The nucleotide sequence of ribosomal 5S RNA from lettuce seeds

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Recently we have proposed new tertiary structure model of lupin 5S rRNA. This structure is based on the five predicted non-canonical nucleic acids base pairs, which existence offers new arrangement of some stems and loops (1). The model accommodates quite well all 5S rRNA from plants, vertebrates and other sources (2). A few years ago we proposed hypothesis that 5S rRNAs conserve the primary structure for some plant species (e.g. *Graminea* or *Solanacea*) but differ for various species of plant of dicotyledon and monocotyledon families. However some exceptions have been observed in *Papilioneacea* (3). Recently we designed several experiments to prove the model (4, 5) and extend it to other 5S rRNAs.

The aim of this paper is to find new sequence data for RNA of *Compositae* species, which is needed for phylogenetic analysis of plants. Also, it is interesting how the new sequence of 5S rRNA fulfil secondary and tertiary structure model of this type of RNA. From nucleotide sequence analysis (3) we have noticed that ribosomal 5S rRNA of sunflower differs significantly from other plant 5S rRNA. Therefore we selected lettuce (*Lactuce sativa*) as the plant of *Compositae* and isolated 5S rRNA from seeds of *Lactuce sativa* by phenol method. The nucleotide sequence of 5S rRNA was determined by limited enzymatic digestions (3). Similarly to the other plant 5S rRNA it is 119 nucleotide long molecule (Fig. 1). In contrast to *Helianthus annuus* 5S rRNA there is no constant adenosine residue in position 116, but cytosine 93 instead uridine was identified. It means that there is only one difference between nucleotide sequences of 5S rRNA of the two plants of the *Compositae*.

It seems that our hypothesis on conservation of 5S rRNA primary structure for some plant species (3) is not totally valid or some mistakes have been made during previous nucleotide sequence analysis. There is also, possibly, another explanation, that these two subfamilies *Tubiflorae* (sunflower) and *Liguliflorae* (lettuce) differentiated early in the evolution of angiosperm plants. Despite this, the lettuce 5S rRNA molecule can be folded well into the secondary structure model, recently proposed by some of us (1), where all constant nucleotides

necessary for tertiary interactions are present. These are: C34, C35, C36, A37, U53 and G85, G86, G87, U88 and A100 respectively (Fig. 1).

It means that lettuce 5S rRNA similar to the other plant 5S rRNA conserves its tertiary structure and further support the model (1).

REFERENCES

1. Joachimiak, A., Nalaskowska, M., Barciszewska, M., Mashkova, T.D. and Barciszewski, J. (1990) *Inter. J. Biol. Macromol.* **12**, 321–327.
2. Sprecht, T., Wolters, J. and Erdman, V. A. (1990) *Nucl. Acids Res.* **18**, 2215–2230.
3. Barciszewska, M., Mashkova, T. D., Kisselev, L.L. and Barciszewski, J. (1985) *FEBS Lett.* **192**, 289–294.
4. Barciszewska, M., Lorentz, S., Erdman, V.A. and Barciszewski, J. (1990) *Biochim. Biophys. Acta* **1087**, 68–72.
5. Barciszewska, M., Lorentz, S., Joachimiak, A., Ulbricht, N., Erdman, V.A. and Barciszewski, J. (1990) *FEBS Lett.* **269**, 83–85.

Figure 1. The secondary structure model of *Lactuca sativa* 5S rRNA.