A New Genetic Defect in Human CYP2C19: Mutation of the Initiation Codon Is Responsible for Poor Metabolism of S-Mephenytoin

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ABSTRACT

The 4'-hydroxylation of the S-enantiomer of the anticonvulsant drug mephenytoin exhibits a genetic polymorphism in humans. This polymorphism shows marked interracial heterogeneity, with the poor metabolizer (PM) phenotype representing 2 to 5% of Caucasian and 13 to 23% of Asian populations. Two defective CYP2C19 alleles, CYP2C19*2 and CYP2C19*3, have been described which account for ~87% of Caucasian and ~99% of Oriental PM alleles. The present study identifies a new allele (CYP2C19*4) in Caucasian PMs which contains an A → G mutation in the initiation codon. A new polymerase chain reaction-restriction fragment length polymorphism genotyping test was developed, and the incidence of this allele was examined in a European Caucasian population which had been phenotyped for mephenytoin metabolism. One of nine putative PMs was heterozygous for CYP2C19*2/CYP2C19*4, which suggests that CYP2C19*4 represents a defective allele. Six of the seven remaining putative PMs available for genotyping were explained by CYP2C19*2. The frequency of the CYP2C19*4 allele in Caucasians was 0.6%. An additional Caucasian PM from a separate study was also heterozygous for CYP2C19*2 and CYP2C19*4. To verify that CYP2C19*4 represents a defective CYP2C19 allele, the initiation codon of the normal CYP2C19 cDNA was mutated to a GTG, and both cDNAs were expressed in yeast. Recombinant CYP2C19 protein was detected by Western blot analysis of colonies transformed with CYP2C19*4 cDNA, but not in those transformed with CYP2C19*2 cDNA. The two cDNAs were also used in an in vitro coupled transcription/translation assay. CYP2C19 protein was translated only from the CYP2C19*1 allele. These data indicate that CYP2C19*4 represents a new PM allele.

Received for publication March 25, 1997.

ABBREVIATIONS: PM, poor metabolizer; EM, extensive metabolizer; PCR, polymerase chain reaction; HI, hydroxylation index; CYP, cytochrome P450; RFLP, restriction fragment length polymorphism.
Methods and Materials

Subjects. An American Caucasian EM subject (CE) and a Can-
dian Caucasian PM subject (CB) were patients about whom infor-
mation was obtained from previously reported studies (de Morais,
1994a, b; Sarich et al., 1997). A European Caucasian population
consisted of the control group (324 unrelated individuals of which
219 were males and 15 were females) from a case-control study
of tobacco-related cancers in smokers (Benhamou et al., 1997). These
individuals were smokers without previous or current malignant
disease recruited from 10 French private or public hospitals and
were predominately male.

Phenotyping. The American and Canadian subjects ingested 100
mg racemic mephenytoin after emptying their bladders and a 0–
8-hr urine sample was collected. The PM phenotype was defined as
a urinary mephenytoin S/R ratio of greater than 0.9, and recovery
of less than 1% of the dose in the urine as 4'-hydroxymephenytoin
(Wedlund et al., 1984, Sarich et al., 1997). S/R ratios were deter-
mined both before and after and acification of the urine to circumvent
misclassification because of the presence of an acid-labile metabolite
in some urines (Wedlund et al., 1987; Zhang et al., 1992).

The European population was given a capsule containing 100
mg racemic mephenytoin and 25 mg dextromethorphan hydrobromide
after emptying their bladders, and a 8- to 12-hr urine sample was
collected. Metabolism of these drugs is mediated by two distinct P450
enzymes (CYP2C19 and CYP2D6), and they can be coadministered
without any interaction (Guttendorf et al., 1996). Metabolism of these
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CYP2C19 genotyping and sequencing of CYP2C19*4.
Genomic DNA was isolated from blood as described previously (Sam-
brook et al., 1989) or using Qiamp blood kits (Qiagen, Chatsworth,
CA) according to the manufacturer's protocol. To identify new genetic
defects of CYP2C19, exons and exon-intron junctions from various
subjects were amplified by PCR with intron-specific primers, and the
PCR products were sequenced on an automated sequencer (Applied
Biosystems, Foster City, CA) with the PRISM Dye Terminator Cycle
Sequencing kit. Genotyping procedures for detection of the
CYP2C19*2 and CYP2C19*3 alleles have been described previously
(Goldstein and Blaisdell, 1996).

A mismatch PCR-RFLP genotyping test was developed for the
CYP2C19*4 allele. This test used a forward PCR primer from the
5'-upstream region with a 1-bp mismatch (underlined) and a 6-bp A
and T overhang on the 5'-end (underlined) (5'-ATTATATTAAACAA-
GAGGAGAAGGCTGCA-3') and a 219-specific reverse primer (5'-
TTGGTTAAGGATTTGTGACA-3') from exon 1 in a method similar
to that described by Wang et al. (1995) for CYP2C9 alleles. The
mismatched primer introduced a PsI site only in the CYP2C19*4
allele. The amplification procedure was similar to that described for
the detection of CYP2C19*2 and CYP2C19*3 (Goldstein and Blais-
dell, 1996) except that the annealing temperature was 57°C for 15
sec, extension time 15 sec and the number of cycles was 40. The
resulting 195-bp products were digested with 4 units of PsI at 37°C
for 2 hr and the fragments were separated on 4% agarose gels.

28-bp fragments after PsI digestion, whereas the 195-bp product
generated from other CYP2C19 alleles remained uncut (see fig. 2).

As a positive control for CYP2C19*4, exon 1 of subject CE was
amplified by PCR as described above. The products were cloned into
the pCRII TA cloning vector (Invitrogen, San Diego, CA), trans-
formed into E. coli DH5α (Life Technologies, Gaithersburg, MD), and
a clone containing the CYP2C19*4 defect selected by sequencing. This clone was reamplified by PCR, and 0.5 ng of gel-purified DNA
was utilized in subsequent PCR tests.

Expression of CYP2C19 in yeast, Western blot, and Northern
blot analyses. The cloning of wild-type CYP2C19*1A cDNA in
pAH5 has been described (Romkes et al., 1991). This cDNA was cloned
in the HindIII site of pUCpUC2C19. A modified CYP2C9 cDNA contain-
ing a TGT as the initiation codon was constructed by replacing the
5'-HindIII-SacI fragment of pUC2C19 with a PCR product generated
by a mutant forward primer (5'-GGGAGGATCCAAATGGATGATCCTT-3')
and the reverse primer (5'-GCGAAGCTTGACACACATCGTGCTTC-3'). The modified cDNA insert was retrieved with HindIII, subcloned into pAH5 and verified by sequencing.

The protease-deficient Saccharomyces cerevisiae strain 334 was
transformed with the wild-type and mutant 2C19 plasmids in
pAH5 and Leu+ transformants selected as described previously
(Faletto et al., 1992). Ten colonies from each transformation were
grown to mid-log phase, and Western blot analysis performed on cell
lysates prepared from 3 × 107 cells with a primary polyclonal antibody
to CYP2C9 which recognizes CYP2C9, CYP2C19 and CYP2C9*1.
Western blot analysis as described previously (Goldstein et al., 1994).
The antibody was a generous gift from Dr. Jerome Lasker, Mount Sinai
School of Medicine. Total RNA (25 μg) isolated from these cultures
(Ausubel et al., 1990) was analyzed by Northern blot analysis with
32P-labeled CYP2C19 cDNA probe which consisted of the complete
CYP2C19 cDNA excised from pAH5 (Romkes et al., 1991).

Coupled in vitro transcription/translation assay.
CYP2C19*1A cDNA was amplified with PCR with the forward primer
(5'-GGGAGATCCAAATGGATGATCCTT-3') and the reverse primer (5'-GCTTCTTCTGATGATCCTT-3'). The PCR
products were digested with EcoRV and SacI and ligated into similarly
digested CYP2C19 in Bluescript. The resultant plasmids containing
the wild-type and the modified GTG codon were digested with
HindIII and BglI, and the inserts ligated into the pSP64 poly(A)
vector (Promega, Madison, WI) which was digested with HindIII and
BamHI. Plasmids were propagated in Escherichia coli DH5α and
sequences confirmed by DNA sequencing.

Plasmid templates (1 μg) were transcribed with SP6 RNA poly-
merase and translated with rabbit reticulocyte lysate in the presence
of [35S]-methionine with the coupled in vitro system (Promega, Mad-
ison, WI). The reaction products were separated on 4 to 20% gradient
polyacrylamide gels (Novex, San Diego, CA) under denaturing and
reducing conditions. The gel was soaked in isopropanol/water/acetic
acid (25:65:10) and then in Amplify scintillant (Amersham, UK),
dried and exposed to X-ray film. Recombinant yeast microsomes
containing CYP2C19 were electrophoresed on the same gel, and a
portion of the gel was subjected to Western blot analysis to verify the
size of the translated protein.

Data analysis. HI values of 62 of the 234 individuals in the
European population were excluded because of either intake of drugs
known to show a metabolic interaction with mephenytoin (five sub-
jects), missing HI values (21 subjects) or recovery of <10% of the
administered dose of both dextromethorphan and 4'-hydroxymephenytoin
(36 subjects). HI values were thus considered reliable for 172 sub-
jects. Blood samples were available for genotyping analysis of 173 of the
234 subjects. Both HI indices and genotype analysis were avail-
able for a total of 130 individuals and were analyzed by frequency
distribution. Frequencies and confidence limits for the CYP2C19
alleles were calculated by methods described by Hahn and Meeker
(1991) with all 173 individuals who were genotyped (346 alleles).
Results

An American subject CE was predicted to be an EM by a HI of 1.68 and S/R ratio of 0.28 which increased to 15 after acidification of the urine. This subject was thought to be homozygous for CYP2C19*1B, and the subject's DNA was sequenced to verify sequence differences between two wild-type alleles, which we are terming CYP2C19*1A (Romkes et al., 1991) and CYP2C19*1B (Richardson et al., 1995; S. M. F. deMorais, J. Blaisdell and J. A. Goldstein, unpublished data). Both alleles have been found to metabolize mephenytoin in cDNA expression systems (Goldstein et al., 1994; Richardson et al., 1995). CYP2C19*1B differs from CYP2C19*1A by an A → G substitution at base pair 991 resulting in the amino acid change I330V (Romkes et al., 1991; Richardson et al., 1995) and a C → T noncoding change at base pair 99 (S. M. F. deMorais, J. Blaisdell and J. A. Goldstein, unpublished data).

Although preliminary sequencing suggested that CE was homozygous for CYP2C19*1B, subsequent sequencing of all exons and exon-intron junctions revealed that CE was heterozygous for an A → G mutation at the first base of exon 1, changing the initiation codon from ATG → GTG (fig. 1). The sequence of the remainder of both alleles was identical with that of CYP2C19*1B. The new allele containing an altered initiation codon was termed CYP2C19*4.

The CYP2C19*4 defect creates a Eco57I restriction endonuclease site in exon 1, and this feature was used in the development of a PCR-RFLP CYP2C19*4 genotyping test (fig. 2). The 285-bp PCR product of exon 1 is undigested in individuals homozygous for the normal ATG (CYP2C19*1A or CYP2C19*1B). Eco57I completely digests the subcloned CYP2C19*4 product, producing 186- and 99-bp fragments. CE was heterozygous for the CYP2C19*4 allele showing all three bands.

The frequency of the three defective CYP2C19 alleles was determined in 173 European Caucasians. Phenotyping data (HI values) were available for 130 of these subjects. The frequency distribution of the HI values indicated that the antimode separating EMs from PMs was not unequivocal (fig. 3). However, comparison of HI values, genotypes, and S/R ratios before and after acidification indicated that HI values $\geq 40$ have approximated the PM phenotype (table 1). Among eight putative PMs available for genotyping, six were explained by the CYP2C19*2 allele. One PM (no. 32006; HI = 47) was heterozygous for CYP2C19*2 and CYP2C19*4 (fig. 1). One putative PM (no. 32080; HI = 43) remained unexplained as a possible outlier. One PM in table 1 was not available for phenotype and is not included in figure 3. Only one additional CYP2C19*4 allele was found out of 173 individuals (an unphenotyped individual no. 32125) (fig. 2). The frequency of CYP2C19*4 was 2 of 346 alleles or $0.006$.
Mutations of CYP2C19 are responsible for a well-known polymorphism in drug metabolism in humans which affects the metabolism of the anticonvulsant agent mephenytoin as well as that of other drugs. Recently, two mutations, CYP2C19*2 and CYP2C19*3 have been shown to account for >99% of Oriental but only ~88% of 37 Caucasian PM alleles, which suggests that other defective alleles contribute to the PM phenotype in Caucasians (de Morais et al., 1994a, b; Sarich et al., 1997; Bresen et al., 1995; Balian et al., 1995; Goldstein et al., 1997; J.A. Goldstein, J. Blaisdell, C. Beyeler and A.K. Daly, unpublished data). The present study identifies a new allele, CYP2C19*4, which contributes to the PM phenotype in Caucasians. This new allele contains an ATG→GTG mutation in the initiation codon.

The defective nature of the CYP2C19*4 allele is shown by the fact that two Caucasian PMs were heterozygous for CYP2C19*2/CYP2C19*4. Although the frequency of CYP2C19*4 is only 0.6% in Caucasians, this allele accounted for the phenotype of 2 of 37 Caucasian PMs. The genetic tests for CYP2C19*2, CYP2C19*3 and CYP2C19*4 now correctly identify ~91% of the defective alleles in 37 Caucasian putative PMs studied in our laboratory (de Morais et al., 1994a, b).
Sarich et al., 1997; Brøsen et al., 1995; Goldstein et al., 1997; and present studies) and predict the phenotype in 86% of these PMs. This may represent an underestimate of the efficiency of the tests because of the possibility of noncompliance in urinary collection and the fact that certain individuals are not available for re-phenotyping.

This is the first example of the utilization of a GTG as the initiation codon in CYP proteins. However, several precedents exist for the initiation of translation from a GTG codon for certain other proteins in bacteria and Drosophila (Shaw and Fulco, 1992; Sugihara et al., 1990), although this codon is often translated with reduced efficiency in these systems. In mammalian systems, a GTG mutation was reported in the initiation codon of the gene which codes for a growth factor protein in two Japanese individuals with Norrie disease (an X-linked recessive disease characterized by bilateral congenital blindness) (Isashiki et al., 1995), and a GTG mutation was also reported in the initiation codon of the gene encoding the G protein of adenylate cyclase in Albright’s hereditary osteodystrophy (Patten et al., 1990). However, the role of the GTG codon in affecting the efficiency of translation of these genes was not investigated.

Mutation of the initiation codon of CYP2C19 cDNA to a GTG in the present study abolished expression of recombinant CYP2C19 in a eukaryotic yeast cDNA expression system, confirming the defective nature of the CYP2C19*4 allele. Because CYP2C19 mRNA levels were similar in yeast transformed with the two cDNAs, these data suggest that the GTG codon produces a marked decrease in the translation of CYP2C19. Results of an in vitro transcription/translation assay also suggest that the GTG codon interferes with translation.

CYP2C19*3 represents ~25% of the PM alleles in Orientals, but it is rare in Caucasians (de Morais et al., 1994a, b; Brøsen et al., 1995; Goldstein et al., 1997). We previously found this allele in 1 of 11 Caucasian PMs from Denmark, but it was not present in 105 American-Caucasians or 97 Saudi Arabians. The present study verifies the presence of this allele in a European Caucasian population with a low frequency of 0.003 (95% confidence limits, 0.001–0.016).

In summary, the present study reports a new PM allele of CYP2C19, in which the initiation codon is changed from an ATG to a GTG. This is the first example of a GTG codon as the initiation codon of a CYP protein. The defective nature of this allele was verified by its lack of expression in a yeast cDNA expression system, the absence of translation in an in vitro coupled transcription/translation assay, and its presence in two previously unexplained PMs of mephenytoin. This mutation accounted for 3% of 37 Caucasian PM alleles, increasing the efficacy of the genetic tests in predicting the PM phenotype to ~86% in Caucasians.
Acknowledgments

The authors thank Richard W. Morris, of Analytical Sciences, Inc., Research Triangle Park, NC for his expert statistical analyses.

References


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