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


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