Extreme sequence conservation characterizes the rabbit H3.3A histone cDNA

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Two distinct subclasses of the replication-independent H3.3 histone genes exist in vertebrates (1, 2). Although both the H3.3A and the H3.3B subclasses encode identical proteins, the untranslated portions of their mRNAs show no sequence similarity. Among members of each subclass, however, the 3' untranslated regions do show a high degree of sequence conservation (2, 3). To further explore these evolutionary relationships, a recombinant clone encoding an H3.3A histone was isolated from a cDNA library made from rabbit jejunum RNA. The coding region of this rabbit H3.3A cDNA shows 97% similarity to the coding region human H3.3A gene (4). Of greater interest is the extremely high degree of sequence conservation observed among the 3' untranslated regions of these H3.3A genes. The 3' UTR of the rabbit cDNA shows 94% similarity to the human 3' UTR and 82% similarity to the chicken H3.3A (1) 3' UTR. More remarkably, the final 154 nucleotides of the human and chicken 3' UTRs are 98% and 92% similar, respectively, to same region in the rabbit cDNA. This strong

evolutionary conservation extending throughout the entire 3' UTR in these vertebrate histone genes indicates that this entire region, especially the distal portion of the untranslated region, must have some as yet undefined evolutionary or functional significance.

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TATACC ATG GCT CGT ACA AAG CAG ACT GCC CGC AAA TCG ACT GGT GGT AAA GCA CCC AGG AAG CAA CTG GCT ACA AAA
      MET Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Thr Lys

GCC GCT CGC AAG AGT GCG CCC TCT ACT GGA GGG GTG AAG AAA CCT CAT CGT TAC AGG CCC GGT ACT GTG GCA CTT CGT
Ala Ala Arg Lys Ser Ala Pro Ser Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala Leu Arg

GAA ATC AGA CGT TAT CAG AAG TCC ACT GAG CTT CTG ATT CGC AAA CTC CCC TTC CAG CGT CTG GTG CGA GAA ATC GCT
Glu Ile Arg Arg Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala

CAG GAC TTC AAA ACA GAT CTG CGC TTC CAG AGC GCA GCT ATT GGT GCT TTG CAG GAG GCA AGT GAG GCC TAT CTG GTT
Gln Asp Phe Lys Thr Asp Leu Arg Phe Gln Ser Ala Ala Ile Gly Ala Leu Gln Glu Ala Ser Glu Ala Tyr Leu Val

GGC CTT TTT GAA GAC ACC AAC CTG TGT GCC ATC CAT GCC AAA CGT GTA ACA ATT ATG CCA AAA GAC ATC CAG CTA GCA
Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala Ile His Ala Lys Arg Val Thr Ile MET Pro Lys Asp Ile Gln Leu Ala

CGC CGC ATA CGT GGA GAA CGT GCT TAA GAATCCACTATGACGGGAACATTTTCATTCTCAAAAATTTTTTTTCTCTTCTTCTGTTATTGGT
Arg Arg Ile Arg Gly Glu Arg Ala .

AGTTCTGAACGTTAGATATTTTTTCCCATGGGTCAAAGGTACCTAAGTATATGATTGCGAGTGGAATAGGGGACAGAAATCAGGTATTGGCAGTTTTTCC
ATTTTCATTTTGTGTGGATTTTAAATATAAATGCGGGGACGTAAAGCATTAATGCAAGTCAAAATGTTTCAGTGAACAAGTTTCAGCAGTTCAACTTTATAA
CAATTATAAATAAACCTGTAAATTTTTCTGGACAATGCCAGCATTTGGATTTTTTAAACAAGTAAATTTCTTATTGACGGCAACTAAATGGTGTGTGATG
CATTTTATCATACAGTAGATTCCATCCATTCACCTATCTTTCTAACTGAGTTGTCTACATGCAAGTACATGTTTTTAATGTTGTCTGTCTTCTGTGCTGTT
CCTGTAAGTTTGCTATTAAATACATTAAACATT
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