Volume 16 Number 6 1988 Nucleic Acids Research

Plant small nuclear RNAs. IV. The structure of U1 RNA from *Chlorella saccharophila*: a phylogenetic support, in terms of RNA structure, for the probable interaction between U1 and U2 and RNPs during the splicing of pre-mRNA

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Submitted January 20, 1988 Accession no.X06880

We have sequenced according to (1) U1 RNA from a photosynthesizing lower eukaryote, the green alga, Chlorella saccharophila. Fig.1 indicates that all regions shown to be (2,3) or supposed to be (4-6) of functional importance in other U1 RNAs (5-7) are present in this molecule, although its sequence similarity to either bean (5) or rat (7) U1 RNA is only 53%. Our data lend phylogenetic support, in terms of RNA structure, to the notion that during the splicing of pre-mRNA U1 and U2 RNPs may interact with each other (4,8-10) and also with some constituents of the splicing complex that may associate interchangeably with both U1 and U2 RNAs.

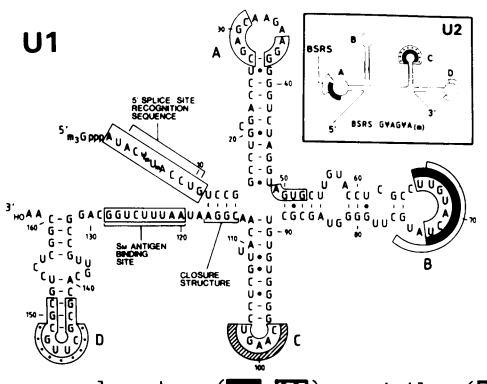

Fig.1. Structure of Chlorella U1 RNA. Evolutionarily highly conserved sequences of identical location in a secondary structure model (11) which accommodates all metazoan (7) and plant (5) U1 RNAs sequenced, are boxed and, wherever feasible (2,3,6), identified. The inset shows the schematic diagram, with the internal loops omitted and with the suggested (12) branch site recognition sequence (BSRS) identified, of a secondary structure model (4) applicable to all metazoan (7) and plant (13) U2 RNAs sequenced. Sequences which are complementary (■,▨) or similar (□) to each other or contain the consensus GYUYGC (◘) in all metazoan and plant U1 and U2 RNAs sequenced, including U2 RNA from Chlorella (unpublished), are indicated.

Acknowledgements: Thanks are due to Dr. M. Uroppa for supplying the alga culture. This work was supported by grants /OKKFT(Tt)/1986/ and OTKA 564/86 to F.S. from the Hungarian Academy of Sciences.

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