

# Functional characteristics of CYP3A4 allelic variants on the metabolism of loperamide in vitro

This article was published in the following Dove Press journal:  
*Infection and Drug Resistance*

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**Background:** Cytochrome P450 3A4 (CYP3A4) appears to be genetically polymorphic, which in turn contributes to interindividual variability in response to therapeutic drugs. Loperamide, identified as a CYP3A4 substrate, is prone to misuse and abuse and has high risks of life-threatening cardiotoxicity.

**Methods:** Thus, this study is designed to evaluate the enzymatic characteristics of 29 CYP3A4 alleles toward loperamide in vitro, including the 7 novel CYP3A4 variants (\*28–\*34). The incubation system (containing CYP3A4 enzyme, cytochrome b5, 0.5–20 μM loperamide, potassium phosphate buffer and nicotinamide adenine dinucleotide phosphate) was subject to 40-mins incubation at 37°C and the concentrations of N-demethylated loperamide were quantified by UPLC-MS/MS.

**Results:** As a result, CYP3A4.6, .17, .20 and .30 showed extremely low activity or no activity and the rest of CYP3A4 variants presented varying degrees of decrements in catalytical activities when compared with CYP3A4.1.

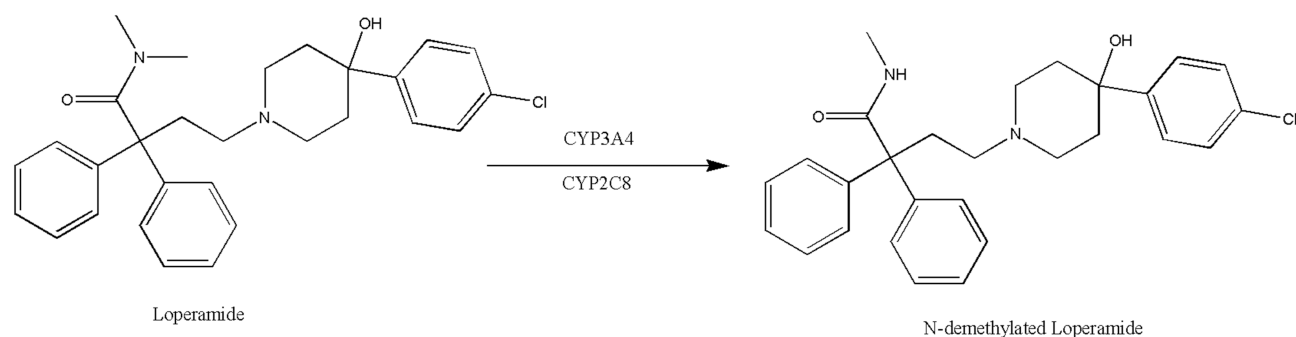
**Conclusion:** As the first study to identify the properties of these CYP3A4 variants toward loperamide metabolism, our investigation may establish the genotype–phenotype relationship for loperamide, predict an individual's capability in response to loperamide, and provide some guidance of clinical medication and treatment for loperamide.

**Keywords:** CYP3A4, genetic polymorphism, interindividual variability, loperamide, misuse and abuse, cardiotoxicity, personalized treatment

## Introduction

Loperamide is routinely prescribed to treat acute and chronic diarrhea.<sup>1</sup> In spite of being a μ-opioid receptor agonist, it is considered not having abuse potential, due to its poor oral bioavailability, extensive first-pass metabolism as well as inability of penetrating across the blood-brain barrier.<sup>1–5</sup> In recent years, however, loperamide use has been on a steep rise, which is used for opioids substitution rather for diarrhea treatment.<sup>4,5</sup> A growing number of clinical cases have been reported to disclose life-threatening cardiac events and death resulted from over-ingestion of loperamide.<sup>5–14</sup> In June 2016, the FDA issued a safety communication aimed to warn about serious heart problems implicated in much higher than the therapeutic doses of loperamide.<sup>15</sup> In Jan 2018, owing to the continually-increasing reports of loperamide-caused events, the FDA issued another communication to foster the safe use of loperamide further by limiting the packaging for loperamide.<sup>16</sup>

Loperamide is subjected to extensive first-pass metabolism in liver to form a principle metabolite, N-demethylated loperamide (DLOP) (Figure 1).<sup>17,18</sup> Although DLOP has a lower cardiotoxicity relative to loperamide, unexpectedly, it can achieve a



**Figure 1** The transformation of loperamide to its main metabolite N-demethylated loperamide (DLOP).

concentration systemically much higher than loperamide, leading DLOP to be an essential contributor to loperamide-associated cardiac events after loperamide.<sup>19</sup> It is evidenced that cytochrome P450 3A4 (CYP3A4) and CYP2C8 play a critical role in this transformation.<sup>20</sup> As the most abundant CYP450 enzyme in human liver, CYP3A4 is speculated to be more responsible for loperamide metabolism.<sup>20,21</sup>

CYP3A4 has an extremely broad substrate spectrum, in charge of the oxidative metabolism of approximately 50% of clinically used drugs.<sup>22</sup> Previous studies have confirmed that CYP3A4 appears genetically polymorphic, causing the wide interindividual variability in CYP3A4 enzymatic activity (up to 60-fold) and further causing the great difference of drugs metabolism, eventually which would result in undesirable side events or subtherapeutic effects.<sup>21–23</sup> Taking loperamide, for example, the risk of loperamide-linked cardiotoxicity may be enhanced among poor metabolizers, especially who experience loperamide misuse or abuse. Therefore, it is imperative to research whether genetic variations of CYP3A4 would affect the enzymatic activities to predict the genotype–phenotype relationship for loperamide.

Hitherto, there are 53 CYP3A4 variants that are identified and named by the Human CYP Allele Nomenclature Committee website (<http://www.cypalleles.ki.se/cyp3a4.htm>). In this study, we aim to investigate the catalytic activity of wild-type CYP3A4\*1, 21 previously reported CYP3A4 variants and 7 novel variants discovered by Hu et al.<sup>21</sup> on the metabolism of loperamide in vitro, which may assist prediction of an individual's capability for responding to loperamide.

## Materials and methods

### Chemicals and materials

Loperamide, DLOP and midazolam (used as internal standard) were purchased from Shanghai Canspec Scientific &

Technology Co., Ltd. (Shanghai, China) Acetonitrile and methanol of analytical grade were bought from Merck (Darmstadt, Germany); formic acid was from Sigma-Aldrich Co. (St. Louis, MO, USA). Ultra-pure water was produced with a Milli-Q reagent system (Millipore, Bedford, MA, USA). The reduced nicotinamide adenine dinucleotide phosphate (NADPH) was purchased from Roche Pharmaceutical Ltd (Basel, Switzerland). Recombinant human CYP3A4 enzymes and purified cytochrome b5 were kind gifts from Beijing Hospital (Beijing, China).<sup>24–26</sup>

### Incubation conditions

The 200- $\mu$ L incubation system involved 100 mM potassium phosphate buffer (pH 7.4), 1 pmol CYP3A4.1 or other CYP3A4 variants, 2 pmol cytochrome b5, 1 mM NADPH and 0.5–20  $\mu$ M loperamide that was sequentially diluted by methanol. The mixture without NADPH went through 5-mins prewarm at 37°C, then with the help of 1 mM NADPH initiated a 40-mins reaction process, and finally was frozen at –80°C to terminate the reaction. 600  $\mu$ L of Acetonitrile and 20  $\mu$ L of midazolam (10  $\mu$ g/mL) were added into the incubation system prior to 2-mins vortex and 10-mins centrifugation at 11,357 $\times$ g, and the supernatant was diluted (1:20) with ultra-pure water for UPLC-MS/MS analysis. Collectively, all incubations were performed in triplicate and data were in the form of mean  $\pm$  SD.

### Equipment and operation conditions

DLOP and midazolam were determined by UPLC-MS/MS, which was equipped with an Acquity UPLC system (Waters Corp., Millipore, Bedford, MA, USA) and a Waters Xevo TQ-S Micro-triple quadrupole mass spectrometer with an electrospray ionization source (Waters Corp., Millipore, Bedford, MA, USA). Analytes were separated on BEH

C18 Column (2.1 mm × 100 mm, 1.7 μm; Waters Corp., Millipore, Bedford, MA, USA) at 40°C. The mobile phase involved ACN (A) and 0.1% formic acid (B) with a gradient elution at 0.35 mL/min for 3.0 mins. The gradient condition was as follow: 70–15% B (0–1.4 mins), 15–70% B (1.4–2.6 mins), and 70% B (2.6–3.0 mins). Multiple reaction monitoring in a positive mode was selected for detecting analytes. The transitions were  $m/z$  463.3→252.1 and  $m/z$  326.1→291.1 for DLOP and midazolam, respectively. Under these circumstances, DLOP and midazolam were well separated and their retention times were 1.39 and 1.16 mins, respectively (Figure 2).

## Statistical analysis

The kinetic parameters ( $K_m$  and  $V_{max}$ ) were calculated via GraphPad Prism 5.0 (GraphPad Software Inc., San Diego, CA, USA) by Michaelis–Menten model to obtain intrinsic clearances ( $Cl_{int}$ ) as the ratio of  $V_{max}/K_m$  and to depict Michaelis–Menten plots. All data were in the form of mean ± SD and subject to one-way ANOVA with Dunnett's test by means of GraphPad Prism 5.0 to compare parameters of wild-type CYP3A4.1 with these of other variants.  $P$ -value below 0.05 means statistic difference.

## Results

Michaelis–Menten kinetics of loperamide for CYP3A4.1 as well as other variants and their corresponding parameters are revealed in Table 1 and Figures 3 and 4. According to the alterations of values in  $V_{max}$ , there are 3 situations: no evident changes between CYP3A4.1 and CYP3A4.3 and .5; significant increments in CYP3A4.7, .8, .11, .14, .16, and .18 compared with CYP3A4.1; remarkable decrements in the remaining variants. According to the alterations of values in  $K_m$ , there are 3 situations: no considerable difference between CYP3A4.1 and CYP3A4.9, .10, .19, .24, .28, .31, and 0.34; moderate increments with  $P<0.05$  in CYP3A4.4, .15, .29 and .32 relative to CYP3A4.1; serious increments with  $P<0.01$  in the remaining variants. According to the comparison of values in  $Cl_{int}$  with CYP3A4.1, there are 2 situations: marginal decrease to 55.06–83.85% observed in CYP3A4.8, .16, .18 and .28; sharp collapse to 7.45–49.65% shown in the rest of CYP3A4 variants. Additionally, the concentrations of DLOP could not be detected for CYP3A4.6, .17, .20 and .30.

Overall, the reductions of  $Cl_{int}$  values could be caused by the changes in  $V_{max}$  and  $K_m$  into 4 situations: similar

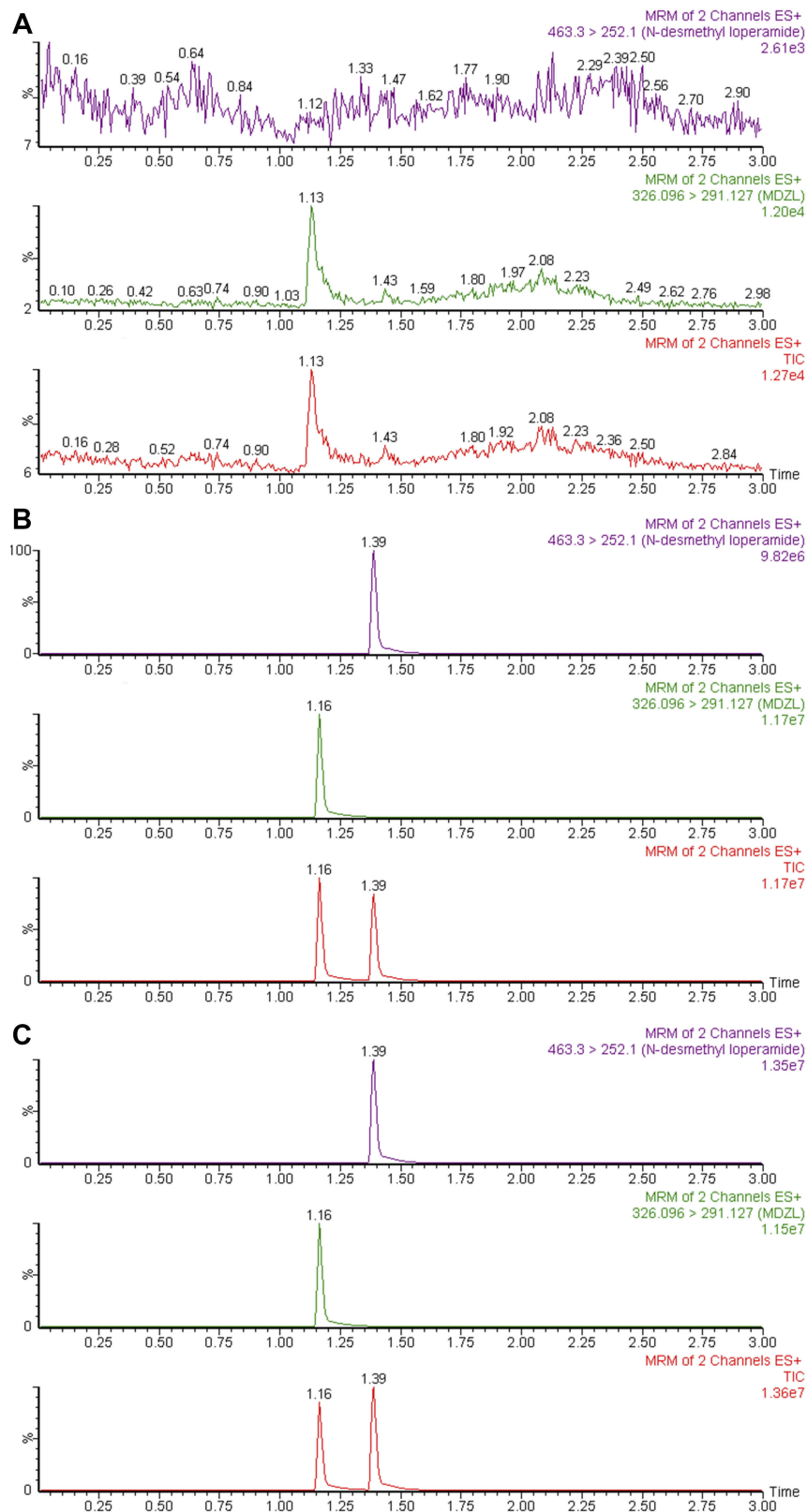
$V_{max}$  versus reduced  $K_m$  (CYP3A4.3 and 0.5); reduced  $V_{max}$  versus similar  $K_m$  (CYP3A4.9, 0.10, 0.19, 0.24, 0.28, 0.31 and 0.34); reduced  $V_{max}$  versus enhanced  $K_m$  (CYP3A4.2, 0.4, 0.12, 0.13, 0.15, 0.23, 0.29, 0.32 and 0.33); increased  $V_{max}$  versus greater-surged  $K_m$  (the rest of CYP3A4 variants).

## Discussion

The huge interindividual variations in drug metabolism may attribute to the collective effect of genetic polymorphisms, regulation of gene expression as well as interactions with therapeutic agents or environmental chemicals.<sup>27</sup> Genetic polymorphisms, one of the influential factors, account for approximately 90% of variances of CYP3A4 enzymatic activities, indicating the great contribution of CYP3A4 genetic polymorphism to the tremendous interindividual variability in response to drugs such as loperamide (a CYP3A4 substrate).<sup>20–22,28</sup> There are no related reports about enzymatic properties of CYP3A4 variants toward loperamide. In addition to the life-threatening cardiotoxicity of loperamide and the epidemic of loperamide misuse and abuse, it is of clinical value to identify the properties to establish the genotype–phenotype relationship to forecast the probability of response or severe toxicity to loperamide.<sup>5,13,29</sup>

A previous study has reported that CYP3A4, CYP2C8, CYP2D6, and CYP2B6 could catalyze loperamide N-demethylation in human liver microsomes.<sup>20</sup> And among them, CYP3A4 and CYP2C8 played more important roles (53% and 38%, respectively) in loperamide N-demethylation.<sup>20</sup> CYP3A4 is the most abundantly expressed enzyme in human liver (accounting for on average approximately 30% of the microsomal P450 pool) and CYP2C8 only accounts for 4.7%.<sup>30</sup> Besides, loperamide exposure was rather increased in the presence of itraconazole (a CYP3A4 inhibitor) with  $P<0.001$  than in the presence of gemfibrozil (a CYP2C8 inhibitor) with  $P<0.05$ .<sup>2</sup> All findings imply that CYP3A4 makes greater contribution to loperamide N-demethylation. Therefore, we primarily investigate the effect of CYP3A4 genetic polymorphisms on the metabolism of loperamide.

In this study, wild-type CYP3A4.1 was set as the control group while CYP3A4.6, .20 and .30 served as negative controls for the functional validation so as to make certain of the reliability and accuracy of this study. Previous experiments confirmed that CYP3A4.6, .20 and .30 were devoid of catalytical function, in agreement with the results in our study, as CYP3A4.6, .20 and .30 carried



**Figure 2** UPLC-MS/MS chromatographs of N-demethylated loperamide and midazolam (10 µg/mL midazolam) in the 200-µL incubation system: **(A)** without loperamide and midazolam; **(B)** with activity-abolished microsomes and spiked with 0.25 µM N-demethylated loperamide; **(C)** incubating with 20 µM loperamide and 1 pmol CYP3A4.1. **Abbreviations:** CYP3A4, cytochrome P450 3A4; MRM, multiple reaction monitoring.

**Table 1** Kinetic parameters for N-demethylated loperamide activity of CYP3A4.1 and other CYP3A4 variants on loperamide metabolism

Variants	V <sub>max</sub> (pmol/min/pmol P450)	K <sub>m</sub> (μM)	Cl <sub>int</sub> (V <sub>max</sub> /K <sub>m</sub> ) (μL/min/pmol P450)
3A4.1	2.079±0.064	2.196±0.218	0.951±0.066
3A4.2	0.568±0.010**	8.023±0.492**	0.071±0.003**
3A4.3	1.777±0.052	5.530±0.290**	0.322±0.007**
3A4.4	1.467±0.018*	3.293±0.019*	0.446±0.003**
3A4.5	2.153±0.131	4.804±0.246**	0.448±0.004**
3A4.6	ND	ND	ND
3A4.7	3.259±0.078**	8.849±0.318**	0.368±0.004**
3A4.8	5.302±0.367**	7.828±1.111**	0.682±0.048**
3A4.9	0.371±0.004**	2.884±0.247	0.129±0.010**
3A4.10	1.180±0.028**	2.500±0.076	0.472±0.003**
3A4.11	2.854±0.021**	17.163±0.229**	0.166±0.003**
3A4.12	0.969±0.042**	4.016±0.346**	0.242±0.010**
3A4.13	0.651±0.014**	5.812±0.249**	0.112±0.002**
3A4.14	4.862±0.226**	10.494±0.711**	0.464±0.016**
3A4.15	1.074±0.054**	3.423±0.313*	0.315±0.013**
3A4.16	10.703±0.430**	15.550±1.370**	0.690±0.033**
3A4.17	ND	ND	ND
3A4.18	9.223±0.116**	11.567±0.319**	0.798±0.012**
3A4.19	0.914±0.042**	2.234±0.394	0.416±0.056**
3A4.20	ND	ND	ND
3A4.23	0.434±0.034**	5.331±0.922**	0.082±0.008**
3A4.24	0.209±0.001**	1.329±0.040	0.157±0.004**
3A4.28	1.230±0.056*	2.356±0.223	0.524±0.026**
3A4.29	1.327±0.009*	3.356±0.045*	0.395±0.003**
3A4.30	ND	ND	ND
3A4.31	0.834±0.004**	2.900±0.167	0.288±0.016**
3A4.32	0.553±0.012**	3.568±0.199*	0.155±0.005**
3A4.33	0.851±0.016**	4.849±0.338**	0.176±0.009**
3A4.34	0.626±0.002**	1.902±0.040	0.329±0.007**

**Notes:** Significantly different from wild-type CYP3A4, \*P<0.05, \*\*P<0.01.

**Abbreviations:** Cl<sub>int</sub>, intrinsic clearance; ND, not determined; CYP3A4, cytochrome P450 3A4.

premature stop codons and then yielded truncated proteins.<sup>21,24,31,32</sup> Apart from CYP3A4.6, .20 and .30, CYP3A4.17 also exhibited extremely weak enzymatic activity without detectable concentrations of DLOP, consistent with the results in lidocaine, ibuprofen, amiodarone, testosterone and chlorpyrifos metabolism.<sup>24,25,33,34</sup> These consistencies indicate that the outcomes in this work are reliable and valid for functional analysis of CYP3A4 variants. Therefore, patients carrying these four variants could be classified as poor metabolizers for loperamide and should be paid more attention in order to avoid loperamide-caused toxicity.

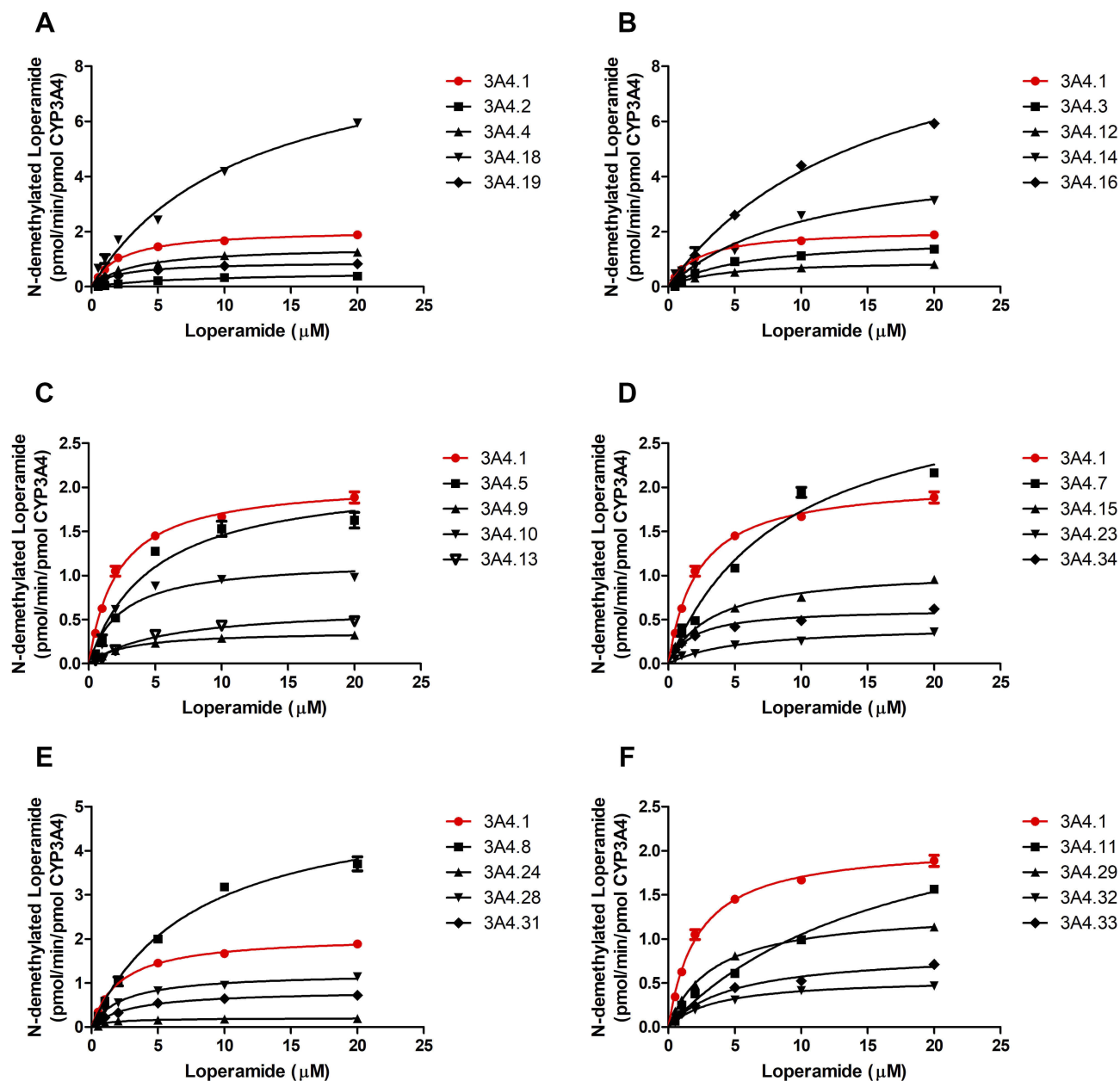
In order to comprehensively expand the understanding of the effects of CYP3A4 genetic polymorphisms on the metabolism of loperamide, we analyzed the remaining CYP3A4 variants in detail. CYP3A4.4, with an allele frequency of 2.4% in Chinese subjects, was point mutation

352A>G in exon 5, which led to the amino acid exchange from Ile to Val in 118 site.<sup>35,36</sup> It showed different catalytic activity with CYP3A4.1 and this difference might attribute to Ile118Val that may have an effect upon the substrate binding.<sup>36</sup>

CYP3A4.18, fairly common in Asians, was previously reported having an increment in turnover numbers for testosterone and chlorpyrifos.<sup>21,34</sup> In this study, a similar result was acquired where CYP3A4.18 was associated with ~4.4-fold higher V<sub>max</sub> value and ~5.3-fold higher K<sub>m</sub> value, resulting in moderately lower catalytic activity.

For CYP3A4.28, .29, .31, .32, .33 and .34, six novel variants detected by Hu et al<sup>21</sup> were collectively demonstrated with decreased intrinsic clearance rate averaged from 16.31% to 55.06% when compared with CYP3A4.1. Specifically, Hu et al predicted that CYP3A4.31 (H324Q), and .32 (I335T) likely have a





**Figure 3** Michaelis–Menten curve of the enzymatic activities of the wild-type CYP3A4 and other CYP3A4 variants on loperamide metabolism. Data are presented as mean  $\pm$  SD of 3 parallel experiments. The variants with designated allele names have been arranged into 6 groups (A–F).

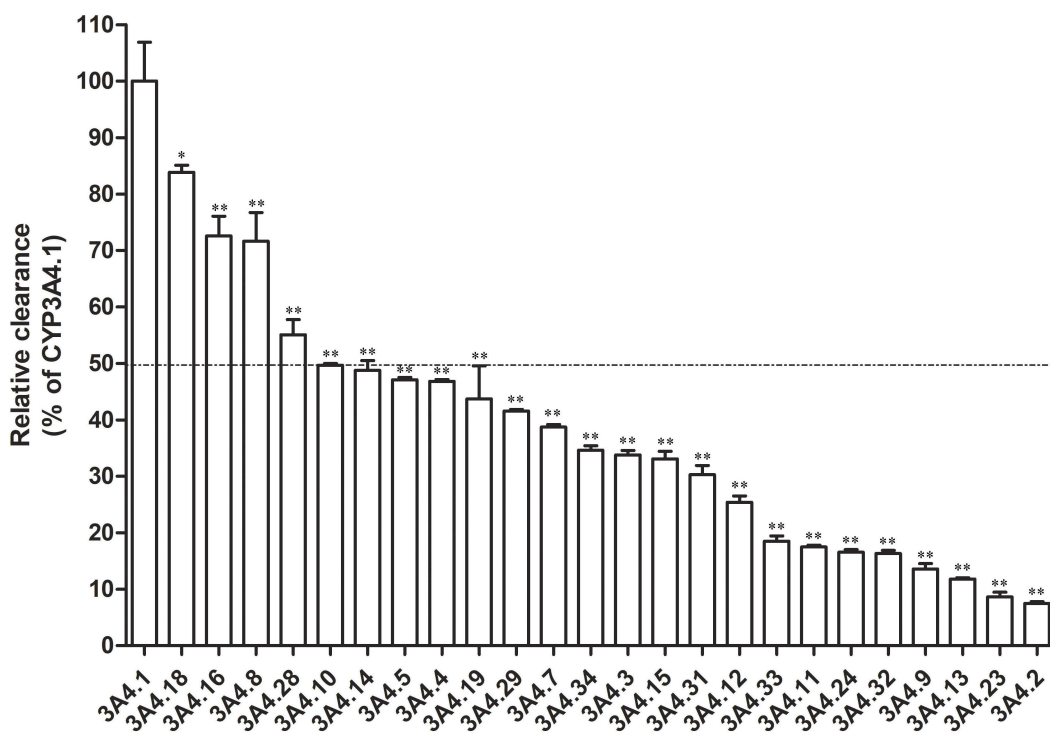
**Abbreviation:** CYP3A4, cytochrome P450 3A4.

damaging effect on enzymatic functions, even though H324Q and I335T were not implicated in the active site for drug-substrate binding.<sup>21,37,38</sup>

For CYP3A4.3 and .8, we speculated that the genetic mutations in CYP3A4 might have an impact on heme incorporation, which in turn altered the enzymatic functions. CYP3A4.3, had a nucleotide exchange of 1334T>C in exon 12, which encoded the amino acid from Met445 to Thr in the conserved heme-binding region.<sup>39</sup> Consequently, CYP3A4.3 presented a massive reduction in  $Cl_{int}$  value

(33.8 $\pm$ 0.78% of wild type) with similar  $V_{max}$  value and increased  $K_m$ , relative to CYP3A4.1. When compared with CYP3A4.1, CYP3A4.8 exhibited lower  $Cl_{int}$  value (71.67 $\pm$ 5.04% of wild type) with  $\sim$ 2.5-fold higher  $V_{max}$  value and  $\sim$ 3.6-fold higher  $K_m$  value. It may result from the substitution of Arg130 with Gln disturbing heme incorporation, in which Arg130 played a pivotal role vital for heme binding.<sup>40,41</sup>

For CYP3A4.11 and .13, we speculated that the genetic mutations in CYP3A4 might alter stability and conformations



**Figure 4** Relative clearance of CYP3A4 variants toward loperamide metabolism compared with the wild type, arranged in the order.

**Notes:** Significant differences between the wild-type CYP3A4 and CYP3A4 variants analyzed by the mean of one-way ANOVA with Dunnett's test, \* $P < 0.05$ , \*\* $P < 0.01$ .  
**Abbreviation:** CYP3A4, cytochrome P450 3A4.

of proteins, which in turn affected the functions. CYP3A4.11 involves a C1088T point mutation where Thr363 is replaced by Met.<sup>42</sup> As previously reported, CYP3A4.11 appeared unstable, probably due to the introduction of the rather large Met at the location of residue 363 disrupting the tertiary structure of the protein in this region.<sup>40</sup> Thus,  $Cl_{int}$  value of CYP3A4.11 was about 5.7-fold lower than that of CYP3A4.1. Likewise, the reduction of CYP3A4.13 enzymatic activity may be caused by destabilization of the protein via perturbing the orderly framework of the structure, in which an amino acid Leu took the place of Pro416.<sup>40</sup>

Interestingly, there were substrate-selective differences of kinetic values observed in CYP3A4.2 that was discovered in white subjects with a frequency of 2.7% and was absent in Chinese or black subjects.<sup>39</sup> This variant involved an amino acid substitution of Ser222Pro that could lead to a significant change in the three-dimensional structure of the enzyme since Pro is a known helix breaker.<sup>39</sup> In comparison with CYP3A4.1, CYP3A4.2 showed a sharp decrement in the intrinsic clearance rate toward loperamide, and this similar decrement was also found in nifedipine, lidocaine and ibuprofen metabolism.<sup>24,33,39</sup> In contrast, CYP3A4.2 exhibited an increased intrinsic clearance rate toward

amiodarone and showed little or no alteration toward testosterone.<sup>25,39</sup> This inconsistency might attribute to the different specificities for these substrates, suggesting that the results from loperamide could not be analogized to other substrates.

## Conclusion

This is the first study performed to elucidate the enzymatic characteristics of 29 CYP3A4 alleles toward the metabolism of loperamide in vitro. Our results find that most of the variants manifest extremely lower enzymatic activities toward loperamide than the wild type, which means patients with these defective alleles may have to pay attention to the dosage when ingesting loperamide. Although the allelic frequencies of these variants are relatively low, considering the large population base in the world as well as the non-standard use and the consequent cardiotoxicity of loperamide, this study can be granted some clinical value in establishing the genotype–phenotype relationship for loperamide, predicting an individual's capability in response to loperamide, and providing some guidance of clinical medication and treatment for loperamide. Additionally, with the existence of substrate specificity, further researches are

warranted to investigate the functional impacts of CYP3A4 genetic polymorphisms on the metabolism of a more various and wider range of CYP3A4 substrates, especially those with high risk of adverse effects or narrow therapeutic window.

## Acknowledgments

The authors thank the members of the Beijing Institute of Geriatrics of the Ministry of Health for their advice and assistance. This study was supported by the Ministry of Science and Technology of the People's Republic of China (No.2017ZX09304026).

## Disclosure

The authors report no conflicts of interest in this work.

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