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The nucleotide sequence of the 5 S rRNA of *Rhodobacter capsulatus* ATCC 23782

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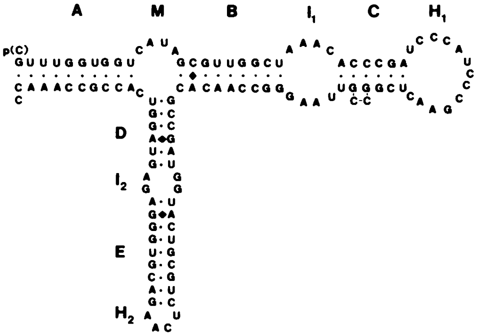
The nucleotide sequence of the 5 S rRNA from *Rhodobacter capsulatus* ATCC 23782 was determined according to (1). It can be fitted into the following secondary structure model (the C at the 5'-terminus is present in submolar amounts; base pairs other than G•C, A•U, G•U are symbolized by losenges) :



Exactly the same model applies to the 5 S RNA of *R. capsulatus* strain NCIB 8254 (2), which shows 8 substitutions with respect to the sequence presented here. With regard to the arrangement of nucleotides in area B-I_1 of the secondary structure, three types of models can be considered for eubacterial 5 S RNAs :

1) A model (3) where helix B bears a bulge on the 3'-proximal strand and where internal loop I_1 has one more base in the 5'-strand than in the 3'-strand.
2) A model where helix B bears a bulge on each strand, and loop I_1 is symmetrical (examples given in (4)).
3) The model shown above, where helix B is devoid of bulges and loop I_1 is symmetrical.

Some eubacterial 5 S RNAs can be fitted in only one of these models, model 3 in the case of *R. capsulatus*. Most, however, can be fitted into model 1 as well as model 2 (4). In *Thiobacillus acidophilus* 5 S RNA, all three models are applicable. We conclude that the secondary structure in area B-I_1 of eubacterial 5 S RNAs is variable and that transitions may occur in certain species.

References

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