Volume 15 Number 15 1987 Nucleic Acids Research

Chicken histone H3.3B cDNA sequence confirms unusual 3′ UTR structure

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Submitted July 1, 1987

Accession no. Y00392

We previously described (1,2) two H3.3 replacement variant chicken histone genes, H3.3A and H3.3B, which code for identical polypeptides but which otherwise differ extensively. Two cDNA clones have been isolated from a chicken liver λgt11 cDNA library which together contain a nearly complete H3.3B cDNA. The cDNA sequence confirms the splice sites previously determined (2), but indicates that the putative poly(A) site estimated from the AATAAA near 1493 was incorrect. In fact, polyadenylation occurs at 1732, downstream from an ATTAAA sequence giving a 3' untranslated region (UTR) of 569 nucleotides (nt). A human H3.3 cDNA (similar to H3.3A) was shown (3) to have a 3' UTR of 520 nt and terminate shortly after two ATTAAA blocks, despite an upstream AATAAA sequence. It appears that the chicken H3.3A poly(A) site may also have been misplaced (4) and this gene should also code for a 3' UTR of 520 nt and use an ATTAAA signal sequence. These results support the proposal (4) that an unusual 3' RNA processing mechanism of functional significance is used for H3.3 genes since the approximate length (>500 nt) of the 3' UTR and the use of the ATTAAA signal sequence have been conserved over the several hundred million years that the H3.3A and H3.3B sequences have been separated.

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  11 GGTAGTTGCG TTCGGAGTTG GTTGTTGTTG GAGCAGCGCA GGCTTCGGTG CGCGGCGATA TCGGCGCTGG TGCGTCCTTT TTCTCTGGGA GGTAAGTGAG 579
 580 AAAAAATGGC CCGTACAAAG CAGACCGCCC GCAAGTCCAC CGGGGGGAAG GCTCCGCGCA AGCAGCTGGC CACCAAGGCG GCCCGGAAAA GCGCTCCCTC 679
 680 TACCGGCGGC GTCAAGAAGC CTCACCGCTA CAGGCCGGGC ACCGTCGCGC TCCGTGAGAT CCGTCGCTAC CAGAAGTCCA CGGAGCTGCT GATCCGCAAG 859
 860 CTGCCCTTCC AGCGGCTGGT CAGGGAAATC GCCCAGGATT TCAAAACGGA CTTGAGGTTC CAGAGCGCGG CCATCGGTGC GCTGCAGGAG GCGAGCGAAG 1047
1048 CGTATCTGGT GGGTCTGTTT GAAGACACAA ACCTGTGCGC CATCCATGCC AAGAGAGTCA CCATCATGCC CAAAGATATC CAGTTGGCTC GCAGGATACG 1147
1148 GGGAGAGAGA GCTTAAGTGA AGGCTGTTTT TATGGTGTTT TGTAGTAAAT TCTGTAAAAT ACTTTGGTTT TAATTTGTGA CTTTTTTGTA AGAAATTGTT 1247
1248 TATAATATGT TGCATTTGTA CTTAAGTCAT TCCATCTTTC ACTCAGGATG AATGCTAAAA GTGACTGTTC ACATAAACCT CAGTGATGTG AGCCTTGTTG 1347
1348 CTCAGGAGTG ACAAGTTGCT AATATGCAGA AGGGATGGGT GATCTTTCTT GCTTCTCATG CATGTTTCTG TATGTTAATG ACTTGTTGGG TAGCTAAACT 1447
1448 TGTAAGGTAC TAGAATTGAT ATAAATGTGT ACAGGGTCCT TTTGCAATAA AACTGGTTAT GACTTGATCC AAGTGTTTAA CAATTGGGGC TGTTAGTCTG 1547
1548 ACCATACATC ACTGTGATCA AATGTGGACT TTTTCAGAGG GTGAAACTAC AACTCTTAAC CACAGTGTAA CTTGCAGTTT CCTAAAAACG TAAACCTGGC 1647
1648 AGCTATAGAA TACACTATGT GCATTTATAA TAGCTATTTT ATATATTGTA GTGTCAACAT TTTTAAATTA AATGTTTTAC ATTCAAAA
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Legend. **Chicken histone H3.3B cDNA sequence.** Numbering corresponds to the genomic sequence described previously (2). Asterisks indicate splice sites between nt 101-571, 712-793, and 946-1035 and the poly(A) site at 1732. The coding region is underlined and the ATTAAA sequence is doubly underlined.

References:

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