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Nucleotide sequence of a mouse vascular smooth muscle alpha-actin cDNA

Bonhong Min, Arthur R.Strauch* and Douglas N.Foster

Biochemistry Program and Departments of Anatomy and Poultry Science, Ohio State University, Columbus, OH 43210, USA

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A cDNA library prepared from mouse smooth muscle-like BC3H1 myocytes (1,2) was screened for vascular smooth muscle (VSM) alpha-actin cDNA probes for use in studies of smooth muscle myogenesis. Dideoxy chain termination sequence analysis of the 1340 bp actin insert from one clone (pM αVSM-2) revealed a unique sequence at the 5' end which corresponded to 6 amino acid residues present at the N-terminus of the nascent VSM alpha-actin polypeptide chain (4). While the 23 bp portion of the 49 bp 5'-untranslated region (5'-UT) immediately 5' to the initiation codon of the mouse cDNA was nearly identical to sequences in both rat (3) and human (5) VSM alpha-actin 5'-UT regions (88% homology), there was only 17% homology to the corresponding sequence in the chicken VSM alpha-actin gene (6). However the 20 bp stretch immediately 5' to the 23 bp region in the mouse cDNA was 85% homologus to a different portion of the chicken 5'-UT encoded by exon 1 indicating that 5'-UT sequences proximal to the upstream promoter region of VSM alpha-actin genes may be evolutionarily conserved. No homology was evident between human, rodent, and bird VSM alpha-actin 3'-UT regions (3,5,6). Interestingly, the 151 bp 3'-UT region of the mouse cDNA did not contain a 37 bp C-rich insertional element that is present in the rat VSM alpha-actin 3'-UT (3) although rat and mouse sequences are 90% conserved 3' to this region.

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                                                          Met Cys Glu Glu Glu Asp Ser Thr  -
   1  GAGAAGCCCAGCCAGTCGCTGTCAGGAACCCTGAGACGCTGCTCCAGCT   ATG TGT GAA GAG GAA GAC AGC ACA GCC
  77  CTG GTG TGC GAC AAT GGC TCT GGG CTC TGT AAG GCC GGC TTC GCT GGT GAT GAT GCT CCC AGG GCT
 143  GTT TTC CCA TCC ATC GTG GGA CGT CCC AGA CAT CAG GGA GTA ATG GTT GGA ATG GGC CAA AAA GAC
 209  AGC TAT GTG GGG GAT GAA GCC CAG AGC AAG AGA GGG ATC CTG ACG CTG AAG TAT CCG ATA GAA CAC
 275  GGC ATC ATC ACC AAC TGG GAC GAC ATG GAA AAG ATC TGG CAC CAC TCT TTC TAT AAC GAG CTT CGT
 341  GTG GCC CCT GAA GAG CAT CCG ACA CTG CTG ACA GAG GCA CCA CTG AAC CCT AAG GCC AAC CGG GAG
 407  AAA ATG ACC CAG ATT ATG TTT GAG ACC TTC AAT GTC CCC GCC ATG TAT GTG GCT ATT CAG GCT GTG
 473  CTG TCC CTC TAT GCC TCT GGA CGT ACA ACT GGT ATT GTG CTG GAC TCT GGA GAT GGT GTG ACT CAC
.539  AAC GTG CCT ATC TAT GAG GGC TAT GCC CTG CCT CAT GCC ATC ATG CGT CTG GAC TTG GCT GGC CGA
 605  GAT CTC ACC GAC TAC CTC ATG AAG ATC CTG ACT GAG CGT GGC TAT TCC TTC GTG ACT ACT GCC GAG
 671  CGT GAG ATT GTC CGT GAC ATC AAG GAG AAG CTG TGC TAT GTA GCT CTG GAC TTT GAA AAT GAG ATG
 737  GCC ACG GCC GCC TCC TCT TCC TCC CTG GAG AAG AGC TAC GAA CTG CCT GAC GGG CAG GTG ATC ACC
 803  ATT GGA AAC GAA CGC TTC CGC TGC CCA GAG ACT CTC TTC CAG CCA TCT TTC ATT GGG ATG GAG TCA
 869  GCG GGC ATC CAC GAA ACC ACC TAT AAC AGC ATC ATG AAG TGT GAT ATT GAC ATC AGG AAG GAT CTC
 935  TAT GCT AAC AAC GTC CTG TCA GGG GGT ACC ACC ATG TAC CCA GGC ATT GCT GAC AGG ATG CAG AAG
1001  GAG ATC ACA GCC CTC GCA CCC AGC ACC ATG AAG ATC AAG ATC ATT GCC CCT CCA GAA CGC AAG TAC
1067  TCT GTC TGG ATC GGT GGC TCC ATC TTG GCT TCG CTG TCT ACC TTC CAG CAG ATG TGG ATC AGC AAA
       -   -   -   -   -   -   -   -   -   -   -   -  Arg Lys Cys Phe End
1133  CAG GAA TAC GAC GAA GCT GGG CCC TCC ATC GTC CAC CGC AAA TGC TTC TAA GTCCCCCCTGCTCTGCCTC
1203  TAGCACACAACTGTGAACGTTTTGTGGATCAGCGCCTCCAGTTCCTTTCCAAATCATTCCTGCCCAAAGCTTTGATTTGTTACTCGT
1290  GGTTTTTTTTAAAAATAAATCAGACATGTGCTACCCTTACCTTGTAAAAAA
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*To whom correspondence should be addressed

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