

A conserved pseudoknot in telomerase RNA

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A conserved secondary structure model has been proposed recently for the telomerase RNAs from six different Tetrahymena and one Glaucoma species (1). In this model four helical regions are present which are all supported by phylogenetic evidence. The templating domain is unpaired in these structures, in agreement with the observation that this region is available for basepairing with complementary DNA oligonucleotides (2). We note that the nucleotides of the loop of helix III are capable of basepairing with a stretch of four bases just upstream of this stem. The pseudoknot thus formed is present in all seven telomerase sequences, and is supported by covariations in three of the four basepairs involved (Table 1). Figure 1 gives the structure of the H-type pseudoknot we propose for the *T.thermophilus* (3).

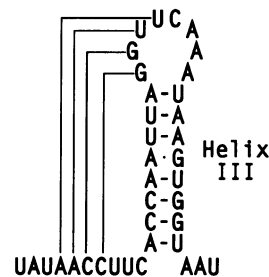


Figure 1. Pseudoknot in telomerase RNA from *T.thermophilus*.

REFERENCES

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Table 1. Alignment of telomerase RNA sequences

<i>T. the:</i>	U <u>AU</u> A CCUUC ACCA <u>UU</u> AG CUU--CAA <u>U</u> AAAGUGGUA
<i>T. mal:</i>	U <u>AU</u> A CCUUC ACCA <u>UU</u> AG CUU--CAA <u>U</u> AAAGUGGUA
<i>T. pyr:</i>	U <u>AU</u> A CCUUC GCCA <u>UU</u> AG CUU--AUA <u>U</u> AAUGGUUC
<i>T. pig:</i>	U <u>AC</u> U CCCUUA ACU <u>UU</u> AG CCA <u>UU</u> AA <u>U</u> AAAUAAA
<i>T. hyp:</i>	U <u>AC</u> U CCCUUA ACU <u>UU</u> AG CCA <u>UU</u> AA <u>U</u> AAAUAAA
<i>T. heg:</i>	U <u>AC</u> U CCCUUA ACU <u>UU</u> AG CCA <u>UU</u> AA <u>U</u> AAAGUUGAA
<i>G. cha:</i>	U <u>AU</u> A CCUUC <u>UU</u> AG CUU--ACA <u>U</u> AAAGUCAC

Alignment of the sequence of 7 telomerase RNAs around helix III (as proposed by (1)). Dashes indicate alignment gaps, bold nucleotides are absolutely conserved residues, underlined nucleotides form helix III and shaded nucleotides form the proposed extra interaction, resulting in the pseudoknot.