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The nucleotide sequences of two rice histone H3 genes

Sheng-Cheng Wu[1,2], Zoltán Végh[1], Xun-Ming Wang[2], Chia-Chen Tan[2] and Dénes Dudits[1]

[1]Institute of Genetics, Biological Research Center, Hungarian Academy of Sciences, H-6701 Szeged, Hungary and [2]Institute of Genetics, Fudan University, Shanghai, China
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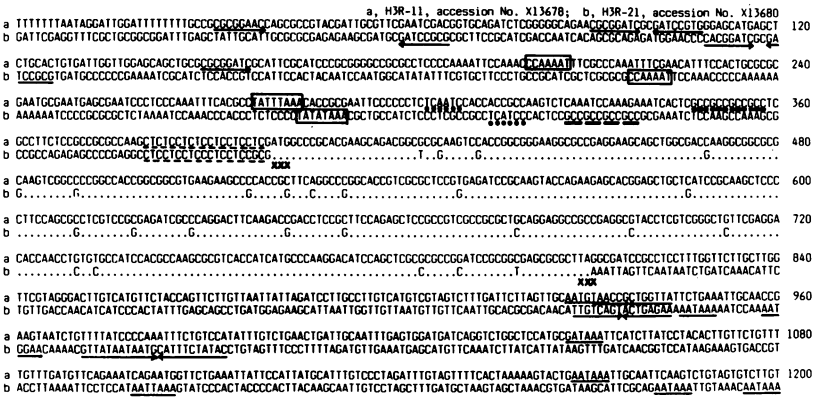
We present here the nucleotide sequences of two rice H3 histone genes, H3R-11(a) and H3R-21(b), from two genomic clones, λRH3-1 and λRH3-2(1), respectively. These two genes are highly conserved in the coding region (Xs indicate the start and stop codons; dots in H3R-21 represent the nucleotides identical to those in H3R-11) and encode an identical protein. This putative protein is identical to those deduced from maize and Arabidopsis H3 genes(2), but surprisingly, it varies with that deduced from a previously published rice H3 gene, pRH3-2(3), by three amino acid changes, though the homology between the coding regions of pRH3-2 and H3R-11 is as high as 96%(3). Despite the high conservation in the coding sequences, H3R-11 and H3R-21 exhibit very little homology in the flanking sequences except several conserved sequence motifs in the 5'flanking regions. Both genes possess more than one copies of plant histone gene-specific octamers, either direct or reverse forms (2, indicated with arrows in either orientations). Two of the octamers in either genes are closely linked and inverted. Other conserved motifs include the TATA and CAAT boxes (framed), the "cap sites" (4, dotted), the CT repeats (shown by dashed lines) adjacent to the start codon and the GCC repeats (marked with black bars) downstream of the "cap site". Instead of the conserved motifs found in animal histone genes(5), the 3' flanking regions of both genes possess several unrelated inverted repeats (shown by arrows) and polyadenylation signal-like sequences (underlined). Whether the rice H3 mRNAs are polyadenylated has yet to be studied.



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