

Recent trends in molecular diagnostics of yeast infections: from PCR to NGS.

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Abstract

The incidence of opportunistic yeast infections in humans is increasing over the last years. These infections are difficult to treat and diagnose, in part due to the large number and broad diversity of species that can underlie the infection. In addition, resistance to one or several antifungal drugs in infecting strains is increasingly being reported, severely limiting therapeutic options and showcasing the need for rapid detection of the infecting agent and its drug susceptibility profiles. Current methods for species and resistance identification lack satisfactory sensitivity and specificity, and often require prior culturing of the infecting agent which delays diagnosis. Recently developed high-throughput technologies such as next generation sequencing or proteomics are opening completely new avenues for more sensitive, accurate, and fast diagnosis of yeast pathogens. These approaches are the focus of intensive research, but translation into the clinics

requires overcoming important challenges. In this review, we provide an overview of existing and recently emerged approaches that can be used in the identification of yeast pathogens and their drug resistance profiles. Throughout the text we highlight the advantages and disadvantages of each methodology and discuss the most promising developments in their path from bench to bedside.

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