scale. *Mycologia* 93:286-296.

T. J. Ward, L. C. Skow, D. S. Gallagher, R. D. Schnabel, C. A. Nall, C. E. Kolenda, S. K. Davis, J. F. Taylor and J. N. Derr. 2001. Differential introgression of uniparentally-inherited markers in bison populations with hybrid ancestries. *Animal Genetics* 32:89-91.

B. J. Ruef, **T. J. Ward**, C. R. Oxner, P. G. Conley, W. C. Brown and A. C. Rice-Ficht. 2000. Phylogenetic analysis with newly characterized *Babesia bovis* hsp70 and hsp90 provides strong support for paraphyly within the piroplasms. *Molecular and Biochemical Parasitology* 109:67-72.

T. J. Ward, J. P. Bielawski, S. K. Davis, J. W. Templeton and J. N. Derr. 1999. Identification of domestic cattle hybrids in wild cattle and bison species: A general approach using mtDNA markers and the parametric bootstrap. *Animal Conservation* 2:51-57.

T. J. Ward, R. L. Honeycutt and J. N. Derr. 1997. Nucleotide sequence evolution at the κ-casein locus: Evidence for positive selection within the family Bovidae. *Genetics* 147:1863-1872.

Last Revised: April 6, 2005