Hypothesis

Sequences in the 3′-terminal coding regions of 5 S and 18 S rRNA genes may contribute to co-ordinated expression of 5 S rRNA and pre(18 S/5.8 S/26 S) rRNA genes

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It has long been known that there is remarkable affinity between 5 S and 18 S rRNA from wheat embryos. Experimental evidence has failed to support the proposition that the extensive complementarity which exists between 3′-terminal regions of the large-subunit (5 S) and small-subunit (18 S) rRNA is involved in uniting the subunits of the ribosome. Alternatively, it is suggested that the degree of complementarity between the 3′-terminal regions of wheat-embryo 5 S and 18 S rRNA may have significance at the level of the genome. It is suggested that common sequences in the 3′-terminal coding regions of 5 S and 18 S rRNA genes may serve to co-ordinate the expression of 5 S rRNA genes with the expression of the remainder of the (18 S/5.8 S/26 S) rRNA genes.

Ribosomal RNA *RNA polymerase* *Wheat enzyme* *Gene control* *5 S RNA* *Pre-rRNA*

1. INTRODUCTION

On the basis of their strong cell-free interaction, we once suggested that base-pairing between 5 S rRNA in the large subunit, and 18 S rRNA in the small subunit, might play a part in bridging the ribosomal subunits of wheat embryos [1]. The highly specific 5 S/18 S rRNA complex is easily formed by briefly heating the constituent molecules in a solution of moderate ionic strength [2,3]. The 'laboratory complex' melts over a narrow range of temperature and is more stable than the naturally occurring complex (5.8 S/26 S rRNA) which is known to be present in eukaryotic ribosomes [4]. An attractive molecular basis, involving base-pairing interaction between the 3′-ends of 5 S and 18 S rRNA, was proposed in support of a possible 'universal' involvement of 5 S/18 S rRNA complexing in the union of ribosomal subunits [5]. However, studies in this laboratory have failed to provide experimental support for the existence of 5 S/18 S rRNA interaction in wheat-embryo ribosomes [6] and independent work in another laboratory has shown that complexing between 3′-ends of 5 S and 18 S rRNA is unlikely to occur in protozoan ribosomes [7]. Although a transient association between 5 S and 18 S rRNA during the attachment of large and small subunit [6] is compatible with the locations of the 3′-ends of the 18 S and 5 S rRNA molecules in *E. coli* ribosomes [8,9], it has been emphasized by others [10,11] that the putative site of interaction between 5 S and 18 S rRNA molecules [5] is, in the case of 5 S rRNA, ordinarily 'protected' through interaction with a specific protein.

2. DISCUSSION

Although the signal affinities between the 3′-ends of the 5 S and 18 S rRNA molecules may or may not play a role in the union of ribosomal subunits, it is of interest to explore the conse-

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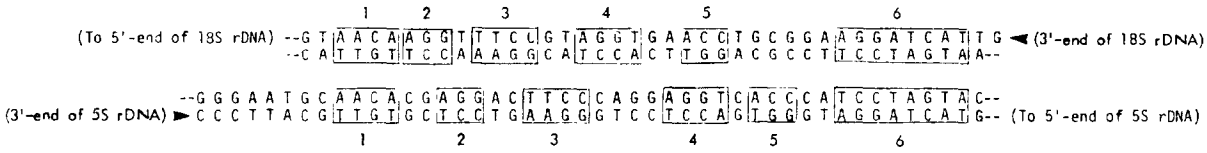

Fig.1. Coding regions of the 3′-terminal regions of 18 S rDNA (upper) and 5 S rDNA (lower) are based on primary structural data for the corresponding 18 S rRNA [20] and 5 S rRNA [21]. Numbered boxes indicate regions of bihelical sequence common to the coding regions of the 18 S and 5 S genes; phosphodiester bridges in the sequences of boxes 1–5 are the same polarity in both genes, but opposite in polarity in the sequence of box 6.

quences of this complementarity at the level of the genome. It is well known that promoter regions for RNA polymerase III are located internally in genes for tRNA and 5 S rRNA [12–17]. It is less well known that there is persuasive evidence, from in vivo studies with wheat embryos, that transcription of the large rRNA precursor by polymerase I requires ongoing transcription by RNA polymerase III [18]. From an examination of the 3′-terminal coding regions within 5 S and 18 S rDNA, it is apparent that the extensive complementarity originally detected by 5 S/18 S rRNA complexing is reflected in the existence of a number of identical bihelical segments common to the two genes. It is not difficult to visualize how such common sequences could serve to co-ordinate the expression of the genes in much the same way that internal promoter sequences direct the transcription of tRNA and 5 S rRNA genes.

As shown in fig.1, there are, near the 3′-ends of the coding sequences in wheat 5 S and 18 S rDNA genes, 5 blocks of identical bihelical sequence in which phosphodiester bridging is the same. There is an additional block of 8 base-pairs (block 6 in fig.1) which is identical in each gene, but in this case, phosphodiester bridging is antiparallel. It would seem that these regions of extensive homology between the 3′-terminal coding regions in 5 S and 18 S rDNA could play a role in co-ordinating expression of the genes, which are located at widely separated sites in the same (and different) chromosomes [19] and are transcribed by different polymerases [18].

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