CANDIDA ALBICANS

SCIENTIFIC CLASSIFICATION	
Kingdom	Fungi
Division	Ascomycota
Class	Saccharomycetes
Order	Saccharomycetales
Family	Saccharomycetaceae
Genus	Candida
Species	C.albicans

(SABHI agar plate culture of the fungus Candida albicans grown at 20°C)

Candida albicans are considered as the most common human fungal pathogen and are also responsible for 50-90% of all cases of candidiasis in humans. Candida albicans is the most virulent member of the CUG clade of yeasts and a common cause of both superficial and invasive infections. They behave as opportunistic pathogens when the host's antimicrobial defenses are lowered. To infect host tissue, the usual unicellular yeast-like form of C. albicans reacts to environmental cues and switches into an invasive, multicellular filamentous form, a phenomenon called dimorphism. One of the most important features of the C. albicans genome is the occurrence of numeric and structural chromosomal rearrangements as means of generating genetic diversity, named chromosome length polymorphisms (contraction/ expansion of repeats),reciprocal translocations, chromosome deletions and trisomy of individual chromosomes. These karyotypic alterations lead to changes in the phenotype, which is an adaptation strategy of this fungus. The genome of C. albicans is highly dynamic, and this variability has been used advantageously for molecular epidemiological studies and population studies in this species.