The nucleotide sequence of a rat vascular smooth muscle α -actin cDNA

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Submitted February 29, 1988

In an attempt to isolate smooth muscle actin specific cDNAs, we screened a whole rat stomach cDNA library (1,2). A single novel clone, pRVQA-19, was isolated and sequenced from single stranded M13 templates using the quasi end labeling technique (3). The entire clone is 1360 bp in length with 5' and 3' untranslated regions (UT) of 45 and 190 bp, respectively. The amino acid sequence encoded by pRVQA-19 is in complete agreement with that proposed for the α -vascular isoform of actin (4). The first amino acid of the mature actin protein coding region is preceded by the previously reported Met-Cys initiator sequence. A possible polyadenylation signal represented by AATAAA appears in the 3' UT region at base pair 1331. The 3' UT region also contains a 93% G/C rich segment which starts at base pair 1181 and extends to base pair 1223.

A comparison of our α -vascular actin cDNA to all other known actin sequences revealed several regions of significant sequence similarity besides the coding region. The human α -vascular smooth muscle actin gene contained a 26 nucleotide stretch of 80% similarity in the 5' flanking sequence immediately preceding the initiation codon, but the corresponding sequence in the chicken α -vascular smooth muscle actin gene showed only 60% similarity. In addition, the chicken α -vascular smooth muscle actin gene contained a second separate sequence of 19 nucleotides further upstream which displayed 74% sequence similarity when compared to the rat. The 3' UT region of our rat α -vascular actin cDNA and the 3' UT region of the chicken α -vascular actin gene show no apparent sequence similarities. By comparison, this region displays 91% sequence conservation when compared to the 3' UT region of the mouse α -vascular actin cDNA (personal communication from Dr. Art Strauch). Interestingly, the mouse α -vascular actin 3' UT region is missing the initial G/C rich segment present in the rat. Since the 3' UT regions of the various isoforms of actin have been implicated in the regulation of expression of these isoforms (5-7), the biological significance of a lack of 3' UT sequence conservation for the α -vascular actins is not clear.

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-42 CCAGCCAGTCCGCCATCAGGAACCTCGAGAAGCTCGCTCCAGCTATGTGTGAAGAGGAGACAGCAAGCTCTGGTGTGTGACAATGGCTCCGGGCTCTGTAAGGCGGGCTTGTCTGGT
MetCysGluGluGluAaspSerThrAlaLeuValCysAaspAsnGlySerGlyLeuCysLysAlaGlyPheAlaGly
76 GATGATGCTCCCGAGGGCTGTTTTCCCATCCATCGTGGGACCTCCAGACACCGAGGATGATGTTGGATGGGCCAAAGACACATATGTGGGGGACAAAGCCGACGACGAGAGA
AaspAaspAlaProArgAlaValPheProSerIleValGlyArgProArgHisGlnGlyValMetValGlyMetGlyGlnLysAaspSerTyrValGlyAaspGluAlaGlnSerLysArg
193 GGGATCTGACCTGAAAGTATCCGATGAACACCGGATCATCCCACTGGGACGACATGGAAGAGATCTGGCACCCTCTCTATACAGAGCTTCGCGTGGCCCCAGAGGAGCAT
GlyIleLeuThrLeuLysTyrProIleGluHisGlyIleIleThrAsnTrpAaspAaspMetGluLysIleTrpHisHisSerPheTyrAsnGluLeuArgValAlaProGluGluHis
310 CCGACTTGTCTAACGAGGCGCGCTGAACCTAAGGCCAACCGGAGAAATGACCCAGATTATGTTTGAGACCTTCAATGTCCCTGCCATGATGTATGGCTATTTCAGGCTGTGCTG
ProThrLeuLeuThrGluAlaLeuProLeuAsnProLysAlaAsnArgGluLysMetThrGlnIleMetPheGluThrPheAsnValProAlaMetTyrValAlaIleGlnAlaValLeu
427 TCCTCTATGCTCTTGAACGTACAACTGGTATTGTGCTGGACCTGGAGATGGCGTGAACACGTGCTCTATATAGGGGCTATGCTCTGCTCTATGCCATCATGGCTCTGGAC
SerLeuTyrAlaSerGlyArgThrThrGlyIleValLeuAaspSerGlyAaspGlyValThrHisAsnValProIleTyrGluGlyTyrAlaLeuPheHisAlaIleMetArgLeuAasp
544 TCGCTGGCGGAGATCTCAGGACTACCTCATGAGACTCTGCTGAGCGTGGCTATTCTCTGCTGACTGCTGAGCGTGAGATCGCTCCGTGACATCAAGGAGAGCTGTGCTAT
LeuAlaGlyArgAaspLeuThrAaspTyrLeuMetHisIleLeuThrGluArgGlyTyrSerPheValThrAlaGluArgGluIleValArgAaspIleLysGluLysLeuCysTyr
661 TCGCTCTGGACTTTGAAATGAGATGGCCACTGCTGCTCTCTCTCTCTCTCTGGAGAGAGCTACGAACTGCTGCTGGCGAGGTGATCACCATCGGGAATGAACGCTTCCGCTGC
ValAlaLeuAaspPheGluAsnGluMetAlaThrAlaAlaSerSerSerLeuGluLysSerThrGluLeuProAaspGlyGlnValIleThrIleGlyAsnGluArgPheArgCys
778 CCGGAGACCCCTTCCAGCCATCTTTTGAATGGATGGGCTGGCGGGCATCCAGAACACCTATACAGCATCATGAAGTGTGATTATGACATCAGGAAGGACCTTATGTCTAAC
ProGluThrGlyPheGlnProSerPheIleGlyMetGluSerAlaGlyIleHisGluThrThrTyrAsnSerIleMetLysCysAaspIleAaspIleArgLysAaspLeuTyrAlaAsn
895 ACGCTCTCTCGGGGGGCACTACCATGTACCCAGGCAATGCTGACAGGATGCAGAGGAGATCAGACCCCTCGCTCCAGCACCATGAAGATCAAGATTATTGCTCTCCAGCAATGC
AsnValLeuSerGlyGlyThrMetTyrProGlyIleAlaAaspArgMetGlnLysGluIleThrAlaGluLeuProSerThrMetLysIleLysIleAlaProProGluArg
1012 AATATTTCTGTCTGGATGGCGGCTCCATCTGCTGCTCTCTACCTTCACGAGATGTGGATCAGCAACAGGAGTATGACGAGCTGGCCCTCCATTTGCTCCAGCCGAAATGC
LysTyrSerValTrpIleGlyGlySerIleLeuAlaSerLeuSerThrPheGlnGlnMetTrpIleSerLysGlnGluTyrAaspGluAlaGlyProSerIleValHisArgLysCys
1129 TTCTAAGTCACGCCCCACCTCGCGCCGCGCCCAACCCCGCGCGCCCGCTCTGCTCTAGCAGACAACTGTGAATGTTTGGATCAGCGCTTCAGTCTTTTCCAAATC
PheEnd
1246 ATTCCTACCTAAAGCTTTGATTGTACTGCTGTGTTTTTTTAAATAATCAGACATGTGCTACCTCTTAA 1319

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This study has been supported by grants from the Ohio Affiliate of the American Heart Association SW 87-35, and NIH HD17000.

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