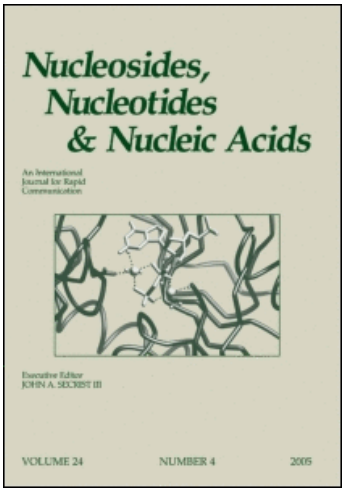

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ON THE SELF-SPLICING COMPLEX OF TETRAHYMENA PRE-rRNA

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Abstract: The base patterns around the splicing site of Tetrahymena pre-rRNA are suggestive of triple strand formation that might mediate and forward self-splicing reactions.

Highly organized and cooperative tertiary biopolymeric structures are not only prerequisites for performing complex molecular functions, but seem, moreover, indicative of molecular hystereses, basal operation modes for oscillations and rhythm generations, memory imprints and information processings in biomesogenic regulations. In poly(deoxy)ribonucleotides these phenomena appear to be intimately connected with triplex arrangements[1-3].

While in self-splicing RNAs internal guide sequences displaying mutual exon-intron recognition facilities have long been discussed in terms of appropriate positioning of reactive parts[4-9] and an informative base triple has been proposed quite recently[9], the base patterns around the splicing site of Tetrahymena pre-rRNA (Figs. 1 and 2) are suggestive of building up even more extended transient triplex organizations. Though at present definite insights into the tracing of the RNA-backbone are still lacking, there are indications of dynamic tertiary domains around the splicing site.

Just in view of RNA dynamics, Figs. 1-3 propose - among other imaginable arrangements - a model that combines overall aligning complexations with forwarding labilizing distortions of the splice sites.

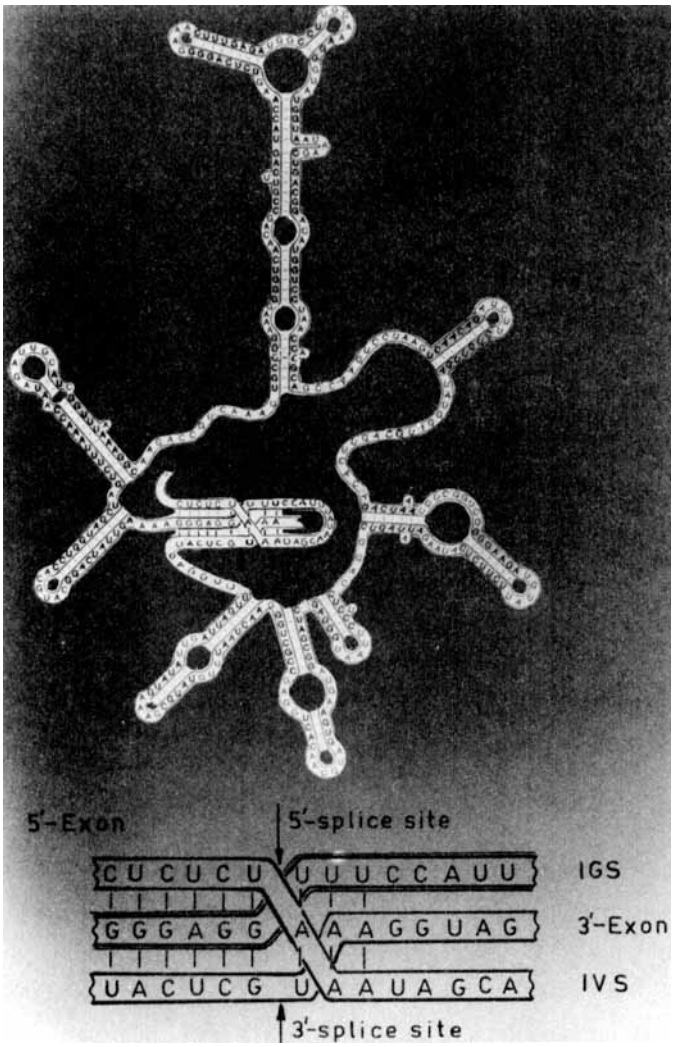

FIG. 1 Tetrahymena pre-rRNA intron as depicted in ref.[5] - modified by visualization of hypothetical triplex formation facilities of internal guide sequence (IGS), intervening sequence (IVS) and the adjacent 5'- and 3'-exon parts around the splice sites

Fig. 1 illustrates the hypothetical course of IGS, IVS and the 5'- and 3'-exons, centring the triplex arrangements along an all-purine leading pattern that switches together with the base-pairing schemes just at the splicing sites. Watson-Crick pairing between antiparallel and Hoogsteen binding to parallel strands seem to a certain degree interchangeable.

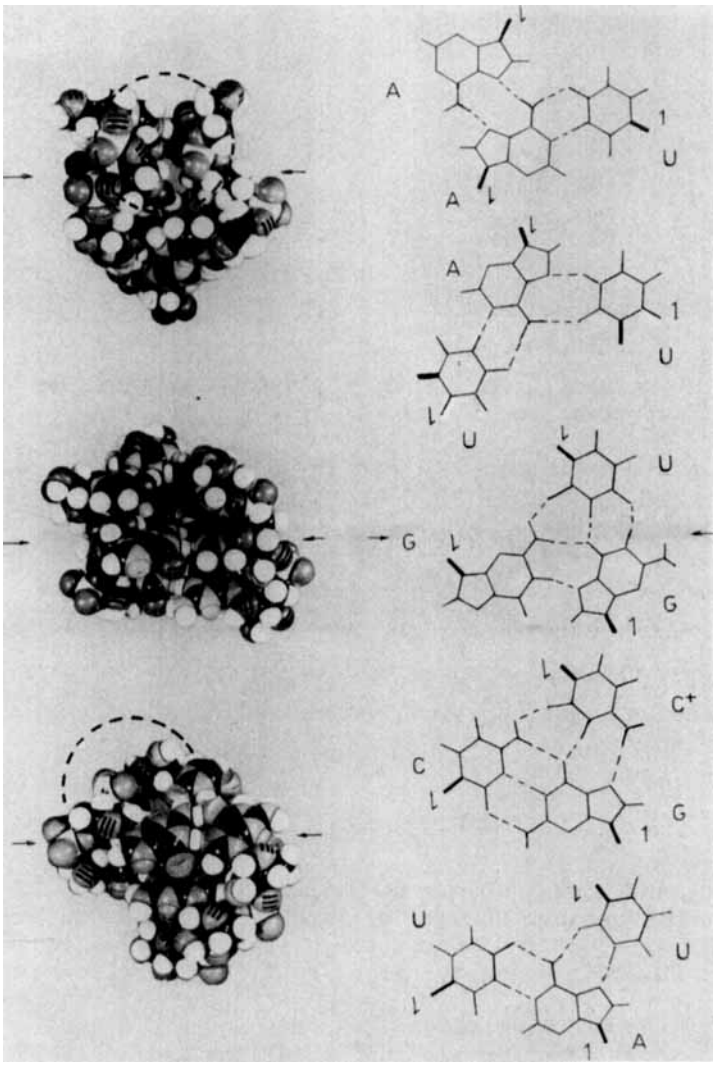

FIG. 2 Cuts of hypothetical mini-triplexes around the (circled) splice sites (top to bottom and left to right): CPK-models of U•A•U/U•G•G/C•G•C^+-triplex viewed from opposite directions and U•G•G/C•G•C^+/U•A•U-triplex down the helix axis; schemes of hypothetical base triples

Fig. 2 envisages the hypothetical triplex arrangements in detail: the here offered structure of the U•G•G-triple in combination with the unconventional appearance of its U•A•U-neighbour (according to recent molecular mechanics calculations, Watson-Crick-pairings between parallel strands are not so unfavourable[10]) force - as is further elucidated in Fig. 3 - the reactive ribose-3'-hydroxy-

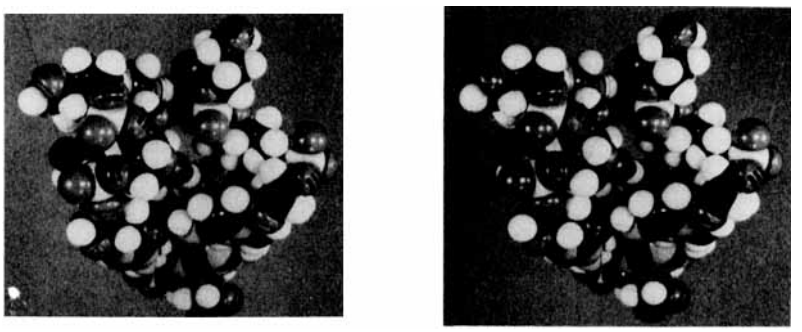

FIG. 3 Mini-triplex from Fig. 2 (top left) in stereo-presentation illustrating the 5'- and 3'-splice sites

phosphate parts of intron-G_{414} and the 3'-terminal U of the 5'-exon into close proximity.

Thus, while models so far emphasized the mutual binding of the guide sequence to parts of the 5'- and 3'-exons, the here presented hypothesis would offer possibilities for a dynamically aligned core region of the splicing complex that would provide cooperative contacts between all partners involved in splicing and exon ligating reactions.

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