Sequence of a histone H2A cDNA from parsley

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We have cloned and sequenced a cDNA for a histone H2A from parsley (Petroselinum crispum). A library of parsley cDNA in lambda gt11 was probed with a cloned fragment originally generated by polymerase chain reaction (PCR). The DNA amplified by PCR was a cDNA preparation made using the downstream PCR oligo primer with a total RNA preparation from parsley cell culture. The PCR upstream primer (a 17-mer, 512-fold degenerate) and the downstream primer (a 17-mer, 128-fold degenerate) were chosen to correspond to highly conserved regions of this nucleosomal protein. The deduced parsley H2A has 149 amino acid residues, which is between the sizes (145 and 151 amino acid residues) of the two known plant H2A variants obtained by direct protein sequencing from wheat (1). The deduced parsley protein sequence is 91% identical to the larger wheat H2A variant. In the region covered by the PCR generated probe, they are 98% identical. Comparison of the parsley deduced H2A sequence with that of chicken (2) and yeast (3) reveals identities of 81% and 79%, respectively (91% and 89% in the region covered by the probe). At the nucleic acid level, the parsley cDNA and chicken H2A cDNA are 66% identical in the probe region, 59% in the coding region and 53% overall. The parsley and yeast cDNAs are 71% identical in the probe region, 68% in the coding region and 61% overall. No plant cDNA or genomic H2A sequences are available for comparison to the parsley sequence.

REFERENCES


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