ARTICLE



Evaluation of the relationship between polymorphisms in *CYP2C19* and the single-dose pharmacokinetics of omeprazole in healthy Chinese volunteers: A multicenter study

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Abstract

The aim of this study was to evaluate the relationship between polymorphisms in CYP2C19 and the single-dose pharmacokinetics (PKs) of omeprazole in healthy Chinese volunteers. A 20 mg single dose of omeprazole (Losec) enteric-coated capsules or tablets was orally administered to 656 healthy subjects from eight subcenters. The polymorphic alleles of *CYP2C19**2, *3, and *17 were determined by Sanger sequencing and Agena mass array. Plasma concentrations of omeprazole were determined by high-performance liquid-chromatography tandem mass spectrometry. PK parameters of area under the concentration versus time curve (AUC)_{0-t}, AUC from zero to infinity (AUC_{0-∞}), maximum plasma concentration (C_{max}), and terminal half-life ($t_{1/2}$) were significantly influenced by *CYP2C19* phenotype (all p < 0.001) and diplotype (all p < 0.001), and the same results were obtained in the subgroup analysis of the effects of diet and dosage form.

This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made. © 2022 The Authors. *Clinical and Translational Science* published by Wiley Periodicals LLC on behalf of American Society for Clinical Pharmacology and Therapeutics. The polymorphisms of *CYP2C19*2*(rs4244285; all PK parameters p < 0.001) and *3(rs4986893; $p_{\text{Cmax}} = 0.020$, and the *p* values of other PK parameters were less than 0.001) were significantly associated with the PKs of omeprazole. For *CYP2C19*17* (rs12248560), only $t_{1/2}$ showed a significant correlation (p = 0.032), whereas other PK parameters did not. The present study demonstrated that the Pks of omeprazole is greatly influenced by *CYP2C19*.

Study Highlights

WHAT IS THE CURRENT KNOWLEDGE ON THE TOPIC?

CYP2C19 is involved in the drug's metabolism and that poor metabolizers have a greater systemic exposure to omeprazole followed by intermediate and then extensive metabolizers.

WHAT QUESTION DID THIS STUDY ADDRESS?

This study aimed to examine the effect of *CYP2C19* polymorphisms on the pharmacokinetics parameters of omeprazole in healthy Chinese volunteers after a single dose by a large sample multicenter study.

WHAT DOES THIS STUDY ADD TO OUR KNOWLEDGE?

The present study demonstrated that the pharmacokinetics (AUC_{0-t}, AUC_{0- ∞}, C_{max} and t_{1/2}) of omeprazole is greatly influenced by *CYP2C19* (rs4244285, rs4986893 and rs1224856).

HOW MIGHT THIS CHANGE CLINICAL PHARMACOLOGY OR TRANSLATIONAL SCIENCE?

In the clinical application of omeprazole, attention should be paid to the effect of *CYP2C19* polymorphisms. If necessary, the clinical therapeutic dose of omeprazole should be guided base on the results of *CYP2C19* gene test.

INTRODUCTION

The commonly prescribed proton-pump inhibitor (PPIs) omeprazole is the first-line treatment against acid-related diseases, such as gastric and duodenal ulcers, gastroe-sophageal reflux disease, nonerosive reflux disease, and Zollinger–Ellison syndrome.¹ Omeprazole is extensively metabolized by the liver P450 cytochrome enzyme *CYP2C19*, whose second metabolic pathway is CYP3A4. Therefore, polymorphisms in *CYP2C19* may affect the pharmacokinetics (PKs) of omeprazole.^{2,3} Due to differences in hepatic enzyme activity, the PKs of omeprazole show extensive interindividual variability that may lead to poor predictability of treatment-related outcomes and adverse effects.⁴ Therefore, this study was conducted to evaluate the effect of CYP2C19 on the PKs of omeprazole in healthy Chinese volunteers.

Among more than 20 *CYP2C19* described alleles, the most frequent ones are *CYP2C19**2 (rs4244285, 681 G>A) and *CYP2C19**3 (rs4986893, 636 G>A), which encode nonfunctional proteins,^{5,6} whereas *CYP2C19**17 (rs12248560, -806 C>T) has been associated with increased metabolic activity.^{7,8} Individuals could be classed into four phenotypes according to the CYP2C19 genotype, as follows: CYP2C19 normal metabolizers (NMs) are characterized by the presence of two normal function alleles (CYP2C19 *1/*1); CYP2C19 intermediate metabolizers (Ims) are characterized by the presence of one normal function allele, and one no function allele (CYP2C19*1/*2 and CYP2C19 *1/*3), or one no function allele and one increased function allele (CYP2C19 *2/*17 and CYP2C19 *3/*17); CYP2C19 poor metabolizers (PMs) are characterized by the presence of two no function alleles (CYP2C19 *2/*2, CYP2C19 *3/*3, and CYP2C19 *2/*3); diplotypes, which are characterized by one normal function allele and one increased function allele (CYP2C19 *1/*17), are classified as rapid metabolizers (RMs).⁹ Previous studies have shown that the area under the concentration versus time curve (AUC) for PPIs is higher in Ims and PMs and lower in ultra metabolizers (UMs) than in extensive metabolizers (EMs) of CYP2C19 polymorphisms in White patients.¹⁰ Compared with African Americans (4%) and Whites (3%), the proportion of PMs in Chinese subjects is very high (17.4–35.0%).^{11,12} The contribution of CYP2C19 polymorphism to PK differences after omeprazole administration in Chinese has been mentioned before,¹³⁻¹⁵ but

the sample size of these studies was small (18–27 cases), and the subjects included in each single-center study were not representative enough. Therefore, a multicenter study with a larger sample size of Chinese people is needed to validate these findings.

The US Food and Drug Administration (FDA)approved drug label for omeprazole (PRILOSEC) notes that CYP2C19 is involved in the drug's metabolism and that PMs have a greater systemic exposure to omeprazole followed by Ims and then EMs.¹⁶ Moreover, the drug labels in Canada, Japan, and Switzerland contain information about the change in efficacy, dosage, and metabolism due to phenotypes.¹⁷ Meanwhile, the Clinical Pharmacogenetics Implementation Consortium (CPIC)¹⁸ and Royal Dutch Pharmacists Association - Pharmacogenetics Working Group (DPWG)¹⁹ have evaluated therapeutic dose recommendations for omeprazole based on CYP2C19 genotype. Patients who are CYP2C19 UMs should receive an increased (about 3-fold higher) dose. However, more data and clinical evidence are needed to update the above treatment recommendations and compensate for the missing data in the Chinese population.

The present study aimed to examine the effect of *CYP2C19* polymorphisms on the PK parameters of omeprazole in healthy Chinese volunteers after a single dose.

MATERIALS AND METHODS

Study design and subjects

Our study population included 656 healthy Chinese adult volunteers from eight single-dose bioequivalence clinical trials of omeprazole. In each original bioequivalence study, blood samples were collected during the period during which the subjects first took the reference preparation Losec and PK parameters AUC versus time curve (AUC_{0-t}), AUC from zero to infinity (AUC_{0-∞}), maximum plasma concentration (C_{max}), time to C_{max} (T_{max}), and terminal half-life ($t_{1/2}$) were calculated. The sample size, dosage, dietary status, blood sample collection time, and PK parameters of each bioequivalence clinical trial are listed in Table 1.

All subjects were found to be healthy on the basis of their physical examination, medical history, vital signs (blood pressure, pulse rate, and temperature), laboratory tests (blood chemistry, hematology, and urine analysis), and 12-lead electrocardiogram. Furthermore, the volunteers were not allowed to take drugs or medications during the study periods.

All these bioequivalence clinical trials were performed in hospitals of China between 2018 and 2020. Our study protocol was approved by the Ethics Committee of Peking University First Hospital as the leading center (No. 2018(21)) and the Ethics Committees of each bioequivalence clinical trials' hospital. Informed written consent was obtained from each subject. The present study was registered at the Chinese Clinical Trial Registry, with a registration number of No. ChiCTR1800016231.

Each subject received a single dose of omeprazole (Losec) with a glass of tap water. Venous blood samples were collected for analysis before dosing and at different times after drug administration. The samples were centrifuged at 1700–3000 g and 4°C, 10 mins after collection, and stored at less than or equal to 60°C.

Genotyping of CYP2C19 polymorphism

The gene detection methods included Sanger sequencing and Agena mass array. The Sanger sequencing process included DNA extraction, polymerase chain reaction (PCR) amplification, and sequencing by ABI3730 analyzer. Agena mass array single-nucleotide polymorphism (SNP) detection, which was performed according to the manufacturer's protocol, included PCR cycling program, shrimp alkaline phosphatase digestion, and single-base extension. Then, extension products were desalted and detected using matrix-assisted laser desorption ionization time-of-flight. Finally, the results were analyzed using TYPER 4.0 software (Agena Bioscience, San Diego, CA). The SNPs, primer sets, and probe sequences that were used in the above assay are shown in Table S1.

Allele frequencies for the variant SNPs were assessed for deviation from Hardy-Weinberg equilibrium using the chi-square test.²⁰ According to the hypothesis testing theory, the alpha value of the acceptance test should be higher or at least not lower than the alpha value of the refusal test. By convention, the value of α was determined as 0.05 in our study. The SNP loci that were in Hardy-Weinberg equilibrium were further analyzed for PKpharmacogenetics (PGx) correlation.

Determination of plasma concentrations and pharmacokinetics analysis

Plasma concentrations of omeprazole (sum of both enantiomers) were determined by ultra-high-performance liquid chromatography-tandem mass spectrometry. The noncompartmental method of Phoenix WinNonlin (Pharsight Co., Mountain View, CA) was used for the analysis of PK parameters.

The C_{max} and the T_{max} were directly estimated from the observed plasma concentration-time data. PK parameters determined after a single dose included the AUC_{0-∞}) and

TABLE 1Overview of subcenter

TADLI		Dietary	Sample		No. of blood	
No.	Subcenter name	status	size	Blood sample collection time	samples	PK parameters
Enteric	Capsules, 20 mg					
1	Jiangsu Province Hospital of Chinese Medicine	Fasting	50	0 h, 0.5 h, 0.75 h, 1 h, 1.25 h, 1.5 h, 1.75 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 6 h, 7 h, 8 h, 10 h, 12 h, 24 h	20	$\begin{array}{c} AUC_{0\text{-t}}, AUC_{0\text{-}\infty\text{+}}\\ C_{max}, T_{max,} t_{1/2} \end{array}$
		Fed	50	0 h, 0.75 h, 1 h, 1.5 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 7 h, 8 h, 10 h, 12 h, 14 h, 24 h	19	
2	The Third Xiangya Hospital of Central South University	Fasting	82	0 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 6.5 h, 7 h, 7.5 h, 8 h, 9 h, 10 h, 12 h, 14 h	18	$\begin{array}{c} AUC_{0\text{-}t}, AUC_{0\text{-}\infty},\\ C_{max}, T_{max}, t_{1/2} \end{array}$
		Fed	95	$\begin{array}{l} 0 \ h, 2 \ h, 2.5 \ h, 3 \ h, 3.5 \ h, 4 \ h, 4.5 \ h, \\ 5 \ h, 5.5 \ h, 6 \ h, 6.5 \ h, 7 \ h, 7.5 \ h, \\ 8 \ h, 9 \ h, 10 \ h, 12 \ h, 14 \ h, 16 \ h, \\ 24 \ h^b \end{array}$	20	
3	Shanghai Public Health Clinical Central	Fed	39	0 h, 0.25 h, 0.5 h, 1 h, 1.5 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 6.5 h, 7 h, 7.5 h, 8 h, 10 h, 12 h, 16 h, 24 h	24	$\begin{array}{c} AUC_{0\text{-t}}, AUC_{0\text{-}\infty},\\ C_{max}, T_{max}, t_{1/2} \end{array}$
4	Wuxi People's Hospital	Fed	58	0 h, 1 h, 1.5 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 7 h, 8 h, 9 h, 10 h, 12 h, 14 h, 16 h	19	$\begin{array}{c} AUC_{0\text{-t}}, AUC_{0\text{-}\infty},\\ C_{max}, T_{max,} \end{array}$
5	Wuhan Jinyintan Hospital	Fed	42	0 h, 0.5 h, 1 h, 1.5 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 6.5 h, 7 h, 8 h, 9 h, 10 h, 12 h, 24 h	20	$\begin{array}{c} AUC_{0\text{-t}},AUC_{0\text{-}\infty},\\ C_{max},T_{max},t_{1/2} \end{array}$
6	Hebei Hospital of Traditional Chinese Medicine	Fasting	40	0 h, 0.25 h, 0.5 h, 0.75 h, 1 h, 1.25 h, 1.5 h, 1.75 h, 2 h, 2.25 h, 2.5 h, 2.75 h, 3 h, 3.33 h, 3.67 h, 4 h, 4.33 h, 4.67 h, 5 h, 5.5 h, 6 h, 8 h, 10 h, 12 h	24	$\begin{array}{c} AUC_{0\text{-}t},AUC_{0\text{-}\infty},\\ C_{max},T_{max,},t_{1/2} \end{array}$
		Fed	37	0 h, 1 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 6.5 h, 7 h, 7.5 h, 8 h, 9 h, 10 h, 11 h, 12 h, 13 h, 14 h, 15 h, 16 h, 18 h	24	
Enteric	tablets, 20 mg					
7	The Second Affiliated Hospital Zhejiang University School of Medicine	Fed	44	0 h, 0.5 h, 1 h, 1.5 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 6 h, 7 h, 8 h, 10 h, 12 h	16	$\begin{array}{c} AUC_{0\text{-}t}, AUC_{0\text{-}\infty},\\ C_{max}, T_{max,}, t_{1/2} \end{array}$
8	The Third Xiangya Hospital of Central South University ^a	Fasting	82	0 h, 0.5 h, 0.75 h, 1 h, 1.25 h, 1.5 h, 1.75 h, 2 h, 2.25 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 6 h, 8 h, 10 h, 12 h	19	$\begin{array}{c} AUC_{0\text{-}t},AUC_{0\text{-}\infty},\\ C_{max},T_{max},t_{1/2} \end{array}$
		Fed	37	0 h, 1.5 h, 2 h, 2.5 h, 3 h, 3.5 h, 4 h, 4.5 h, 5 h, 5.5 h, 6 h, 6.5 h, 7 h, 7.5 h, 8 h, 10 h, 12 h, 14 h	18	

Abbreviations: AUC_{0-t} , area under the concentration versus time curve; $AUC_{0-\infty}$, AUC from zero to infinity; C_{max} , maximum plasma concentration; NA, not available; PK, pharmacokinetic; T_{max} , time to C_{max} ; $t_{1/2}$, terminal half-life.

^aThe same subcenter, but another form.

^bForty-five cases did not collect blood samples of 16 h and 24 h.

 $t_{1/2}$. Due to the different design of blood sampling points in the two subcenters, AUC_{0-t} was not included in the PK-PG correlation study, and AUC_{0-∞} was used instead.

Statistical analysis

TABLE 2 The frequencies of SNPs and results of the Hardy-Weinberg tests

The PK-PG correlation analyses were performed using SPSS version 25.0 (SPSS, Chicago, IL). Subjects were grouped according to the detection results of a single SNP, genotypes, or metabolic phenotypes. The Mann-Whitney U test was used to evaluate the significance of differences in PK parameters between the two genotypic groups. Data from three or more different genotypic groups were compared using the Kruskal-Wallis H test. The significance of the differences in PK parameters (including C_{max} , T_{max} , $t_{1/2}$, T_{max} AUC_{0-t}, and AUC_{0-∞}) among different SNPs, genotypes, and metabolic phenotypes were determined, and the subgroup analyses were performed according to

dosage form and dietary status. Any p less than 0.05 was considered to be statistically significant.

RESULTS

CYP2C19 polymorphism distribution

The allele frequencies and genotype frequencies are shown in Table 2. The gene mutation frequencies of *CYP2C19**2 (rs4244285, 681G>A), *CYP2C19**3 (rs4986893, 636G>A), and *CYP2C19**17 (rs12248560, -806C>T) were 31.1%, 5.56%, and 0.84%, respectively. Hardy-Weinberg equilibrium test results showed that all the detected SNPs were in Hardy-Weinberg equilibrium (p > 0.05, Pearson test). The distributions of diplotype and phenotypic frequencies of *CYP2C19* are summarized in Table 3. The assignment of predicted *CYP2C19* phenotype based on genotype was referred to as CPIC guidance.¹⁸

SNP	Allele	Number of cases (%)	Genotype	Number of cases (%)	Pearson's P
CYP2C19*2	G	904 (68.9)	GG	322 (49.09)	0.054
	А	408 (31.1)	GA	260 (39.63)	
			AA	74 (11.28)	
CYP2C19*3	G	1239 (94.44)	GG	585 (89.18)	0.981
	А	73 (5.56)	GA	69 (10.52)	
			AA	2 (0.3)	
CYP2C19*17	С	1301 (99.16)	CC	645 (98.32)	0.829
	Т	11 (0.84)	СТ	11 (1.68)	

Abbreviation: SNPs, single-nucleotide polymorphisms.

TABLE 3	The distributions of diplotype	and phenotypic frequen	cies of CYP2C19
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Metabolic phenotypes	The definition of metabolic phenotypes	Sample size (n, %)	Diplotypes	Sample size (n, %)
RM	An individual carrying one normal function allele and one increased function allele	6 (0.91)	*1/*17	6 (0.91)
NM	An individual carrying two normal function alleles	263 (40.09)	*1/*1	263 (40.09)
IM	An individual carrying one normal function	294 (44.82)	*1/*2	241 (36.74)
	allele and one no function allele or one		*1/*3	48 (7.32)
	increased function allele and one no function allele		*2/*17	2 (0.30)
	function ancie		*3/*17	3 (0.46)
РМ	An individual carrying two no function	93 (14.18)	*2/*2	74 (11.28)
	alleles		*2/*3	17 (2.59)
			*3/*3	2 (0.30)

Abbreviations: IM, intermediate metabolizer; NM, normal metabolizer; PM, poor metabolizer; RM, rapid metabolizer.

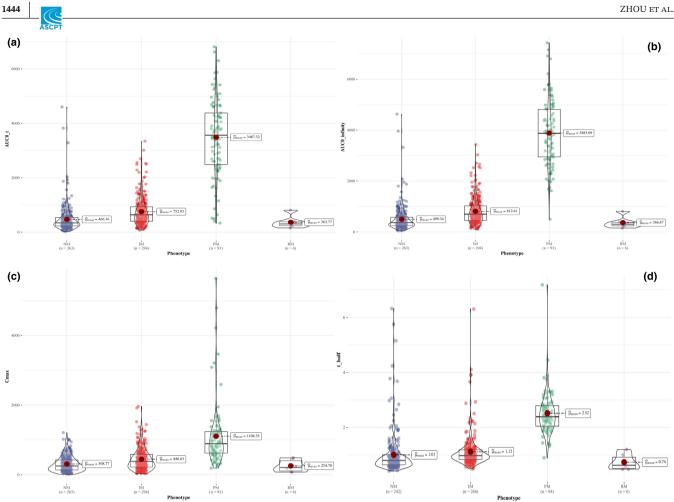


FIGURE 1 Scatter plot of omeprazole pharmacokinetic parameters according to diplotype (a) area under the concentration versus time curve (AUC_{0.t}), (b) AUC from zero to infinity (AUC_{0- ∞}), (c) maximum plasma concentration (C_{max}), (d) time to C_{max} (T_{max}), (e) terminal halflife $(t_{1/2})$

Effect of CYP2C19 polymorphism on pharmacokinetics

The differences of AUC_{0-t}, AUC_{0- ∞}, C_{max}, and t_{1/2} among GG, GA, and AA of CYP2C19*2 (rs4244285) were significantly different (AUC0-t, AUC0- ∞ , C_{max}, and t_{1/2} were all p < 0.001), whereas there was no statistically significant difference in T_{max} (p = 0.092). The relative AUC_{0-t}, $AUC_{0-\infty}$, C_{max} , and $t_{1/2}$ value in the GG, GA, and AA were 1:1.86:6.47, 1:1.83:6.68, 1:1.48:3.40, and 1:1.18:2.46, respectively. The differences in AUC_{0-t}, AUC_{0- ∞}, C_{max}, and t_{1/2} among GG, GA, and AA of CYP2C19*3 (rs4986893) were statistically significant ($pc_{max} = 0.02$, the other p < 0.001), whereas there was no statistically significant difference in T_{max} (p = 0.998). The relative AUC_{0-t}, AUC_{0- ∞}, C_{max}, and $t_{1/2}$ value in the GG, GA, and AA were 1:1.55:4.09, 1:1.56:4.25, 1:1.25:1.88, and 1:1.18:2.32, respectively. For CYP2C19*17 (rs12248560), compared with CC, only the reduction in $t_{1/2}$ was statistically significant in the CT group (p = 0.032), whereas the decreases in AUC_{0-t}, AUC_{0-∞}, C_{max}, and T_{max} were not statistically significant $(pAUC_{0-t} = 0.141, pAUC_{0-\infty} = 0.108, pC_{max} = 0.278 \text{ and}$ $pT_{max} = 0.135$). The mean (\pm SD) PK parameters of every SNP are summarized in Table S2.

The AUC_{0-t}, AUC_{0- ∞}, C_{max}, and t_{1/2} of nine diplotype groups were significantly different (all p < 0.001), but the T_{max} was not (p = 0.098), The difference was summarized in Figure 1. The relative AUC_{0- ∞} values in the *1/*17, *1/*1, *3/*17, *2/*17, *1/*3, *1/*2, *2/*2, *2/*3, and *3/*3 were 0.73, 1, 1.10, 1.39, 1.62, 1.64, 7.59, 8.45, and 8.90, respectively. AUC_{0-t}, C_{max} , and $t_{1/2}$ also followed this trend. The T_{max} value was achieved at 1.33–4.60 h after administration in all subjects. The mean $(\pm SD)$ PK parameters of omeprazole in the nine diplotype groups are summarized in Table 4 and the pairwise comparisons of each group are shown in Table S3. In the pairwise comparisons of AUC_{0-t} , AUC_{0- ∞}, C_{max}, and t_{1/2}, *1/*2, *2/*2, *1/*3, and *2/*3 vs *1/*1, *2/*2 and *2/*3 vs *1/*2, *2/*2, and *2/*3 vs *1/*3, *2/*2, and *2/*3 vs *1/*17 were significantly different.

Compared with NM CYP2C19 *1*1, the AUC_{0-t}, AUC_{0- ∞}, C_{max}, and t_{1/2} of IMs and PMs were significantly increased, whereas they were decreased in the RM group.

The difference is summarized in Figure 2. The relative AUC_{0-t} value in the RM, NM, IM, and PM was 0.78, 1, 1.61, and 7.48, the relative AUC_{0-∞} value in the RM, NM, IM, and PM was 0.73, 1, 1.63, and 7.78, the relative C_{max} value in the RM, NM, IM, and PM was 0.83, 1, 1.45, and 3.58, and the relative t_{1/2} value in the RM, NM, IM, and PM was 0.73, 1, 1.11, and 2.50, respectively. The T_{max} value was achieved at 3.89–4.45 h after administration in all groups. The PK parameters of omeprazole in the four phenotype groups are summarized in Table 5, and the pairwise comparisons of each group are shown in Table S3. In the pairwise comparisons, the AUC_{0-∞} of the PM group significantly differed from all other groups ($p_{PM-RM} < 0.001$, $p_{PM-NM} < 0.001$, and $p_{PM-IM} < 0.001$), and the IM and NM groups also significantly differed ($p_{IM-NM} < 0.001$).

Subgroup analysis of different dietary states

Of the 656 healthy subjects included in the study, 254 took omeprazole on an empty stomach (no food intake within 8 h), and 402 took omeprazole after a high-fat meal. The PK parameters between the fasted group and the fed group are shown in Table S4. The differences in PK parameters between the fasting and postprandial groups were significantly different. The same results were obtained in fasted and fed subgroups. There were statistically significant differences in AUC_{0-t} (p < 0.001), AUC_{0- ∞} (p < 0.001), C_{max} (p < 0.001), and t_{1/2} (p < 0.001) among the different CYP2C19 phenotypes, whereas there were no statistically significant differences in T_{max} ($p_{fasted} = 0.553$ and $p_{fed} = 0.287$) among the different CYP2C19 phenotypes. The PK parameters of the different metabolic phenotypes in each subgroup are shown in Table S5.

Subgroup analysis of different drug dosage forms

Of the 656 healthy subjects, 537 were taking enteric-coated capsules, and 119 were taking enteric-coated tablets. The differences in PK parameters between the fasting and postprandial groups were significantly different (Table S4). The same results were obtained in enteric-coated capsules and tablets subgroups. There were statistically significant differences in AUC_{0-t} (p < 0.001), AUC_{0-∞} (p < 0.001), C_{max} (p < 0.001), and t_{1/2} (p < 0.001) among the different CYP2C19 phenotypes, but there was no significant difference in T_{max} ($p_{enteric-coated capsules} = 0.107$ and $p_{enteric-coated tablets} = 0.601$) among the different CYP2C19 phenotypes. The PK parameters of different metabolic phenotypes in each subgroup are shown in Table S6.

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	n^*1/n^1 ($n=263$)	n^*1/n^2	n^*1/n^3 ($n = 48$)	(n=6)	$^{*}2/^{*}3$ $(n=17)$	*2/*2 $(n = 74)$	$*^{3/*17}$ (<i>n</i> = 3)	*2/*17 (<i>n</i> = 2)	*3*3 (n = 2)	<i>p</i> value
AUC _{0-t} , h*ng/ml	466.2 ± 493.2	466.2 ± 493.2 766.4 ± 529.4	707.8 ± 490.3	363.8 ± 232.6	3908 ± 1560	3379 ± 1421	544.8 ± 14.52	507.3 ± 150.3	3913 ± 493.0	0.000*
$AUC_{0-\infty}, h^*ng/ml$	499.3 ± 498.4	499.3 ± 498.4 817.8 ± 524.4	808.0 ± 545.9	366.5 ± 233.4	4221 ± 1453	3790 ± 1311	547.0 ± 14.47	693.0 ± 109.6	4444 ± 793.4	0.000*
C _{max} , ng/ml	309 ± 227	449 ± 309	440 ± 390	255 ± 180	1040 ± 550	1130 ± 992	310 ± 129	530 ± 344	884 ± 575	0.000*
$t_{1/2}$, h	1.01 ± 0.76	1.01 ± 0.76 1.12 ± 0.62	1.41 ± 0.71	0.74 ± 0.29	2.54 ± 0.70	2.51 ± 0.82	0.86 ± 0.13	0.90 ± 0.09	2.88	0.000*
Abbreviations: AUC, area under the curve: C maximum plasma concentration: t biological half-life: T time to reach maximum plasma concentration.	der the curve: C	maximum plasma c	oncentration: t. /3. b	iological half-life: T	time to reach	maximum plasma c	concentration.			

The difference was statistically significant (p < 0.05)

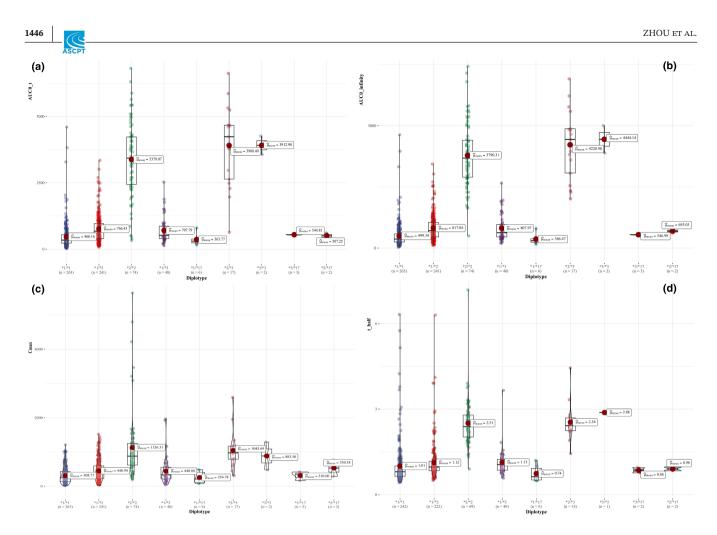


FIGURE 2 Scatter plot of omeprazole pharmacokinetic parameters according to phenotype (a) area under the concentration versus time curve (AUC_{0-t}), (b) AUC from zero to infinity (AUC_{0- ∞}), (c) maximum plasma concentration (C_{max}), (d) time to C_{max}(T_{max}), (e) terminal half-life (t_{1/2})

	RM (<i>n</i> = 6)	NM (<i>n</i> = 263)	IM (<i>n</i> = 294)	PM (<i>n</i> = 93)	p value
AUC _{0-t} , h*ng/ml	363.77 ± 232.56	466.16 ± 493.21	519.18 ± 752.83	3487.32 ± 1440.13	0.000*
1331.02 AUC _{0-∞} , h*ng/ml	366.47 ± 233.42	499.34 ± 498.44	812.61 ± 523.39	3883.09 ± 1331.02	0.000*
C _{max} , ng/ml	254 ± 180	308 ± 227	447 ± 322	1110 ± 916	0.000*
t _{1/2} , h	0.74 ± 0.29	1.01 ± 0.76	1.12 ± 0.60	2.52 ± 0.79	0.000*

 TABLE 5
 Pharmacokinetic parameters of omeprazole (mean ± SD) according to CYP2C19 phenotype

Abbreviations: AUC, area under the curve; C_{max} , maximum plasma concentration; IM, intermediate metabolizer; NM, normal metabolizer; PM, poor metabolizer; RM, rapid metabolizer; $t_{1/2}$, biological half-life; T_{max} , time to reach maximum plasma concentration.

^{*}The difference was statistically significant (p < 0.05).

DISCUSSION

In the present study, we found significant differences in the AUC_{0-t}, AUC_{0- ∞}, C_{max}, and t_{1/2} of omeprazole in healthy Chinese volunteers with different genotypes. This multicenter, large sample study examined the effect of *CYP2C19* polymorphisms on the PK parameters of omeprazole in healthy volunteers.

Herein, we investigated the correlation between PG and PK based on a bioequivalence study. The bioequivalence

study of generic drugs has been widely carried out in China over recent years. There are multiple pharmaceutical companies conducting bioequivalence studies for generic drugs at the same stage. According to the policy requirements of China, the reference drugs for a bioequivalence study of generic drugs should be selected from the "Reference Listed Drug for Generic Drugs." For omeprazole in the present study, the generic reference drug from different manufacturers is Losec (AstraZeneca UK Limited). Herein, we used an opportunity to include the bioequivalence study of omeprazole conducted across eight different pharmaceutical companies as a subcenter and successfully obtained a large sample size of 656 volunteers. To the best of our knowledge, this is the largest such study to date. This is an innovation in research methodology and organizational form with Chinese characteristics, which can verify the effect of gene polymorphisms on PKs in more subjects with lower cost, shorter time, and better quality. Conducting genetic polymorphism studies with healthy subjects has many advantages, such as controlling for confounding factors, like disease and drug interactions, reducing the effect of individual differences, and providing a more realistic and accurate correlation to PG and PK.

The CYP2C19 phenotypes tend to differ in relation to race. Loss of CYP2C19 *2, CYP2C19 *3, and other functiona, which are responsible for PM alleles, is mainly found in Asians.²¹ CYP2C19 *2 has an allele frequency of 25-30% in Asians, about 15% in Europeans and Africans, and about 60% in Oceanians.^{9,18} The allele frequency of CYP2C19 *2 in our study is 31.1%, which is consistent with the 1000 Genomes and previous reports.²² CYP2C19 *3 has an allele frequency of about 15% in Oceanians, 0.04% in Whites,²² and 2–7% in Asians,⁹ which allele frequency is 5.56% in our study. The increased function allele CYP2C19 *17 is most common in European, African, and Near Eastern populations, with an allele frequency of about 20%.^{9,23} However, the allele frequency in our study of Chinese participants is only 0.84%. PM status has been found in 2.5-3.5% of Whites, 2% of American Blacks, and ~20% of Asians.²² Of the 656 subjects enrolled in this study, the proportion of PM status was 11.59%. Therefore, it is still necessary to carry out a study with a large sample size in the Chinese population to clarify the correlation between omeprazole PK characteristics and CYP2C19 in the Chinese population, regardless of previous studies conducted in other populations.

The classification of *CYP2C19* predicted phenotypes in this study was defined according to the latest CPIC guidelines.⁹ Compared with the historical classification, the main change lies in the attribution of *1/*17. This classification is more scientific, detailed, and clear than the DPWG guidelines²³ and previous studies of the same type.¹⁵

Our results showed a statistically significant difference in the PK parameters AUC_{0-t} , $AUC_{0-\infty}$, C_{max} , and $t_{1/2}$ of different *CYP2C19* metabolizers after oral administration of 20 mg omeprazole in healthy Chinese volunteers. These findings are consistent with previous studies that have reported on populations including European, Saharan, and Asian populations.^{8,24–26} Of these, the most representative was the $AUC_{0-\infty}$ that reflects the extent of drug clearance, which was significantly increased in PM, 9.6, 7.5, and 6.5 times in RM, NM, and IM, respectively. This result, which is consistent with previous studies,²⁷ complements the relevant data of the NM group as well as more PK parameters. The C_{max} of the response drug efficacy and safety was also significantly increased in PM, 4.4-fold RM, 3.6-fold NM, and 2.5-fold IM, respectively. When grouped according to different genotypes, the AUC_{0-t}, AUC_{0-∞}, C_{max}, and t_{1/2} were also significantly different, which is consistent with the results of a previous study in a White population.⁷

The present study has some limitations. First, the efficacy of omeprazole was not evaluated. As a drug that inhibits gastric acid secretion, this study failed to evaluate and analyze intragastric PH or symptom relief as an effective outcome for more clinical application value. Second, we obtained PK parameters rather than all plasma concentration test results, thus failing to visually show the concentration-time curve of different genotypes and broader the population-by-population PK modeling.

In conclusion, our study demonstrated that the PKs of omeprazole is greatly influenced by CYP2C19 in Chinese healthy subjects. In the clinical application of omeprazole, attention should be paid to the effect of CYP2C19 polymorphisms.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

S.Z., R.X., and X.Z. wrote the manuscript. Y.C., X.Z., and Q.X. designed the research. X.Z., X.H., J.H., J.Y., M.L., Y.D., D.Y., Y.L., Q.Z., G.Y., F.L., S.G., Q.H., H.L., F.G., and X.M. performed the research. S.Z., R.X., and Q.X. analyzed the data. Q.X. and Y.C. contributed new analytical tools.

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1448

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SUPPORTING INFORMATION

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