Comparative Genomics of *Candida albicans* and *Candida dubliniensis*.

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The two pathogenic yeasts *Candida albicans* and *Candida dubliniensis* are closely related, but they differ in their virulence. *C. albicans* is found in many niches and frequently causes disseminated disease as well as mucosal infections. Its niches in the host are varied. *C. dubliniensis,* first identified in 1995, is found most frequently in mucosal infections in AIDS patients. Although the two species differ in some phenotypes, such as maximum growth temperature, they are quite similar at the genomic level. They contain approximately the same amount of DNA, and their genes have high similarity at the DNA level and at the protein level. Approximately 95% of the *C. dubliniensis* genes are close orthologues of genes in *C. albicans*, and there is extensive synteny of genes in the two organisms.

The contrast between the genomic similarity and the difference in virulence suggests that the genetic *differences* between the two organisms may cast light on the mechanisms of pathogenicity of *C. albicans*. Recently the sequence of *C. dubliniensis* has become available (http://www.sanger.ac.uk/sequencing/Candida/dubliniensis/) and orthologues to *C. albicans* genes are available at the Candida Genome Database (http://www.candidagenome.org/). For this reason a genomic comparison is informative. Differences and similarities in chromosome organization, comparison of gene families, repeated DNA, and centomeres and centromere function will be addressed. These comparisons allow inferences to be drawn about the role of some gene family members in the pathogenecity and suggest experiments to test these inferences. The genomic comparison also gives some insight into the common ancestor of these closely related species.