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Published in:
Clinical and Translational Science (Print)

DOI:
10.1111/cts.12423

Publication date:
2016

Document version
Publisher's PDF, also known as Version of record

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Citation for published version (APA):

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ARTICLE

Population Pharmacokinetics of Methylphenidate in Healthy Adults Emphasizing Novel and Known Effects of Several Carboxylesterase 1 (CES1) Variants

YK Lyauk1−∗, C Stage2, TK Bergmann3,4, L Ferrero-Milliani5, D Bjerre5, R Thomsen6, KP Dalhoff7, HB Rasmussen5 and G Jürgens1

The aim of this study was to identify demographic and genetic factors that significantly affect methylphenidate (MPH) pharmacokinetics (PK), and may help explain interindividual variability and further increase the safety of MPH. d-MPH plasma concentrations, demographic covariates, and carboxylesterase 1 (CES1) genotypes were gathered from 122 healthy adults and analyzed using nonlinear mixed effects modeling. The structural model that best described the data was a two-compartment disposition model with absorption transit compartments. Novel effects of rs115629050 and CES1 diplotypes, as well as previously reported effects of rs71647871 and body weight, were included in the final model. Assessment of the independent and combined effect of CES1 covariates identified several specific risk factors that may result in severely increased d-MPH plasma exposure.


Study Highlights

WHAT IS THE CURRENT KNOWLEDGE ON THE TOPIC?

✔ Large unexplained IIV is observed in the PK of MPH. The CES1 SNP rs71647871 GA has been reported to substantially increase MPH plasma exposure. The effect of CES1 diplotypes on MPH metabolism is unknown.

WHAT QUESTION DID THIS STUDY ADDRESS?

✔ First, this study developed a d-MPH population PK model that included the effects of CES1 variants and demographic covariates. Second, the model was used to assess the independent and combined effects of covariates on d-MPH plasma exposure.

WHAT THIS STUDY ADDS TO OUR KNOWLEDGE

✔ This analysis reveals the effects of rs115629050 TG and CES1 diplotypes on d-MPH PK. It also confirms the effect of rs71647871 GA and body weight. Additionally, it illustrates the considerable d-MPH plasma exposure increases caused by the independent or combined presence of CES1 variants.

HOW THIS MIGHT CHANGE CLINICAL PHARMACOLOGY OR TRANSLATIONAL SCIENCE

✔ These findings may eventually contribute to the quantitative guidance of individual dosing recommendations based on specific CES1 variants or variant combinations, and lead to increased safety with MPH.

Methylphenidate (MPH), a central nervous system stimulant, is the most commonly prescribed drug for the treatment of patients with attention deficit hyperactive disorder.1,2 It is also prescribed for other conditions, such as narcolepsy in adults as well as depression in the elderly and patients with advanced illness.3−5 A significant increase in MPH prescription has occurred in developed countries over recent years.6−8

The pharmacokinetics (PK) of MPH have been reported to display large unexplained interindividual variability (IIV)9−11 and certain studies indicate a 30-fold difference in MPH serum concentrations 1 h postdose12 and up to a sevenfold difference in maximal concentrations.13 The study of MPH PK is relevant from a clinical perspective due to significant correlation between MPH concentration and clinical response.14,15 Furthermore, a linear relationship between MPH dose and the development of adverse effects has been reported,16 and, hence, MPH-related adverse effects may be concentration-dependent. Adverse effects during MPH treatment are common and are in the majority of cases categorized as mild to moderate.17 They include insomnia, anorexia, anxiety,16 as well as cardiovascular effects in terms of increases in heart rate and blood pressure.18,19 However, due to their sympathomimetic activity,20 case reports of serious adverse

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[Correction added on 1 November 2016, after first online publication: The supporting information was updated].

Received 26 May 2016; accepted 5 September 2016; published online on 18 October 2016. doi:10.1111/cts.12423
effects, such as sudden cardiac death, stroke, myocardial infarction, and hypertension, have raised concerns regarding stimulants’ cardiovascular safety.\textsuperscript{21,22} It has been hypothesized that pharmacogenetic factors may predispose certain individuals to a higher risk of harmful adverse effects during treatment and, hence, further research that may lead to increased safety with MPH has been encouraged.\textsuperscript{17}

Human metabolism of MPH is predominantly mediated by carboxylesterase 1 (CES1), a serine esterase, which des-esterifies MPH to ritalinic acid in the liver.\textsuperscript{23} Approximately 80% of orally administered MPH is recovered in urine as ritalinic acid, whereas minor metabolites of MPH or ritalinic acid each account for a nonsignificant amount.\textsuperscript{24} In recent years, differences in CES1 have been found to affect the PK of several drugs metabolized by CES1, in particular MPH.\textsuperscript{13,25-27} A nonsynonymous single nucleotide polymorphism (SNP), rs71647871 GA (p.Gly143Glu) with a reported frequency of 3.7% in Caucasians, has been identified to significantly influence MPH PK.\textsuperscript{13} It has been found to cause a reduction in the catalytic activity of CES1; consequently, MPH metabolism is reduced and substantially elevated MPH plasma exposure is observed in carriers.\textsuperscript{13} Apart from the aforementioned, no studies have yet been able to identify other CES1 SNPs that impact MPH PK. Considering the crucial role of CES1 in MPH metabolism, it is plausible that additional CES1 SNPs that impact MPH PK may exist. In addition to CES1 SNPs, CES1 gene structure has also been found to influence the PK of CES1-metabolized drugs. A study involving the CES1-metabolized compound, irinotecan, has shown the presence of CES1A2 to have a significant effect on its PK,\textsuperscript{28} and it is therefore of interest to investigate the impact of CES1A2 on MPH metabolism. CES1A2 is a hybrid gene with a reported allele frequency of 14.4% in Caucasians consisting of the upstream portion of the nonfunctional pseudogene CES1P1 (also referred to as CES1A3) and a duplicated segment of CES1.\textsuperscript{29} The latter is commonly designated CES1A1 to distinguish it from CES1A2. One of three possible CES1 diplotypes can be present in a given individual: two CES1A1 and two CES1P1, which is the most frequent; two CES1A1, one CES1P1, and one CES1A2; or two CES1A1 and two CES1A2.\textsuperscript{30}

Until now, studies that have reported an association between CES1 variants and MPH PK have done so while focusing on one variant at the time through noncompartmen-tal methods, and have therefore not considered any potential combined variant effect. This is of interest to investigate given that CES1 variants resulting in altered drug metabolism may be due to SNPs and potentially structural CES1 differences. Use of population PK modeling for assessing the impact of genetics on drug PK holds several advantages. Covariate model development was performed using a simultaneous analysis of the effects of several demographic and/or genetic covariates, as well as clinical trial simulation, which may illustrate the risk associated with a particular effect or combination of effects.\textsuperscript{31} Furthermore, in the presence of nonlinearity or variability in drug bioavailability, model-based phenotype allows a higher probability to detect SNP effects than other phenotypes.\textsuperscript{32} Presently, population-based analyses of MPH are few\textsuperscript{9,33,34} and none have, to this date, included CES1 variants as covariates, despite their reported effect on MPH metabolism\textsuperscript{13} and the metabolism of other CES1-metabolized compounds.\textsuperscript{28} Therefore, the aim of this work is to build on recent CES1 pharmacogenetic findings and develop an MPH population PK model, which (i) identifies significant effects of demographic covariates as well as different types of CES1 variants on PK parameters and their IIV, and (ii) can determine the independent and potential combined effects of covariates on MPH plasma exposure.

METHODS

PK data from two previously conducted clinical studies (NCT02135263 and NCT02147535) at Bispebjerg Hospital, Copenhagen, Denmark, were aggregated for analysis. Both study protocols were reviewed and approved by an ethical review board. The studies were conducted in accordance with all applicable regulatory and Good Clinical Practice guidelines and followed the ethical principles originating in the Declaration of Helsinki. All participants were fasting overnight and MPH was administered 1 h following a standardized breakfast. Two participants did not receive the standard meal due to lactose intolerance and a food delivery issue. Study I involved 44 healthy adult volunteers who were administered a single dose of 10 mg MPH (Ritalin; Novartis, Basel, Switzerland). Plasma samples from each subject were collected predose and 0.5, 1, 1.5, 2, 2.5, 3, 4, 6, 8, 10, 24, and 33 h postdose. Study II involved 78 healthy adult volunteers who were administered a single dose of 10 mg MPH (Ritalin), followed by the collection of a single plasma sample from each subject 3 h postdose. All subjects were Caucasians and their demographic characteristics are presented in detail in Supplementary Table S1. All participants were CES1 genotyped using DNA extracted from saliva samples. Details regarding the genetic analysis are presented in the Supplementary Material, along with the genetic characteristics of participants in the two studies (Supplementary Table S2).

$d$-MPH and $l$-MPH plasma concentration analysis is described in the Supplementary Material. Population PK modeling was performed using nonlinear mixed-effects modeling software (NONMEM, version 7.3; ICON Development Solutions, Ellicott City, MD) and the first-order conditional estimation with interaction method. In total, 503 $d$-MPH plasma concentrations collected from 122 healthy adults were analyzed and handling of data below the quantification limit is presented in the Supplementary Material. Model development procedure and criteria are presented in detail in the Supplementary Material. The following covariates were investigated: body weight, body mass index, gender, and a total of nine CES1A1 SNPs that result in nonsynonymous amino acid substitutions in CES1, as well as CES1 diplotypes. Covariate model development was performed using a stepwise procedure with a forward inclusion $p$ value $< 0.05$ (objective function value [OFV] decrease $> 3.841$, 1 degree of freedom) and a backward elimination $p$ value $< 0.005$ (OFV increase $> 7.879$, 1 degree of freedom). In order to explore the effect of CES1 variants in which subjects in the studied population presented missing genotype data, methods for handling missing covariate data were considered. As
Figure 1 Schematic diagram of the structural d-methylphenidate (MPH) pharmacokinetic model along with model-incorporated covariates. d-MPH passes through three transit compartments (TCs) into an absorption compartment, where it is absorbed into the central compartment and distributed to the peripheral compartment. d-MPH undergoes elimination from the central compartment to d-ritalinic acid (CL/F). kₜᵢᵣ is the transit rate constant and is defined as (number of TCs + 1) divided by mean transit time. kₐᵢ is the absorption rate constant. V_d_central/F and V_d_peripheral/F represent apparent central and peripheral volumes of distribution, respectively. Q/F is the apparent inter-compartmental clearance. Dotted circles and arrows indicate covariates and the parameters they affect, respectively. CES1, carboxylesterase 1.

RESULTS

The final d-MPH PK model was a two-compartment model with absorption transit compartments and first-order elimination from the central compartment. The parameter estimation process and covariance step both converged successfully using the first-order conditional estimation method with interaction. Three significant digits were requested in the parameter estimates. The structural model along with PK parameters and covariates that influence them are shown in Figure 1. The final parameter estimates are shown in Table 1, along with nonparametric 95% confidence intervals obtained through bootstrapping. The estimated number of transit compartments was originally 3.05 (data not shown) but was fixed to the value of 3.0 in subsequent models to aid model stability and successful convergence. No significant changes to the model fit and parameter estimates were observed doing so. IIV was estimated for apparent oral clearance (CL/F), central volume of distribution (V_d_central/F), and mean transit time (MTT) in a full variance-covariance matrix, containing both diagonal and nondiagonal elements. A proportional error model was used to describe unexplained residual variability.

The final model included allometrically scaled body weight using a fixed value of 0.75 for CL/F and apparent inter-compartmental clearance (Q/F) and 1 for V_d_central/F and apparent peripheral volume of distribution (V_d_peripheral/F). Estimation of allometric exponents for these parameters was evaluated; however, no significant change in OFV or parameter estimates was obtained. The effects of the CES1 genetic covariates rs71647871, rs115629050, and CES1 diplotypes were included on CL/F. Genotype information regarding CES1 diplotypes, rs71647871, and rs115629050 was missing in 0.8%, 5%, and 42%, respectively, of the total studied population. Missing data were considered as being missing not at random and was handled using the EXTRA (or EST) method.

Gender was included on MTT due to the improvement of model fit assessed through decrease of OFV and improvement of visual diagnostics. Incorporation of the aforementioned covariates reduced the OFV by 104.3 points, reduced unexplained CL/F IIV by 15.0%, and increased the proportion of explained CL/F IIV to total CL/F IIV from zero.
to 50.1% compared with the base model without covariates. OFV drop, CL/F IIV reduction, and proportion of explained CL/F IIV to total CL/F IIV increase for the stepwise addition of each covariate is shown in Table 2. The two model-included CES1A1 SNPs, rs71647871 and rs115629050, were not correlated as observed in a linkage disequilibrium analysis (Supplementary Figure S1) and both could therefore be incorporated in the model. Permutation testing results for the model-inclusion of covariates are shown in Supplementary Table S3.

The equations that describe the typical values of the final model parameters are:

\[
\begin{align*}
\text{MTT} &= \theta_1 \times (1 + \text{Gender} \times \theta_b) \\
\text{CL/F} &= \theta_4 \times (1 + \text{rs71647871} \times \theta_b) \\
&\quad \times (1 + \text{One CES1A2} \times \theta_1) \\
&\quad \times (1 + \text{Two CES1A2} \times \theta_2) \\
&\quad \times (1 + \text{rs115629050} \times \theta_14) \\
&\quad \times \left(\frac{\text{WT}}{70}\right)^{0.75}
\end{align*}
\]

\[
\begin{align*}
\text{Vd_{central}/F} &= \theta_b \times \left(\frac{\text{WT}}{70}\right) \\
\text{Q/F} &= \theta_b \times \left(\frac{\text{WT}}{70}\right)^{0.75} \\
\text{Vd_{peripheral}/F} &= \theta_7 \times \left(\frac{\text{WT}}{70}\right)
\end{align*}
\]

The variables Gender, rs71647871, rs115629050, one CES1A2, and two CES1A2 are equal to zero and take on the value of one for individuals that possess the gender or genotype reported in Table 1. WT represents the body weight of the individual subject. Goodness of fit plots and a visual predictive check for the final model are shown in Figures 2 and 3, respectively.

Results of the Monte-Carlo simulations highlighting the independent effects of each model-incorporated covariate on d-MPH plasma exposure are shown in Figure 4. Significant increases in d-MPH plasma exposure compared with a wild-type reference population were observed for carriers of rs71647871 GA (143%), two CES1A2 (70%), as well as rs115629050 TG (68%), whereas a minor increase was seen for carriers of one CES1A2 (22%). Populations consisting of 50 kg as well as 100 kg individuals were simulated to

Table 1 Final d-MPH population PK parameter estimates

<table>
<thead>
<tr>
<th>Model parameter</th>
<th>NONMEM estimate (RSE%)</th>
<th>Bootstrap estimate (RSE%)</th>
<th>Nonparametric (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Structural model</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(\theta_1): MTT ((/h))</td>
<td>0.505 (13.7)</td>
<td>0.521 (16.3)</td>
<td>(0.371–0.707)</td>
</tr>
<tr>
<td>(\theta_2): No. of transit compartments (fixed)</td>
<td>3</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>(\theta_3): (k_d) ((/h))</td>
<td>0.418 (18.8)</td>
<td>0.430 (134.0)</td>
<td>(0.370–1.304)</td>
</tr>
<tr>
<td>(\theta_4): CL/F ((/L/h))</td>
<td>233.0 (3.6)</td>
<td>231.7 (4.5)</td>
<td>(214.0–251.8)</td>
</tr>
<tr>
<td>(\theta_5): Vd_{central}/F ((/L))</td>
<td>97.6 (28.6)</td>
<td>101.8 (63.7)</td>
<td>(47.6–288.7)</td>
</tr>
<tr>
<td>(\theta_6): Q/F ((/L/h))</td>
<td>70.1 (47.8)</td>
<td>74.3 (38.7)</td>
<td>(49.9–175.3)</td>
</tr>
<tr>
<td>(\theta_7): Vd_{peripheral}/F ((/L))</td>
<td>252 (30.9)</td>
<td>260.7 (64.5)</td>
<td>(198.2–453.2)</td>
</tr>
<tr>
<td>Covariate effects</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(\theta_8): Female gender on MTT</td>
<td>0.925 (44.3)</td>
<td>0.852 (42.7)</td>
<td>(0.297–1.831)</td>
</tr>
<tr>
<td>(\theta_9): Missing data rs71647871 on CL/F</td>
<td>–0.587 (6.9)</td>
<td>–0.585 (8.8)</td>
<td>(–0.677 to –0.473)</td>
</tr>
<tr>
<td>(\theta_{10}): Missing data rs71647871 on CL/F</td>
<td>–0.157 (46.9)</td>
<td>–0.161 (54.6)</td>
<td>(–0.330 to –0.00164)</td>
</tr>
<tr>
<td>(\theta_{11}): One CES1A2 on CL/F</td>
<td>–0.182 (31.9)</td>
<td>–0.184 (36.8)</td>
<td>(–0.307 to –0.0475)</td>
</tr>
<tr>
<td>(\theta_{12}): Two CES1A2 on CL/F</td>
<td>–0.410 (22.5)</td>
<td>–0.408 (25.6)</td>
<td>(–0.583 to –0.192)</td>
</tr>
<tr>
<td>(\theta_{13}): Missing data CES1A diplotype on CL/F</td>
<td>–0.535 (8.0)</td>
<td>–0.533 (11.3)</td>
<td>(–0.663 to –0.440)</td>
</tr>
<tr>
<td>(\theta_{14}): rs115629050 (TG) on CL/F</td>
<td>–0.403 (26.1)</td>
<td>–0.399 (31.4)</td>
<td>(–0.714 to –0.180)</td>
</tr>
<tr>
<td>(\theta_{15}): Missing data rs115629050 on CL/F</td>
<td>0.090 (79.6)</td>
<td>0.0913 (86.8)</td>
<td>(–0.0623 to 0.262)</td>
</tr>
<tr>
<td>Weight exponent on CL/F (fixed)</td>
<td>0.75</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Weight exponent on Vd_{central}/F (fixed)</td>
<td>1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Weight exponent on Q/F (fixed)</td>
<td>0.75</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Weight exponent on Vd_{peripheral}/F (fixed)</td>
<td>1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>IIV (%CV)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MTT</td>
<td>62.1 (27.7)</td>
<td>60.8 (29.3)</td>
<td>(43.1–78.8)</td>
</tr>
<tr>
<td>CL/F</td>
<td>21.6 (15.4)</td>
<td>21.0 (17.6)</td>
<td>(17.3–24.4)</td>
</tr>
<tr>
<td>Vd_{central}/F</td>
<td>90.1 (27.1)</td>
<td>87.7 (38.5)</td>
<td>(54.7–123.5)</td>
</tr>
<tr>
<td>Residual variability</td>
<td>0.184 (9.6)</td>
<td>0.181 (10.2)</td>
<td>(0.144–0.218)</td>
</tr>
<tr>
<td>Proportional error</td>
<td>0.184 (9.6)</td>
<td>0.181 (10.2)</td>
<td>(0.144–0.218)</td>
</tr>
</tbody>
</table>

CES1, carboxylesterase 1; CI, confidence interval; CL/F, apparent oral clearance; CV, coefficient of variation; IIV, interindividual variability; MPH, methylphenidate; MTT, mean transit time; PK, pharmacokinetic; Q/F, apparent intercompartmental clearance; RSE, relative standard error; Vd_{central}/F, central volume of distribution. \(k_d\), absorption rate constant; NONMEM, non-linear mixed effects modeling software. 2,000 nonparametric bootstrap CI were generated.
Table 2: Effect of each included covariate on the objective function value, decrease in unexplained d-MPH apparent clearance (CL/F) IIV, and increase in explained d-MPH CL/F IIV

<table>
<thead>
<tr>
<th>Model</th>
<th>OFV decrease</th>
<th>Unexplained CL/F IIV decrease (% CV)</th>
<th>Explained CL/F IIV increase (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model A: Base model + body weight</td>
<td>20.068</td>
<td>1.6</td>
<td>10.2</td>
</tr>
<tr>
<td>Model B: Model A + rs71647871</td>
<td>38.874</td>
<td>8.6</td>
<td>19.3</td>
</tr>
<tr>
<td>Model C: Model B + rs115629050</td>
<td>15.888</td>
<td>2.3</td>
<td>10.5</td>
</tr>
<tr>
<td>Model D: Model C + gender</td>
<td>12.693</td>
<td>0.40</td>
<td>1.5</td>
</tr>
<tr>
<td>Final model: Model D + CES1 diplotype</td>
<td>16.820</td>
<td>2.1</td>
<td>8.6</td>
</tr>
</tbody>
</table>

CL/F, apparent oral clearance; CV, coefficient of variation; IIV, interindividual variability; MPH, methylphenidate; OFV, objective function value. Base model represents the final structural model without covariates. Unexplained CL/F IIV was assessed through NONMEM’s OMEGA output. Explained CL/F IIV was calculated as explained CL/F IIV divided by total CL/F IIV (total CL/F IIV being the sum of unexplained and explained CL/F IIV and is subject to change during model development), and explained and total parametric variability estimates were obtained from pvar in Perl-Speaks-NONMEM (PsN).

Figure 2: Diagnostic plots for the final d-methylphenidate (MPH) population pharmacokinetic model. Top left corner: Observed d-MPH plasma concentrations (DV) vs. population predictions (PRED). Top right corner: Observed d-MPH plasma concentrations (DV) vs. individual predictions (IPRED). Bottom left corner: Conditionally weighted residuals (CWRES) vs. PRED. Bottom right corner: CWRES vs. time after dose.

Explore the effect of low or high body weight, respectively, on d-MPH exposure. A 29% d-MPH exposure increase and 24% d-MPH exposure decrease was observed for individuals of 50 and 100 kg, respectively. However, differences in body weight did not alter the effects of the CES1 variants to a significant extent compared with their independent effects in 70 kg individuals (Supplementary Table S4 and Supplementary Figure S2).

The simulation results investigating the effect of the physiologically plausible simultaneous presence of two or more CES1 variants on d-MPH plasma exposure are shown in Figure 5. Twofold to sevenfold plasma d-MPH exposure increases resulting from different variant combinations were observed. In order to estimate the frequency of occurrence of CES1 variants as well as their plausible combined presence in individuals, a simulation of a large virtual population...
Figure 3 Visual predictive check for the final d-methylphenidate (MPH) population pharmacokinetic model. Solid lines represent the 5th, 50th, and 95th percentiles of the observed data. Dashed lines represent the 5th, 50th, and 95th percentiles of the simulated data. Shaded areas represent 95% confidence intervals around the 5th, 50th, and 95th percentiles of the simulated data.

Figure 4 Forest plot of the simulated independent effect of each model-included covariate. Effects are expressed as d-methylphenidate (MPH) plasma exposure (area under the curve \([AUC]_{0-\infty}\)) relative to a reference population (70-kilogram male adults, carrying the wild-type carboxylesterase 1 \([CES1]\) variants \(rs71647871\) GG, \(rs115629050\) GG, and no \(CES1A2\)). The independent effect of each covariate is investigated, keeping all other characteristics similar to the reference population. Median \([AUC]_{0-\infty}\), followed by 95% prediction intervals in brackets, are reported for each population, consisting of 5,000 virtual individuals.

Figure 5 Forest plot of the physiologically plausible simulated combined effects of model-included covariates. Effects are expressed as d-methylphenidate (MPH) plasma exposure (area under the curve \([AUC]_{0-\infty}\)) relative to a reference population (70-kilogram male adults, carrying the wild-type carboxylesterase 1 \([CES1]\) variants \(rs71647871\) GG, \(rs115629050\) GG, and no \(CES1A2\)). The combined effects of each covariate are investigated, keeping all other characteristics similar to the reference population. Median \([AUC]_{0-\infty}\), followed by 95% prediction intervals in brackets, are reported for each population, consisting of 5,000 virtual individuals.

\((n = 100,000)\) was performed (Supplementary Tables S5 and S6). It was found that approximately 4.1% of the total simulated population showed a d-MPH plasma exposure increase between twofold and threefold while carrying \(CES1\) variants or variant combinations. It is to be noted that 5.4% of individuals (234 of 4,339 subjects) presenting a plasma exposure increase between two to threefold were carriers of the wild-type \(CES1\) genotype (Supplementary Table S6). Furthermore, approximately 1.3% of the virtual population consisting of 100,000 individuals showed a larger than threefold plasma exposure increase while carrying \(CES1\) variants or combinations. In comparison, only 0.3% of the total simulated population showed a larger than threefold elevated d-MPH exposure while carrying the wild-type \(CES1\) genotype (Supplementary Table S6). Thus, these results indicate that a small minority of a given Caucasian population undergoing treatment with MPH may be predisposed to experience substantially higher d-MPH plasma exposure owing directly to specific \(CES1\) variants or variant combinations. Subsequently, such patients may potentially have a higher risk of adverse effects during MPH treatment.

DISCUSSION

This study is the first to examine the population PK of d-MPH while including effects of both demographic covariates and \(CES1\) variants. Model-based analyses investigating the PK
of MPH are limited and none have included information concerning CES1. Rs71647871 GA (p.Gly143Glu) was found to significantly reduce d-MPH apparent oral CL/F and this is in accordance with previously reported findings. Its effect has also been identified on the PK of several other CES1-metabolized drugs. Incorporation of rs71647871 was found to decrease d-MPH CL/F unexplained IV and increase explained CL/F IV to a greater extent than inclusion of other covariates. This indicates that rs71647871 is a very important covariate in determining MPH PK interindividual differences. The simulated independent presence of rs71647871 GA resulted in a 2.4-fold increase in d-MPH plasma exposure, and, hence, this variant could potentially be considered an adverse effect risk factor during MPH treatment.

This study found that rs115629050 TG (p.Ala270Ser) significantly reduces d-MPH CL/F and this is, to our knowledge, the first time this has been reported. Model incorporation of this variant was found to reduce unexplained and increase explained d-MPH CL/F IV to a reasonable level compared with the inclusion of other model-included covariates. Simulations showed that rs115629050 TG resulted in approximately 68% higher d-MPH plasma exposure in carriers compared with the wild-type genotype. The only current evidence, which supports the observed effect of this CES1A1 SNP, are in silico CES1 functional annotation predictions, performed using different software packages, and a total of nine different scoring methods (Supplementary Table S7). For rs115629050 TG, the scores were equal to or greater than those of rs71647871 GA in six of the nine approaches (Supplementary Table S8). However, in vitro studies regarding the impact of CES1 variants on a series of CES1-metabolized angiotensin-converting enzyme inhibitors have not been able to identify the effect of rs115629050 TG on drug metabolism. These conflicting results may arise from differences in CES1 affinity to the aforementioned angiotensin-converting enzyme inhibitors and MPH, resulting in a lack of effect of rs115629050 TG. Furthermore, it should be noted that extrapolation of in vitro results to clinical study observations is difficult. Additional studies need to be performed to confirm the effect of rs115629050 TG on CES1 activity and MPH PK.

CES1 diplootypes were associated with significantly lower estimates of d-MPH CL/F. Furthermore, model-inclusion of CES1 diplootypes decreased unexplained and increased explained d-MPH CL/F IV to a reasonable level compared with the other model-included covariates. Simulations indicated that two CES1A2 copies resulted in approximately 70% higher d-MPH plasma exposure in carriers compared with the wild-type genotype, whereas one CES1A2 copy yielded an approximately 22% increase. These findings are in conflict with those from a study with CES1-metabolized irinotecan, in which presence of CES1A2 resulted in an increase in systemic clearance. Additionally, a clinical PK study involving oseltamivir found no effect associated with CES1 diplootypes. Therefore, additional studies need to be performed to confirm the effect of CES1 diplootypes on CES1 activity and MPH PK.

Body weight was not found to alter the observed effects of model-included CES1 variants to a significant extent. This may imply that when adjusting dose according to weight, carriers of plasma exposure-increasing CES1 variants, included in the current study, may still experience significantly increased MPH plasma exposures, and potentially be in higher risk of adverse effects. A preliminary study investigating the body weight-based daily dose required for symptom reduction in patients with attention deficit hyperactive disorder, has shown that significantly lower MPH doses were needed in patients carrying rs71647871 GA compared with noncarriers. The completion of similar studies focusing on CES1 variants identified in this study is of interest to establish the clinical relevance of the findings.

To date, only rs71647871 GA has been reported to have significant impact on MPH PK, yet these findings have revealed that significant increases in d-MPH exposure may also occur due to other CES1 variants. Within a large population, it is possible for several genetic and/or demographic covariates to co-occur in individuals. Through simulation, it was observed that the simultaneous presence of several different CES1 variants may result in severe increases in d-MPH plasma exposure, ranging from twofold to sevenfold. Such elevated exposures may put patients in high risk of developing adverse effects, which could potentially be serious as well as sudden. In this context, diagnosed or undiagnosed preexisting conditions (e.g., congenital heart disease) may further contribute to the occurrence of such aforementioned events. In adults, a significant increase in the use of stimulants to treat attention deficit hyperactive disorder has been observed. Compared with children, adult patients may present risk factors that are more prevalent (e.g., coronary atherosclerosis, hypertension, smoking, or concomitant use of other drugs) and may, therefore, be predisposed to a higher risk of serious complications during treatment. A recent study has indicated a significant increase in risk of ventricular arrhythmia and sudden death in adults treated with MPH compared with nonusers, although it was not possible to determine a causal effect due to lack of a dose-response relationship. However, in light of the current study’s findings, it could hypothetically be more appropriate to consider a dose-concentration-response relationship, given that individuals with different genotypes may experience markedly different concentrations with the same dose. Despite the preliminary low incidence estimate of CES1 variant combinations that result in substantial exposure increases, it is important to consider the widespread use of MPH. Hence, the reported variants and combinations have cause to be taken into clinical consideration, along with the individual patient’s possible preexisting clinical risk or family history. It is important to note, however, that improvement of clinical outcome as well as cost-effectiveness need to be evaluated before routine pretreatment screening of patients’ CES1 genotype can be implemented in MPH treatment. Considering the high cost of genetic sequencing and reported low incidence estimates of risk factor CES1 variants in a large population, implementation of CES1 screening is not currently expected to be cost-effective; however, with evolving technology and decreasing prices of genetic assays, CES1 screening may be a viable tool in the future. Clinical implementation of CES1 testing could on the other hand potentially occur in specific cases (e.g., should specific patients...
exhibit unexpected dose-dependent adverse effects at standard therapeutic doses). In such cases, CES1 genotyping could be used as a diagnostic tool to clarify if patients are carriers of risk factor CES1 variants, and thereby help guide MPH dose adjustment.

In this study, large amounts of missing data were observed for several CES1A1 SNPs (Supplementary Table S2). Missing genotype data were in a large part due to a limitation of the genetic analysis, which is not able to provide sequence information downstream exon 5 in CES1A1 if CES1A2 is present. To the best of our knowledge, no assays currently exist that can overcome the limitation of the current method. The high sequence homology among CES1A1, CES1P1, and CES1A2 renders it difficult to develop methods that can differentiate between the three genes. Taking the aforementioned limitation of the genetic analysis into account, as well as the proportion of different missing genotypes, in this study, missing data were considered as being missing not at random. The EXTRA (or EST) method, which quantifies the effect of missing covariate data through full maximum likelihood modeling and adds a parameter for each covariate containing missing data, was therefore chosen due to its precise and unbiased parameter estimates when dealing with missing not at random data, as well as its ease of implementation in stepwise covariate procedures. Genotype information regarding rs115629050, located in CES1A1 exon 7, was found to be missing in 42% of the study population, which was high compared with the amount of missing data observed in the other final model-included CES1 variants. However, for low (10%) and high (50%) levels of missing categorical covariate data, the EXTRA method has been shown to perform similarly well, yielding estimates of PK parameters and covariate effects with adequately low bias and imprecision. Other limitations possibly include that all carriers of rs115629050 TG as well as a large part of single CES1A2 carriers were present in the very sparsely sampled study II (Supplementary Table S2), and this may have influenced accurate estimation of the effect of these variants on d-MPH CL/F. When analyzing sparse data containing missing covariate data, a higher bias/imprecision for the covariate effect magnitude may be observed. This may have implications for the simulation results in this study, and these should therefore be viewed as preliminary. However, concerning type I errors associated with final model-inclusion of these covariates, the actual significance levels for their exclusion from the final model were found to be lower than the threshold applied in this study (Supplementary Table S3). Therefore, rs115629050 and CES1 diplotype were ultimately kept in the final model. Furthermore, despite having applied methods for dealing with missing covariate data, it cannot be ruled out that the currently reported CES1A diplotype effect on d-MPH CL/F is caused by the presence of SNPs downstream CES1A1 exon 5 that affect MPH PK. Therefore, due to the previously mentioned conflicting findings with other CES1-metabolized drugs, possibly inaccurate/imprecise reported covariate effect magnitude, and possible presence of unidentifiable CES1A1 SNPs downstream exon 5 in subjects carrying CES1A2, additional studies are needed to confirm the effects of rs115629050 TG and CES1 diplotype on CES1 activity and MPH PK. Last, in light of the presented results, the need for novel genetic assays that are able to determine SNPs in all CES1A1 exons yet still distinguish CES1A1 from CES1A2, is greater than ever before. Additional study limitations are described in the Supplementary Material.

To conclude, the presented work has developed a population d-MPH PK model that includes the effects of CES1 variants. Novel effects of CES1 variants on MPH PK were revealed and require further investigation. This study has contributed to a better understanding of factors, which may be determinants of interindividual differences in MPH PK. Through additional studies, it may also contribute to the accurate estimation of variability in MPH response, as well as the risk of adverse effects, which in rare cases may be serious. Last, the need for novel and more informative CES1 assays has also been made clear.

Acknowledgments. The authors thank Paolo Denti and the Pharmacometrics Research Group at the Division of Clinical Pharmacology at the University of Cape Town, who generously supplied us with advice, guidance, and code examples during the model development process; Ron Keizer, for his input on missing covariate data handling and associated modeling; and Stefanie Hennig at the University of Queensland, Brisbane, Australia, for her input on explaining parametric variability.


Conflict of Interest. The authors declared no conflict of interest.

Source of Funding. The study was part of the Individualized Drug Therapy Based on Pharmacogenomics: Focus on Carboxylesterase 1 (INDICES) project, funded by grant 10-092792/DSF from the Danish Council for Strategic Research, Program Commission on Individuals, Disease, and Society.
A single nucleotide variation in the human carboxylesterase 1 (CES1) gene may influence the pharmacokinetics of methylphenidate (MPH). MPH is a central nervous system stimulant primarily used to treat attention deficit hyperactivity disorder (ADHD). The pharmacokinetics of MPH are affected by the CES1 genotype, which can result in increased or decreased MPH levels due to differences in drug metabolism. This variation can lead to differences in therapeutic response and side-effect profiles, particularly in terms of cardiovascular risk.

**References**


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