CASE REPORT

UGT1A1*28 and *6 polymorphisms and nilotinib-induced unconjugated hyperbilirubinemia in a Japanese patient with chronic myelogenous leukemia

Kohichi Takada · Tsutomu Sato · Satoshi Iyama · Kaoru Ono · Yusuke Kamihara · Kazuyuki Murase · Yutaka Kawano · Tsuyoshi Hayashi · Koji Miyanishi · Yasushi Sato · Masayoshi Kobune · Rishu Takimoto · Junji Kato

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Abstract Nilotinib, a second-generation tyrosine kinase inhibitor of BCR-ABL, has shown superior efficacy compared with imatinib for the treatment of chronic myelogenous leukemia (CML). Unconjugated hyperbilirubinemia has been the most frequent adverse event with laboratory abnormality observed in clinical trials of nilotinib. The homozygosity for uridine diphosphate glucuronosyltransferase (UGT) 1A1*28 polymorphism has been reported to increase the risk of nilotinib-induced unconjugated hyperbilirubinemia in Caucasians. However, the frequency of UGT1A1*28 is low in Asians, including Japanese. On the other hand, the UGT1A1*6 allele mutation, which is extremely rare in Caucasians, is more frequent than the UGT1A1*28 allele in the Japanese population. Herein, we present a patient with CML who developed grade 3 unconjugated hyperbilirubinemia after being treated with nilotinib. We found that the patient was heterozygous for both UGT1A1*28 and *6. Our findings suggest that the compound heterozygosity for UGT1A1*28 and *6 could be a cause of unconjugated hyperbilirubinemia during nilotinib treatment.

Keywords Nilotinib · Hyperbilirubinemia · UGT1A1 · Polymorphism

K. Takada · T. Sato · S. Iyama · K. Ono · Y. Kamihara · K. Murase · Y. Kawano · T. Hayashi · K. Miyanishi · Y. Sato · M. Kobune · R. Takimoto · J. Kato (☒) Fourth Department of Internal Medicine, Sapporo Medical University School of Medicine, South-1, West-16, Chuo-ku, Sapporo, Hokkaido 060-8543, Japan e-mail: jkato@sapmed.ac.jp

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Introduction

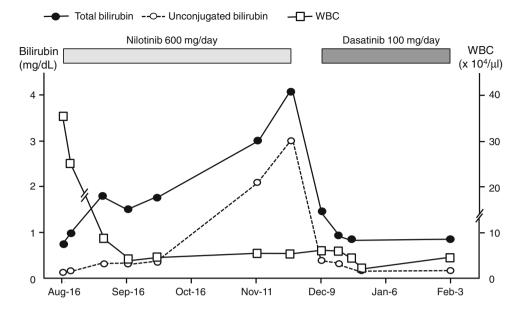
Randomized phase 3 trials have revealed that nilotinib and dasatinib, second-generation tyrosine kinase inhibitors (2nd TKIs) of BCR-ABL, have superior efficacy compared with imatinib for the first-line treatment of chronic myelogenous leukemia in the chronic phase (CML-CP) [1, 2]. Currently, both these 2nd TKIs are available as the first-line treatment in newly diagnosed CML-CP. Their profiles of adverse effect are characteristic. Common adverse events (AEs) of nilotinib include myelosuppression, transient unconjugated hyperbilirubinemia, and rashes. In clinical studies of the setting for frontline treatment of CML-CP with nilotinib, 7–16 % patients had grade 3 or 4 hyperbilirubinemia [3, 4].

As for the risk factor of developing nilotinib-induced hyperbilirubinemia, the uridine diphosphate glucuronosyltransferase (UGT) 1A1 promoter polymorphism has been noticed recently. UGT1A1 catalyzes glucuronidation of hepatic bilirubin in humans. A (TA)₇ repeat polymorphism (termed the *28 mutation) in a TATA element in the promoter region, in place of the more common (TA)₆ repeat, reduces UGT1A1 expression and causes the benign elevation of unconjugated bilirubin. The homozygosity for this UGT1A1*28 mutation was reportedly associated with an elevated risk of nilotinib-induced hyperbilirubinemia in Caucasians [5]. However, the distribution of *UGT1A1*28* differs greatly between Caucasians and Japanese, namely, the frequency of UGT1A1*28 is high in Caucasians, whereas it is low in Asians, including Japanese [6, 7]. On the other hand, another low-activity allele 211G > A (G71R) in exon 1 (termed the *6 mutation) was frequently found in an Asian population [8].

Herein, we present a patient with CML-CP who developed grade 3 unconjugated hyperbilirubinemia after being



Fig. 1 Clinical course of the patient. *WBW* white blood cells



treated with nilotinib. She was not homozygous for *UGT1A1*28* but heterozygous for both *UGT1A1*28* and *6. This is the first case that suggests that the compound heterozygosity for *UGT1A1*28* and *6 increases susceptibility to nilotinib-induced unconjugated hyperbilirubinemia.

Case report

In August 2011, a 26-year-old Japanese woman was diagnosed with CML-CP. She was started on nilotinib 300 mg twice daily (Fig. 1). Two days later, she suffered from headache, which spontaneously improved. She achieved complete hematological remission within 4 weeks. Her serum total bilirubin started to elevate during the same period, then gradually increased. Fourteen weeks later, her serum total bilirubin concentration reached 4.1 mg/dL, of which unconjugated bilirubin was 3.0 mg/dL. Other laboratory data including liver function tests were within normal ranges. We suspected a nilotinib-induced hyperbilirubinemia, and stopped nilotinib treatment. Two weeks after stopping administration of nilotinib, her total bilirubin concentration returned to normal. Then the administration of dasatinib (100 mg/day) was started. She tolerated dasatinib well without any significant AE. She achieved complete cytogenetic remission after 7 months of treatment with nilotinib and dasatinib.

We performed *UGT1A1* genotyping in our patient with written informed consent using the Invader®UGT1A1 Assay Kit (Sekisui Medical, Co., Ltd., Tokyo, Japan) according to the manufacturer's instructions. We found that she was a heterozygote for two polymorphisms, *UGT1A1*28* and *6.



Discussion

UGT1A1 is a key enzyme in bilirubin conjugation and, in the absence of hemolysis, defects in this enzyme can cause an isolated unconjugated hyperbilirubinemia, such as Gilbert's syndrome (GS) or Crigler-Najjar syndrome. GS is characterized by mild hyperbilirubinemia, normal values in standard hepatic biochemical tests, and normal hepatic histology other than a modest increase in lipofuscin pigment in some patients. The UGT1A1*28 polymorphism, found in the promoter area of UGT1A1, is the most frequent cause of GS in Caucasians. It was Singer et al. [5] who reported that nilotinib-induced hyperbilirubinemia may be associated with UGT1A1*28 polymorphism. Individuals with the UGT1A1*28 homozygous genotype were found to be at elevated risk of nilotinib-induced hyperbilirubinemia, with the observed relative risk varying between 4.5 and 18.0. The allele mutation UGT1A1*28 occurs at frequencies up to 40 % in the Caucasian population and is seen in the Japanese population at lower rates (9-13 %). On the other hand, the UGT1A1*6 allele, which is extremely rare in Caucasians, is more frequent than the UGT1A1*28 allele in Japanese people [8–10]. Taking account of the frequency of UGT1A1 polymorphisms in the Japanese population, we might have to consider the influence of UGT1A1*6 polymorphism on nilotinib-induced unconjugated hyperbilirubinemia. Actually, our patient with nilotinib-induced unconjugated hyperbilirubinemia was not homozygous for UGT1A1*28 but heterozygous for both UGT1A1*28 and *6.

Accumulating evidence about the effects of *UGT1A1* polymorphism on irinotecan helps support our hypothesis that *UGT1A1*6* is associated with nilotinib-induced unconjugated hyperbilirubinemia. Irinotecan, an anticancer

agent that inhibits topoisomerase I, is widely used in the treatment of colorectal, gastric, and lung cancers. However, adverse drug reactions such as severe diarrhea and neutropenia limit the dose of this drug. Irinotecan is metabolized by carboxylesterase to form an active metabolite, 7-ethyl-10-hydroxycamptothecin (SN-38), which, in turn, is subsequently conjugated by UGT1A1 to yield an inactive form, SN-38 glucuronide (SN-38G). It has been demonstrated that genetic polymorphisms of *UGT1A1* are associated with the occurrence of AEs in irinotecan chemotherapy. In Caucasians, *UGT1A1*28* has been noted as a major mutant allele which causes AEs of irinotecan [11–14]; however, *UGT1A1*6* is significantly associated with severe neutropenia in Japanese patients who received irinotecan therapy [10, 15, 16].

The possible involvement of *UGA1A1*6* in nilotinib-induced unconjugated hyperbilirubinemia might be also suggested by a report by Kim et al. [17], which presented a Korean patient with nilotinib-induced unconjugated hyperbilirubinemia who was heterozygous for both *UGT1A1*60* and *6.

The mechanism by which nilotinib and the *UGT1A1* genotype interact to cause an increased rate of hyperbilirubinemia is not fully defined. Preclinical studies revealed that nilotinib was not glucuronidated by UGT1A1; however, nilotinib inhibited UGT1A1 activity itself (unpublished data) [5]. Recently, Fujita et al. [18] also identified that nilotinib was a potent noncompetitive inhibitor of UGT1A1 activity. Therefore, a plausible explanation of nilotinib-induced hyperbilirubinemia in patients with a *UGT1A1* mutant allele such as *UGT1A1*28* or *6 is that the lower activity of UGT1A1 due to allele mutation would be decreased further by its inhibitor, nilotinib.

The way in which one should manage CML when nilotinib induces unconjugated hyperbilirubinemia has been uncertain. Rosti et al. [19] suggested that physicians should maintain nilotinib dose intensity without dose reductions, after presenting a successfully managed case of nilotinib-induced hyperbilirubinemia. With three interruptions of nilotinib treatment, that patient achieved a complete molecular response by a year. They concluded that hyperbilirubinemia and its management did not spoil the effectiveness of nilotinib; however, long-term follow-up would be needed to confirm the safety and efficacy of nilotinib for patients with CML complicated by hyperbilirubinemia. In addition, National Comprehensive Cancer Network (NCCN) guidelines recommend withholding nilotinib treatment when patients have grade 3 or 4 hyperbilirubinemia until the grade returns to less than 1 [20]. We also recommend to stopping nilotinib treatment until the bilirubin concentration return to normal in a safe pharmaceutical use.

Another choice may be switching TKI from nilotinib to dasatinib as presented in our report. In a clinical study for frontline treatment of CML-CP with dasatinib (the DASISION trial), the incidence of hyperbilirubinemia was only 1 %. In vitro analysis also confirmed that the inhibitory effect of dasatinib against UGT1A1 is ten times less than that of nilotinib [18]. This is a plausible reason why nilotinib but not dasatinib induced hyperbilirubinemia in the present case. The possibility that dasatinib induces its characteristic adverse effects anew should be considered; however, dasatinib was safely administrated 2 weeks after withholding nilotinib in our case.

Taken together, for individualized nilotinib treatment, genotyping of *UGT1A1*6* as well as *28 would be beneficial in Japanese patients to avoid unconjugated hyperbilirubinemia and helpful in making the choice between nilotinib and dasatinib for CML-CP treatment.

Conflict of interest We declare that there are no financial supports or relationships that may pose conflict of interest.

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