Chromosomal variations in *Candida albicans*

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We report here the separation of chromosomal DNA molecules from the diploid pathogenic yeast *C. albicans* by field inversion gel electrophoresis (FIGE). Our earlier work on *C. albicans* ATCC strain 10261 revealed a pulsed field gel electrophoretic pattern of six bands, two of which were possibly doublets (2). In the present study we found that FIGE gave superior resolution with uniform DNA mobility between lanes, and therefore could be used to examine the possibility of electrophoretic karyotype variation in this asexual yeast. The extension of our study to other strains of *C. albicans* showed that local clinical isolates, strain 22114 (from M.D. Richardson, Birmingham, England) and our ATCC 10261 reference strain exhibit considerable differences in their FIGE banding patterns (Figure). However, certain similarities are apparent, especially in bands 5 and 6. Probing Southern blots with *C. albicans* DNA probes which complement the HIS3, ADE2 and URA3 genes in *S. cerevisiae* gave results supporting this conclusion. Close examination of the variant chromosomes, including further probing, suggested that they may have had common origins, but have undergone rearrangements which involve either one or both homologues of a diploid pair. However, we do not believe that *C. albicans* chromosomes are overly unstable, since ATCC 10261 strains freeze-dried in 1960 and 1965 gave the same banding pattern as an ATCC 10261 strain in laboratory culture for the last 15 years. Thus, FIGE electrophoretic patterns could be a valuable means of characterizing and identifying *C. albicans* strains. The molecular basis of these chromosomal variations and their phenotypic and medical consequences are of obvious interest. Finally, we recommend the use of type strains for the rational genetic analysis of *C. albicans*.

**Figure:** Yeast chromosomal DNA molecules resolved by FIGE.

Lanes a–e are *C. albicans* (a: 22114; b: 1346/6; c: W4112; d: 255/6; e: ATCC 10261), lane f is *Saccharomyces cerevisiae* 2180 (truncated pattern). Running conditions were 160 V, 22 hrs, 1% agarose, 7°C with ramp switching times over the run of forward 10–60 s and backward 3–20 s. DNA was prepared and bands are numbered according to Ref. 2.

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