NUCLEOTIDE SEQUENCE OF *DROSOPHILA MELANOGASTER* 5S RNA: EVIDENCE FOR A GENERAL 5S RNA MODEL

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1. Introduction

The position of 5S ribosomal RNA among biological molecules is somewhat particular since its precise function is still largely unknown although the molecule is a fundamental constituent of ribosomes and has been extensively studied. It is reasonable to expect that 5S RNA molecules from different organisms fulfill the same function(s); the structural analysis of a number of different 5S RNAs should help to point out which are their common features: hopefully these will be involved in the function(s) of the molecule. Such common elements can be found at the level of primary structure, or possibility at the level of secondary structure: different 5S RNA molecules with largely different sequences may be able to form similar secondary structures, as in the case of tRNA molecules. The proposals which have been made so far for a common 5S RNA model [1] are based on the consideration of three different eukaryotic sequences: vertebrate 5S RNA, plant 5S RNA and Yeast 5S RNA. The determination of new and quite different 5S RNA sequences can provide new possibilities for testing these hypotheses. In this paper we report the nucleotide sequence of *Drosophila* 5S RNA, discuss its relationship with other 5S RNA sequences and show that it can be folded into a secondary structure very similar to that which has been proposed on an experimental basis for *Chlorella* 5S RNA [2,3]; as pointed out recently, similar models are applicable to vertebrate and possibly Yeast 5S RNAs [1]. The knowledge of the sequence of *Drosophila* 5S RNA also makes it possible to study such topics as the expression of 5S RNA genes during development or the mechanism which maintains sequence homogeneity in a cluster of repeated genes, using the special genetic advantages of this system.

The complete derivation of the sequence and the results of experiments designed to test the model of secondary structure will be reported elsewhere.

2. Materials and methods

Drosophila cells (subline F6 of the KC cell line established by Echalier and Ohanessian [4] were grown in suspension culture and labelled with ^{32}P, the RNA was extracted as previously described [5]. 5S RNA was purified by two successive electrophoreses in acrylamide gel slabs and was sequenced using standard fingerprinting techniques [6]; partial digests were fractionated either by two-dimensional acrylamide gel electrophoresis [7] or by homochromatography [6].

3. Results

The sequence determined for Drosophila 5S RNA is shown in fig.1. Although there are in *Drosophila* approx. 200 copies of the 5S RNA gene per haploid genome [8], the 5S RNA preparations which we analyzed were largely homogeneous, at least at the level of resolution of the fingerprint technique. This does not however mean that the 200 5S RNA genes are identical since we do not know whether all of them are transcribed in cultured *Drosophila* cells; nor can we exclude the

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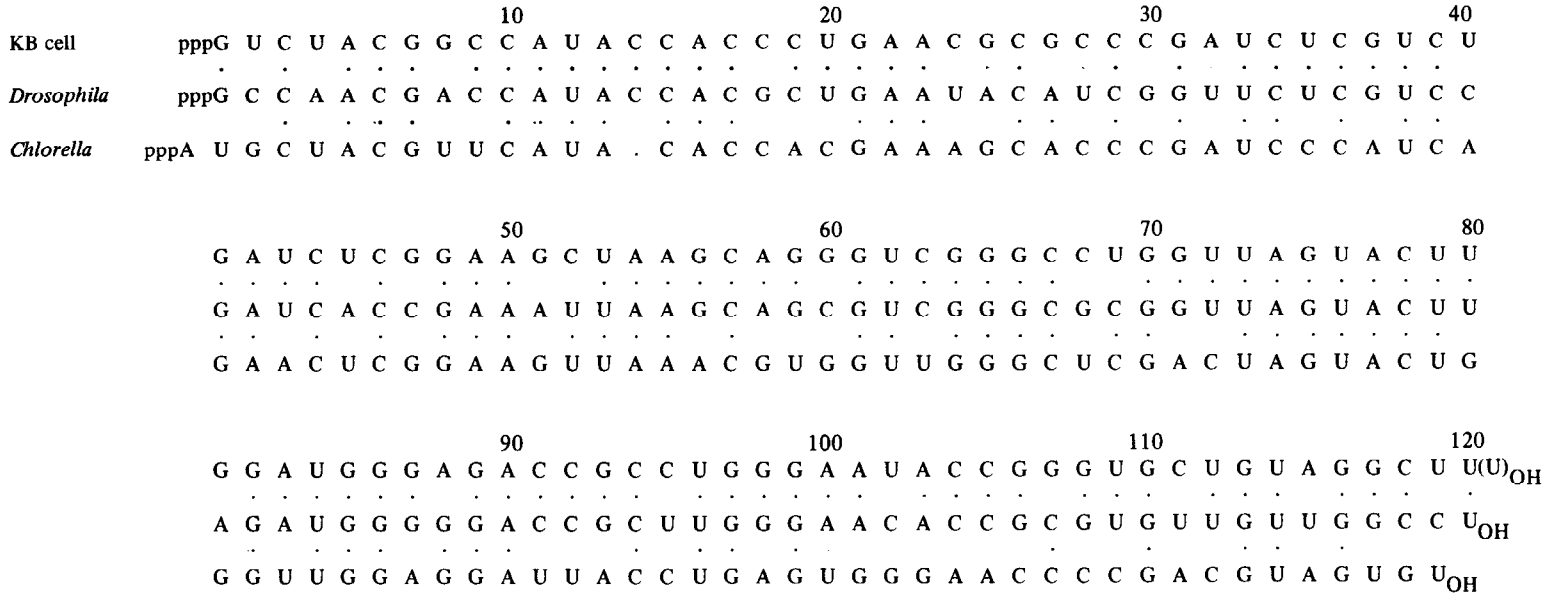
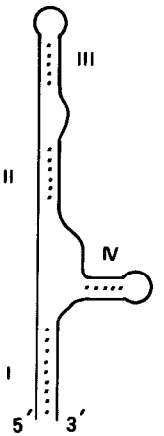


Fig.1. Nucleotide sequence of *Drosophila* 5S RNA compared with human (top) and *Chlorella* 5S RNA sequences One or two gaps respectively, have been introduced to maximize homology. The $_{64}$GGGCGC sequence could be GCGGGC; also one G more or less may be present before $\underset{90}{A}$. These changes would not alter either the homology or the possible pairing scheme.

Table 1
Possible base-paired regions in *Drosophila* 5S RNA

Region	Possible regions in human 5S RNA	Regions found in *Chlorella* 5S RNA ( )	Possible regions in *Drosophila* 5S RNA
I	1 9 pppG U C U A C G G C HO(U)U U C G G A U G U C G 118 110	3 10 pppA U G C U A C G U U OH U G U G A U G C A G 117 110	1 9 pppG C C A A C G A C HO U C C G G U U G U U G 118 110
II	16 21 A C C C U G U G G G A C 62 57	16 21 A C C A C G U G G U G C 62 57	16 21 A C G C U G U G C G A C 62 57
III	30 33 C C G A G G C U 48 45	29 32 C C G A G G C U 48 45	28 32 U C G G U A G C C A 49 45
IV	67 72 C C U G G U G G G C C A 108 103	80 84 G G G U U C C C A A 108 104	67 72 C G C G G U G C G C C A 108 103



Possible base paired regions in *Drosophila* 5S RNA. The possible base paired regions are indicated for human, *Chlorella* and *Drosophila* 5S RNA. It is remarkable that in spite of large sequence divergence the base pairing possibilities have remained very similar.

existence of small amounts (less than 10%) of different sequences.

Fig.1 also shows how this sequence compares with vertebrate 5S RNA (in this case from human KB cells) and *Chlorella* 5S RNA – the sequences are quite different but clearly related.

When the sequence is examined with respect to its base pairing possibilities, it becomes quite obvious that it can be arranged in a secondary structure extremely similar to that which was derived for *Chlorella* 5S RNA from partial hydrolysis data. All four base-paired regions found in *Chlorella* 5S RNA can be found at approximately the same position in the *Drosophila* sequence. Thus, in spite of large differences in the sequences of the two molecules, the secondary structures which can be formed are very similar. It is very unlikely that this could be due to chance; since moreover, vertebrate 5S RNAs can be folded according to a similar scheme, the case for this model seems quite convincing. The analysis of partially digested molecules by two-dimensional acrylamide gel electrophoresis and/or homochromatography, provides further evidence for this model (J. Benhamou and B. R. Jordan, manuscript in preparation). It does seem that a general 5S RNA model is now emerging, ten years after the first proposal of an essentially correct tRNA model [9]. This should help considerably in the elucidation of the function(s) of the molecule as well as in the study of its interaction with the other constituents of the ribosome.

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