

Molecular cloning and nucleotide sequences of cDNAs for histone H1 and H2B variants from wheat

Ping Yang¹, Masaaki Katsura¹, Takuya Nakayama¹, Koji Mikami² and Masaki Iwabuchi^{1,2,*}

¹Department of Botany, Faculty of Science, Kyoto University, Kyoto 606 and ²Division of Developmental Biology, National Institute for Basic Biology, Okazaki 444, Japan

Submitted June 24, 1991

EMBL accession nos X59872, X59873

Recombinant phages containing full-length cDNAs encoding plant histone H1 and H2B were plaque-isolated from a wheat seedling cDNA library through screenings using synthesized oligonucleotides corresponding to the highly conserved amino acid sequences in wheat and several animal H1 and H2B variants (1, 2).

The H1 cDNA clone (1028 bp) contains an open reading frame of 708 bp which is flanked by the 5'-noncoding sequence of 71 bp and the 3'-untranslated sequence of 233 bp containing a 16 bp poly(A) tail. The cloned H1 consists of 236 amino acid residues and has a molecular weight of 24 kDa and thereby it surely belongs to the H1.1 variant, a major group of wheat H1 variants (1). The amino acid composition of this variant much resembles those of pea and maize H1 variants (3, 4) with high numbers of lysine, alanine and proline (58, 67 and 27 residues, respectively) and a high lysine/arginine ratio (58/5). The region containing first 52 residues is so-called 'nose', which is subdivided into an acidic domain (residues 1–25) and a basic domain (residues 26–52). The conserved central globular region (residues 53–116) is followed by the basic 'tail' region (residues 117–236) that contains the AAKPK motifs and its homologs similar to those of the pea and maize H1 variants (3, 4).

The complete sequence (712 bp) of a H2B cDNA contains an open reading frame of 456 bp which is flanked by the 5'-noncoding sequence of 64 bp and the 3'-noncoding sequence of 177 bp followed by a 15 bp poly(A) tail. Since the cloned

H2B consists of 152 amino acid residues and has a molecular weight of 16.4 kDa, it surely belongs to the H2B.2 variant, a major group of wheat H2B variants (5). The H2B has high numbers of lysine and alanine (31 and 22 residues, respectively) and a high lysine/arginine ratio (31/4). The basic N-terminal region (residues 1–61) contains the AEK motifs and its homologs as other wheat H2B variant (6). The highly conserved hydrophobic region extends from residues 62 to 152.

In both clones, the codon usage is strongly biased as this is in plant H3 and H4 genes and a putative poly(A) signal for plant H3 and H4 genes (7) is not present in the 3'-untranslated regions.

This is the first report on the histone H2B cDNA and the second report on the complete histone H1 cDNA in higher plants.

REFERENCES

1. Brandt, W.F. and von Holt, C. (1986) *FEBS Lett.* **194**, 282–286.
2. von Holt, C., Strickland, W.N., Brandt, W.F. and Strickland, M.S. (1979) *FEBS Lett.* **100**, 201–218.
3. Gantt, S. and Key, J.L. (1987) *Eur. J. Biochem.* **166**, 119–125.
4. Razafimahatratra, P., Chaubet, N., Philipps, G. and Gigot, C. (1991) *Nucl. Acids Res.* **19**, 1491–1496.
5. Spiker, S. (1982) *J. Biol. Chem.* **257**, 14250–14255.
6. Brandt, W.F., Rodrigues, J.de.A. and von Holt, C. (1988) *Eur. J. Biochem.* **173**, 547–554.
7. Wu, S.-C., Györgyey, J. and Dudits, D. (1989) *Nucl. Acids Res.* **17**, 3057–3063.

*To whom correspondence should be addressed at Department of Botany, Faculty of Science, Kyoto University, Kyoto 606, Japan