Plant small nuclear RNAs. III. The complete primary and secondary structure of broad bean U2 RNA: phylogenetic and functional implications

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We report for the first time the entire nucleotide sequence of a plant (broad bean (Vicia faba L.) U2 RNA. It perfectly fits (Fig. 1) into a secondary structure model (1) which accommodates all fully sequenced higher eukaryotic U2 RNAs (for reference see (2)) including that from the higher plant, Arabidopsis thaliana (P. van Kan and W. Filipowicz, personal communication).

The 5' half of the molecule compares very well with its consensus sequence (3). The high evolutionary conservation of this part of U2 RNA and the presence of some highly conserved nucleotides in the right half of the molecule (especially in the loops) suggest that besides the very 5' end of U2 RNA (4) there are some more extended structural constraints on this RNA species for it to be functional in pre-mRNA splicing.

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Fig. 1. Primary and secondary structure of broad bean U2 RNA. Nucleotides that are identical (disregarding modifications) in all U2 RNAs from higher eukaryotes (ref. (2)) are boxed.