A NOVEL CANDIDA ALBICANS LIBRARY

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Technology description

Candida albicans is one of the most frequently encountered fungal pathogens, causing a wide variety of infections ranging from mucosal infections in healthy immunocompetent people to life-threatening systemic infections in immunocompromised individuals such as those with AIDS and those undergoing immunosuppressive therapy or chemotherapy. When individuals with compromised immune system are infected, it is fatal in nearly one in three cases. The limited number of safe and effective antifungal drugs underscores the importance of understanding the genetic pathways underlying the pathogenicity of C. albicans.Because it is diploid and lacks a well-characterized sexual cycle, C. albicans poses a challenge for genetic analysis. UCSF researchers have recently carried out a genome-wide insertional mutagenesis of C. albicans. They have generated a library that represents one of the largest collections of mutant C. albicans, approximately 20,000 strains, each with an independent Tn7-based transposon insertion. There is an average of one insertion per 2.5kb of haploid genome.This library has been validated in a genetic screen that identified 300 genes, the haploinsufficieny of which affect the transition between single cell and filamentous growth, a feature of C. albicans associated with pathogenicity. Six of the genes identified were previously known to affect filamentous growth in C. albicans, validating the approach and suggesting that the library will prove useful for screening of genes associated with other functions.

Application area

The potential uses of this C. albicans library include:
Identification of genes involved in signal-response pathways
Identification of genes that affect the expression of a reporter gene
Identification of genes necessary for pathogenesis in animal models
Identification of loss-of-function mutations that cause resistance to antifungal drugs
Identification of the targets of antifungal drugs through the isolation of hypersensitive insertion mutants

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