Journal Club

Genome sequencing suggests sexual reproduction in *Candida albicans*

Meiosis is the hallmark process of sexual reproduction. Haploid cells are produced by the reduction of homologous chromosomes in diploid parental cells. The recent identification of a mating-type-like (MTL) locus in the human pathogenic yeast *Candida albicans* strongly suggests that this fungus, which has been historically thought of as being asexual, does in fact have a sexual cycle. The lack of knowledge of a sexual cycle in *C. albicans* has hindered the ability to carry out conventional genetic analyses on this organism. Recently, however, shotgun sequencing of the diploid *C. albicans* genome has been completed to 10.4 haploid genome equivalents (http://sequence-www.stanford.edu/group/candida). With this sequence, as well as the sequence of *Saccharomyces cerevisiae* and higher eukaryotic organisms, genome comparisons should provide an insight into the possibility that *C. albicans* uses a complete sexual cycle.

Tzung *et al.*[1] recently carried out such a genomic comparison between *C. albicans*, *S. cerevisiae* and some higher eukaryotes to search for homologues of genes known to be involved in meiosis. These investigators focused their search to genes crucial for mating and meiosis in budding yeast, as well as regulators known to be involved in cellular reproduction in higher eukaryotes. Using the BLASTP program, output was sorted and E-values of $1e^{-6}$ were used to assign homologues. Each sequence was also evaluated individually because there were some instances where biological data implied the presence of a particular homologue despite the lack of a gene with significant sequence homology. [Supplementary data summarizing the findings are available on the *PNAS* website (http://www.pnas.org)]. The genes identified were categorized according to their associated function: (1) mating differentiation; (2) nutritional control; (3) cell type control; (4) initiation of meiosis; (5) checkpoint control and progression through meiosis; (6) recombination and formation of synaptonemal complexes; and (7) spore wall morphogenesis and ascus formation. Five hundred genes analyzed by genome-wide transcriptional analysis of sporulation in *S. cerevisiae* were used as a reference point to begin the analysis.

The presence of known *S. cerevisiae* homologues in *C. albicans* suggests similarities in the sexual cycle between these two fungi and the lack of known homologues of some genes highlights the interesting differences between them. With the identification of genes encoding homologues implicated in meiosis in *C. albicans*, a detailed functional characterization of each component should help to identify the role of these proteins and confirm the presence of a sexual cycle in this important human pathogen.

1 Tzung, K. *et al.* (2001) Genomic evidence for a complete sexual cycle in *Candida albicans*. *Proc. Natl. Acad. Sci. U. S. A.* 98, 3249–3253

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Recognition of virus-infected cells by NK cells

Recognition of infected cells has previously only been characterized for the major histocompatability complex (MHC)-class I binding, negative regulatory receptors of natural killer (NK) cells. With these receptors, a reduction in MHC class I at the cell surface releases inhibition of NK cell function and allows killing of infected cells. Recently Mandelboim *et al.*[1] demonstrated specific recognition of certain viral haemagglutinins by NKp46, one of the activating receptors of NK cells. Recognition involves a sialic acid on a carbohydrate group on NKp46 and is required for lysis of infected cells. However, other cellular receptors might also be involved.

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Although sendai virus and influenza virus were studied by Mandelboim *et al.*, other virus groups also use sialic acid as their cellular receptor. NKp46 might therefore be involved in recognition of a broad range of viruses.

1 Mandelboim, O. *et al.* (2001) Recognition of haemagglutinins on virus-infected cells by NKp46 activates lysis by human NK cells. *Nature* 409, 1055–1060

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Microbial genomics

Caulobacter crescentus genome sequence

Workers at The Institute for Genomic Research (TIGR) and their collaborators have recently reported the 4-Mb genome sequence of *Caulobacter crescentus*, an α-proteobacterium that grows in a dilute aquatic environment and provides a bacterial model for cellular differentiation[1]. The *C. crescentus* genome sets records for having the highest numbers of two-component signal transduction proteins (105) and TonB-dependent outer membrane proteins (65) and encodes 16 sigma factors. The genome contains multiple clusters of genes for functions essential for survival in a nutrient-poor habitat (for example, chemotaxis, aromatic degradation and the use of plant-derived carbon sources). Comparative analyses revealed important similarities with the *Rickettsia prowazekii* and *Pseudomonas aeruginosa* genomes.

1 Nierman, W.C. *et al.* (2001) Complete genome sequence of *Caulobacter crescentus*. *Proc. Natl. Acad. Sci. U. S. A.* 98, 4136–4141

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