

cDNA and deduced amino acid sequences of a male dominant P-450Md mRNA in rats

Kiyoshi Nagata, Hiroyuki Sasamura, Masaaki Miyata, Miki Shimada, Yasushi Yamazoe and Ryuichi Kato

Department of Pharmacology, School of Medicine, Keio University, Tokyo 160, Japan

Submitted June 29, 1990

EMBL accession no. X53477

A λgt11 library constructed from hepatic mRNA of a 10 week-old male rat was screened with P-450-male specific antibody (1) and a new cDNA designated P-450Md cDNA, was isolated and sequenced. The deduced amino acid sequence of P-450Md cDNA displayed the highest similarity (60%) to those of P-450 (M-1) (2) or P-450f (3). The cysteine residue that attached to haem iron with the enzyme active site and the polyadenylation signal are underlined. The mRNA hybridized with a specific oligonucleotide probe displayed a male dominant expression in adult rats.

ACKNOWLEDGEMENTS

This work was supported by Grants-in-Aid from the Ministry of Education, Science and Culture, and from the Japan Health Science Foundations.

REFERENCES

1. Kamataki,T. et al. (1983) *Arch. Biochem. Biophys.* **225**, 758–770.
2. Yoshioka,H. et al. (1987) *J. Biol. Chem.* **262**, 1706–1711.
3. Gonzalez,F.J. et al. (1986) *J. Biol. Chem.* **261**, 10667–10672.

GTGAGCCAATGGCCCTTTCATTCTGGGATTTGGCTTCTGTTGGTTCTATGGAATCAGCACCATGTCAGAAGGAAGCTCCCACCTGGTCCACTCCTCTACCAA	120
MetAlaLeuPheIlePheLeuGlyIleTrpLeuSerCysLeuValPheLeuTrpAsnGlnHisHisValArgArgLysLeuProProGlyProThrProLeuProI	38
lePheGlyAsnIleLeuGlnValGlyValLysAsnIleSerLysSerMetCysMetLeuAlaLysGluTyrGlyProValPheThrMetTyrLeuGlyMetLysProThrValLeuT	78
ATGGATATGAAAGTATTGAAAGAACGCTCTGATTGACCGGGGAGAAGAGTTCTGATAAAATGCATTGCAATGCTCAGTAAAGTCAGGCCAAGGGTAGGCATTGCTTCAGCAATGGAG	360
yrGlyFyrGluValLeuLysGluAlaLeuIleAspArgGlyGluGluPheSerAspLysMetHisSerSerMetLeuSerGlnGlyLeuGlyIleValPheSerAsnGlyG	118
AAATATGGAAACAAACACGGCGTTCTCCCTATGGCTTAAGGTATGGGATGGGAAAGAGAACTATTGAAAACCGAATTCAAGGAGGAAGTTGTTTATCTGCTGGAAGCACTGAGAA	480
luIleTrpLysGlnThrArgArgPheSerLeuMetValLeuArgSerMetGlyMetGlyLysArgThrIleGluAsnArgIleGlnGluGluValValTyrLeuLeuGluAlaLeuArgL	158
AAACCAATGGTCCCCGTGTGACCCAGCTCCCTCTGGCCTGTGTTCCCTGCAATGTCATCTCAGCACCCTTGACTACAGTGATGAGAAATTCCAAAAATTCA	600
ysThrAsnGlySerProCysAspProSerPheLeuAlaCysValProCysAsnValIleSerSerPheGlnHisArgPheAspTyrSerAspGluLysPheGlnLysPheI	198
TAGAGAAATTCCATACAAAATTGAAATTTGACATCTCCTGGGCCAGTTGTCAGTGCCTATCCTGTTCTATACTATCTCCGGGAATCCATAACAAATTCTAAAGATGTGACTG	720
leGluAsnPheHisThrLysIleGluIleLeuAlaSerProTrpAlaGlnLeuCysSerAlaTyrProValLeuTyrLeuProGlyIleHisAsnLysPheLeuLysAspValThrG	238
AACAGAAAAAGTCATCTGATGGAAATAAACAGGCATCGAGCATCTCTGAACCTCAGTAACCCCTCAGGACTTTATTGACTATTCTCTGATTAATGAAAGGAAACACAATGAA	840
luGlnLysLysPheIleLeuMetGluIleAsnArgHisArgAlaSerLeuAsnLeuSerAsnProGlnAspPhenleAspTyrPheLeuIleLysMetGluLysGluLysHisAsnGluL	278
AGTCTGAATTTACCATGGACACCTGATAGTCACCATAGGTGATCTTTGGAGCAGGAACAGAGACAACGAGTCCACCATAAAATATGGGCTTGTGCTGAAGTACCCAGAGG	960
ysSerGluPheThrMetAspAsnLeuIleValThrIleGlyAspLeuPheGlyAlaGlyThrGluThrThrSerSerTyrGlyLeuLeuLeuLeuLysTyrProGluV	318
TCACAGCTAAAAATTCAAGGAAAGAAATTACTCGCGTGATTGGTAGACACCGGGAGACCCCTGCATGCAGGGACAGGAACACATGCCCTATACGGATGCTGCTGATGAGATCCAGAGATA	1080
alThrAlaLysIleGlnGluGluIleThrArgValIleGlyArgHisArgArgProCysMetGlnAspArgAsnHisMetProTyrThrAspAlaValLeuHisGlnArgTyrI	358
TTGATTTGTCCTCATTCCCTGCCTCGTAAGACAACGCAAGGATGTTGAGGATACACATCCCAAGGGACAAGCGTAAATGGCATGCTGACTTCTGCCCTGCACGATGACA	1200
leAspPheValProIleProLeuProArgLysThrThrGlnAspValGluPheArgGlyTyrHisIleProLysGlyThrSerValMetAlaCysLeuThrSerAlaLeuHisAspAspL	398
AAGAATTCCCCAACCCAGAGAAGTCGACCCGCCACTTCTCGATGAGAAAGCAACTCAAGAAGAGTACTTCTGACTTCTCAGCAGGAAGAAGAGCCTGATTGGAGAAG	1320
ysGluPheProAsnProLysPheAspProGlyHisPheLeuAspGluLysGlyAsnPheLysLysSerAspTyrPheMetAlaPheSerAlaGlyArgArgAlaCysIleGlyGluG	438
GTTCAGCCCGATGGAGATGTTCTTAATCCTGACCGCATTTACAGCATTTACTTTAAACCTCTGTCATGCAATCCAGAGGACATCGACACAACCCAGTTCAACCTGGTTATTGCTG	1440
lyLeuAlaArgMetGluMetPheLeuIleLeuThrSerIleLeuGlnHisPheThrLeuLysProLeuValAsnProGluAspIleAspThrProValGlnProGlyLeuLeuSerV	478
TGCCCGCACCTTGAGGCTCTGTTCAAGCAGGCTCTGAAGCAGGATAGCTCTGCTTCAACAGATGACTGAGACCCCTGCTACTTGTGAGCAACAGGTCCCTGCTGTACCTGTA	1560
alProProProPheGluLeuCysPheIleProVal	489
ACTGGCAGTCCTCTGAATGGCAGGGATGCTACCTCTGAACGTGCTACATTTCATTCTGTAACCAGTCAATTCTTGTGAAACCAGTCAATTTCATATGTGAAAAACTTCAGTGTGACTA	1680
ATAAAGTTTTTGTAGTGTATGTCAGAAAAAAA	1715