The CYP2C19 intron 2 branch point SNP is the ancestral polymorphism contributing to the poor metabolizer phenotype in livers with CYP2C19*35 and CYP2C19*2 alleles

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Running Title Page

Running Title:  CYP2C19 nonfunctional SNP rs12769205 alters splicing

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Abbreviations:  CYP, cytochrome P450; LD, linkage disequilibrium; IGV, integrative genomic viewer; NMD, nonsense mediated decay; PM, poor metabolizer; PTC, premature termination codon; REHH, relative extended haplotype homozygosity; SNP, single nucleotide polymorphism; SV, splice variant; YRI, Yorubans.
ABSTRACT

CYP2C19 rs12769205 alters an intron 2 branch point adenine leading to an alternative mRNA in human liver with complete inclusion of intron 2 (exon 2B). rs12769205 changes the mRNA reading frame, introduces 87 amino acids, and leads to a premature stop codon. The 1000 genomes project indicated rs12769205 is in LD with rs4244285 on CYP2C19*2, but found alone on CYP2C19*35 in Blacks. Minigenes containing rs12769205 transfected into HepG2 cells demonstrated this SNP alone leads to exon 2B and decreases CYP2C19 canonical mRNA. A residual amount of CYP2C19 protein was detectable by quantitative proteomics with tandem mass spectrometry in CYP2C19*2/*2 and *1/*35 liver microsomes with an exon 2 probe. However, an exon 4 probe, downstream of rs12769205, but upstream of rs4244285, failed to detect CYP2C19 protein in livers homozygous for rs12769205 demonstrating rs12769205 alone can lead to complete loss of CYP2C19 protein. CYP2C19 genotypes and mephenytoin phenotype were compared in 104 Ethiopians. Poor metabolism of mephenytoin was seen in persons homozygous for both rs12769205 + rs4244285 (CYP2C19*2/*2), but with little effect on mephenytoin disposition of CYP2C19*1/*2, CYP2C19*1/*3 or CYP2C19*1/*35 heterozygous alleles. Extended haplotype homozygosity tests of the Hapmap Yorubans (YRI) showed both haplotypes carrying rs12769205 (CYP2C19*35 and CYP2C19*2) are under significant natural selection, with CYP2C19*35 having a higher REHH score. The phylogenetic
tree of the YRI CYP2C19 haplotypes revealed rs12769205 arose first on CYP2C19*35 and that rs4244285 was added later creating CYP2C19*2. In conclusion, rs12769205 is the ancestral polymorphism leading to aberrant splicing of CYP2C19*35 and CYP2C19*2 alleles in liver.
INTRODUCTION

CYP2C19 is an important drug-metabolizing enzyme that plays a critical role in the metabolism as well as drug-drug interactions of a variety of drugs, including proton pump inhibitors, anti-epileptics, anti-platelet drugs, and anti-depressants (Li-Wan-Po et al., 2010; Shah et al., 2012; Shirasaka et al., 2013). Similar to a variety of other CYP family members, CYP2C19 activity is polymorphic, with sub-populations of poor metabolizers, intermediate metabolizer, extensive metabolizer and ultra-rapid metabolizer (Wedlund, 2000; McGraw and Waller, 2012; Hicks et al., 2013). Multiple allelic variants of CYP2C19 have been described. CYP2C19*1 represents the wild-type allele. The frequent rs4244285 polymorphism, defining the CYP2C19*2 allele, creates an exon 5 aberrant splice site, altering the reading frame of the mRNA leading to a premature stop codon and a non-functional protein (de Morais et al., 1994a).

There are numerous reports linking the CYP2C19*2 allele to altered substrate clearance (Hirota et al., 2013; Hicks et al., 2013; Owusu et al., 2014). Over 34 CYP2C19 variant alleles have been identified in a cytochrome P450 database (http://www.cypalleles.ki.se/cyp2c19.htm). In addition, a recent study of 2203 African Americans (Gordon et al., 2014) found that CYP2C19 had the highest number of putative novel functional variants compared with 11 other drug metabolizing CYP genes. This result was interesting because it was recently reported that the CYP2C19*2 nonfunctional allele may have been positively selected in human evolution (Janha...
et al., 2014), and that inactivation of CYP2C19 might have afforded some survival advantage.

Conversely, because CYP2C19 loss-of-function alleles confer increased risks for serious adverse cardiovascular events among clopidogrel treated patients, Clinical Pharmacogenetic Implementation Consortium (CPIC) Guidelines were issued for CYP2C19 genotype-directed drug therapy (Scott et al., 2013).

In an effort to identify additional function-disrupting CYP2C19 alleles, we sequenced CYP2C19 in human livers and identified a branch point SNP (rs12769205; gene position 12662A>G) in intron 2 of CYP2C19 that leads to intron 2 retention. Interestingly, rs12769205 is found in combination with rs4244285 (the SNP that defines all CYP2C19*2 alleles) and 12662A>G is likely part of all CYP2C19*2 alleles. However, rs12769205 is also found without rs4244285 on CYP2C19*35 (allele designation assigned by the CYP allele nomenclature committee). In this report, we have investigated the functional consequence of rs12769205, whether CYP2C19*35 is also under natural selection, and whether CYP2C19*35 is the ancestral CYP2C19 nonfunctional allele, arising before CYP2C19*2.
MATERIALS AND METHODS

**Human liver tissue.** A total of 335 human livers from 272 White and 63 Black donors were processed through the St. Jude Liver Resource at St. Jude Children’s Research Hospital and were provided by the Liver Tissue Procurement and Distribution System (National Institutes of Health National Institute of Diabetes and Digestive and Kidney Diseases Contract N01-DK92310) and by the Cooperative Human Tissue Network. The St. Jude Children's Research Hospital Institutional Review Board approved the use of these human tissues for research purposes.

**RNA isolation and cDNA preparation.** Total RNA was extracted from human livers with rs4244285 and rs12769205 genotypes using TRIzol reagent (Invitrogen, Cat. No. 15596-026). 500 ng RNA was used to prepare cDNA using Invitrogen Thermoscript™ RT-PCR System (Cat no. 11146-024).

**Genotyping of CYP2C19 alleles in human livers.** Genomic DNA from human livers was isolated using a DNeasy tissue kit (Qiagen Cat no. 69506). Genotyping of the rs4244285 and rs12769205 SNPs was performed by direct DNA sequencing. Primers used for PCR amplification and sequencing of rs4244285 were (FP) 5’-CAACCAGAGCTTGGCATATTG-3’ and (RP) 5’-TGATGCTTACTGGATATTCATGC-3’; and for rs12769205 were (FP)
5’-AAAAATATGAATCTAAGTCAGGCTTAGT-3’ and (RP) 5’-GGAGAGCAGTCCAGAAAGGTCAGTGATA-3’. A general 25 µL PCR mixture consisted of 50 ng gDNA, 1 µM primers and Platinum PCR supermix (Invitrogen Cat No. 11306-016). For quality control, minor allele frequencies (MAFs) for rs4244285 and rs12769205 were compared to existing population genotype data from the Exome Variant Server (http://evs.gs.washington.edu/EVS/) for Whites and Blacks. The observed and reported MAFs values were in agreement.

**Sequencing of CYP2C19 exons from genomic DNA.** CYP2C19 exons were PCR amplified in a 25 µL PCR mixture consisting of 50 ng gDNA, 1 µM primers and Platinum PCR supermix mix (Invitrogen Cat No. 11306-016) and sequenced using CYP2C19 specific primers (Supplemental Table 1).

**Genotyping of African livers for CYP2C19*2 at the cDNA level.** To confirm the CYP2C19*2 genotype assignments obtained by DNA sequencing we also genotyped the eight African livers used for subsequent analysis of the transcripts at the cDNA level using the primers and method reported by de Morais et al 1994a.
CYP2C19 cDNA amplification. Various portions of CYP2C19 were PCR amplified from human liver cDNA using the following primer pairs and products were either directly sequenced or analyzed on 2% agarose gels. (1) Exon 4 (FP) (5’-ATTGAATGAAAAACATCAGGATTG-3’) and exon 6 (RP) (5’-GTAAGTCAGCTGCAGTGATTA-3’) (de Morais et al., 1994a). CYP2C19*1 and CYP2C19*2 generate 284 and 244 bp products, respectively. (2) Exon 2 (FP) (5’-GAAGAGGCCATTTCCCACCT-3’) and exon 4 (RP) (5’-TTTCTGGAAAAATGAGGA-3’). Livers with and without rs12769205 generate 438 bp (retaining 169 bp intron 2) and 269 bp products, respectively. (3) Exon 2 (FP) (5’-GAAGAGGCCATTTCCCACCT-3’) and exon 6 (RP) (5’-GTAAGTCAGCTGCAGTGATTA-3’) primers. CYP2C19*1 generates the canonical 597 bp product. CYP2C19*35 generates products of 766 bp (containing exon 2B) and 695 bp (exon 2B plus 70 bp deletion in exon 4). CYP2C19*2 generates products with the 40 bp deletion of exon 5 (557 bp) and additionally containing exon 2B with or without the 70 bp deletion in exon 4 (726 bp and 655 bp, respectively).

Sequencing the full length CYP2C19*35 cDNA and its alternative transcripts. First, cDNA from the CYP2C19*1/*35 liver was used as template and PCR amplified with exon 2 and 6 primers (above), the PCR products were cloned into pCR 2.1 TOPO vector using the TOPO TA
Cloning® Kit (Invitrogen Cat No. 450641), and products transformed into One Shot® Top 10 Chemically Competent cells (Invitrogen Cat no. 1427548) and grown on LB-ampicillin plates. Forty individual colonies were picked and colony PCR carried out using M13 primers (FP) 5´-GTAAAACGACGGCCAG-3´ and (RP) 5´-CAGGAAACAGCTATGAC-3´, and the PCR products directly sequenced using the same primers.

Second, to determine whether the CYP2C19*35 allele carried other polymorphisms in the coding region, the full length CYP2C19*35 cDNA from the CYP2C19*35 liver was PCR amplified using FP 5´-TTGTGGTCCTTGTGCTCTGTCTC-3' and RP 5´-GGAATGAAGCACAGCTGA-3' and the PCR product cloned into TOPO TA vector and sequenced using M13 primers mentioned above. The sequences obtained were then aligned using a software suite for sequence analysis (DNASTAR SeqMan Pro version 9.0.4. 39, 418).

CYP2C19 genotypic data mining from 1000 genomes server (Phase 3 data). rs4244285 and rs12769205 genotypes were downloaded for CEU, All Africans and CHB in the 1000 genomes browser (http://browser.1000genomes.org/index.html) to generate visual genotypes and study the linkage between these two alleles in different ethnic groups.

Linkage Disequilibrium Analysis. Pairwise linkage disequilibrium (LD) was calculated for 85
CEU, 246 Africans, 88 YRI and 97 CHB from the 1000 genomes browser and displayed using Haploview 4.2 software (Barrett et al., 2005). The D', along with its corresponding Logarithm of Odds (LOD) score, and r^2 LD values were determined between rs4244285, and rs3758580, rs4417205 and rs12769205 SNPs.

**Generation of CYP2C19 Minigenes.** The RHGlo minigene plasmid (Singh and Cooper 2006) was generously provided by Dr. Thomas A. Cooper (Baylor College of Medicine, Houston, TX). A 264 bp fragment consisting of the last 87 nucleotides of CYP2C19 intron 4 and full length exon 5 was amplified from the DNA of a CYP2C19*2/*2 human liver using PCR primers (FP) 5’-ATATATGTCGACAGTTTTAATTACAACCAGAGCTTG-3’ (having a SalI site (underlined)) and (RP) 5’-ATATATCTCGAGCTTTCTCCATTTTGATCAGGAAGC-3’ (having XhoI site (underlined)), and used to replace the SalI/XhoI fragment of the RHGlo plasmid to generate the CYP2C19*2 minigene. The CYP2C19*2 minigene was used as template to perform site directed mutagenesis to create the CYP2C19*1 wild type minigene using the QuikChange II site directed mutagenesis kit (Agilent Technologies Cat no. 200523) and primers (SDM-FP) 5’-CCCCACTATCATTTTATCTCAGGGGAAATCACAAATTACTTAA-3’ and (SDM-RP) 5’-TTAAGTATTTTGTTATGTTTCCCCGGAATATAATAATCATGATAGTGGG-3’. The CYP2C19 exon 2/intron 2/exon 3 minigenes were generated by PCR amplifying this region.
from human liver DNAs with either CYP2C19*1 or CYP2C19*35 genotypes using primers (FP) 5’-ATATATGGATCCCTCTCTGAAAAATCTATGGCCCTG-3’ (having a BamHI site (underlined)) and (RP) 5’-ATATATCTCGAGCCTTGGTTTTTCTCAACTCC-3’ (having XhoI site (underlined)). The 482 bp amplified CYP2C19 fragments were used to replace the BamHI/XhoI fragment of the RHCglo plasmid to generate either CYP2C19*1 or rs12769205 minigenes. The sequences of all minigenes were confirmed by DNA sequencing.

**Minigene Transfection Assays.** HepG2 human hepatoblastoma cells were cultured in minimal essential media supplemented with 10% fetal bovine serum, 1% penicillin, and 1% streptomycin, and maintained in a humidified incubator at 37°C in an atmosphere of 5% CO₂. For transfection studies, 150,000 cells per well were seeded in 12 well culture dishes. Twenty four hours later cells were transfected with 1000 ng of different minigene plasmids using LipoJet *in vitro* DNA and siRNA transfection kit (Ver. II, SignaGen laboratories Cat. No. SL100468). Forty-eight hours later cells were washed with phosphate-buffered saline and harvested with TRIzol reagent (Invitrogen Cat. No. 15596-026). First-strand cDNA was prepared using 500 ng RNA and oligo (dT) primers (catalog no. 11146-016, ThermoScript RT-PCR system; Invitrogen). PCR amplification was performed using (FP) RSV5U 5’-CATTCACCACATGGGTGC-3’ and (RP) TNIE4 5’-AGGTGCTGCGCCCGGGCTGCTGC-3’ that both anneal to the vector expressed exons in
order to selectively amplify only the plasmid expressed mRNA transcripts (Singh and Cooper 2006). The amplified PCR fragments were electrophoresed on 1% agarose gel.

**Quantitative PCR analysis.** Q-real time PCR was used to quantitate the amount of canonical \(CYP2C19\) transcript generated by the \(CYP2C19\) wild type and rs12769205 minigenes. The forward primer RSV5U 5’-CATTCACCACATTGGTGTGC-3’ annealed in the vector and the reverse primer 5’-CCATTGCTGAAAACGATTCCAA-3’ annealed across the \(CYP2C19\) exon 2 -3 junction to specifically amplify only the canonical \(CYP2C19\) transcript generated from the minigene. GAPDH primers were (FP) 5’-GGACCACCAGCCCCAGCAAGAG-3’ and (RP) 5’-GAGGAGGGGAGATTCAGTGTGGTG-3’. Real-time PCR quantification was carried out using the SYBR GreenER quantitative PCR supermix (catalog no. 11760-100; Invitrogen) and amplifications run on an ABI PRISM 7900HT Sequence Detection System (PE Applied Biosystems, Foster City, CA). The Ct values were analyzed by the comparative Ct method to obtain relative mRNA expression levels.

**CYP2C19 peptide quantification.** CYP2C19 was quantified using three different surrogate peptides, (1) exon 2 specific peptide (IYGPVFTLYFGLER); (2) exon 8 specific peptide (GTTLTSLTSVLHDK); and (3) exon 4 specific peptide (ASPCDPTFLGCAPCNVICSIFQK).
The surrogate peptides for LC-MS/MS quantification were selected based on previously reported criteria (Prasad et al., 2014). Trypsin digestion and sample preparation for LC-MS/MS analysis of the genotype-defined pooled HLM (human liver microsomal) samples was performed using a previously reported protocol (Edson et al., 2013; Wang et al., 2015) with few modifications. Briefly, the pooled HLM sample (60 μL) was denatured and reduced with 40 μL of ammonium bicarbonate digestion buffer (100 mM, pH 7.8) and 10 μL of 100 mM dithiothreitol at 90 °C (5 min). The sample was then alkylated by adding 20 μL iodoacetamide (200 mM) at room temperature for 20 min. The protein was then extracted using addition of ice-cold methanol (500 μL), chloroform (200 μL) and water (400 μL). The mixture was vortexed, centrifuged at 12000x g for 5 min, and the upper layer was removed. The protein pellet was washed with 500 μL ice-cold methanol followed by centrifugation at 12000g for 5 min. The final protein pellet was dissolved in ammonium bicarbonate (40 μL) and 3% sodium deoxycholate (10 μL) before digestion by trypsin (protein:trypsin ratio of 25:1) at 37 °C for 16 h. The reaction was quenched by addition of 20 μL of heavy peptide 2 (GTTILTSLTSVLHDNK[^13C_6,^15N_2]) internal standard solution (prepared in 70% acetonitrile in water containing 0.1% formic acid) and 10 μL of the neat solvent (70% acetonitrile in water containing 0.1% formic acid). The samples were centrifuged at 4000g for 5 min. All of the HLM samples were digested and processed in triplicates.

The CYP2C19 surrogate peptides were then quantified using triple-quadrupole LC-MS.
instruments (Xevo TQ-S coupled to ACQUITY UPLC (Waters)) in ESI positive ionization mode.

Approximately 10 µg of the trypsin digest (5 µL) was injected onto the column (Acquity UPLC®
HSS T3 1.8 µm, 2.1 x 100 mm, Waters) and eluted at 0.3 mL/min. A mobile phase consisting of
water containing 0.1% formic acid (A) and acetonitrile containing 0.1% formic acid (B) was used.

A flow rate of 0.3 mL/min was used with a gradient elution starting from 3% B and kept until 2.0
min, followed by gradient program (B concentration) of 3% to 15% (2.0-4.0 min), 15% to 25%
(4.0-10 min) and 25% to 50% (10.0-14 min), and his was followed by washing with 80% mobile
phase B for 0.9 min, and re-equilibration for 4.9 min. The peak retention times were confirmed
by spiking either peptide standards (peptides 1 and 2) and/or trypsin digested CYP2C19 protein
standard (gratis sample from Dr Nina Isoherranen). MS/MS analysis was performed by
monitoring the surrogate peptides and the internal standard using instrument parameters provided
(Supplemental Table 2). LC/MS/MS data were processed using the MassLynx 4.1 (Waters,
Milford, MA) by integrating the peak areas generated from the ion chromatograms for the
surrogate peptides and normalized by the internal standard response. Peak response for two
transitions from each peptide was averaged for quantification of samples and the relative protein
quantification was reported as the mean and standard deviation (SD) of peak area ratio values
obtained in at least three experiments.
Ethiopian cohort (n=104). Details of the healthy unrelated Ethiopian subjects of both sexes living in Ethiopia who participated in this study were described previously (Persson et al., 1996; Aklillu et al., 2002). The study received ethics approval from the Human Ethics Committees at Huddinge University Hospital, Karolinska Institutet, Stockholm, Sweden and the National Ethics committees at the Ethiopian Science and Technology commission, Addis Ababa, Ethiopia.

CYP2C19 phenotyping of the Ethiopian cohort. Details on CYP2C19 phenotyping of the Ethiopian cohort has been previously published (Persson et al., 1996; Aklillu et al., 2002; Sim et al., 2006). Briefly, the subjects received 100 mg racemic mephenytoin (Mesantoin® Sandoz Pharmaceuticals, Basel, Switzerland) after emptying their bladder just before bedtime. Total urine was collected for 0-8 h after drug intake. Volume and pH were measured and 20 mL aliquots were stored at -20°C until analysis. The concentration ratio of S and R-mephenytoin was measured by gas chromatography as described previously (Sanz et al., 1989). Urine samples with S/R ratio > 0.6 were reanalyzed after acid treatment (Tybring & Bertilsson, 1992). Subjects with an S/R ratio greater than 0.9 and not increasing above 1.4 after acid treatment were assigned as poor metabolizers.
CYP2C19 genotyping of the Ethiopian cohort. Ten mL venous blood sample was taken from each subject into an EDTA-containing vacutainer tube and DNA was isolated from peripheral leukocytes using a guanidinium-isothiocynate method. Genotyping for CYP2C19*2 and CYP2C19*3 was done using allele specific PCR as described previously (de Morais et al., 1994a and 1994b; Persson et al., 1996). Genotyping for CYP2C19*17 was performed as described previously (Sim et al., 2006). CYP2C19*35 (rs12769205) was genotyped using a custom Taqman SNP genotyping assay (Item Number 4331349) from Life Technologies. Taqman genotyping assay was done using a QuantStudio 12K Flex- Real-Time PCR system (Life Technologies Holding Pte Ltd, Singapore). The final volume for each reaction was 10 µL, consisting of TaqMan fast advanced master mix (Applied Biosystems, USA), TaqMan 1X drug metabolism genotyping assays mix (Applied Biosystems, USA) and 20 ng genomic DNA. The PCR profile consisted of an initial step at 60°C for 30 sec, hold stage at 95°C for 10 min. and PCR stage for 40 cycles - step 1 at 95°C for 15 sec, and step 2 at 60°C for 1 min, and post read stage at 60°C for 30 sec.

Preparation of RNA-sequencing libraries. Liver RNA was isolated at SJCRH. Liver RNA was shipped to the Baylor College of Medicine Human Genome Sequencing Center (BCM-HGSC) where it was analyzed for integrity and used for RNA-Seq library preparation and sequencing as described in detail in a separate report (Chhibber A et al., communicated).
reads were sent to the St Jude Children’s Research Hospital Computational Biology team for analysis.

**RNA-Seq analysis.** FASTQ sequences were mapped to the hg19 genome by STRONGARM. STRONGARM is a pipeline that employs STAR (Dobin et al., 2012), Tophat2 (Kim et al., 2013), and other mappers and was developed for the Pediatric Cancer Genome Project (Downing et al., 2012). Mapped reads were counted with HTSEQ (Theodor et al., 2014) coverage files and gene level FPKM values were then computed and data was visualized using IGV (Robinson et al., 2011). Exon junction data was extracted through the RNApeg pipeline (Edmonson et al., in preparation).

**Haplotypes, relative extended haplotype homozygosity (REHH), and ancestral analysis.**

The Sweep program (http://www.broadinstitute.org/mpg/sweep/) was used to determine haplotypes and to generate relative extended haplotype homozygosity (REHH) plots in order to look for positive selection in the YRI population and then in other African Populations. All 216 chromosomes from the YRI in the 1000 Genomes phase 3 data (release #20130502) were used (compared to the recent Janha et al., 2014, that used 120 Yoruban chromosomes). The coordinates were lifted from hg19 to hg17 using the liftover program.
(https://genome.ucsc.edu/cgi-bin/hgLiftOver) and then data in chr10:96486608-96688055 (hg17 coordinates) were used for subsequent analysis, totaling 201,447 bp. SNP positions rs12769205, rs4244285, rs4417205 and rs3758580 defined the core haplotypes. REHH plots were generated from rs77989980 (downstream of CYP2C18) to rs9332103 (upstream of CYP2C9). For ancestral analysis, the Sweep program predicts the chimp allele to be the ancestral allele for all SNPs from the HapMap Release 16. Where ancestral information was available, the ancestral core haplotype was predicted and a phylogenetic tree of haplotypes was then created.
RESULTS

A polymorphic CYP2C19 alternative mRNA retaining intron 2. PCR amplification of the CYP2C19 cDNA from exon 2 to exon 4 revealed the expected 269 bp product in all livers, but an additional 438 bp product polymorphically expressed in some (Fig 1). Direct sequencing of the 438 bp fragment showed complete intron 2 retention generating exon 2B. All livers expressing the CYP2C19 alternative mRNA with exon 2B also carried a unique intron 2 SNP rs12769205, but no other SNP in intron 2 or in exons 2 or 3 was found after sequencing exon 2 through exon 3 in genomic DNA. Sequencing of the entire CYP2C19 cDNA revealed that the rs12769205 was also found in those carrying the CYP2C19*2 allele.

rs12769205 is in LD with rs4244285 on CYP2C19*2 but occurs independently on the CYP2C19*35 allele in some Blacks. To observe the frequency of rs12769205 in different populations and determine whether rs12769205 ever occurred independent of CYP2C19*2, rs4244285 and rs12769205 genotypes were retrieved from different populations (Fig 2) in the 1000 genome project database-phase 3 (http://browser.1000genomes.org/index.html) and plotted (Fig 2 A-D). The rs4244285 and rs12769205 SNPs appeared to be linked in CYP2C19*2 in 99 White descendants of Northern Europeans (CEU), but rs12769205 did occur independent of rs4244285 on a new allele (CYP2C19*35) in 11/108 Black descendants of Yoruban West
Africans (YRI), and in 29/661 All Africans (that includes the YRI group). CYP2C19*2 and CYP2C19*35 appeared to be linked in 103 Asians (CHB). Next, we examined visual genotypes of rs4244285 and rs12769205 in each of the seven African populations representing the African super population in the 1000 Genomes project (Supplemental Figure 1). The rs12769205 SNP had the highest frequency in YRI and the lowest frequency in the Esan in Nigeria. Interestingly, there were individuals in the ESN, GWD, LWK and MSL population that were CYP2C19*35 homozygous, but CYP2C19*2 heterozygous, and even one YRI CYP2C19*35 homozygous, but CYP2C19*1 homozygous. The CYP2C19*2/*35 diplotypes as well as CYP2C19*2 and CYP2C19*35 allele frequency data in different populations is provided (Supplemental Table 3). To determine if the SNPs were in LD, the D’, along with its corresponding Logarithm of Odds (LOD) score, and r² LD values were determined between rs4244285 and rs12769205 SNPs in all populations. Haploview (Barrett et al, 2005) analysis showed that the D’/LOD = 1.0 (Supplemental Figure 2) for all pairwise comparisons of the two SNPs in all populations (note: the LD values in the Supplemental Figure 2 are scaled from 1.0 to 100 for visual clarity). The D’ of 1.0 indicates that the CYP2C19*2 rs4244285 is co-inherited with rs12769205 (on the CYP2C19*2 haplotype) 100% of the time. The high correlation coefficients (r² ≥ 0.6) between the two SNPs confirm they are significantly linked in each population. The r² value is lower than the D’ because the allele frequencies of rs4244285 and rs12769205 are not identical -
rs12769205 is more frequent in YRI because rs12769205 can be found on CYP2C19*35 that lacks rs4244285. These results prompted us to genotype human livers from White and Black donors. rs12769205 and the rs4244285 appeared to be in LD in Whites (Fig 2E) and African Americans (Fig 2F) with the CYP2C19*2 genotypes and there was a single African American who had rs12769205 (CYP2C19*35) without rs4244285. This liver was further analyzed to determine if exon 2B occurred when only rs12769205 was present.

**CYP2C19*35 (rs12769205) alone leads to exon 2B.** First, the CYP2C19*2 aberrant spliced mRNA (deletion of the first 40 bp of exon 5) was confirmed by PCR amplification of CYP2C19 exons 4 to 6 in all samples with the rs4244285 genotype (Fig 3A). Next, CYP2C19 exons 2 to exon 4 (Fig 3B) were amplified in the same samples yielding both the canonical 269 bp product and a 438 bp amplicon retaining intron 2 (exon 2B). CYP2C19*2 exon 2B occurred in all livers that carried rs12769205 either alone (CYP2C19*35, lane 6), or in livers with rs4244285 (CYP2C19*2 lanes 3, 4, 5, 8). Moreover, the relative abundance of canonical 269 bp product was always lower in amount in livers with the rs12769205 genotype. Lanes 3, 4, and 6 and lanes 5 and 8 indicate the smaller amount of residual wild-type mRNA amplified in samples heterozygous and homozygous for rs12769205, respectively, compared to samples 1, 2 and 7 homozygous for the CYP2C19*1 genotype.
Alternative mRNAs in livers carrying the rs12769205 allele. *CYP2C19* was amplified from exons 2 to 6 and the PCR products sized on agarose gels to further determine the structure of all hepatic *CYP2C19* alternative mRNAs in livers with the rs12769205 and rs4244285 polymorphisms. Samples homozygous for *CYP2C19*/*1 yielded the single 597 bp wild-type product (Fig 4). *CYP2C19* PCR products from samples heterozygous for rs4244285 and rs12769205 yielded the 597 bp wild-type product, but other bands were difficult to resolve. To unambiguously identify the alternative mRNAs arising from rs12769205, *CYP2C19* exons 2-6 were amplified from the sample heterozygous for *CYP2C19*/*35, the products were TOPO TA cloned, and individual clones sequenced. Only transcripts represented in 5% or more of clones are reported: 52/72 were wild type; 14/72 had aberrant exon 2B, and 4/14 of those lacked the first 71 bp of exon 4. These *CYP2C19*/*35 mRNAs corresponded to the WT (597 bp), SV1 (766 bp) and SV2 (695 bp) bands, respectively (Fig 4). The partial deletion of 71 bp of exon 4 (which alters the reading frame and truncates the protein after amino acid 165) appears to be a passenger splice variant as there were no additional SNPs associated with this spliced transcript.

This strategy also allowed the unambiguous identity of the *CYP2C19* mRNAs from samples homozygous for rs12769205 and rs4244285: the alternative mRNAs shared the 40 bp deletion of exon 5 (SV1-3); SV2 and SV3 had exon 2B and SV3 had an additional 71 bp deletion of exon 4.
There was only a small amount of correctly spliced CYP2C19 WT transcript in livers homozygous for rs12769205 and rs4244285 and this can be seen in Fig 1 (lanes 16-17) and Fig 3.

**Sequencing CYP2C19 from a CYP2C19*1/*35 liver.** To determine whether the CYP2C19*35 allele carried other polymorphisms, the full length CYP2C19*35 cDNA from the CYP2C19*35 liver was amplified, cloned into the TOPO TA vector and sequenced (Supplemental Table 4). The CYP2C19*35 mRNA contained exon 2B with the causative rs12769205, the common non-synonymous Ile331Val, and the synonymous Pro33Pro. Additional variations were discovered on the other allele but are the focus of another manuscript.

**In Silico and In vitro analysis of the effect of rs12769205 on CYP2C19 splicing.** The online bioinformatics resource Human Splicing Finder Version 2.4.1 (Desmet et al., 2009) was used to analyze intron 2 for splicing consensus sequences. The program identified a ctcctAg sequence 23 bp upstream of the end of intron 2 as the optimal branch point motif (recognized by the highest number of matrices) having a consensus value of 73.05 (on a 0-100 score range), while rs12769205 will disrupt the branch point sequence decreasing the value to 43.42 (Gooding et al., 2006).
To test whether the rs12769205 branch point SNP alone leads to exon 2B, and to confirm that rs4244285 leads to a 40 bp deletion of exon 5, CYP2C19 minigenes were constructed using the RHCglo minigene vector (Singh and Cooper 2006). Two minigenes contained exons 2 and 3 and intron 2 and differed only by rs12769205 (Fig 5A), and two minigenes contained exon 5 and the last 87 bp of intron 4 and differed only by rs4244285 (CYP2C19*2) (Fig 5B). HepG2 cells were transfected with the four minigenes and RNA from the transfected cells was used for RT-PCR analysis using primers residing in the flanking minigene exons. The CYP2C19*1 intron 2 minigene generated the expected wild-type transcript, whereas the rs12769205 variant generated a larger transcript containing insertion of intron 2 and one other smaller alternatively spliced fragment (Fig 5A). Q-PCR quantitation of the amount of residual wild-type transcript from the minigene revealed a 40% decrease in the amount of wild-type transcript from the rs12769205 vs. CYP2C19*1 minigene. As expected, the CYP2C19*1 exon 5 minigene generated the correctly spliced exon 5 transcript, whereas the rs4244285 minigene demonstrated the 40 bp deleted fragment at the start of exon 5 (Fig 5B).

Can next-generation RNA sequencing analysis of CYP2C19 in human livers identify the 40 bp exon 5 deletion and the exon 2B splicing events? Twenty-four liver samples that had undergone next-generation RNA sequencing were analyzed for alternative CYP2C19 mRNAs
and results visualized with the integrative genomic viewer (IGV). As is typical of RNA-Seq IGV results, there is non-uniformity in the exon peaks in part due to non-uniformity of read coverage (even when the transcripts have very similar concentrations), sequence specific read variability, and the transcriptional complexity for multigene family members, such as the CYPs. In general, the intron 2 retention (Fig 6A) and the 40 bp deletion in exon 5 (Fig 6B) was apparent by IGV in mRNA samples heterozygous for rs12769205 and rs4244285, although it was much more apparent in some samples where CYP2C19 was more highly expressed. However, it would be difficult to accurately call either of the CYP2C19 alternative mRNAs in some samples, for example the second sample from the top in Fig 6, due to low read coverage and non-uniformity of the exon architecture. Moreover, while visual inspection of each sample revealed there might be a small insertion of intron 2, when exon/intron junction analysis software was used to identify novel transcripts, the software did not call the novel exon 2B junction.

**Quantitation of CYP2C19 protein in pooled human liver microsomes with different CYP2C19 genotypes.** CYP2C19 was quantified in pooled human liver microsomes with different CYP2C19 genotypes by trypsin digestion and LC-MS/MS analysis using three different surrogate peptides specific for CYP2C19 exons 2, 4 and 8 (Fig 7A). In theory, (a) the probes detect not just the amount of full length CYP2C19, but truncated in-frame CYP2C19 translated
from the splice variant mRNAs; and (b) because rs12769205 will frame shift the CYP2C19 protein after exon 2, and rs4244285 will frame shift the protein in the middle of exon 5, the exon 2 and 4 probes could distinguish between the functional effects of rs12769205 in intron 2 (downstream of exon 2 but upstream of exon 4 probe), and rs4244285 in exon 5 (downstream of both exon 2 and 4 probes) on the abundance of the residual CYP2C19 wild-type protein. As expected, CYP2C19 was detected with all exon probes in CYP2C19*1/*1 livers. The amount of CYP2C19 protein detectable with the exon 2 probe in pooled livers homozygous for CYP2C19*2/*2 or heterozygous for CYP2C19*1/*35 was only 10% and 2%, respectively, of the amount of protein in CYP2C19*1/*1 pooled livers (Fig 7B). The peptide quantity of CYP2C19 exon 4 and exon 8 was 95% and 81.5%, respectively, (relative to exon 2) in CYP2C19*1/*1 samples. No wild-type CYP2C19 protein was detected in the CYP2C19*2/*2 or CYP2C19*1/*35 livers with either the exon 4 or exon 8 probe. The absence of detectable protein in the CYP2C19*1/*35 liver was surprising and suggested that person carried an additional deleterious allele. That novel allele is the subject of a separate publication. Nevertheless, the absence of detectable CYP2C19 protein in the CYP2C19*2/*2 livers with the exon 4 (but not exon 2) probe demonstrates that intron 2 rs12769205 has a functional effect on the CYP2C19 protein independent of the effect of the rs4244285. In fact, it suggests that rs12769205, because it leads to insertion of exon 2B and creates 87 altered amino acids followed by a stop codon,
confers the loss of CYP2C19 protein in CYP2C19*2/*2 livers because of its primacy (before rs4244285) in the RNA splicing event.

Relationship of CYP2C19 genotype to activity in Ethiopians. Data on S-mephenytoin hydroxylation phenotype and CYP2C19 genotypes for CYP2C19*2, CYP2C19*3 and CYP2C19*17 among 104 Ethiopians was already available from earlier studies and the detailed information about the cohort has been published (Persson et al., 1996; Aklillu et al., 2002; Sim et al., 2006). We genotyped this in vivo cohort for the new CYP2C19*35 allele to perform a phenotype genotype association analysis (Fig 8). Compared to CYP2C19*1/*1 individuals, those persons heterozygous for one nonfunctional CYP2C19 allele, either CYP2C19*1/*35 (p=0.22) or heterozygous for CYP2C19*1/*3 (p=0.16) did not show a significant increase in S/R-mephenytoin plasma concentrations, while those heterozygous for both rs12769205 and rs4244285 together (CYP2C19*1/*2) (p=0.039) did. As expected, persons homozygous for rs12769205 and rs4244285 together were poor mephenytoin metabolizers, but there were no persons homozygous for rs12769205 alone (CYP2C19*35/*35) to conclusively determine the independent functional effect of this SNP in vivo.

Extended haplotype homozygosity at the CYP2C19 locus in Yorubans and other African
populations. It was recently reported that the CYP2C19*2 nonfunctional allele may be under positive selection with CYP2C19 inactivation conferring an evolutionary advantage in Africa (Janha et al., 2014). To investigate if the signal for selection could be attributed to rs12769205, we used Sweep, a program that uses large scale analysis of haplotype structure in the genome to detect evidence of natural selection, to reanalyze CYP2C19*2 in 108 YRI and included rs12769205. We first used Sweep to determine CYP2C19 haplotype structure. Sweep detected haplotype blocks 1, 2 and 3 (defining CYP2C19*1, CYP2C19*2 and CYP2C19*35, respectively) (Fig 9A). CYP2C19*2 rs4244285 is carried only on haplotype 2, while SNP rs12769205 is carried on haplotypes 2 (CYP2C19*2) and 3 (CYP2C19*35). Sweep then used the long range haplotype test to analyze the haplotypes for long range linkage disequilibrium. CYP2C19 Haplotypes 2 and 3 in YRI both displayed extended homozygosity as seen by the high relative extended haplotype homozygosity (REHH) scores (Fig 9B). The REHH plots for the three haplotypes, with the core for the haplotypes centered on the genomic position of the CYP2C19*2 variant, shows that both CYP2C19*2 (containing both rs4244285 and rs12769205) and CYP2C19*35 (containing only rs12769205) showed long range LD, suggesting the haplotypes rose rapidly to a high frequency before recombination could break down associations with nearby markers (Sabeti et al., 2002).

The region of longest extended homozygosity and highest REHH of 10 was seen 68-95 kb
from the core with Haplotype 3 (rs12769205 alone on CYP2C19*35), while across the same region for Haplotype 2 with rs12769205 + rs4244285 (CYP2C19*2) the REHH was 5.5-2.5. Indeed, the significant REHH for both haplotypes 2 and 3 suggests rs12769205, both alone on CYP2C19*35 and together with rs4244285 on CYP2C19*2, confers an evolutionary advantage to these alleles.

The highest REHH scores were 3’ of CYP2C19. Although the most distal 3’ intergenic SNPs flanking CYP2C19 did not extend into CYP2C9, we determined whether either CYP2C9*2 or CYP2C9*3 were on these long range CYP2C19 extended haplotypes. However, none of the 108 YRI from the HapMap project carried either the CYP2C9*2 (rs1799853) or CYP2C9*3 (rs1057910) nonfunctional SNPs demonstrating that it is the two CYP2C19 haplotypes with rs12769205 that are under natural selection.

Sweep was next used to construct a phylogenetic tree of the CYP2C19 haplotypes (Fig 9C). The haplotypes closer to the ancestral haplotype are at the top of the figure. CYP2C19*35 is calculated to be closer than CYP2C19*2 to the ancestral haplotype, and hence CYP2C19*35 is the ancestral haplotype, and rs12769205 arose before rs4244285.

Next we performed the same analysis on the 396 individuals who represented other African populations (LWK, Luhya in Webuye, Kenya; GWD, Gambian in Western divisions in the Gambia; MSL, Mende in Sierra Leone; and ESN, Esan in Nigeria) still living on the African
continent. The same three CYP2C19 haplotypes were present in the other African populations, and at a similar frequency to the YRI (Supplemental Figure 3). Likewise, the combined other African populations displayed extended homozygosity for CYP2C19*35, as evidenced by the high REHH (7.6, at 95.4 kb from the core). Finally, Sweep ancestral tree analysis generated a CYP2C19 phylogenetic tree for the other African populations that was identical to that generated for the YRI, again showing the haplotype with rs12769205 alone in the ancestral haplotype, with rs4244285 added later to generate CYP2C19*2.
DISCUSSION

We discovered that rs12769205 disrupts the branch site in *CYP2C19* intron 2 creating a novel exon 2B. This alternative *CYP2C19* mRNA will generate a nonfunctional protein since insertion of exon 2B creates an out-of-frame protein with 87 novel amino acid residues followed a premature termination codon (PTC), resulting in a truncated 197 amino acid protein. Several lines of evidence showed that rs12769205 leads to intron 2 retention (exon 2B): (a) all livers with rs12769205 generated *CYP2C19* exon 2B; (b) *in silico* splice site strength analysis predicted rs12769205 perturbed the fidelity of intron 2 branch point splice site recognition; and (c) minigenes with rs12769205 transfected into HepG2 cells showed intron 2 inclusion.

Interestingly, rs12769205, that alone defines *CYP2C19*<sup>35</sup>, was found together with rs4244285 on the *CYP2C19*<sup>2</sup> allele. *CYP2C19*<sup>2</sup> was discovered in 1994 (de Morais et al., 1994a) and rs4244285, which clearly leads to altered splicing of exon 5, was the single variant thought to contribute to the *CYP2C19*<sup>2</sup> poor metabolizer phenotype. Clearly both rs12769205 and rs4244285 are functionally important as they can individually alter the *CYP2C19* reading frame and produce a premature stop codon resulting in a truncated nonfunctional protein. This leads to the obvious question of whether rs12769205 and rs4244285 contribute equally to the PM phenotype in livers with *CYP2C19*<sup>2</sup>. Because we did not have any individuals homozygous for *CYP2C19*<sup>35</sup>, we cannot at this time determine, using RNA, whether the residual pool of WT
CYP2C19 transcript differed between those homozygous for the CYP2C19*2 vs. CYP2C19*35 alleles. To address this question we took two approaches. First, we used peptide probes to quantify the amount of remaining CYP2C19 wild-type protein in persons carrying CYP2C19*2 and *35 alleles. While the exon 2 probe (upstream of both rs12769205 and rs4244285) detected residual CYP2C19 protein in livers homozygous for CYP2C19*2 or with CYP2C19*35, the exon 4 probe failed to detect CYP2C19 protein in the same livers. Since the exon 4 probe is downstream of intron 2 rs12769205, but upstream of exon 5 rs4244285, this result suggests the intron 2 SNP can lead to complete loss of CYP2C19 protein due to its primacy in the RNA splicing event. Second, we used extended haplotype homozygosity statistics and uncovered significant evidence that the haplotypes with rs12769205 alone (CYP2C19*35) and with rs4244285 on CYP2C19*2 have undergone positive selection, and that natural selection was not limited to YRI but was seen across African populations, having probably arisen in earlier human ancestors from which all other groups of Africans descended. Notably, the magnitude of evolutionary pressure for both haplotypes with rs12769205 was as great as that exerted on the human genome by infectious diseases (Janha et al., 2014), and implies that rs12769205 on both haplotypes confers an evolutionary advantage. Indeed, the signature of positive selection on the haplotype with rs12769205 alone (CYP2C19*35) reinforces that this polymorphism has a significant functional effect independent of rs4244285.
Ancestry analysis showed that, on an evolutionary timescale, rs12769205 is the original CYP2C19 deleterious polymorphism that arose first on CYP2C19*35, and then later added rs4244285 to create the new haplotype (CYP2C19*2). While it is possible that the gain of rs4244285 added to CYP2C19*2 nonfunction, evidence for natural selection on the haplotype with rs12769205 alone, suggests it is sufficient to create the no function allele.

In vivo analysis was unable to conclusively demonstrate that rs12769205 alone contributes to the mephenytoin PM phenotype in Ethiopians because only persons heterozygous for CYP2C19*35 were available, and there were no persons with CYP2C19*35 paired with another poor metabolizer allele, and there was only a modest effect of the heterozygous genotype (intermediate phenotype) on mephenytoin disposition. Poor metabolism of mephenytoin was seen in persons homozygous for both rs12769205 + rs4244285 (CYP2C19*2/*2). However, there was only a moderate effect of any of the heterozygous PM genotypes (CYP2C19*1/*2, CYP2C19*1/*35, or CYP2C19*1/*3) on mephenytoin disposition. Indeed, persons with CYP2C19 intermediate phenotypes (e.g., CYP2C19*1/*2) are the most challenging populations to address for proposing clinical pharmacogenetic implementation consortium (CPIC) guidelines (drug and dose recommendations) because of the wide interindividual variability in residual CYP2C19*1 activity (Scott et al., 2013). Consequently, the most informative subjects,
individuals homozygous for *CYP2C19*35, or heterozygous for *CYP2C19*35 and another *CYP2C19* PM allele, need to be CYP2C19 phenotyped before comparisons can be made with *CYP2C19*2/*2 poor metabolizers and before any *CYP2C19*35 genotype directed recommendations can be made.

The discovery that rs12769205 leads to alternative *CYP2C19* splicing adds to the growing list of hepatic CYPs where we have identified SNPs leading to polymorphic splicing (*CYP3A5*3, *CYP3A5*6 and *CYP2B6*6 (Kuehl et al., 2001; Lamba et al., 2003) and nonfunctional alleles. Sakabe and de Souza (2007) proposed that intron retention happens when introns and flanking exons are small. *CYP2C19* exons 2 and 3, 163 nt and 150 nt, respectively, are not large; and, while the average *CYP2C19* intron size is 11,092 nt (range 169 – 38,498 nt), Intron 2 is the smallest (169 nt) and is 6.8x smaller than the next smallest intron (Intron 4, 1161 nt). *CYP2C19* rs12769205 is an interesting example of a branch point SNP leading to intron retention. There are numerous hereditary disease alleles where polymorphisms in branch point motifs lead to loss of splicing activity (Taggart et al., 2012). The branch point signal, located upstream of the polypyrimidine tract, is one of three obligatory signals required for appropriate pre-mRNA splicing. Approximately 96% of branch points fall between -15 and -55 nt relative to the 3’-splice site, with the peak at position -24 nt, and the *CYP2C19* Intron 2 rs12769205 branch
point A is located at -23 bp relative to the 3’-splice site. This SNP would disrupt the invariant branch point adenine, a nucleotide that is absolutely required to engage in a 2’-5’ phosphodiester bond with the 5’ end of the intron after the first catalytic step of the splicing reaction (Corvelo et al., 2010).

Since we have a large liver resource, it would be extremely useful to have a high-throughput RNA sequencing and analysis pipeline that could identify novel alternative splicing of ADME genes, like CYP2C19, that might be caused by sequence variation. This resource is the ideal tissue to look for the consequence of any sequence variant that could lead to alternative splicing because (a) many ADME genes are highly expressed in liver; (b) liver is one of the tissues that generates the highest number of alternative mRNAs per genes; and (c) alternative splicing can show tissue specificity. Hence, any polymorphism with the potential to cause alternative splicing has the best chance of being detected in liver tissue. In theory, RNA-Seq analysis can discover new mRNA transcripts and it would be incredibly valuable if the analysis tools could unambiguously call novel transcripts, such as the inclusion of exon 2B, and report those livers that had these novel transcripts. The assembly of CYP2C19 mRNAs from short RNA-Seq reads is complicated by the high percent similarity with other neighbor CYP2C family members. For example, exon 3 in CYP2C19, shows 99, 95 and 97 percent identity with 2C9, 2C8 and 2C18, respectively; and intron 2 in CYP2C19 shows 96% identity with CYP2C9.
intron 2. Regardless, visual inspection of the IGV views of CYP2C19 assembled exons 2-3 revealed that there might be inserted nucleotides between these exons (Fig 6). However, the IGV views still required visual analysis of the results, and that we already had PCR results to guide this analysis. The exon junction program analysis (data not shown) correctly called the novel CYP2C19*2 exon 4/5 junction, but that was because the CYP2C19*2 alternative mRNA was already in the reference database. The exon junction program did not observe a novel junction at exon 2 in rs12769205 livers, and would require that the transcript with exon 2B, first, be added to the reference database as the current programs don’t have a reliable intron retention caller (D. Finkelstein, personal communication). Hence, because RNA-Seq requires a reference mRNA, and because small RNAs and long non-coding RNAs can also inhabit introns, identification of polymorphic alternative mRNAs, particularly those with intron retention, may not yet be unequivocally identified by these high throughput approaches. An additional complicating factor is that, while CYP2C19 is a highly expressed gene in human liver, the alternative CYP2C19 transcripts generated by rs12769205 +/- rs4244285 ultimately lead to premature termination codons (PTC) and these will trigger accelerated alternative mRNA degradation through nonsense-mediated decay (NMD), decreasing the amount of alternative mRNA. Indeed, it has been suggested that the rate of intron retention in mRNA transcripts is higher than reported because NMD filters off some mRNA transcripts (Aten et al., 2013).
Importantly, it also makes the identification of alternative mRNAs linked to PTCs and NMD (those that are linked to functional consequences) harder to identify by an RNA-Seq approach.
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Author Contributions:

*Participated in research design:* Schuetz, Chaudhry, Thummel

*Conducted experiments:* Chaudhry, Prasad, Aklillu, Sim

*Contributed new reagents or analytic tools:* Prasad

*Performed data analysis:* Schuetz, Chaudhry, Fohner, Prasad, Finkelstein, Fan, Wu, Wang, Aklillu,

*Wrote or contributed to the writing of the manuscript:* Schuetz, Chaudhry, Prasad, Finkelstein, Wang, Aklillu, Thummel
DMD # 64428

References:


Chhibber A, French CE, Yee SW, Gamazon ER, Theusch E, Qin X, Webb A, Papp AC, Wang A,


Taggart AJ, DeSimone AM, Shih JS, Filloux ME, and Fairbrother WG (2012). Large-scale


Footnotes

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Figure Legends:

Figure 1. *CYP2C19*<sup>*35* (rs12769205) leads to aberrant intron 2 retention (exon 2B). (A)

*CYP2C19* cDNA was amplified from human liver cDNAs by PCR using primers in exon 2 and exon 4 and the wild-type product (269 bp) and alternatively spliced product (438 bp) analyzed on agarose gel. Homozygous wild-type (Lanes 1-7 are *CYP2C19*/*1/*1), rs12769205 heterozygous (lanes 8-15) and homozygous (lanes 16-17) variant genotypes are indicated by the open, half-filled and filled boxes, respectively. Lanes marked M and –ve  represent the 100 bp DNA ladder and a negative control, respectively. (B) The 438 bp fragment was excised from the gel and directly sequenced and the resulting electropherogram and nucleotide sequence are shown. The cartoon illustrates the amplification strategy, the insertion of exon 2B in samples with rs12769205, and the location of rs12769205 at the branch point adenine -23 nt upstream of the Intron 2 splice acceptor site.

Figure 2. Visual genotypes of rs12769205 and rs4244285 in different populations (1000 genomes phase 3 data) and Liver samples. Visual genotypes for rs12769205 and rs4244285 in 1000genomes samples (genotypes downloaded from http://browser.1000genomes.org/index.html): (A) 99 White (CEU), (B) 108 Yoruban (YRI), (C) 661 all Africans, and (D) 103 Han Chinese in Beijing, China (CHB); and in the St Jude Liver
Bank (SJLB) samples from (E) 272 White and (F) 63 African Americans. Grey, orange and red boxes indicate homozygous wild-type, heterozygous and homozygous variant genotypes, respectively. // lines indicate not all subjects are shown for that particular diplotype and population.

**Figure 3. Effect of rs4244285 and rs12769205 on CYP2C19 splicing.** (A) Eight liver samples were analyzed by PCR for (A) the CYP2C19 exon 5-40 bp deletion, caused by rs4244285, using primers in exons 4 and 6, and (B) the CYP2C19 exon 2B insertion, caused by rs12769205, using primers in exons 2 and 4 and the products analyzed on agarose gels. Arrows indicate the migration of the canonical and splice variant bands. Homozygous wild-type, heterozygous and homozygous variant genotypes are indicated by the open, half-filled and filled boxes, respectively. In Panel B, the smaller residual amount of the 269 bp wild-type mRNA is seen in rs12769205 heterozygous (Lanes 3, 4, and 6) or homozygous (lanes 5, 8) samples compared to samples 1, 2 and 7 homozygous for the CYP2C19*1/*1 genotype.

**Figure 4. Structure of alternative CYP2C19 mRNAs in livers with rs4244285 and rs12769205 genotypes.** CYP2C19 was PCR amplified using exon 2 and 6 primers, in liver samples with indicated genotypes and the products analyzed on agarose gels. Arrows indicate
the migration of the canonical and splice variant bands. Genotypes are illustrated as depicted in Fig 3 legend. The cartoon illustrates the structures of the canonical exons (open boxes), novel exon 2B (gray box) and partial deletions of 40 bp and 71 bp at the start of exon 5 and exon 4 (black boxes), respectively in the splice variant (SV) transcripts.

**Figure 5. RT-PCR analysis of minigene mRNA products.** (A) Exon2-intron2-exon3

Minigenes: Two minigenes contained \textit{CYP2C19} exon 2 + intron 2 + exon 3 (differing only by rs12769205A>G) that replaced the \textit{BamH1/Xho1} fragment (minigene exon (Em)) of the RHCglo minigene. (B) Exon 5 minigenes: Two minigenes contained the last 87 nucleotides of \textit{CYP2C19} intron 4 and all of exon 5 (differing only by rs4244285) that replaced the \textit{SalI/Xho1} fragment of the RHCglo minigene. HepG2 cells were transfected with each of the four plasmids and minigene mRNA products were analyzed by RT-PCR using the RSV5U/TNIE4 primers and the products analyzed on agarose gels. The rs12769205 minigene generated a transcript with the exon 2B insertion (A), and the rs4244285 minigene generated a transcript with the 40 bp exon 5 deletion (B).

**Figure 6. Integrative genomic viewer (IGV) visualization of human liver \textit{CYP2C19} mRNA.**

RNA-Seq results for human livers that were heterozygous (half filled box) or homozygous
wild-type (open box) for: (A) rs12769205 were visualized across CYP2C19 exons 2-Exon3; and (B) rs4244285 were visualized across exon 5. Due to differences in CYP2C19 read coverage, IGV was scaled between 0-50 for six of the liver samples, and between 0-250 for one sample. Panel A shows that only samples heterozygous for rs12769205 had RNA sequences with intron 2 included. Panel B shows that only samples heterozygous for rs4244285 had a decreased signal across the first 40 bp of exon 5, indicative of the heterozygous deletion of this region of the mRNA transcript.

Figure 7. CYP2C19 peptides downstream of exon 2 failed to detect residual CYP2C19 wild-type protein in CYP2C19*2 and CYP2C19*35 liver microsomes. (A) The location of the peptide probes used relative to CYP2C19 exons and to rs12769205 and rs4244285. (B) Expression of CYP2C19 protein quantified in pooled human liver microsomes from CYP2C19*1/*1, CYP2C19*2/*2, and CYP2C19*1/*35 livers using exon 2, exon 4 and exon 8 specific peptide probes. Results are graphed relative to CYP2C19 protein in CYP2C19*1/*1 pooled liver microsomes (100%). >LLOQ, less than the lower limit of quantitation.

Figure 8. CYP2C19 activity in 104 Ethiopians with different CYP2C19 genotypes. S/R-mephenytoin ratio is plotted for each CYP2C19 diplotype group. Box plots indicate the 25th
and 75th percentile, and the bold line within the box represents median and whiskers represent the range after excluding the outliers. Statistical analyses were performed using R version 3.1 (http://www.rproject.org). A general linear model was used to obtain p-values for each group compared to the \textit{CYP2C19}^*1/*1 group. N, number of subjects.

\textbf{Fig 9.} \textit{CYP2C19} haplotype frequencies, extended haplotype homozygosity, and ancestral tree in 216 YRI chromosomes. (A) Sweep was used to determine \textit{CYP2C19} haplotypes (SNP positions rs12769205, rs4244285, rs4417205 and rs3758580) and their frequencies. The “.” in the observed haplotypes represents nucleotides that match the ancestral allele. “GCG” below the SNP rsIDs are the Sweep predicted ancestral allele nucleotides based on the HapMap Release 16. (B) Relative extended haplotype homozygosity (REHH) for each \textit{CYP2C19} haplotype with the core of the haplotypes centered on rs4244285. Both haplotypes containing SNP rs12769205 either alone (haplotype 3 (green, \textit{CYP2C19}*35)), or with rs4244285 (haplotype 2 (orange, \textit{CYP2C19}*2)) show extended haplotype homozygosity REHH. (C) Phylogenetic tree of the \textit{CYP2C19} haplotypes. Haplotypes closer to the ancestral are at the top of the figure. The area of the squares is proportional to the frequency of the haplotype. The gray squares represent haplotypes not present in the data, but that are missing links in the phylogeny. The program determined the ancestral root of the tree was \textit{CYP2C19}*1.
A.

rs12769205

438 bp
Intron 2 retention

269 bp
Wild Type

B.

CYP2C19*1

Ex 2

Ex 3

Ex 4

269 bp

*rs12769205

Ex 2

Ex 2B

169 nt

TCCTAGTG

Ex 3

Ex 4

438 bp

-23 bp

Intron 2

Exon 3

Fig. 1
A. rs4244285 G>A
   - 40 bp deleted

B. rs12769205 A>G
   - 169 nt
   - 438 bp Int2 retention
   - 269 bp Wild Type

Fig. 3
Fig. 4
Fig. 6

A. CYP2C19 intron 2 retention
   rs12769205

B. CYP2C19 exon 5 partial deletion
   rs4244285
Fig. 8

The figure shows the distribution of S/R-mephenytoin ratio across different CYP2C19 diplotypes. The box plots compare the ratio for each diplotype group, with statistical significance indicated by p-values.

- *1/*1 (n=44): p=0.03
- *17/*17 (n=3): p=0.087
- *1/*17 (n=24): p=0.039
- *1/*2 (n=10): p=0.22
- *1/*35 (n=7): p=0.68
- *2/*17 (n=6): p=0.56
- *35/*17 (n=2): p=0.16
- *1/*3 (n=1): p=0.16
- *2/*2 (n=3): p=0.56
- *2/*3 (n=3): p=0.16

Statistical significance levels are indicated as follows:

- p=2.16e-10
- p=1.33e-10
A.

<table>
<thead>
<tr>
<th>rs12769205</th>
<th>rs4244285</th>
<th>rs4417205</th>
<th>rs3758580</th>
</tr>
</thead>
<tbody>
<tr>
<td>GCG</td>
<td></td>
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</tr>
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</table>

1. 78% A..C CYP2C19*1
2. 17% GAGT CYP2C19*2
3. 6% G.GC CYP2C19*35

B.

REHH

-19 = 5' Distance (Kb)

-38.5 -11.7 15.1 41.9 68.7 95.4

Fig. 9
Drug Metabolism Disposition

The CYP2C19 intron 2 branch point SNP is the ancestral polymorphism contributing to the poor metabolizer phenotype in livers with CYP2C19*35 and CYP2C19*2 alleles

Supplemental Table 1: Primers used for PCR amplification and sequencing of *CYP2C19* exons from genomic DNA.

<table>
<thead>
<tr>
<th>Exons</th>
<th>FP/RP</th>
<th>Primer sequence</th>
<th>PCR amplified fragment size (base pairs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exon 1</td>
<td>FP</td>
<td>5’-AGTGGGCCCTAGGTGATTGGCCACTT-3’</td>
<td>410</td>
</tr>
<tr>
<td></td>
<td>RP</td>
<td>5’-TCAAAAGTATTTTACTTTACAATGATCTC-3’</td>
<td></td>
</tr>
<tr>
<td>Exon 2-3</td>
<td>FP</td>
<td>5’-AAAATATGAATCTAAGTCAGGCTTAGT-3’</td>
<td>607</td>
</tr>
<tr>
<td></td>
<td>RP</td>
<td>5’-GGAGAGCAGTCCAGAAAGGTCTAGTGATA-3’</td>
<td></td>
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<tr>
<td>Exon 4</td>
<td>FP</td>
<td>5’-TGCTTTTTAAGGGAATTTCATAGG-3’</td>
<td>383</td>
</tr>
<tr>
<td></td>
<td>RP</td>
<td>5’-AAAATGTACTTCAGGGCTTG-3’</td>
<td></td>
</tr>
<tr>
<td>Exon 5</td>
<td>FP</td>
<td>5’-CAACCAGAGCTTGCCATATTG-3’</td>
<td>409</td>
</tr>
<tr>
<td></td>
<td>RP</td>
<td>5’-TGATGCTTACTGGATATTCATGC-3’</td>
<td></td>
</tr>
<tr>
<td>Exon 6</td>
<td>FP</td>
<td>5’-AAAACTGGCACAAGACAGGGATG-3’</td>
<td>456</td>
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<tr>
<td></td>
<td>RP</td>
<td>5’-AAATTGGGACAGATTCAGCTGCG-3’</td>
<td></td>
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<tr>
<td>Exon 7</td>
<td>FP</td>
<td>5’-AATTGCTAGAAACAATGTTCCATTTC-3’</td>
<td>327</td>
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<tr>
<td></td>
<td>RP</td>
<td>5’-AGAGGGTAAGACTCATACTTGTA-3’</td>
<td></td>
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<tr>
<td>Exon 8</td>
<td>FP</td>
<td>5’-CCACTGTTTTCTTAAACCTTCGTGA-3’</td>
<td>284</td>
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<td></td>
<td>RP</td>
<td>5’-GAAGGCACATGTAAGTTCACACTGA-3’</td>
<td></td>
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<tr>
<td>Exon 9</td>
<td>FP</td>
<td>5’-ATCTACTCATCCCTCCTATGATTCCACCG-3’</td>
<td>529</td>
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<tr>
<td></td>
<td>RP</td>
<td>5’-ATGTGGCACTCAATGTAATTATAGA-3’</td>
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</table>
Supplemental Table 2: Optimized MS/MS parameters of CYP2C19 surrogate peptides used for protein quantification

<table>
<thead>
<tr>
<th>Peptide</th>
<th>Amino acid position</th>
<th>Parent ion (V)</th>
<th>Product ion (V)</th>
<th>Cone (V)</th>
<th>CE (eV)</th>
</tr>
</thead>
<tbody>
<tr>
<td>IYGPVFTLYFGLER (exon 2)</td>
<td>838.2</td>
<td>998.3</td>
<td>52</td>
<td>28</td>
<td></td>
</tr>
<tr>
<td></td>
<td>838.2</td>
<td>1145.4</td>
<td>52</td>
<td>28</td>
<td></td>
</tr>
<tr>
<td>GTTILTSLTSLTVLHDNK (exon 8)</td>
<td>567.3</td>
<td>664.4</td>
<td>35</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td></td>
<td>567.3</td>
<td>607.8</td>
<td>35</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>C[160]NVIC[160]SIIFQK* (exon 4)</td>
<td>1434.68</td>
<td>535.32</td>
<td>60</td>
<td>42</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1434.68</td>
<td>989.44</td>
<td>60</td>
<td>42</td>
<td></td>
</tr>
</tbody>
</table>

*C[160] indicates S-carbamidomethylated cysteine after alkylation of native peptide.
Supplemental Table 3: *CYP2C19*2/*35 diplotype and *CYP2C19*2 and *CYP2C19*35 allele frequencies in different populations (1000 genome-Phase 3 data)

<table>
<thead>
<tr>
<th>Diploptype</th>
<th>All Africans*</th>
<th>Yorubans (YRI)</th>
<th>Caucasians (CEU)</th>
<th>Chinese (CHB)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n =661</td>
<td>n=108</td>
<td>n=99</td>
<td>n=103</td>
</tr>
<tr>
<td><em>CYP2C19</em>1/*1</td>
<td>430</td>
<td>66</td>
<td>75</td>
<td>41</td>
</tr>
<tr>
<td><em>CYP2C19</em>1/*2</td>
<td>174</td>
<td>26</td>
<td>22</td>
<td>55</td>
</tr>
<tr>
<td><em>CYP2C19</em>1/*35</td>
<td>28</td>
<td>10</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><em>CYP2C19</em>2/*35</td>
<td>5</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><em>CYP2C19</em>2/*2</td>
<td>23</td>
<td>5</td>
<td>2</td>
<td>7</td>
</tr>
<tr>
<td><em>CYP2C19</em>35/*35</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Allele Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>CYP2C19</em>1</td>
</tr>
<tr>
<td><em>CYP2C19</em>2</td>
</tr>
<tr>
<td><em>CYP2C19</em>35</td>
</tr>
</tbody>
</table>

*All Africans includes all seven populations of African descent (YRI, ASW, ACB, ESN, GWD, LWK and MSL) as defined in Supplemental Figure 1.
### Supplemental Table 4: Full length sequencing of the CYP2C19*35 cDNA

<table>
<thead>
<tr>
<th>SNP rsID</th>
<th>Liver Genotype observed</th>
<th>CYP2C19*35 allele</th>
<th>Gene position</th>
<th>mRNA Position</th>
<th>Location in intron</th>
<th>Exon</th>
<th>Amino acid change</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs17885098</td>
<td>CT</td>
<td>T</td>
<td>99C&gt;T</td>
<td>99C&gt;T</td>
<td>-</td>
<td>Ex 1</td>
<td>Pro33Pro</td>
</tr>
<tr>
<td>rs12769205</td>
<td>AG</td>
<td>G</td>
<td>12662A&gt;G</td>
<td>-</td>
<td>Ex 3-23A&gt;G</td>
<td>Int 2</td>
<td>-</td>
</tr>
<tr>
<td>rs3758581</td>
<td>GG</td>
<td>G</td>
<td>80161A&gt;G</td>
<td>991A&gt;G</td>
<td>-</td>
<td>Ex 7</td>
<td>Ile331Val</td>
</tr>
</tbody>
</table>
Supplemental Figure 1: Visual genotypes of rs12769205 and rs4244285 in populations of African descent (1000 genomes phase 3 data). Visual genotypes for rs12769205 and rs4244285 in 1000 genomes samples (genotypes downloaded from http://browser.1000genomes.org/index.html). The populations of African descent are each listed with the number of individuals (n) and the CYP2C19*35 minor allele frequency. Grey, orange and red boxes indicate homozygous wild-type, heterozygous and homozygous variant genotypes, respectively.
Supplemental Figure 2: Linkage disequilibrium (LD) map for the common CYP2C19 allelic variants in the YRI population. (Left panel) A LD map of the CYP2C19 SNPs rs4244285, rs3758580, rs4417205 and rs12769205 in the YRI population was created using Haploview 4.2. The red squares show complete LD with statistical significance ($|D'| = 1$, LOD $> 2$). (Right panel) $R^2$ LD values. The black squares show the SNPs have the highest correlation with each other, the gray boxes indicate a correlation of 0.65. The LD values in the figure are scaled from 1.0 to 100 for visual clarity.
Supplemental Figure 3: CYP2C19 haplotype frequencies, extended haplotype homozygosity, and ancestral tree in other African populations in the 1000 genome project.

The African populations (excluding YRI) living on the African continent (LWK, Luhya in Webuye, Kenya; GWD, Gambian in Western divisions in the Gambia; MSL, Mende in Sierra Leone; and ESN, Esan in Nigeria) were combined (n=396). (A) Sweep was used to determine CYP2C19 haplotypes (SNP positions rs12769205, rs4244285, rs4417205 and rs3758580) and their frequencies were determined (see Fig. legend 9). (B) Relative extended haplotype homozygosity (REHH) for each CYP2C19 haplotype with the core of the haplotypes centered on rs4244285. Both haplotypes containing SNP rs12769205 either alone (haplotype 3 (green, CYP2C19*35)), or with rs4244285 (haplotype 2 (orange, CYP2C19*2)) show extended haplotype homozygosity REHH. (C) Phylogenetic tree of the CYP2C19 haplotypes. Haplotypes closer to the ancestral are at the top of the figure. The area of the squares is proportional to the frequency of the haplotype. The gray squares represent haplotypes not present in the data, but that are missing links in the phylogeny. The program determined the ancestral root of the tree was CYP2C19*1.