Individual Differences in Urinary Cotinine Levels in Japanese Smokers: Relation to Genetic Polymorphism of Drug-metabolizing Enzymes

Mihi Yang, Naoki Kunugita, Kyoko Kitagawa, Seung-Ho Kang, Brian Coles, Fred F. Kadlubar, Takahiko Katoh, Koji Matsuno, and Toshihiro Kawamoto

Department of Environmental Health [M. Y., N. K., K. K., T. K.], School of Health Science [T. K.], and Research Center for Common Use [K. M.], University of Occupational and Environmental Health, Kitakyushu 807-8555, Japan; Department of Preventive Medicine, Seoul National University, Seoul, 110-799, Korea [M. Y.]; Department of Statistics, Ewha Womans University, Seoul 120-750, Korea [S-H. K.]; and Division of Molecular Epidemiology, National Center for Toxicological Research, Jefferson, Arkansas 72079 [B. C.]

Abstract

Urinary cotinine, one of the main metabolites of nicotine, has been widely used as a biomarker for assessment of direct or passive exposure to cigarette smoke. However, there is wide variation of the cotinine level among smokers who smoke the same number of cigarettes. To use urinary cotinine as a proper exposure-biomarker for cigarette smoke, interindividual variations of cotinine formation must be considered. Therefore, we studied the effects of genetic polymorphisms in drug metabolic enzymes on urinary cotinine levels among 190 male Japanese smokers (ages 19–66 years; mean, 40.6 years). Genetic polymorphisms in cytochrome P-450 (CYP1A1, CYP2A6, CYP2E1), and aldehyde dehydrogenase 2 (ALDH2) were determined by analyzing DNA isolated from peripheral blood. Cotinine in morning spot urine was analyzed by high-performance liquid chromatography. Lifestyle, i.e., smoking, alcohol consumption, and intake of coffee or tea, was examined using a questionnaire. The number of cigarettes smoked and CYP2A6 polymorphism were significantly associated with the urinary cotinine level. Especially, the urinary cotinine levels was drastically lower in CYP2A6-deleted homozygous (CYP2A6*4/*4) subjects than in CYP2A6*I/allele-positive subjects. The polymorphism in the CYP2E1 5'-flanking region was related to the urinary cotinine level in intermediate smokers (who smoke 11–20 cigarettes/day; P < 0.01). Polymorphisms in CYP1A1 or ALDH2, and consumption of alcohol, coffee, or tea were not associated with the urinary cotinine level.

Introduction

Urinary cotinine levels have been widely used to assess direct or passive exposure to cigarette smoke, and as a motivation tool for smokers who are trying to stop smoking (1, 2). However, it is reported that there are variations in cotinine levels in smokers who smoke the same number of cigarettes (3). Thus, to use urinary cotinine as an accurate exposure-biomarker for smoking, the causes of variation in urinary cotinine levels should be determined.

One source of interindividual variation in the metabolism of xenobiotics is polymorphism of the genes that encode metabolic enzymes (4). Among the enzymes that are induced by smoking and involved in cotinine bioproduction, cytochrome P-450 IAI (CYP1A1), CYP2A6, CYP2D6, and CYP2E1 are known to be genetically polymorphic (5–9). In addition, lifestyle factors, e.g., alcohol drinking and coffee or tea consumption, may induce expression of these enzymes and affect nicotine metabolism. For example, CYP2E1 is known to be induced by alcohol intake (10–11). Furthermore, there is an association between alcohol consumption and genetic polymorphism in aldehyde dehydrogenase 2 (ALDH2) in Japanese populations (12).

Kitagawa et al. (5) reported that urinary cotinine excretion in CYP2A6-deleted homozygous subjects was approximately one-seventh that of individuals who were CYP2A6*1I-positive, indicating an effect of a genetic polymorphism on nicotine metabolism. This conclusion was based on a small population, and therefore we reported here a more extensive study to investigate the effects of lifestyle and genetic polymorphisms in the above mentioned metabolic enzymes on urinary cotinine levels.

Materials and Methods

Subjects. The study subjects were 190 male students and office workers who were current smokers living in southwestern Japan during 1997–1999, and who had smoked at least one cigarette during the 24 h before urine sampling. The mean age was 40.6 years (range, 19–66 years). Peripheral blood and morning spot urine specimens were collected from each study subject. One hundred forty-nine of the subjects filled out a questionnaire concerning lifestyle, i.e., smoking, alcohol consumption, coffee/tea intake, and dietary habits. All of the subjects gave their informed consent to be included in the study.

Analysis of Urinary Cotinine and Creatinine. Urinary cotinine was analyzed by the method described by Takeda et al. (13) with a minor modification. In brief, 1 ml of each urine sample was hydrolyzed with 0.33 ml of 3 N NaOH and extracted with 3 ml of CH3Cl. After centrifugation (1500 rpm for 5 min), 1.5 ml of the CH3Cl layer was transferred to an HPLC3.

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3 The abbreviation used is: HPLC, high-performance liquid chromatography.
vial and evaporated. The residue was dissolved in water and analyzed by HPLC (Hitachi L-6210 Intelligent Pump, 655A-40 Auto Sampler, 6554–52 Column Oven, L-4200 UV-VIS Detector, D-2500 Chromato-Integrator). HPLC parameters were as follows: column, TOSOH TSK-gel ODS-80TM; column temperature, 50°C; mobile phase, a mixture of acetonitrile/water (15/85) containing 20 mM potassium dihydrogen phosphate and 3 mM sodium 1-decanesulfonate (pH 4.5); flow rate, 1.0 ml/min. Absorbance was monitored at 254 nm.

**Determination of Genotypes.** Genomic DNA was isolated from the buffy coat fraction of each blood sample using an automated DNA extractor (Applied Biosystems Inc., Model 340A) after complete digestion with protease K. The genotyping of each metabolic enzyme was performed as follows. The genetic polymorphism of CYP1A1 in exon 7, which is the substitution of codon 462 [ATT (Ile) to GTT (Val)], was analyzed by the method described by Oyama et al. (14). Genotypes were classified as “Ile/Ile” (the dominant homozygote), “Ile/Val,” and “Val/Val” (the rare homozygote).

Genotypes of CYP2A6 were determined by the PCR-RFLP method developed by Kitagawa et al. (5). The alleles of CYP2A6 were classified into CYP2A6*1, CYP2A6*2, CYP2A6*3, and the deletion, CYP2A6*4.

The RsaI polymorphism of CYP2E1, which is attributable to substitution of C to T at nucleotide 1019 of the 5’ flanking region of the gene, was determined by the method of Kawamoto et al. (12), and classified as the predominant homozygous allele (c1/c1), the heterozygous allele (c1/c2), and the rare homozygous allele (c2/c2).

The genetic polymorphism of ALDH2 in exon 12, which consists of an amino acid substitution from Glu to Lys at codon 487, was classified into ALDH2*1/*1, ALDH2*1/*2, and ALDH2*2/*2 according to the method of Kawamoto et al. (15).

**Materials.** Cotinine was obtained from Aldrich Chem. Co. (Milwaukee, WI). Protease K, Taq polymerase, dNTPs, restriction enzymes (HincII, Mspl, Dael, XcmI, RsaI, and MboII) and other chemicals were purchased from Wako Pure Chemical Industries, Ltd. (Osaka, Japan).

**Statistical Analysis.** To study the correlation between urinary cotinine levels and number of cigarettes smoked, Spearman correlation analysis was used. Lifestyle and genotypes of the drug-metabolizing enzymes were quantified as follows: (a) alcohol, i.e., frequency of alcohol drinking: rare, 0; 0–1 day/week, 1; 2–4 days/week, 2; ≥5 days/week, 3; (b) coffee and tea: not taken, 0; 0–1 cup/day, 1; 1–2 cups/day, 2; ≥3 cups/day, 3; (c) CYP1A1: Ile/Ile, 0; Ile/Val or Val/Val, 1; (d) CYP2A6: *1/*1, *1/*4, or *1/unknown variant, 0; *4/*4, 1; (e) CYP2E1: c1/c1, 0; c1/c2 or c2/c2, 1; and (f) ALDH2: *1/*1, 0; *1/*2 or *2/*2, 1. We used Spearman rank correlation to study the significance of effects of lifestyle or genetic polymorphisms on urinary cotinine levels. The Mann-Whitney U test was used to compare urinary cotinine levels with the genotypes of CYP2A6 and CYP2E1.

**Results**

**Correlation between Extent of Smoking and Urinary Cotinine.** Urinary cotinine was significantly correlated with the number of cigarettes smoked (Fig. 1; Spearman correlation coefficient (Rho), 0.319; P = < 0.001). Correction for creatinine slightly improved the Rho value (r, 0.323). When we included nonsmokers who were in the same university or coworkers of the smoking subjects (n = 248) to the present study population, the Rho value was increased to 0.719.

The use of nicotine intake, i.e., “nicotine content × cig-

![Fig. 1. Relationship between urinary cotinine level and number of cigarettes smoked during the 24 h before urine sampling. Spearman Rho, 0.319; P < 0.001.](image-url)
between lifestyle or genetic polymorphisms and the urinary cotinine level, with adjustment for the number of cigarettes smoked. It shows that polymorphisms of CYP2A6 and CYP2E1 affect individual variation of the urinary cotinine level. Coffee or tea intake was associated with the number of cigarettes smoked (0.05, \( P < 0.1 \)); however, it was not significantly related to the urinary cotinine level. Because alcohol induces CYP2E1, we examined the effect of alcohol consumption on the relationship between CYP2E1 polymorphism and urinary cotinine. We found that among subjects who drank 2–4 days/week, the CYP2E1-c1/c2 or c2/c2 type subjects had higher urinary cotinine levels than c1/c1 type subjects (\( P < 0.051 \)); however, this trend was not seen among drinkers with other drinking habits.

On the other hand, alcohol consumption was associated with ALDH2 polymorphism, i.e., the ALDH2*1/*1 type subjects had higher alcohol consumption than the ALDH2*1/*2 or ALDH2*2/*2 type subjects (\( P < 0.001 \)). However, alcohol consumption was not associated with the number of cigarettes smoked or with the urinary cotinine level.

**Discussion**

**Relationship between Number of Cigarettes Smoked and Urinary Cotinine.** There have been several reports in which the correlation coefficient between urinary cotinine level and daily cigarette consumption varied from 0.39 to 0.99, and was generally greater than 0.75 (1, 19). However, one-half of the subjects in these reports were nonsmokers whose urinary cotinine levels were very low, near zero, or below the detection limit. On the other hand, a study that was restricted to smokers showed a correlation coefficient of 0.32 between the urinary cotinine level and the number of cigarettes smoked (20). This value is very similar to those determined in our study, i.e., 0.319 for Spearman’s Rho and 0.283 for the simple correlation coefficient (Fig. 1). When nonsmokers were included in our study, the correlation coefficient increased to 0.72, a value similar to that found in other studies in which the subjects included both smokers and nonsmokers. Thus, inclusion of nonsmokers results in a higher correlation coefficient between the number of cigarettes smoked and urinary cotinine.

These results indicate that, although urinary cotinine appears to distinguish smokers from nonsmokers, it is not a reliable quantitative measure of the extent of cigarette smoke exposure. In addition to cigarette smoking, some other factors appear to affect the level of urinary cotinine. These factors may include induction of nicotine metabolic enzymes in smokers (21). That is, heavy smokers metabolize nicotine primarily by pathways other than C-oxidation to cotinine, resulting in attenuation of the relationship between urinary cotinine and the number of cigarettes smoked.

### Table 1 Allele frequency of CYP1A1, CYP2A6, CYP2E1, and ALDH2 in the study subjects

<table>
<thead>
<tr>
<th>Gene</th>
<th>Total (%)</th>
<th>Genotype n (%)</th>
<th>Allele frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>CYP1A1</td>
<td>149 (100.0)</td>
<td>Ile/Ile 85 (57.0) Ile/Val 54 (36.3) Val/Val 10 (6.7)</td>
<td>0.752 0.248</td>
</tr>
<tr>
<td>CYP2A6</td>
<td>190 (100.0)</td>
<td><em>1 positive</em>1 181 (95.3) *1/*4 9 (4.7)</td>
<td>0.780 0.217 0.003*9</td>
</tr>
<tr>
<td>CYP2E1</td>
<td>190 (100.0)</td>
<td>c1/c1 118 (62.1) c1/c2 62 (32.6) c2/c2 10 (5.3)</td>
<td>0.784 0.216</td>
</tr>
<tr>
<td>ALDH2</td>
<td>149 (100.0)</td>
<td>*1/*1 84 (56.4) *1/*2 59 (39.6) *2/*2 6 (4.0)</td>
<td>0.762 0.238</td>
</tr>
</tbody>
</table>

* Subjects who have at least one *1 allele, *1/*1 or *1/*4 (one case was a heterozygote of *1 and an unknown variant allele).
* Allelic frequencies were computed by assuming that the Hardy-Weinberg equilibrium holds.

Fig. 2. Effects of CYP2A6 genetic polymorphism on the urinary cotinine level according to smoking status.
Factors That May Cause Individual Variation in Nicotine Intake. In addition to the number of cigarettes smoked, the time between the last cigarette and urine collection, the nicotine contents of different brands of cigarettes, the depth of inhalation of tobacco smoke and other details of smoking behavior may affect the nicotine intake. However, the use of "number of cigarettes smoked" rather than "(nicotine content) / (cigarettes smoked)" as a measure of nicotine exposure did not appear to be a confounding factor in this study. Although the presence of nicotine in foods such as eggplants, potatoes, and some tea plants has been reported (1, 22–23) and could pose a potential source of nicotine, these dietary sources of nicotine were not considered in this study as the levels are too small to significantly affect urinary cotinine levels in active smokers.

Rao et al. (21) reported that the individuals whose genotypes were CYP2A6*1/*2, CYP2A6*2/*2, or CYP2A6*1/*4 smoked fewer cigarettes than the CYP2A6*1/*1 type individuals but had the same intensity of smoking as CYP2A6*1/*1 individuals. They found individuals with CYP2A6 duplication, CYP2A6*1/*1 plus duplication, had an increase in smoking intensity. However, CYP2A6 polymorphisms did not affect smoking status in the present study, i.e., subjects smoked 21.5 ± 8.9 cigarette/day in the CYP2A6*1-positive group versus 16.2 ± 9.1 cigarette/day in the CYP2A6*4/*4 group.

Individual variability in the kinetics of nicotine metabolism may also contribute to individual differences in nicotine addiction or stimulation (24). However, lifestyle factors that induce metabolic enzymes, e.g., consumption of coffee, tea, or alcohol, did not affect the urinary cotinine level (Table 2). Thus, those lifestyle factors may not induce variation in cotinine bioformation.

Effect of Genetic Polymorphisms on Variation of Urinary Cotinine. Among the P450 enzymes, CYP2A6 was reported to have the highest nicotine C-oxidation activity at low nicotine concentration (25). In addition, we previously reported a remarkable decrease of urinary cotinine excretion in homozygously CYP2A6-deleted subjects (5). Moreover, the present study showed that the CYP2A6 genetic polymorphism is related to the urinary cotinine level adjusted for the number of cigarettes smoked (Table 2), and, thus, CYP2A6 genetic polymorphism is an indispensable biomarker if urinary cotinine is to be used for monitoring cigarette smoking.

![Fig. 3. Effects of CYP2E1 genetic polymorphism on urinary cotinine levels according to smoking status among CYP2A6*1-positive subjects.](chart.png)

### Table 2 - Relationship between lifestyle or genetic polymorphisms and urinary cotinine adjusted for cigarettes smoked per 24 hours

<table>
<thead>
<tr>
<th>Lifestyle or gene</th>
<th>Spearman’s Rho</th>
<th>P</th>
<th>Spearman’s Rho</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alcohol</td>
<td>0.113</td>
<td>0.136</td>
<td>0.129</td>
<td>0.089</td>
</tr>
<tr>
<td>Coffee/tea</td>
<td>0.059</td>
<td>0.513</td>
<td>0.071</td>
<td>0.430</td>
</tr>
<tr>
<td>CYP1A1</td>
<td>0.102</td>
<td>0.205</td>
<td>0.082</td>
<td>0.310</td>
</tr>
<tr>
<td>CYP2A6</td>
<td>-0.283</td>
<td>&lt;0.001*</td>
<td>-0.228</td>
<td>0.002*</td>
</tr>
<tr>
<td>CYP2E1</td>
<td>0.166</td>
<td>0.022b</td>
<td>0.132</td>
<td>0.068</td>
</tr>
<tr>
<td>ALDH2</td>
<td>-0.124</td>
<td>0.127</td>
<td>-0.057</td>
<td>0.485</td>
</tr>
</tbody>
</table>

*Statistical significance, P < 0.01.

bStatistical significance, P < 0.05.
(26). Similarly, individuals with the c2/c2 allele showed higher expression of CYP2E1 mRNA than c1/c1 type subjects (9). Moreover, our previous epidemiological study showed that CYP2E1-c1/c2 or c2/c2 subjects have higher naphthol bioformation than c1/c1 type subjects (2). Thus, the c2 allele can be considered as a predictor of “rapid” CYP2E1-mediated oxidation activity, probably because of increased transcription of the gene. In the present study, in intermediate smokers, higher urinary cotinine levels were found in CYP2E1-c1/c2 or c2/c2 subjects than in c1/c1 subjects (Fig. 3). When alcohol consumption, an inducer of CYP2E1, was considered, there were also higher urinary cotinine levels in CYP2E1-c1/c2 or c2/c2 subjects than in c1/c1 subjects among intermediate (2–4 days/week) drinkers. These results are the first demonstration that genetic polymorphism in the CYP2E1 5′-flanking region affects nicotine metabolism; however, this effect was not seen among nondrinkers, light (0–1 day/week), or heavy (>5 days/week) drinkers. Thus, to clarify the effects of CYP2E1 polymorphism on cotinine biotransformation, additional studies would be required in a larger number of subjects.

On the other hand, there was no relationship between polymorphism of CYP1A1 or ALDH2 and urinary cotinine. Thus, CYP1A1, and ALDH2 are not likely to play important roles in cotinine bioproduction.

Recently, genetic polymorphisms in the dopamine transporter (SLC6A3) and D2 dopamine receptor (DRD2) have been reported to influence the initiation of smoking and nicotine dependence (27). In addition to these two polymorphisms, CYP2A6 and CYP2E1 polymorphisms may induce individual variability in smoking cessation or nicotine addiction, because they affect cotinine biotransformation.

In addition to genetic polymorphisms, there may be several other factors that cause interindividual variability in nicotine metabolism. For example, metabolism of cotinine to 3-hydroxycotinine (23), enzyme induction by diet or smoking itself, and variation in urinary pH could affect urinary cotinine biotransformation. These are potential variables that should be addressed in future studies.

In summary, the effects of lifestyle and genetic polymorphisms of drug metabolic enzymes on the urinary cotinine level were studied in male Japanese smokers. The number of cigarettes smoked and the CYP2A6 polymorphism were significantly associated with the urinary cotinine level. Polymorphism in the CYP2E1 5′-flanking region also affected the urinary cotinine level, particularly in intermediate smokers who smoked 11–20 cigarettes/day. Thus, interindividual variability in nicotine metabolism appears to be an important factor that limits the quantitative application of urinary cotinine as a biomarker of tobacco smoke exposure.

References
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