The nucleotide sequence of a human smooth muscle (enteric type) γ-actin cDNA

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Mammalia have at least six actin isoforms. We report here the nucleotide sequence of the human smooth muscle (enteric type) γ-actin (SMγA) cDNA, which was isolated as the sixth human actin gene. A λgt11 cDNA library constructed from the human stomach was screened with a 100 bp DdeI-SmaI DNA fragment around the amino-terminal region of SMγA prepared from a genomic clone (1), because amino-terminal sequences are the most variable regions of actin isoforms and only different between two smooth muscle actin isoforms (2). An isolated cDNA clone (pHSMγAc-5) was 1273 bp long with 5′ and 3′ untranslated regions of 54 bp and 77 bp, respectively. The amino acid sequence (376 residues) deduced from the nucleotide sequence was compatible with that of SMγA except for amino acid 359 (2), where Glu was substituted for Pro (double underlined). This substitution was also reported in mouse and rat SMγA genes (3, 4). Among human, mouse and rat SMγA cDNAs, deduced amino acid sequences are completely identical but nucleotide sequences in the coding regions show about 92% similarity. Recently, we determined the nucleotide sequence of the human SMγA gene (1), which was identical with that of cDNA except for four nucleotide substitutions (underlined). But, since they do not cause any amino acid replacements, they may be polymorphic changes in the human gene.

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GAACCTCTCATACCCTCGGTGCTCCAGTCCCCAGCTCACTCAGCCACACACACCATGTGTGAAGAGGAGACCACCGCGCTCGTGTGTGACAATGGCTCTG  100
                                                          MetCysGluGluGluThrThrAlaLeuValCysAspAsnGlySerG

GCCTGTGCAAGGCAGGCTTCGCAGGAGATGATGCCCCCCGGGCTGTCTTCCCCTCCATTGTGGGCCGCCCTCGCCACCAGGGTGTGATGGTGGGAATGGG  200
lyLeuCysLysAlaGlyPheAlaGlyAspAspAlaProArgAlaValPheProSerIleValGlyArgProArgHisGlnGlyValMetValGlyMetGl

CCAGAAAGACAGCTATGTGGGGGATGAGGCTCAGAGCAAGCGAGGGATCCTAACTCTCAAATACCCCATTGAACACGGCATCATCACCAACTGGGATGAC  300
yGlnLysAspSerTyrValGlyAspGluAlaGlnSerLysArgGlyIleLeuThrLeuLysTyrProIleGluHisGlyIleIleThrAsnTrpAspAsp

ATGGAGAAGATCTGGCACCACTCCTTCTACAATGAGCTGCGTGTAGCACCTGAAGAGCACCCCACCCTGCTCACAGAGGCTCCCCTAAATCCCAAGGCCA  400
MetGluLysIleTrpHisHisSerPheTyrAsnGluLeuArgValAlaProGluGluHisProThrLeuLeuThrGluAlaProLeuAsnProLysAlaA

ACAGGGAAAAGATGACCCAGATCATGTTTGAAACCTTCAATGTCCCTGCCATGTACGTCGCCATTCAAGCTGTGCTCTCCCTCTATGCCTCTGGCCGCAC  500
snArgGluLysMetThrGlnIleMetPheGluThrPheAsnValProAlaMetTyrValAlaIleGlnAlaValLeuSerLeuTyrAlaSerGlyArgTh

GACAGGCATCGTCCTGGATTCAGGTGATGGCGTCACCCACAATGTCCCCATCTATGAAGGCTATGCCCTGCCCCATGCCATCATGCGCCTGGACTTGGCT  600
rThrGlyIleValLeuAspSerGlyAspGlyValThrHisAsnValProIleTyrGluGlyTyrAlaLeuProHisAlaIleMetArgLeuAspLeuAla

GGCCGTGACCTCACGGACTACCTCATGAAGATCCTCACAGAGAGAGGCTATTCCTTTGTGACCACAGCTGAGAGAGAAATTGTGCGAGACATCAAGGAGA  700
GlyArgAspLeuThrAspTyrLeuMetLysIleLeuThrGluArgGlyTyrSerPheValThrThrAlaGluArgGluIleValArgAspIleLysGluL

AGCTGTGCTATGTGGCCCTGGATTTTGAGAATGAGATGGCCACAGCAGCTTCCTCTTCCTCCCTGGAGAAGAGCTATGAGCTGCCAGATGGGCAGGTTAT  800
ysLeuCysTyrValAlaLeuAspPheGluAsnGluMetAlaThrAlaAlaSerSerSerSerLeuGluLysSerTyrGluLeuProAspGlyGlnValIl

CACCATTGGCAATGAGCGCTTCCGCTGCCCTGAGACCCTCTTCCAGCCTTCCTTTATTGGCATGGAGTCCGCTGGAATTCATGAGACAACCTACAATTCC  900
eThrIleGlyAsnGluArgPheArgCysProGluThrLeuPheGlnProSerPheIleGlyMetGluSerAlaGlyIleHisGluThrThrTyrAsnSer

ATCATGAAGTGTGACATTGACATCCGTAAGGACTTATATGCCAACAATGTCCTCTCTGGGGGCACCACCATGTACCCTGGCATTGCTGACAGGATGCAGA 1000
IleMetLysCysAspIleAspIleArgLysAspLeuTyrAlaAsnAsnValLeuSerGlyGlyThrThrMetTyrProGlyIleAlaAspArgMetGlnL

AGGAGATCACAGCCCTGGCCCCCAGCACCATGAAGATCAAGATTATTGCTCCCCCAGAGCGGAAGTACTCAGTCTGGATCGGGGGCTCTATCCTGGCCTC 1100
ysGluIleThrAlaLeuAlaProSerThrMetLysIleLysIleIleAlaProProGluArgLysTyrSerValTrpIleGlyGlySerIleLeuAlaSe

TCTCTCCACCTTCCAGCAGATGTGGATCAGCAAGCCTGAGTATGATGAGGCAGGGCCCTCCATTGTCCACAGGAAGTGCTTCTAAAGTCAGAACAGGTTC 1200
rLeuSerThrPheGlnGlnMetTrpIleSerLysProGluTyrAspGluAlaGlyProSerIleValHisArgLysCysPheEnd

TCCAAGGATCCCCTCGAGACTACTCTGTTACCAGTCATGAAACATTAAAACCTACAAGCCTTAAAAAAAAAAA  1273
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