Sequence of a locus on chromosome VII encompassing a tRNA^{Lys} gene in *Saccharomyces cerevisiae*

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The yeast *Saccharomyces cerevisiae* contains two major forms of tRNA^{Lys} (1, 2). Both are comprised of 76 nucleotides but differ at 21 sites, including the wobble position of the anticodon. One has the anticodon C-U-U and decodes specifically A-A-G. The other has the anticodon U-U-U, which, based on wobble rules, would be expected to decode both A-A-A and A-A-G codons. However, the U residue in the wobble position is modified to 5-methoxycarbonylmethyl-2-thiouridine (3), which apparently eliminates the ability to decode the synonymous A-A-G codon (reviewed in ref. 4). This accounts for the requirement for two distinct tRNA^{Lys} molecules. tRNA^{Lys} (C-U-U) is the predominant form (1), which is consistent with A-A-G as the preferred lysine codon (5, 6).

Genes encoding both of these molecules have been cloned from yeast. A tRNA^{Lys} (U-U-U) gene was cloned from a DNA bank by hybridization to a tRNA-encoding probe (7). Sequence analysis revealed two structural features common to many yeast tRNA genes: a repetitive element, *sigma*, is located 16 bp from the 5' end of the gene and a 23 bp intron is present 3' to the anticodon. The tRNA^{Lys} (C-U-U) gene was found within a transposition hotspot on chromosome V, which was cloned using the Ty4 transposable element as a probe (8). This gene was identified within a region containing two complete Ty elements, multiple solo repetitive elements, and three different tRNA genes. As for tRNA^{Lys} (U-U-U), a repetitive element, in this case *delta*, was found just upstream of the structural gene. The coding region was not interrupted by an intron.

While sequencing the promoter region of the *SUA5* gene (9) we have identified another tRNA^{Lys} gene. The sequence of the 772 bp *HindIII*-*NheI* fragment located upstream of the *SUA5* ORF revealed a 73 bp sequence that is colinear with the tRNA^{Lys} (C-U-U) gene (8). Sequence polarity indicates that transcription would occur divergently with respect to *SUA5*. Unlike either of the other tRNA^{Lys} genes, the flanking sequence is devoid of any repetitive sequence elements. The gene does not contain an intron and, like other tRNA genes, it does not encode the 3' terminal -C-C-A sequence of the mature tRNA.

A physical map of the tRNA^{Lys}-*SUA5*-*PMR1* locus is presented in Figure 1. The *pmr1* locus had been mapped previously (10). Combined with the physical map, this places the tRNA^{Lys} gene on the left arm of chromosome VII, tightly linked to *lys5*.

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Figure 1. Physical map of the tRNA^{Lys}-*SUA5*-*PMR1* locus. This region is tightly linked to *lys5* on the left arm of chromosome VII, as determined previously by three-factor crosses using the *pmr1*, *lys5* and *aro2* markers (10).

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