SI Materials and Methods

The *C. albicans* TER gene was identified by screening a genomic phage lZAPII library (1) for sequences that hybridized to oligonucleotide probes matching the *C. albicans* telomeric repeat sequence. Approximately 20,000 plaques were screened by hybridization at 49°C in sodium phosphate buffer (2) to a mixture of three ^{32}P-labeled 20-mers, each a truncated permutation of the 23-bp *C. albicans* telomeric repeat: MMCa7-1 (ACGGATGTCTAACTTCTTGG), MMCa7-2 (CTTCTTGGTGTACGGATGTC), and MMCa7-3 (GTCTAACTTCTTGGTGTACG). DNA from the 18 phage clones identified as positives after both primary and secondary screening were then prepared and analyzed by restriction enzyme cleavage and Southern blotting. Five phage clones that hybridized most strongly to the *C. albicans* telomeric probe were identified by rewashing filters at 60°C after hybridization at 49°C. Two clones had very low yields of DNA and were not followed further. The remaining three were found to be nonidentical but to contain the same cloned region. A 96-bp *Tsp*509 I restriction fragment from one of these clones was subcloned and sequenced, and it was shown to contain a 28-bp region of perfect homology to *C. albicans* telomeric sequence, suggesting that it encodes a portion of TER.

Total cellular RNA (isolated by RNeasy mini kit; Qiagen, Valencia, CA) was used for Northern blotting and 5′- and 3′-end RACE analyses of Ter1. Mapping of the 3′ end entailed polyA tailing, cDNA synthesis, and PCR amplification (3). The first two steps were done as described previously using primer T18Bam (5′-GCCGGGATCCT$_{18}$-3′) (4). cDNAs were then subjected to two rounds of PCR amplification, first using the primers T18Bam and CaTER2463 (5′-GACAACAGGCTTTTATTCGT-3′, within *TER1*), and then using T18Bam and the nested primer CaTER2723 (5′-GGGAGTACTGGTGGATTTC-3′). Products were sequenced directly to obtain the 3′ ends. Mapping of the 5′ end entailed cDNA synthesis, ligation of an anchor primer to the 3′ end of the cDNA, amplification with the primers CAL1773 (5′-GGATGTCTAACTTCTTGGTG-3′) and RA21 (complementary to the anchor primer; 5′-GCGGCCGCTTATTAACCCTCACTAA-3′), and direct sequencing, as described previously (4).

1. Miyasaki SH, White TC, Agabian N (1994) *J Bacteriol* 176:1702-1710.

2. Church GM, Gilbert W (1984) *Proc Natl Acad Sci USA* 81:1991-1995.

3. Lingner J, Keller W (1993) *Nucleic Acids Res* 21:2917-2920.

4. Tzfati Y, Knight Z, Roy J, Blackburn E (2003) *Genes Dev* 17:1779-1788.