NATIONAL CENTER FOR AGRICULTURAL UTILIZATION RESEARCH

Microbial Genomics & Bioprocessing Research

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Research

Molecular Systematics and Taxonomy of Yeasts
Current research in my laboratory focuses on characterizing the phylogenetic diversity of ascomycetous yeasts and developing molecular tools for rapid strain identification and prediction of agriculturally and biotechnologically significant properties of those species. Yeasts are nearly ubiquitous in nature and are essential for the production of numerous foods and beverages as well as for various industrial and biotechnological processes. Yeasts are common spoilage organisms of foods and beverages as well as accounting for 80% of human and animal mycotic infections. Despite the enormous importance of yeasts, species identification has been problematic. Traditional methods rely on phenotypic characters such as cellular morphology and reactions on various growth tests. Molecular genetic comparisons have shown that morphology and growth reactions are often strain variable and therefore unreliable for recognizing species (Kurtzman and Fell, 1998). Gene sequence comparisons offer a relatively rapid alternative that allows resolution of both close and distant relationships. Research shows certain yeast clades to be sparsely populated and this has been largely attributed to absence of undiscovered taxa rather than lack of divergence (Kurtzman, 2001). Consequently, an improved understanding of yeast biodiversity is highly dependent on discovery of missing taxa, and a phylogenetic framework for classification will provide a prediction of the utility of new taxa.

Selected Publications

Kurtzman, C.P. 2005. Description of *Komagataella phaffii* sp. nov. and the transfer of *Pichia pseudopastoris* to the methylotrophic yeast genus *Komagataella*.
Int. J. Syst. Evol. Microbiol. 55:973-976.

Kurtzman CP, Robnett CJ, Ward JM, Brayton C, Gorelick P, Walsh TJ. 2005. Multigene phylogenetic analysis of pathogenic candida species in the *Kazachstania* (*Arxiozyma*) *telluris* complex and description of their ascosporic states as *Kazachstania bovina* sp. nov., *K. heterogenica* sp. nov., *K. pintolopesii* sp. nov., and *K. slooffiae* sp. nov. J. Clin. Microbiol. 43:101-111.

Vaughan-Martini A, **Kurtzman CP**, Meyer SA, O'Neill EB. 2005. Two new species in the *Pichia guilliermondii* clade*: Pichia caribbica* sp. nov., the ascosporic state of *Candida fermentati*, and *Candida carpophila* comb. nov. FEMS Yeast Res. 5:463-469.

Kurtzman, C.P. 2003. Phylogenetic circumscription of Saccharomyces, Kluyveromyces and other members of the Saccharomycetacease, and the proposal of the new genera Lachancea, Nakaseomyces, Naumovia, Vanderwaltozyma and Zygotorulaspora. FEMS Yeast Res. 4:233-245

Kurtzman, C.P. and Robnett, C.J. 2003. Phylogenetic relationships among yeasts of the "Saccharomyces complex" determined from multigene sequence analyses. FEMS Yeast Res. 3:417-432.

Tomaszewski, E.K., Logan, K.S., Snowden, K.F., **Kurtzman**, C.P. and Phalen, D.N. In Press. Phylogenetic analysis identifies the 'megabacterium' of birds as a novel anamorphic ascomycetous yeast, Macrorhabdus ornithogaster gen. nov., sp. nov. Int. J. Syst. Evol. Microbiol. 53.

Gimenez-Jurado, G., **Kurtzman**, C.P., Stramer, W.T. and Spencer-Martins, I. In Press. Metschnikowia vanudenii and Metschnikowia lachancei spp., nov., two novel species from flowers and associated insects in North America. Int. J. Syst. Evol. Microbiol. 53.

Kurtzman, C.P., Fell, J.W., Robert, V., and Boekhout, T. 2003. Methods to identify yeasts. In: Yeasts in Food, T. Boekhout and V. Robert (eds.), chap. 3. pp. 69-121. B. Behr's Verlag GMBH & Co., Hamburg, Germany.

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Published by the Microbiology Society, Microbial Genomics is a Gold Open Access, peer-reviewed journal publishing cutting edge, pioneering research into genomic approaches to microbiology, fully supported by Open Data and innovative, collaborative services. We cover topics including, but not limited to: -Microbial evolution (including viruses) -Population genomics and phylogeography -Outbreaks and epidemiological investigations -Ecosystems, community and niche interactions -Host pathogen, host commensal, host... Engineered microbes can produce appreciable amounts of scarce natural compounds, thereby facilitating the synthesis of the target novel compound and potent derivatives, as well as the validation of their activities (Matsumura et al., 2018).Â While many of the biological activities of microbial natural products and biologics are well known, new advances and insights continue to be discovered. Genomic technologies have revolutionized microbiology research, enabling us to characterize microbial communities and reveal the diversity of microorganisms not seen before due to their inability to be isolated by culture. Genomics is expanding our knowledge of how pathogens interact with their hosts, how they relate to each other, and how drug resistance genes spread within a community. Thermo Fisher Scientific offers a broad range of genomic technologies to characterize microbes. Our optimized platforms for next-generation sequencing, Sanger sequencing using capillary electrophoresis, and real-time PCR offer highly effective approaches to analyzing viruses, bacteria, fungi, and other eukaryotic microorganisms and microbial communities.