Short Communication

Close Association of UGT1A9 IVS1+399C>T with UGT1A1*28, *6, or *60 Haplotype and Its Apparent Influence on 7-Ethyl-10-hydroxycamptothecin (SN-38) Glucuronidation in Japanese

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ABSTRACT:

The anticancer prodrug, irinotecan, is converted to its active form 7-ethy10-hydroxycamptothecin (SN-38) by carboxylesterases, and SN-38 is inactivated by UDP-glucuronosyltransferase (UGT1A1)-mediated glucuronidation. UGT1A9 also mediates this reaction. In a recent study, it was reported that the UGT1A9 IVS1+399 (I399C>T) polymorphism is associated with increased SN-38 glucuronidation both in vitro and in vivo. However, its role in UGT1A9 expression levels and activity is controversial. Thus, we evaluated the role of I399C>T in SN-38 glucuronidation using 177 Japanese cancer patients administered irinotecan. I399C>T was detected at a 0.63 allele frequency. This polymorphism was in strong linkage disequilibrium (LD) with UGT1A10, UGT1A7, UGT1A9, and UGT1A10, known to glucuronidate SN-38 (Gagné et al., 2002; Saito et al., 2007).

The UGT1A gene complex consists of 9 active first exons including UGT1A10, I9A, I7A, and I1A (in this order) and common exons 2 to 5. One of the 9 first exons can be used in conjunction with the common exons (Tukey and Strassburg, 2000). The UGT1A1 N-terminal domains (encoded by the first exons) determine substrate-binding specificity, and the C-terminal domain (encoded by exons 2 to 5) is important for binding to UDP-glucuronic acid. The 5’- or 3’-flanking region of each exon 1 is presumably involved in regulation of its expression. Substantial interindividual differences have been detected in mRNA and protein levels and enzymatic activity of the UGT1A isofoms (Fisher et al., 2000; Saito et al., 2007).

SN-38 glucuronidation is thought to be mediated mainly by UGT1A1, and its genetic polymorphisms affecting irinotecan pharmacokinetics and adverse reactions have been already identified. The TA-repeat polymorphism, −54−39(A/T), TAA>A(TA), TAA (UGT1A1*28 allele), is associated with lower promoter activity, resulting in reduced SN-38 glucuronidation (Beutler et al., 1998; Iyer et al., 1999). The single nucleotide polymorphism (SNP) 211G>A (Gly71Arg, *6 allele), found mainly in East Asians, causes reduced protein expression levels and SN-38 glucuronidation activity (Gagné et al., 2002; Jinno et al., 2003). Another SNP in the enhancer region of UGT1A1, −3279T>G (*60 allele), is also a causative factor for reduced expression (Sugatani et al., 2002). Allele frequencies have been reported for *28 (0.09–0.13), *6 (0.15–0.19), and *60 (0.26–0.32) in Japanese and Chinese populations and for *28 (0.30–0.39), *6 (*0), and *60 (0.44–0.55) in whites (Saito et al., 2007).

In a previous study, in the Japanese population, we defined haplotype *28 as the haplotype harboring the *28 allele, haplotype *6 as that harboring the *6 allele, and haplotype *60 as that harboring the *60 allele (and without the *28 or *6 allele) (Sai et al., 2004; Saeki et al., 2006). Note that most of the *28 haplotypes concurrently harbored the *60 alleles, and that the *28 and *60 alleles were exclusively present on the different chromosomes (Sai et al., 2004; Saeki et al., 2006). We have also revealed that the haplotype *28, *6, or *60 was associated with reduced SN-38 glucuronidation (SN-38G/SN-38 area under concentration-time curve (AUC) ratios, an in vivo parameter for UGT1A activity) and decreased in SN-38 AUC/ dose were apparent (P < 0.0001), these effects were no longer observed after stratified patients by UGT1A1*6, *28, or *60 haplotype. Thus, at least in Japanese populations, influence of I399C>T on SN-38 glucuronidation is attributable to its close association with either UGT1A1*6, *28, or *60.

Irinotecan is an important drug for treatment of various tumors including lung, colon, and gastric (Smith et al., 2006). The infused drug is metabolized to its active form 7-ethyl-10-hydroxycamptothecin (SN-38) by carboxylesterases, and SN-38 is inactivated by glucuronidation. At least four UDP-glucuronosyltransferase (UGT) isoforms, namely UGT1A1, UGT1A7, UGT1A9, and UGT1A10, are known to glucuronidate SN-38 (Gagné et al., 2002; Saito et al., 2007).

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ABBREVIATIONS: SN-38, 7-ethyl-10-hydroxycamptothecin; UGT, UDP-glucuronosyltransferase; SNP, single nucleotide polymorphism; SN-38G, SN-38 glucuronide; AUC, area under concentration-time curve; I399, UGT1A9 IVS1+399; LD, linkage disequilibrium.

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SN-38 glucuronidation activity by this SNP is significant among subjects without UGTA1A*28. Sandanaraj et al. (2008) have also reported that I399C/C patients showed higher SN-38 AUC than C/T and T/T patients. With the same UGTA1A diplootypes, patients with I399TT (and UGTA9 −126_−118T>C>T G) have shown higher SN-38G Cmax than I399CT (and T>C>T G) patients. UGTA9*1b (UGTA9 −126_−118T>C>T G) has been shown to have no effect on UGTA9 expression levels (Girard et al., 2006; Ramirez et al., 2007; Sandanaraj et al., 2008). Thus, two groups did suggest that I399T allele was associated with higher glucuronidation activity. However, using human liver microsomes, Ramirez et al. (2007) showed that I399C/T had no significant effect on both UGTA9 mRNA levels and glucuronidation activities for two UGTA9 substrates. Therefore, the roles of I399C>T in UGTA9 activities as well as SN-38 glucuronidation remain inconclusive.

In the present report, we reveal the linkage of I399C>T with UGTA1A, UGTA7, and UGTA9 polymorphisms and analyze its association with the SN-38G/SN-38 AUC ratio and SN-38 AUC/dose (per dose) to clarify its role in SN-38 glucuronidation.

Materials and Methods

Patients. One hundred and seventy-seven patients (data for one patient was unavailable) were described previously (Saeki et al., 2006). Hardy-Weinberg equilibrium were determined previously (Saeki et al., 2006). Genotyping and Haplotype Analysis. Genomic DNA was extracted from whole blood of 177 irinotecan-administered patients (Saeki et al., 2006). UGTA9 IVS1+399C>T (rs2741049) was genotyped using the TaqMan SNP Genotyping Assay kit (C_9096281_10) according to the manufacturer’s instructions (Applied Biosystems, Foster City, CA). The UGTA1A*28 allele (−54_−39A(TA)2, TAA>A(TA)2, TAA), UGTA9*6 allele [211G>A (Gly71Arg)], UGTA9*60 allele (−3279T>G), UGTA7*2 haplotype [387T>G, 391C>A and 392G>A (Asn129Lys and Arg131Lys)], UGTA7*3 haplotype [387T>G, 391C>A, 392G>A, and 622T>C (Asn129Lys, Arg131Lys, and Trp208Arg)] and UGTA9*1b allele (−126_−118T>C>T G) were determined previously (Saeki et al., 2006). Hardy-Weinberg equilibrium analysis of I399C>T, linkage disequilibrium (LD) analysis of the UGTA9, UGTA7, and UGTA9 polymorphisms, and haplotype estimation with an expectation-maximization algorithm were performed using SNPAlyze version 7.0 software (Dynacom, Chiba, Japan).

Pharmacokinetics. Pharmacokinetic data for the 176 irinotecan-treated patients (data for one patient was unavailable) were described previously (Minami et al., 2007). In brief, heparinized blood was collected before irinotecan administration and at 0, 0.33, 1, 2, 4, 8, and 24 h after the first and second infusion of irinotecan. SN-38 and SN-38G plasma concentrations were measured by high-performance liquid chromatography, and AUC was calculated using the trapezoidal method in WinNonlin version 4.01 (Pharsight, Mountain View, CA).

Statistical Analysis. Gene dose effects of I399C>T and UGTA9 haplotypes (*28, *6, *60) were assessed by the Jonckheere-Terpstra test using StatExact version 6.0 (Cytel Inc., Cambridge, MA). Multiplicity adjustment was conducted with the false discovery rate. The significant difference was set at p = 0.05 (two-tailed).

Results

Linkages of UGTA9 IVS1+399 (I399C)>T with Other Polymorphisms. In our patients, I399C>T was detected at a 0.636 allele frequency, which is almost the same as those in the HapMap data (rs2741049) for Japanese (0.663) and Han Chinese (0.633) populations, but higher than those for Europeans (0.383) and Sub-Saharan Africans (Yoruba) (0.417). Genotype distribution for this SNP was in Hardy-Weinberg equilibrium (p = 0.418). LD analysis was performed between I399C>T and the previously determined genotypes, UGTA9*1b, UGTA7*2 and *,3, and UGTA1A*28, *6, and *60, which were detected at >0.1 frequencies in Japanese populations (Saeki et al., 2006). When assessed by the ID’s value, I399C>T was in complete LD with UGTA7 387T>G, 391C>A and 392G>A (UGTA7*2, ID’ = 1.000); in strong LD with UGTA9 −126_−118T>C>T G (UGTA9*1b, 0.987), UGTA7 622T>C (UGTA7*3, 0.977), and UGTA9 211G>A (UGTA9*6, 0.864); and in moderate LD with UGTA9 −3279T>G (UGTA9*60, 0.554), but weakly associated with UGTA9 −34_−39A(TA)2, TAA>A(TA)2, TAA (UGTA9*28, 0.252). In r2 values, the I399C>T was in strong LD with UGTA7*2 (r2 = 0.976) and UGTA9*1b (0.916), in moderate LD with UGTA7*3 (0.478), but weak in LD with UGTA9*6 (0.261) and UGTA1A*60 (0.208), and in little LD with UGTA1A*28 (0.018).

Haplotypic Analysis. Haplotype analysis was performed using the 9 polymorphisms including I399C>T. As shown in Fig. 1, 95% (123/129) of the I399C alleles were linked with the UGTA9 −126_−118T>A alleles, and 100% (225/225) of the T alleles were linked with the T alleles (UGTA9>1b). The associations of I399C alleles were completely (129/129) linked with the UGTA7 387T>G, 391A, and 392A alleles. The 40% (51/129) and 60% (78/129) of the I399C alleles were linked with UGTA9*2 and UGTA7*3 haplotypes, respectively. We also found that 98% (126/129) of the I399C alleles were linked with the UGTA9>1b allele (UGTA1A*6, 211G>A), *28 (54_−39A(TA)2, TAA>A(TA)2, TAA) or *60 (−3279T>G). According to the UGTA9 haplotype definition by Sai et al. (2004), 42% (54/129), 36% (46/129), 19% (25/129) and 1% (1/129) of the I399C alleles were linked with the UGTA9 haplotypes *6a (harboring *6 allele), *60a (harboring *60 allele), *28b (harboring *60 and *28 alleles), and *28d (harboring *28 allele), respectively. On the other hand, 85% (191/225) of the T alleles were linked with the UGTA1A wild-type haplotype *1.

Association Analysis. The associations of I399C>T with irinotecan pharmacokinetic parameters were then analyzed using the estimated haplotypes. First, association with SN-38G/SN-38 AUC ratio, an in vivo parameter of UGTA1A activity (Sai et al., 2004; Minami et al., 2007; Sandanaraj et al., 2008), was analyzed. UGTA7*2 had unchanged activity for SN-38 glucuronidation (Gagné et al., 2002), and neither UGTA9*1b nor UGTA9*3 had significant effects on the SN-38G/SN-38 AUC ratio in this study (Minami et al., 2007). On the other hand, the UGTA1A*6, *28, and *60 haplotypes were associated with the reduced SN-38G/SN-38 AUC ratios (Minami et al., 2007). Although effects of the haplotype *28 and *6 were more striking, haplotype UGTA1A*60, harboring only the *60 allele without the *28 allele, was weakly associated with the reduced ratio. To remove even this weak effect and clarify the real effect of I399C>T, UGTA1A*60 was also considered as low-activity haplotype in this analysis. Namely, we analyzed the associations of I399C>T with the AUC ratio within the groups stratified by the UGTA9 haplotypes, UGTA1A*28 (*28b and *28d), *6 (*60a), and *60 (*60a) (combined and shown as UGTA1A*4+).
increase in the SN-38G/SN-38 AUC ratio was observed \( (p < 0.0001, \text{Jonckheere-Terpstra test}) \) (Fig. 2A). However, this trend was obviously dependent on biased distributions of UGT1A1 haplotypes; e.g., 96% of the I399C/C patients were homozygotes for UGT1A1*28, *6, or *60, and “UGT1A1*28, *6, or *60”-dependent reduction of SN-38G/SN-38 AUC ratio was found within the I399T/T genotypes \( (p < 0.05) \). As shown in Fig. 2B, UGT1A1*28, *6, or *60 (UGT1A1*)-dependent reduction in the SN-38/GSN-38 ratio was observed when patients were stratified by these three haplotypes. However, no significant effect of I399C>T was found within the stratified patients \( (p > 0.05 \text{ within the } \sim/-, \sim/+, or +/- patient group in Fig. 2B) \). As for SN-38 AUC/dose (SN-38 AUC values adjusted by the doses used), a similar UGT1A1 haplotype dependence was observed. Although the I399T-dependent reduction of SN-38 AUC/dose was detected \( (p < 0.0001) \), biased distributions of the UGT1A1*28, *6, or *60 were again evident, and the UGT1A1 + haplotypes-dependent increase was significant within the I399 C/T and T/T patients \( (p < 0.01 \text{ and } p < 0.05, \text{respectively}) \) (Fig. 2C). Moreover, no significant effect of I399C>T on SN-38 AUC/dose was found when stratified by the UGT1A1 haplotypes \( (p > 0.05 \text{ within the } \sim/-, \sim/+, or +/- patient group in Fig. 2D) \).

**Discussion**

In the present study, LD between I399C>T and UGT1A1, UGT1A7, or UGT1A9 polymorphisms in Japanese populations was shown for the first time. Moreover, the apparent effect of I399C>T on SN-38 glucuronidation in Japanese cancer patients was suggested to result from its close association with UGT1A1*28, *6, or *60. As for the influence of I399C>T on UGT1A9 activity, conflicting results have been reported. Girard et al. (2006) have shown that I399C>T was associated with increased UGT1A9 protein levels and enzyme activity toward an UGT1A9 probe drug propofol using 48 human liver microsomes derived mainly from whites. In contrast, using human liver microsomes from 46 white subjects, Ramírez et al. (2007) have revealed that the I399C>T had no significant effects on UGT1A9 mRNA levels and in vitro glucuronidation activities toward the two UGT1A9 substrates, flavopiridol and mycophenolic acid. Furthermore, another report has demonstrated that I399C>T had no influence on the pharmacokinetic parameters (such as AUC and C_{max}) of mycophenolic acid in 80 Japanese renal transplant recipients (Inoue et al., 2007). Thus, these latter two studies did suggest that the I399C>T polymorphism has no effect on UGT1A9 enzymatic activity. Note that, at least for Japanese populations, no study has reported that I399C>T affects UGT1A9 activity.

As for the influence of I399C>T on SN-38 glucuronidation, a possible enhancing effect has been suggested. Girard et al. (2006) have shown an increasing effect of I399C>T on SN-38 glucuronidation, and that this SNP did not show any close linkages with the UGT1A1*28 or *60 allele \( (r^2 < 0.06) \). In addition, Sandanaraj et al. (2008) have reported that in 45 Asians consisting of Chinese (80%), Malay (18%), and others (2%), I399C/C patients had higher SN-38 AUC than C/T and T/T patients. Again, this SNP was not in LD with UGT1A1*28, *6, or *60 allele \( (r^2 > 0.09) \). Furthermore, association of I399T with increased SN-38G C_{max} has been observed even after stratified patients by UGT1A1 genotypes, although the study sample size was small. These findings suggest that the I399T
allele was associated with increased glucuronidation activity for SN-38 without linkages with the UGT1A1 polymorphisms. Our data demonstrate that an increase in SN-38G/SN-38 AUC ratio (i.e., increased glucuronidation activity) was also found with I399C/H11022; however, after stratified patients by the UGT1A1*6, *28, or *60 haplotypes (haplotype+/+), homozygotes or compound heterozygotes for either UGT1A1*28, *6, or *60; +/+, homozygotes or compound heterozygotes for either UGT1A1*28, *6, or *60; B and D, UGT1A1−/−, −/+, and +/+ patients were further divided by I399 C/C, C/T, and T/T genotypes. Gene dose effects of I399C>T and the UGT1A1+ haplotype were assessed by the Jonckheere-Terpstra test.

In irinotecan therapies, genetic polymorphisms leading to increases in SN-38 AUC, which closely correlates with increased risk of severe neutropenia (Minami et al., 2007), are clinically important. The current study also demonstrated no significant influence of I399C>T on SN-38 AUC/dose after stratified patients by UGT1A1 haplotypes. Consistent with this finding, no influence of this SNP was observed on the incidence of grade 3 or 4 neutropenia after irinotecan therapy in our population (data not shown). Recently, genetic testing of UGT1A1*6 and *28, which are related to severe neutropenia in Japanese populations, has been approved for clinical application in Japan. This study indicates that there is no clinical necessity for additional genotyping of I399C>T, at least in Japanese populations.

In conclusion of this study, the apparent influence of I399C/T on SN-38 glucuronidation is attributable to its close association with UGT1A1*6, *28, or *60 in the Japanese population. Furthermore, additional genotyping of I399C>T for personalized irinotecan therapy seems to be clinically irrelevant for Japanese populations.

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