Complete nucleotide sequence of *Candida albicans* 5.8S rRNA coding gene and flanking internal transcribed spacers

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Repeated sequences, like the 5.8S rRNA and its flanking regions in *C.albicans*, can be of particular interest as PCR targets; this is especially true if variations in sequence or length of these regions occur between members of a same genus or species (1). We therefore cloned ribosomal repetitive units of two *C.albicans* strains and determined the sequence of their respective Internal Transcribed Spacers (ITS) and 5.8S rRNA. This was achieved by using the Sequenase procedure (USB) with four different primers, one located in the 18S rRNA (sense, 1702–1727), one located in the 25S rRNA (antisense, 91–109), and two located in the 5.8S rRNA (sense, 32–49; antisense 141–158).

The 5' and 3' ends of the region encoding the 5.8S rRNA were identified by comparison with the equivalent gene from closely related fungi (2, 3). The length of this region encoding the 5.8S rRNA in *C.albicans* is 158 bp. The two ITS (ITS 1 and 2) located between 18S and 5.8S and 5.8S and 25S rRNA are respectively 138–139 bp, depending on the strain, and 151 bp long. Only three mismatches were observed between the sequence from the two *C.albicans* strains, one in the 5.8S rRNA coding gene and two in ITS 1. We found that the 5.8S rRNA of *C.albicans* is very closely related to those of other fungi like *Saccharomyces cerevisiae* (2) (95.0% homology), *Schizosaccharomyces pombe* (3) (90.0% homology) and *Neurospora crassa* (4) (92.5% homology). In particular, nucleotides involved in the base pairing between the 5.8S rRNA and the 25S rRNA (5) are highly conserved. We have previously shown that these nucleotides involved in pairing are identical in the 25S rRNA of *C.albicans* and *S.cerevisiae* (6). This also holds true in the complementary 5.8S sequence except for one substitution in the 3' region of the 5.8S.

The predicted 5.8S rRNA secondary structures of *C.albicans* and *S.cerevisiae* (2) are highly similar. As already described (7), the differences between these two rRNA coding genes occur mainly in non-pairing regions or in the stem-loop closest to the 3' end of the 5.8S rRNA. In this stem-loop, four nucleotide's substitutions were observed in *C.albicans* compared to *S.cerevisiae*, but the proposed base pairing remained identical (2).

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Ca62	AAACTTTCAA	CAACGGATCT	CTTGTTCTC	GCATCGATGA	AGAACGCAGC	GAAATGCGAT
Ca4						
Sc						
Sp		G		*		
Ca62	ACGTAATATG	AATTGCAGAT	ATTC*GTGAA	TCATCGAATC	TTTGAACGCA	CATTGGGCCC
Ca4					T	
Sc		G	*	C		
Sp		G	*	C		*
Ca62	TCTGG*TATT	CCGGAGGGCA	TGCCTGTTTG	AGCGTCGTTT		
Ca4						
Sc	CT		A G		A	
Sp	TG	T C A	AA *		T A	

Figure 1. Base differences between the 5.8S rRNA nucleotide sequence of *Candida albicans* and two other fungi. The sequence was determined for two strains of *C.albicans*, 62-1 (as it appears in GenBank) and 4-1. Sc, *Saccharomyces cerevisiae*; Sp, *Schizosaccharomyces pombe*. *, deleted nucleotide.

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