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Molecular Evolutionary Biology of *Fusarium*

Research in my laboratory focuses on several aspects of the evolutionary biology of *Fusarium*, a large genus of filamentous fungi that represents the single most important group of mycotoxigenic plant pathogens. Fusaria have also emerged within the past two decades as opportunistic pathogens of severely immuno-compromised patients. Members of this genus produce an amazing diversity of toxic secondary metabolites, such as trichothecenes (potent inhibitors of eukaryotic protein synthesis and virulence-associated factors towards sensitive plant hosts), fumonisins (suspected carcinogens) and estrogenic compounds, which pose a serious threat to human and plant health and food safety. One of the primary goals of my research program is to develop molecular epidemiological tools for the rapid detection and identification of the most important fusarial pathogens of plants and humans. To achieve this objective, we have been using multilocus sequence typing (MLST) to identify species limits and to examine their population biology. Knowledge of species limits is essential for understanding their geographic distribution, host range and toxin potential. This information is critical in order to establish successful molecular surveillance programs for economically devastating plant diseases such as *Fusarium* Head Blight (FHB) of wheat and barley and Sudden Death Syndrome (SDS) of soybean (for publications, see below). Just within the past decade, FHB endemics in the upper Midwest of the U. S. have accounted for approximately 3 billion dollars in losses to U. S. agriculture because of low yields and price discounts due to toxin contaminated grain. Research in my laboratory has shown that both of these diseases are caused by several genetically distinct species that are non-indigenous to the United States. Our phylogenetic epidemiological studies are directed at minimizing the threat of inadvertent introductions of foreign FHB and SDS pathogens into the U. S. We are also using MLST to characterize the genetic diversity of medically important fusaria as part of a multi-institution collaborative study. Lastly, some of

my research has focused on the evolution of the Zygomycota and true morels (for publications, see below).

Selected Publications

Evolution of *Fusarium* Head Blight (FHB) and trichothecene mycotoxins

O'Donnell, K., Cigelnik, E. and Casper, H. H. 1998. Molecular phylogenetic, morphological, and mycotoxin data support reidentification of the Quorn mycoprotein fungus as *Fusarium venenatum*. *Fungal Genetics and Biology* 22:57-67.

O'Donnell, K., Kistler, H. C., Tacke, B. K. and Casper, H. C. 2000. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab. *Proc. Natl. Acad. Sci. USA* 97:7905-7910.

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

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

O'Donnell, K., Ward, T. J., Geiser, D. M., Kistler, H. C. and Aoki, T. 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 Genet. Biol.* 41:600-623.

Gale, L. R., Bryant, J. D., Calvo, S., Giese, H., Katan, T., O'Donnell, K., Suga, H., Taga, M., Usgaard, T. R., Ward, T. J. and Kistler, H. C. 2005. Chromosome complement of the fungal plant pathogen *Fusarium graminearum* based on genetic and physical mapping and cytological observations. *Genetics* 171:1-17.

Evolution of the *Fusarium solani* species complex [including Sudden Death Syndrome (SDS) of soybean]

O'Donnell, K. 2000. Molecular phylogeny of the *Nectria haematococca* - *Fusarium solani* species complex. *Mycologia* 92:919-938.

Aoki, T., O'Donnell, K., Homma, Y. and Lattanzi, A. R. 2003. Sudden death syndrome of soybean is caused by two morphologically and phylogenetically distinct species within the *Fusarium solani* species complex, *F. virguliforme* in North America and *F. tucumaniae* in South America. *Mycologia* 95:660-684.

Aoki, T., O'Donnell, K. and Scandiani, M. 2005. Sudden Death Syndrome of soybean in South America is caused by four species of *Fusarium*: *Fusarium brasiliense* sp. nov., *F. cuneirostrum* sp. nov., *F. tucumaniae* and *F. virguliforme*. *Mycoscience* 46:162-183.

Evolution of the *Gibberella fujikuroi* species complex [mycotoxigenic phytopathogens including most fumonisins toxin producers]

O'Donnell, K. and Cigelnik, E. 1997. Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. *Mol. Phylogenet. Evol.* 7:103-116.

Nirenberg, H. and O'Donnell, K. 1998. New *Fusarium* species and combinations within the *Gibberella fujikuroi* species complex. *Mycologia* 90:434-458.

O'Donnell, K., Cigelnik, E. and Nirenberg, H. 1998. Molecular systematics and phylogeography of the *Gibberella fujikuroi* species complex. *Mycologia* 90:465-493.

O'Donnell, K., Nirenberg, H. I., Aoki, T. and Cigelnik, E. 2000. A multigene phylogeny of the *Gibberella fujikuroi* species complex: Detection of additional phylogenetically distinct species. *Mycoscience* 41:61-78.

Schweigkofler, W., O'Donnell, K. and Garbelotto, M. 2004. Detection and quantification of airborne conidia of *Fusarium circinatum*, the causal agent of pine pitch canker, from two California sites by using a real-time PCR approach combined with a simple spore trapping method. *Appl. Environ. Microbiol.* 70:3512-3520.

Evolution of the *Fusarium oxysporum* species complex [wilt pathogens of many economically important plants]

O'Donnell, K., Kistler, H. C., Cigelnik, E. and Ploetz, R. C. 1998. Multiple evolutionary origins of the fungus causing Panama disease of banana: Concordant evidence from nuclear and mitochondrial gene genealogies. *Proc. Natl. Acad. Sci. USA* 95:2044-2049.

Baayen, R. P., O'Donnell, K., Waalwijk, C., Bonants, P. J. M., Cigelnik, E., Kroon, P. N. M. and Roebroek, E. J. A. 2000. Gene genealogies and AFLP analyses within the *Fusarium oxysporum* complex identify monophyletic and non-monophyletic formae speciales causing wilt and rot disease. *Phytopathology* 90:891-900.

Baayen, R. P., O'Donnell, K., Breeuwsma, S., Geiser, D. M. and Waalwijk, C. 2001. Molecular relationships of fungi within the *Fusarium redolens*-*F. hostae* clade. *Phytopathology* 91:1037-1044.

Skovgaard, K., Nirenberg, H. I., O'Donnell, K. and Rosendahl, S. 2001. Evolution of *Fusarium oxysporum* f.sp. *vasinfectum* races inferred from multigene genealogies. *Phytopathology* 91:1231-1237.

O'Donnell, K., Sutton, D. A., Rinaldi, M. G., Magnon, K. C., Cox, P. A., Revankar, S. G., Sanche, S., Geiser, D. M., Juba, J. H., van Burik, J.-A. H., Walsh, T. J., Francesconi, A., Anaissie, E. J., Padhye, A. and Robinson, J. S. 2004. Genetic diversity of human pathogenic members of the *Fusarium oxysporum* complex inferred from gene genealogies and AFLP analyses: Evidence for the recent dispersion of a geographically widespread clonal lineage and nosocomial origin. *J. Clin. Microbiol.* 42:5109-5120.

Schroers, H.-J., Baayen, R. P., Meffert, J. P., Hooftman, M. and O'Donnell, K. 2004. *Fusarium foetens*, a new species pathogenic to begonia elatior hybrids (*Begonia x hiemalis*) and the sister taxon of the *Fusarium oxysporum* species complex. *Mycologia* 95:393-406.

Web-based Identification of *Fusarium*

Geiser, D. M., del Mar Jiménez-Gasco, M., Kang, S., Makalowska, I., Veeraraghavan, N., Ward, T. J., Zhang, N., Kuldau, G. A. and O'Donnell, K. 2004. FUSARIUM-ID v.1.0: A DNA sequence database for identifying *Fusarium*. *Europ. J. Plant Pathol.* 110:473-479.

Evolution of the Zygomycota

O'Donnell, K., Cigelnik, E. and Benny G. L. 1998. Phylogenetic relationships among the Harpellales and Kickxellales. *Mycologia* 90:624-639.

Voigt, K., Cigelnik, E. and O'Donnell, K. 1999. Phylogeny and PCR identification of clinically important Zygomycota based on nuclear rDNA sequence data. *J. Clin. Microbiol.* 37:3957-3964.

Benny G.L. and O'Donnell, K. 2000. *Amoebidium parasiticum* is a protozoan, not a Trichomycete. *Mycologia* 92:1133-1137.

Tanabe, Y., O'Donnell, K., Saikawa, M. and Sugiyama, J. 2000. Molecular phylogeny of parasitic Zygomycota (Dimargaritales, Zoopagales) based on nuclear small subunit ribosomal DNA sequences. *Mol. Phylogenet. Evol.* 16:253-262.

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

James, T. Y. and O'Donnell, K. Zygomycota. 2004. Tree of Life.
<http://tolweb.org/tree?group=Zygomycota>.

Taylor, J. W., Spatafora, J., O'Donnell, K., Lutzoni, F., James, T., Hibbett, D. S., Geiser, D., Bruns, T. D. and Blackwell, M. 2004. The Fungi. Pp. 171-194. *In*: Cracraft, J. and Donoghue, M. J. (Eds) Assembling the Tree of Life. Yale University Press.

Evolution of Morels and Truffles (Ascomycota)

O'Donnell, K., Cigelnik, E., Weber, N. S. and Trappe, J. M. 1997. Phylogenetic relationships among ascomycetous truffles and the true and false morels inferred from 18S and 28S ribosomal DNA sequence analysis. *Mycologia* 89:48-65.