Global patterns of genetic diversity and signals of natural selection for human ADME genes

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Genetic polymorphisms in many genes related to drug absorption, distribution, metabolism and excretion (ADME genes) contribute to the high heterogeneity of drug responses in humans. However, the extent to which genetic variation in ADME genes may contribute to differences among human populations in drug responses has not been studied. In this work, we investigate the global distribution of genetic diversity for 31 core and 252 extended ADME genes. We find that many important ADME genes are highly differentiated across continental regions. Additionally, we analyze the genetic differentiation associated with clinically relevant, functional polymorphism alleles, which is important for evaluating potential among-population heterogeneity in drug treatment effects. We find that ADME genes show significantly greater variation in levels of population differentiation, and we find numerous signals of recent positive selection on ADME genes. These results suggest that genetic differentiation at ADME genes could contribute to population heterogeneity in drug responses.

INTRODUCTION

An individual’s response to drug treatment is an essential aspect of the therapeutic outcome, as aberrant drug responses can lead to a lack of therapeutic effect or adverse drug response (ADR). Moreover, drug response is highly variable both at the intra-population and inter-population levels (1). ADR incidents due to poor understanding of variability in drug response can have severe medical and economic consequences (2).

Many factors can influence one’s response to drug therapy, including age, gender and genotype. Genes involved in absorption, distribution, metabolism and excretion (ADME) of drugs, and various drug target genes comprise the most important genetic determinants (3,4). Based on metabolic properties in vivo, the ADME proteins can be generally classified into three groups (5,6): phase I metabolizing enzymes, which primarily consist of the cytochrome P450 enzymes and carry out enzymatic oxidation, reduction and hydrolysis reactions that expose or add functional groups to produce polar molecules; phase II metabolizing enzymes, which add endogenous compounds to the molecules after phase I metabolism and further increase solubility, and include arylamine N-acetyltransferase (NAT), cytosolic glutathione S-transferases (GST), etc.; and drug transporters, which include efflux transporters [e.g. the ATP binding cassette (ABC) proteins] and uptake transporters [e.g. the solute carrier proteins (SLC)], and play key roles in drug absorption, distribution and excretion in the human body(7).

Genetic polymorphisms in the ADME genes are known to contribute significantly to variation in drug response (8). For example, genetic variants can alter the drug response phenotypes by changing the expression level (e.g. CYP2D6), the protein coding sequence (e.g. CYP2C9) or the mRNA splicing form (e.g. CYP3A5) of ADME genes (9–13). Functional genetic polymorphisms have also been discovered and analyzed in many other common ADME genes, including CYP1A1, CYP1A2, CYP2E1, CYP3A4, ABCB1, SLCO1B3, UGT2B7 and UGT2B15 (11,12,14–17). As a result, genetic tests for relevant ADME polymorphisms are becoming increasingly common; according to a recent study by the Federal Drug Administration, approximately one quarter of the prescriptions written in the USA in 2006 contained pharmacogenetic labeling (18).

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Substantial genetic differences and phenotypic variation may also occur for the ADME genes across different populations. Recent genome-wide genetic diversity studies have demonstrated significant population structure at both global and local levels (19–21). Ample evidence exists for strong inter-population differences in drug responses for specific genes, such as CYP2C9, CYP2D6 and NAT2, and for drugs such as clopidogrel, mercaptopurine, omeprazole, warfarin etc. (13,22–24). However, development and clinical trials of drugs in use today were predominantly carried out in populations of European ancestry from the USA or Europe. Many countries, especially in the developing world, rely on US FDA/European Medicines Agency (EMEA) guidelines for safety levels and optimal therapeutic dosages. A comprehensive understanding of the inter-ethnic genetic differences in the ADME genes and their impact on drug response is therefore crucial to guide the effective global prescription of drugs.

Nonetheless, most pharmacogenetic studies to date have focused on a limited number of ADME genes in a limited number of populations; only a few studies investigated population differentiation in ADME genes at the global or continental scale. One such study found substantial allele frequency differences among statistically inferred clusters of ancestry as well as ethnically labeled groups (25). Another investigated the genetic diversity pattern of CYP2D6 across 52 worldwide populations and found that the CYP2D6 genetic diversity distribution did not differ from that of random markers (26). This analysis was subsequently extended to three P450 enzymes—CYP2C9, CYP2C19 and CYP2D6—in more populations, and revealed that the three genes have distinctive global diversity patterns (27). Analysis of the SLCO1B1 gene revealed a similar pattern of SLCO1B1 global genetic diversity, compared with other genomic markers (28). Finally, the most comprehensive study to date of ADME genes genotyped 167 polymorphisms in 27 ADME genes in East Asian, European and African groups (29). However, the general population differentiation pattern of ADME genes remains unclear as only a limited numbers of SNPs were analyzed for each gene. A systematic and comprehensive worldwide survey of the general patterns of genetic diversity is needed to reveal the population differentiation patterns for each gene and for the ADME genes as a group.

Moreover, many ADME genes play important roles in defense against xenobiotics. These genes might have undergone substantial local selective pressures during early human migrations throughout different geographical regions. Natural selection leaves specific signals in the genetic diversity patterns around the selected loci, such as high/low population differentiation levels, skewed allele frequency spectra and/or extended haplotype homozygosity (30). Indeed, evidence of recent positive selection has been reported for numerous ADME genes, such as ABCB1 (31), CYP3A5 (32,33), NAT2 (34,35) and several ABC transporters (25). Therefore, a systematic survey of signals natural selection in ADME genes may help explain the inter-population differentiation patterns in the ADME genes. It may also help identify additional functional polymorphisms (36).

In this study, we systematically analyze the patterns of genetic diversity and signals of natural selection in 283 ADME genes (31 core and 252 extended ADME genes) in 62 global populations. We further discuss how the inter-population genetic diversity profiles and potential functional polymorphisms might impact the response to various drug compounds. This study is the first to systematically investigate worldwide population differentiation and potential signals of natural selection in a comprehensive list of ADME genes. Follow-up research based on this framework may help evaluate the portability of specific drugs across different populations.

RESULTS

We obtained genome-wide SNP data for different populations from two data sources. The first is Human Genome Diversity Panel (CEPA-HGDGP) (19), and the second is HapMap 3 data set (37). A total of 580 612 SNPs were used, analyzed in 1951 individuals from 62 populations, and which were further assigned into seven continental regions, namely Africa, Middle East, Europe, South/Central Asia, East Asia, Oceania and America (see Supplementary Material, Table S1). We defined the ADME gene lists according to the PharmaADME database (4,38). The proposed ADME consensus genes are divided into two lists—the core gene list and the extended gene list. The core genes are deemed to be the most important as they are directly involved in drug metabolism and/or have a significant impact on drugs pharmacokinetic profile. The extended genes include other genes thought to be associated with drug metabolism. The PharmaADME consensus has been used in previous studies (4), and the core gene list has been adopted by several commercial genotyping products (e.g. Affymetrix DMET®, Illumina VeraCode® ADME and TaqMan® DME).

Given the significance of the core ADME genes in both research and industry, we investigated whether this group of genes has a different global population differentiation pattern when compared with the extended genes and to control genic and non-genic regions. In total, we studied 31 core ADME genes and 252 extended ADME genes (see Supplementary Material, Table S2).

Global population differentiation in ADME genes

To investigate global differentiation among ADME genes, we calculated the weighted average $F_{st}$ of multiple sites from haplotypes of each gene across all 62 populations (hereafter referred to as GA-$F_{st}$, see Materials and Methods) for the core ADME genes and extended genes. Genes in high LD were concatenated into single loci (see Materials and Methods). GA-$F_{st}$ value measures population differentiation based on the full polymorphism composition of a genomic region. High GA-$F_{st}$ values indicate that the haplotype composition is substantially different among different populations, suggesting that the functional variants associated with specific haplotypes are also distributed heterogeneously across populations. On the other hand, genes with low GA-$F_{st}$ may have limited genetic as well as functional heterogeneity across populations. The GA-$F_{st}$ values vary widely among the ADME genes, with the maximum GA-$F_{st}$ found in the core
gene CYP3A5 at 0.310, and the minimum of 0.0526 in the extended gene SLC04C1 (Supplementary Material, Table S3).

Under neutral evolution, population differentiation is influenced solely by random genetic drift (which increases differentiation) versus migration (which decreases differentiation), and these are expected to have the same average effect across the genome. On the other hand, natural selection impacts population differentiation in a locus-specific manner: local positive selection tends to increase population differentiation, whereas negative or balancing selection tends to decrease population differentiation. GA-$F_{st}$ is therefore often used to detect departures from evolutionary neutrality (39–41). In this study, we sampled 500 random non-genic regions which are expected to be mainly influenced by neutral demographic processes (see Materials and Methods).

Figure 1 shows the comparison of the GA-$F_{st}$ distribution of the non-genic regions, and those of the two ADME gene groups (the core and extended ADME genes). It is apparent from Figure 1 that compared with the GA-$F_{st}$ distribution of the non-genic regions, those of the two ADME gene groups have a much bigger range. The $F$-test of equal variance is highly significant between the core genes (0.130 ± 6.2%, mean ± SD) and non-genic regions ($P$-value = $5.267 \times 10^{-9}$, Table 1). The average GA-$F_{st}$ value is significantly higher in the extended ADME genes (Mann–Whitney $U$-test $P$-value = 0.005, Table 1) than in the non-genic regions. Although the average GA-$F_{st}$ value for core ADME genes does not differ significantly from that for non-genic regions (Table 1), this is likely to reflect limited power due to the small number of core ADME genes, as the average GA-$F_{st}$ value for core ADME genes is actually larger than that for extended ADME genes (Table 1). These results strongly suggest an excess of positive selection on the ADME genes.

To determine whether the ADME genes are under a stronger influence of selection than other genes in the genome, we compared the two ADME gene categories against a group of randomly sampled genes (see Materials and Methods) and between each other. The mean GA-$F_{st}$ values do not differ significantly among the three gene categories (Table 1). However, the core ADME genes have a significantly higher variance in the GA-$F_{st}$ distribution than both the extended ADME genes ($F$-test $P$-value = 0.001) and the random genes ($F$-test $P$-value = 0.012). Moreover, the difference in the variance in the GA-$F_{st}$ distribution for the extended ADME genes versus the random genes approaches, but does not reach, statistical significance ($F$-test $P$-value = 0.067, Table 1). These results together suggest that while most of
the ADME-related alleles were not more influenced by natural selection than the other genes in the genome, some core genes do show more evidence of selection, which led to greater variance in the distribution of GA-$F_{st}$ values.

We use the lowest and highest 1% of the non-genic GA-$F_{st}$ values as the cutoffs for evidence of departure from neutrality, which are 0.0503 and 0.2032, respectively. No ADME genes have GA-$F_{st}$ values lower than the lower cutoff, whereas three core genes (CYP3A4, CYP1A2 and CYP3A5) and 12 extended genes (ALDH2, GSTCD, CYP3A7, CYP3A43, ABC12, SLC28A2, ABC11, PPARA, CYP26A1, CYP26C1, CES2 and CYP1B1) are above the upper cutoff (Supplementary Material, Table S3). These genes are thus candidates for functional heterogeneity across ethnic groups.

**Pairwise population differentiation in ADME genes**

The GA-$F_{st}$ values indicate the overall degree of population differentiation in the ADME genes. It is also desirable to know how exactly are the inter-population differences distributed, e.g. whether the global differentiation is mainly explained by a few outlier populations, or by differences among major geographical regions. To answer this question, we used the pairwise weighted average $F_{st}$ for the multiple sites from haplotypes of each gene (hereafter referred as PA-$F_{st}$, see Materials and Methods) to measure the differentiation between each pair of populations. The PA-$F_{st}$ values are plotted as contour maps (Fig. 2 and Supplementary Material, Fig. S1). In these contour maps, PA-$F_{st}$ values are represented as boxes of black/white gradients, where darker gradients represent higher PA-$F_{st}$ values. Each population was also assigned to one of the seven continental regions as mentioned above (Supplementary Material, Table S1). We observed various kinds of pairwise population differentiation patterns among different ADME genes. It seems most of these patterns can be described as differentiation among the seven continental regions. To formally evaluate whether the variances among continental regions are higher than those among populations within a region, we carried out an analysis of molecular variance (AMOVA) and compared the variances between the two levels with an F-test (see Materials and Methods). Indeed, most ADME genes are more differentiated among regions than within regions (see Supplementary Material, Table S3 for details).

Some typical population differentiation patterns in the ADME genes are presented in Figure 2. CYP3A4 (Fig. 2A) shows distinct differences in the genetic profiles between African and non-African populations (F-test $P$-value $= 0.006$). CYP1A2 (Fig. 2B) exhibits strong differences between European and non-European populations (F-test $P$-value $= 0.001$). East Asians are clearly differentiated from other populations at NAT2 (F-test $P$-value $= 0.002$, Fig. 2C). On the other hand, significant differentiation does not always occur only between continental regions. For example, UGT2B7 (Fig. 2D) seems to be as highly differentiated among populations within continental regions as among continental regions (F-test $P$-value $= 0.106$). The inter-population differentiation for UGT2B7 is especially high in East Asia and America (Fig. 2D). This suggests that for drugs processed by such genes, there may be significant differences in drug response even among closely related ethnic groups.

In some cases, no strong differences can be observed among populations or regions. For example, NAT1 shows low PA-$F_{st}$ values across all pairwise comparisons ($P$-value $= 0.031$), which implies that its sequence is highly conserved among human populations (Fig. 2E). Still, many of the PA-$F_{st}$ patterns for ADME genes are strongly different from neutral patterns (Fig. 2F), suggesting that natural selection has played a major role in shaping the population differentiation of ADME genes. Genes with high-population differentiation may indicate substantial diversity in drug response, and care has to be taken when a drug metabolized or transported by these genes is to be applied to groups with very different genetic profiles.

**Global population differentiation of functional ADME SNPs**

All the above analyses are based on general patterns of genetic variation in each gene. However, the genetic variants most relevant to clinical application are the functional variants that directly affect enzyme efficacy or expression. We first looked for high-frequency non-synonymous SNPs, which are assumed to have higher potential functional impact on the drug response profile. Eighteen candidate SNPs (SNP1–18, Table 2) were identified and many have been previously reported to have functional significance (see references in Table 2). We further included two reported functional SNPs in non-coding regions (SNP19, 20, Table 2). Finally, six additional candidate SNPs were added from the PHARMADME core ADME SNP list (http://www.pharmaadme.org/). For any candidate SNPs that are not represented in our merged genotyped data, we found tagging SNPs (see Materials and Methods). We then studied the global population differentiation for these

<table>
<thead>
<tr>
<th>Gene</th>
<th>PA-$F_{st}$ Mean</th>
<th>PA-$F_{st}$ Mean</th>
<th>$U$-test $P$-value</th>
<th>Ratio of variance</th>
<th>$F$-test $P$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Core genes</td>
<td>0.109</td>
<td>0.109</td>
<td>0.005</td>
<td>1.861</td>
<td>5.267 x 10^-9</td>
</tr>
<tr>
<td>Extended genes</td>
<td>0.119</td>
<td>0.119</td>
<td>0.012</td>
<td>1.861</td>
<td>5.267 x 10^-9</td>
</tr>
</tbody>
</table>

**Table 1.** The results of statistical tests of the significance of differences in the distribution of GA-$F_{st}$ values among ADME core genes, extended genes, randomly selected genes and non-genic regions

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candidate functional SNPs and tested whether the GA-Fst of the specific genes predicts the population differentiation of these functional SNPs.

The 26 candidate functional SNPs are listed in Table 2. The GS-Fst values (0.109 ± 6.4%) of these SNPs fall in a similar range as the GA-Fst values of the ADME genes. Two SNPs,
rs776746 (in CYP3A5) and rs4149117 (in SLCO1B3), are of particular interest for their high GS- $F_{st}$ values (0.332 and 0.208). They therefore may contribute significantly to inter-ethnic variation in response to drugs metabolized by these genes.

More interestingly, we found that the GS- $F_{st}$ values of these functional SNPs strongly correlate with the GA-$F_{st}$ of their respective genes ($r^2 = 0.80$; Fig. 3). This suggests that the population differentiation level of the functional SNPs can be well interrogated by the GA-$F_{st}$ of the corresponding gene. In the absence of full characterization of potential functional variants, the GA-$F_{st}$ patterns of ADME genes may therefore provide an indirect assessment for potential inter-population variation in drug responses.

### Detecting local natural selection in the ADME genes

The PA-$F_{st}$ analyses revealed highly variable patterns of ADME genetic differentiation among worldwide populations, and many of them are incompatible with neutral expectations. To formally analyze the signatures of selection in the ADME genes, we applied two commonly used statistics: lnRsb and composite likelihood ratio (CLR) (see Materials and Methods). The lnRsb method has been shown to possess good power to detect recent positive selection, with higher power toward fixed or nearly fixed sweeps (42). The CLR test is a model-based approach, which preferentially detects fixed sweeps (43). Therefore, lnRsb is used here to describe the distribution of putative signals of positive selection, and CLR is used for validating fixed sweeps.

In general, we found that a substantial fraction of ADME genes exhibit evidence of recent positive selection. There is good agreement between the results of the lnRsb and CLR tests, which supports the reliability of the analysis (Fig. 4 and Supplementary Material, Fig. S2). Figure 4 shows the signals of positive selection in the core ADME genes in different populations. In the African populations, signals of selection identified by lnRsb seem to occur sporadically in different genes and populations. Nonetheless, the CLR test supports the indication of selection on DPYD in the Mandenka and Luhya populations, and on ABCB1 in the African American and Yoruba populations. Less clear patterns in the African populations may result from the overall high level of population differentiation in Africans. On the other hand, signals of selection in the non-African populations seem to depend highly on the geographic region. Specifically, the phase I drug metabolizers CYP2E1, CYP3A4, and CYP3A5, phase II drug metabolizers GSTP1 and NAT1, as well as the drug transporters ABCB1 and SLCO1B1 show rather consistent signals of positive selection across the Middle East, Europe and Central South Asia. In East Asia, the signals of selection are less consistently shared among all the populations. But signals are found in numerous populations for the phase I drug metabolizers CYP2C8, CYP2C9, CYP2D6, CYP2E1, CYP3A4 and CYP3A5, the phase II drug metabolizers GSTM1, GSTP1 and UGT1A1, as well as the drug transporter ABCB1. The two drug transporters SLCO2A1 and SLCO2A2 appear to be selected in multiple American populations (Fig. 4).

Several genes also exhibit significant signals in the CLR test, including CYP2E1 (in Russian and Brahui) and
**DISCUSSION**

Genetic polymorphisms account for a substantial proportion of inter-individual and inter-ethnic heterogeneity for drug responses (45). Nonetheless, the development and clinical tests of the majority of drugs currently in use were conducted in cohorts of limited ethnic diversity, with a strong bias towards European ancestry. A comprehensive understanding of population differentiation in the genetic determinants of drug response is vital for guiding the extrapolation of drug usage to diverse ethnicities. We systematically addressed this issue by examining the global and local population differentiation profiles in 283 ADME genes across 62 worldwide ethnic groups. We further conducted a full scan for evidence of natural selection on ADME genes. Our results provide insights into the evolution of genetic diversity patterns in the ADME genes and provide new candidates for important functional variants.

We found that ADME genes have very different population differentiation patterns both globally and regionally. Some genes have high global population differentiation levels (e.g. CYP3A5), while others are more conserved (e.g. SLC04C1 and NAT1). For many genes, the high differentiation across populations mainly reflects differentiation among continental regions. However, for some genes, global diversity mostly reflects differentiation within a single continental region, such as Africa, Europe or East Asia (Fig. 2). It is worth emphasizing that the population differentiation of functional variants strongly correlates with the average differentiation (GA-Fst) based on all SNPs within the gene (Fig. 4). This suggests that the allele frequency differences of functional variants can be estimated by examining their surrounding common polymorphisms. High GA-Fst values for a gene, therefore, may imply the existence of functional variants contributing to inter-ethnic heterogeneity in drug responses.

Various lines of evidence suggest that natural selection has influenced many ADME genes. The GA-Fst has a much wider distribution in the ADME genes than in the random neutral regions (Fig. 1), suggesting enrichment for signals of both positive selection and negative/balancing selection. PA-Fst maps also revealed clear departures from neutrality in many genes. Moreover, two formal tests of positive selection, the lnRsb and CLR tests, revealed widespread signals of recent positive selection. These signals tend to be continental specific for a given gene (Fig. 5 and Supplementary Material, Fig. S6). A potential explanation for the enrichment of signals of selection is that from an evolutionary viewpoint, the ADME genes are mainly involved in defense against xenobiotics. The varying environments and diets encountered during the recent migrations of humans out-of-Africa might have exerted strong selection pressures on various ADME genes. Local adaption consequently resulted in high differentiation of the ADME genes across different ethnic groups.

A potential caveat to these results is that many of the groups examined in this study have small sample sizes; 10 of the 62 populations have less than 10 individuals. While larger sample sizes would improve the overall power of our analyses, small sample sizes alone do not account for our results. The global GA-Fst value is calculated as the weighted average of the population specific Fst values, therefore populations with small sample size contribute less to the GA-Fst values. Indeed, after removing all the populations with sample sizes less than 10, the main GA-Fst pattern remains unchanged (see Supplementary Material, Table S4). The PA-Fst values could, in principle, be more affected by small population sizes. However, the pairwise Fst patterns were examined in the context of continental regions, such that individual PA-Fst values are unlikely to change the general patterns. Finally, for the tests of positive selection, small sample size does not dramatically reduce the power of the tests used here (21).

Many ADME genes examined in this study play pivotal roles in response to daily drug therapies, and some of them also exhibit high population differentiation and/or strong evidence of selection. This could contribute to variation in therapeutic outcomes and to elevated risks of adverse reactions across populations. To examine this more closely, we summarized various factors concerning drug response for each core ADME gene, including its substrates, GA-Fst value, PA-Fst summary pattern and signals of positive selection. Table 3 gives this summary for the six genes of interest: CYP1A2, CYP2C19, CYP2C9, CYP3A4, NAT1 and ABCB1. The data for the remaining genes are listed in Supplementary Material, Table S3.

![Figure 3. The scatter plot of GA-Fst versus GS-Fst for functionally important SNPs.](https://academic.oup.com/hmg/article-abstract/20/3/528/560401/18/January/2019)
CYP3A4 and CYP3A5 are located near each other in the chromosomal region 7q21.1. CYP3A4 metabolizes an estimated 50% of the currently used drugs (46,47). Both CYP3A genes show strong population differentiation globally (GA-Fst 0.223 and 0.310, respectively; CYP3A5 has the highest GA-Fst of all ADME genes). In agreement with a previous study (48), we find strong signals of selection on CYP3A4 and CYP3A5 in many Eurasian populations. For example, in CYP3A4, there are 27 populations with significant lnRsb signals and 7 populations with significant CLR signals. The allele frequency spectrum for CYP3A5 shows a clear selection sweep signal in multiple Eurasian populations. Previously, an intron SNP (rs776746) was found to completely interrupt the CYP3A5 expression by alternative splicing, which might explain the strong signal of selection in this region (49). Other candidate causal SNPs in CYP3A4 have been proposed but no clear conclusions were obtained (48).

Details of the PA-Fst contour maps show that the genetic diversity of CYP3A genes mainly comes from high differentiation between Africans and non-Africans (Fig. 2). Given the wide substrate spectrum of CYP3A4, Africans may have some general differences in drug responses from non-Africans. Therefore, special care should be taken when CYP3A substrates are given to individuals of African ancestry.

CYP2C9 is another important drug metabolizer. It carries out the metabolism of anti-inflammatory, antidiabetic drugs, such as celecoxib, lornoxicam, diclofenac, ibuprofen etc. Warfarin, one of the major substrates used as an anticoagulant, is also metabolized by CYP2C9, and at a significantly higher rate in Europeans than in African-Americans or Asians (50). The GA-Fst value for CYP2C9 is low (0.067) and there is no clear indication of population differentiation either globally or specifically between Europeans and African/Asians (51). The very broad substrate spectrum of CYP2C9 suggests that general drug resistance phenotypes may exhibit non-negligible differences between individuals of African versus non-African ancestry.

NAT2 is one of the NAT genes in humans involved in detoxification of a large number of chemicals. Many genetic polymorphisms influence NAT2 activity, resulting in the phenotype of either slow or rapid metabolizer. The GA-Fst of NAT2 is not extreme (0.128), although East Asians do tend to differ from the other populations in pairwise comparisons (Fig. 2C). However, signals of selection come from various other continental regions but not East Asia (Fig. 5). It is therefore of interest to study the detailed distribution of the genetic variants of NAT2 in Asian populations and test how they influence general detoxification in East Asians.

In conclusion, we have identified a significant tendency for ADME genes to exhibit more variation than other regions of the genome in the amount of differentiation among human
populations. There is a strong correlation between the population differentiation of functionally significant SNPs and the population differentiation of other SNPs in such genes, suggesting that GA-$F_{st}$ values for genes can help identify functional SNPs. We have also identified numerous signals of recent positive selection in ADME genes. Further investigation of these signals should help in avoiding adverse drug reactions in particular populations, and illuminate important selective events in the history of human populations.

To fully appreciate how ethnicity would influence ADME gene diversity and function, one promising strategy is to carry out deep sequencing in all ADME genes in various ethnic groups. This becomes feasible with the development of next-generation sequencing technologies (54,55). In the future, cohort studies of comprehensive drug–response phenotypes supported with full genetic information should enable a systematic understanding of the ethnicity/drug–response interplay.

**MATERIALS AND METHODS**

**Genetic data**

The genome-wide SNP data analyzed here are from two primary data sources, namely the Human Genome Diversity Panel (CEPH-HGDP) (19) and the phase III Hapmap (http://hapmap.ncbi.nlm.nih.gov/). The CEPH-HGDP panel includes 940 individuals from 51 populations, while the phase III Hapmap data are from 1011 individuals from 11 populations. These 62 globally distributed populations were further grouped into seven continental regions: Africa, Middle East, Europe, South/Central Asia, East Asia, Oceania and America. The population ID, location and sample size are listed in Supplementary Material, Table S1.

**Phasing and merging data sets**

The HGDP-CEPH individuals were previously genotyped with Illumina HumanHap 650K Beadchips, resulting in genotypes for approximately 650,000 SNPs (56). After downloading the data, we phased the data with fastPHASE (57), using the parameters “-Ku100 -Kl5 -Ki10” to determine the number of haplotype clusters (all other parameter values used the default settings). The phased data were then merged in PLINK (58) with haplotype data from phase III Hapmap, and non-overlapping SNPs were removed. The merged data set thus consists of haplotypes for 580,612 SNPs in 1952 individuals from 62 populations.

**Inferring ancestral states**

In some analyses, such as identifying recent selective sweeps, it is desirable to specify the ancestral and derived alleles of each SNP. To do so, SNP annotations were created using the TAMAL database, based chiefly on data from UCSC genome browser files (59). Using the physical position of the SNP in the human genome, the aligned chimpanzee and macaque allele information were obtained, and the ancestral allele of the human SNP was defined if one of the human alleles was identical to both the chimpanzee and the macaque allele at the corresponding position. In the merged data set, there are 461,461 SNPs for which the ancestral allele could be identified by this procedure.

**Obtaining gene information for ADME genes**

The ADME gene lists were obtained from the PharmaADME database (4,38). The PharmaADME consortium consists of individuals from academia and the pharmaceutical and genomic technology industries (www.PharmaADME.org). Our analyses were based on two sets of ADME genes: the core set, containing the most important genes in drug metabolism, and the extended set, containing other drug metabolism-related genes (4,38). ADME genes located on sex chromosomes were excluded, resulting in 31 core ADME genes and 252 extended ADME genes (Supplementary Material, Table S2). Gene coordinate information was obtained from the Refseq database to infer the start and end position for each gene (60).

Two additional groups of genes/regions were defined to compare to the ADME genes. The first consists of 500 randomly selected non-genic regions, selected to be at least 200 kb away from any RefSeq genes (http://www.ncbi.nlm.nih.gov/RefSeq/) and matching the physical size distribution of the ADME genes. For the set of random genes, 500 random genes were directly sampled from the RefSeq database without replication.

**Population differentiation and $F_{st}$ estimation**

Three $F_{st}$ Statistics, namely $F_{st}$ averaged across all sites within a gene over all populations (GA-$F_{st}$), pairwise $F_{st}$ averaged across all sites within a gene between each pair of populations (PA-$F_{st}$) and $F_{st}$ calculated per site (GS-$F_{st}$) were all obtained with Arlequin v.3.11(61). The $F_{st}$ for a single site is equivalent...
Table 3. Summary information for several core ADME genes of interest

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Example substrates</th>
<th>GA-$F_{st}$</th>
<th>Global diversity pattern</th>
<th>Populations with InRsb signals</th>
<th>Populations with SweepFinder signals</th>
</tr>
</thead>
<tbody>
<tr>
<td>CYP1A2</td>
<td>Amitriptyline, imipramine, clozapine, caffeine etc.</td>
<td>0.277</td>
<td>EU-others</td>
<td>LWK, MKK</td>
<td>NA*</td>
</tr>
<tr>
<td>CYP2C19</td>
<td>Amitriptyline, antiepileptics, nordazepam, diazepam, phenytoin etc.</td>
<td>0.085</td>
<td>AM-others</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>CYP2C9</td>
<td>Celecoxib, lornoxicam, lornoxicam, diclofenac, ibuprofen etc.</td>
<td>0.067</td>
<td>AM-others</td>
<td>Cambodian, Miaozu, Mongola, Oroqen, Pygmies, Tuja, Yizu, Yoruba, YRI</td>
<td>NA</td>
</tr>
<tr>
<td>CYP3A4</td>
<td>Diltiazem, nifedipine, felodipine, verapamil, ciclosporin etc. (approximately 50% of all current clinical used drugs)</td>
<td>0.223</td>
<td>AF-others</td>
<td>Adygei, Bedouin, Brahui, Burusho, Daar, Druze, Hazara, Kalash, Makrani, Mozabite, Naxi, Orqen, Palestinian, Pathan, Russian, Sardinian, Sindhi, Tu, Tuscan, Uygur, Yakut, CEU, GIH, LWK, MEX, MKK, TSI</td>
<td>NA</td>
</tr>
<tr>
<td>NAT2</td>
<td>Sulfamethazine, retigabine, hydralazine, sulfasalazine, ribavirin etc.</td>
<td>0.128</td>
<td>EA-others</td>
<td>Adygei, Bedouin, Colombian, Italian, LWK, MEX, MKK</td>
<td>NA</td>
</tr>
<tr>
<td>ABCB1</td>
<td>Colchicine, tacrolimus, quinidine, etoposide etc.</td>
<td>0.115</td>
<td>AF-others</td>
<td>Adygei, Balochi, Bedouin, Brahui, Burusho, Colombian, Druze, Hazara, Italian, Japanese, Makrani, Mozabite, Naxi, Orqen, Papuan, Pathan, Russian, Sardinian, Sindhi, Tu, Tujia, Xibo, Yakut, ASW, CEU, GIH, YRI</td>
<td>Pathan, Sindhi, MEX</td>
</tr>
</tbody>
</table>

*AF,’AM’,‘EA’ and ‘EU’ in column four indicate Africa, America, East Asia, Europe, respectively. ‘NA’ in columns five and six means no signal of selection was found.

Table S2 provides similar information for the other core genes.

*AF, ’AM’, ‘EA’ and ‘EU’ correspond to the unbiased $F_{st}$ described by Weir and Cockerham (62), and the $F_{st}$ for a haplotype is simply a weighted average $F$-statistic over the corresponding loci. A non-parametric test (e.g. Mann–Whitney U-test) was used to evaluate the significance of differences between $F_{st}$ distributions among ADME gene sets, randomly selected genes and no-genic regions. Similarly, an $F$-test was used to evaluate the significance of differences between the variance of the various $F_{st}$ distributions. All significance tests were performed using the R package (http://www.r-project.org/).

Based on the HapMap LD database, we concatenated two neighboring genes into a single locus if any pair of SNPs, one from either gene, had an LD value ($r^2$) higher than 0.5 in any of the HapMap LD populations. Thus, in GA-$F_{st}$ distributions, there are 28 ADME core genes (or groups) and 221 ADME extended genes (or groups) (Fig. 1).

The PA-$F_{st}$ values were also calculated with the Arlequin package. In particular, a $62 \times 62$ PA-$F_{st}$ matrix was calculated among the 62 populations. Each PA-$F_{st}$ value was assigned into one of the following bins: $<0.01$, $0.01–0.05$, ..., $0.25–0.30$, $>0.30$. Each bin was then represented by a gray scale gradient in the contour maps, where the darker gradients represent higher PA-$F_{st}$ values.

To evaluate whether the genetic variance among the seven continental regions is significantly different from the genetic variance among populations within each region, AMOVA was carried out using Arlequin, and an $F$-test was used to assess the statistical significance of the variance components.

Selection of candidate functional SNPs

We first identified all the non-synonymous SNPs from the HapMap phase II data (http://hapmap.ncbi.nlm.nih.gov/), which are located within the ADME genes and have minor allele frequencies higher than 0.05 in each of the three groups—Yoruba (YRI), Central Europeans (CEU) and Chinese-Japanese combined (CHB, JBT). Based on these criteria, we identified 18 non-synonymous SNPs. We further included one intronic SNP (SNP19 in Table 2, rs776746 in CYP3A5), which disrupts transcript splicing (63), and one 5′-UTR SNP (SNP20 in Table 2, rs7662029 in the proximal promoter region of UGT2B7), which modulates the transcription of UGT2B7 (64). The pharmaADME consortium also proposed a list of core candidate functional SNPs (http://www.pharmaadme.org/), within which 22 SNPs have minor allele frequencies higher than 0.05 in all three HapMap II groups (YRI, CEU and CHB-JBT). Sixteen of these overlap with the 20 functional SNPs identified above (SNP1–14, SNP19 and SNP20 in Table 2); the other six SNPs were also added to the list of candidate functional SNPs (Table 2). For any candidate SNPs that are not represented in our merged genotyped data, we identified corresponding tagging SNPs with high $r^2$-value (at least 0.8) with the SNP of interest.

Detecting signals of selection

Two approaches were used to detect signals of recent positive selection. The first is based on the idea that unusually long haplotype homozygosity, associated with a high allele frequency, is unexpected under neutrality but is expected with strong positive selection (42). Here, we used a modified InRsb approach, which is based on comparing the EHH of the same allele in different populations, to identify candidate regions that have experienced recent local selection (42). We used the same procedure described previously to identify candidate regions (21), except that we used a cutoff of 1% to...
identify the top SNPs, and candidate regions were defined as having at least five top SNPs within a 100 kb region.

The second approach used to identify signals of recent positive selection is based on the maximum CLR statistic, which uses the spatial distribution of allele frequencies along the genome and compares the hypothesis of a complete selective sweep against the null hypothesis of no sweep. We used the SweepFinder program (65) to carry out these calculations. Given that the alternative hypothesis is a complete sweep, this test has the most power to detect complete or near-complete sweeps, but may lack power to detect partial sweeps. We used a strict cutoff for the empirical P-value of 0.01, to consider a signal as a significant indication of positive selection.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG online.

Conflict of Interest statement. None declared.

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REFERENCES


