The use of yeast genetic diversity for agricultural and biotechnological applications

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Abstract

Many yeasts have been shown to be effective for biocontrol of field, greenhouse, and storage diseases of agricultural crops. Yeasts are generally regarded as safe for a wide variety of applications and some species establish large populations on leaf and fruit surfaces, resulting in disease control through competitive exclusion of pathogens. Yeasts that are used for biocontrol include ascomycetes assigned to the subphylum *Saccharomycotina*, dimorphic ascomycetes that are members of the subphylum *Pezizomycotina* and species classified in various subphyla of the *Basidiomycota*. This great diversity of species presents a challenge for identification, which must be correct to ensure product safety as well as to protect intellectual property. Over the past decade, all described yeasts have received a barcode through use of diagnostic gene sequences resulting in far more accurate strain identification than is possible from phenotypic characterization. Phylogenetic relationships determined from gene sequence analysis can be used to predict which species may be effective for biocontrol and for other biotechnological applications. Relationships among biocontrol species are discussed and examples of phylogenetic predictions for discovery of biotechnological applications are presented.