Prolonged Unconjugated Hyperbilirubinemia Associated With Breast Milk and Mutations of the Bilirubin Uridine Diphosphate-Glucuronosyltransferase Gene

Yoshihiro Maruo, MD, PhD*; Kashiro Nishizawa, MD, PhD§; Hiroshi Sato, PhD‡; Hiroko Sawa, MD*; and Morimi Shimada, MD, PhD*

ABSTRACT. Objective. Breast milk jaundice is a common problem in nursing infants. It has been ascribed to various breast milk substances, but the component or combination of components that is responsible remains unknown. During our study of defects of the bilirubin uridine diphosphate-glucuronosyltransferase gene (UGT1A1) in patients with hereditary unconjugated hyperbilirubinemia (Crigler-Najjar syndrome and Gilbert’s syndrome) and neonatal hyperbilirubinemia, we encountered a prolonged case associated with breastfeeding; after cessation of breastfeeding, the infant’s bilirubin level became normal. Genetic analysis revealed a missense mutation identical to that found in patients with Gilbert’s syndrome, which usually causes jaundice after puberty. We analyzed the bilirubin UGT1A1 of infants with prolonged unconjugated hyperbilirubinemia associated with breast milk to ascertain whether genetic factors are involved.

Patients and Methods. We analyzed 17 breastfed Japanese infants with apparent prolonged jaundice (total serum bilirubin concentrations above 171 μmol/L [10 mg/dL]) 3 weeks to 1 month after their birth. Except for jaundice, the infants were healthy and did not show evidence of hemolytic anemia, liver dysfunction, or hypothyroidism. After cessation of breastfeeding, the serum bilirubin concentration began to decrease in all cases. When breastfeeding was resumed, serum bilirubin concentration again became elevated in some infants, but the concentration fell to within normal by 4 months of age. We analyzed the polymerase chain reaction-amplified exon, promoter, and enhancer regions of UGT1A1 by direct sequencing.

Results. Sixteen infants had at least one mutation of the UGT1A1. Seven were homozygous for 211G→A (G71R), which is the most common mutation detected in the East Asian population, and the mutant enzyme had one third of the normal activity. G71R is the most common missense mutation we found in our analyses in the East Asian population, and the mutant enzyme had one third of the normal activity. One was heterozygous for 356T→G (Y119D) and homozygous for 211G→A. Six were heterozygous for 211G→A. One was heterozygous for both 211G→A and a TATA box mutation (ATA)7TAA. One had a heterozygous mutation in an enhancer region (C→A at −1353). We did not detect a homozygous (ATA)7TAA mutation, which was the most common cause of Gilbert’s syndrome in European population, in this study of Japanese infants with prolonged hyperbilirubinemia triggered by breast milk.

Conclusions. The results indicate that defects of UGT1A1 are an underlying cause of the prolonged unconjugated hyperbilirubinemia associated with breast milk. One or more components in the milk may trigger the jaundice in infants who have such mutations. The mutations we found were identical to those detected in patients with Gilbert’s syndrome, a risk factor of neonatal nonphysiologic hyperbilirubinemia and a genetic factor in fasting hyperbilirubinemia. Pediatrics 2000;106(5).

ABBREVIATIONS. BMJ, breast milk jaundice; UGT1A1, bilirubin uridine diphosphate-glucuronosyltransferase gene.

Breast milk jaundice (BMJ) was first described in 1963,1,2 and is a problem that pediatricians frequently encounter in nursing infants. BMJ is characterized by prolonged unconjugated hyperbilirubinemia in otherwise healthy infants, is related to ingestion of breast milk, and often results in serum bilirubin levels >171 μmol/L (10 mg/dL), with danger of brain damage in severe cases.3 The condition has been ascribed to breast milk components such as pregnane-3β,20α-diol,4 nonesterified fatty acids,5 and glucuronidase,6 but it is not known exactly which component or combination of components is responsible.7–9

During our study of defects of the bilirubin uridine diphosphate-glucuronosyltransferase gene (UGT1A1) in patients with hereditary unconjugated hyperbilirubinemia (Crigler-Najjar syndrome and Gilbert’s syndrome)10,11 and neonatal hyperbilirubinemia,12 we encountered a prolonged case associated with breastfeeding; after cessation of breastfeeding, the infant’s bilirubin level became normal. Genetic analysis revealed a missense mutation identical to that found in patients with Gilbert’s syndrome, which usually causes jaundice after puberty.13 Furthermore, Grunébaum et al14 suggested that there may be a genetic factor in the cause of BMJ. Here, we analyzed UGT1A1 in Japanese infants with the pro-
longed unconjugated hyperbilirubinemia associated with breast milk and showed that missense mutations of the gene are an underlying cause of the condition; breast milk may trigger the hyperbilirubinemia in carriers of such mutations.

**METHODS**

**Patients**

We analyzed 17 Japanese infants who developed prolonged apparent jaundice and had total serum bilirubin concentrations above 171 μmol/L (10 mg/dL) after the third week of life (Table 1). All the infants were nursed with breast milk. Six cases were discovered during the third to fourth week of life when the parents visited our office concerned about the prolonged jaundice (cases 1, 6, 8, 9, 12, and 15). Prolonged jaundice in the other 11 infants was detected at an obligatory health check 1 month after birth (cases 2–5, 7, 10, 11, 13, 14, 16, and 17). Their total and indirect acting bilirubin concentrations ranged from 1.8% to 8.7% of the mmol/L and from 164 to 533 mmol/L, respectively. The direct bilirubinemia was also detected in our previous studies for Gilbert’s syndrome and Crigler-Najjar syndrome type II.10,11,19 G71R is the most common polymorphism in the Japanese population and is considered to be clinically silent.12

**RESULTS**

Sixteen of the 17 infants had at least 1 UGT1A1 mutation (Table 2). Fifteen had missense mutations.

### TABLE 1. Characteristics and Blood Examination of Infants With BMJ

<table>
<thead>
<tr>
<th>Case</th>
<th>Sex</th>
<th>Birth Weight (Grams)</th>
<th>At Visit or an Obligatory Health Check (From Three Weeks to One Month Old)</th>
<th>At Four Months Old</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Bilirubin* (μmol/L)</td>
<td>Hb (Grams/dL)</td>
</tr>
<tr>
<td>1</td>
<td>Female</td>
<td>3276</td>
<td>478 (465)</td>
<td>13.3</td>
</tr>
<tr>
<td>2</td>
<td>Male</td>
<td>3098</td>
<td>352 (336)</td>
<td>13.8</td>
</tr>
<tr>
<td>3</td>
<td>Male</td>
<td>2660</td>
<td>343 (333)</td>
<td>10.2</td>
</tr>
<tr>
<td>4</td>
<td>Female</td>
<td>3110</td>
<td>270 (259)</td>
<td>10.5</td>
</tr>
<tr>
<td>5</td>
<td>Male</td>
<td>3066</td>
<td>176 (160)</td>
<td>12.5</td>
</tr>
<tr>
<td>6</td>
<td>Female</td>
<td>2162</td>
<td>383 (372)</td>
<td>11.5</td>
</tr>
<tr>
<td>7</td>
<td>Female</td>
<td>1895</td>
<td>321 (300)</td>
<td>11.5</td>
</tr>
<tr>
<td>8</td>
<td>Male</td>
<td>2726</td>
<td>543 (533)</td>
<td>12.4</td>
</tr>
<tr>
<td>9</td>
<td>Female</td>
<td>2808</td>
<td>330 (318)</td>
<td>11.7</td>
</tr>
<tr>
<td>10</td>
<td>Male</td>
<td>2240</td>
<td>176 (164)</td>
<td>13.2</td>
</tr>
<tr>
<td>11</td>
<td>Female</td>
<td>3250</td>
<td>314 (297)</td>
<td>12.0</td>
</tr>
<tr>
<td>12</td>
<td>Male</td>
<td>3272</td>
<td>487 (422)</td>
<td>12.0</td>
</tr>
<tr>
<td>13</td>
<td>Female</td>
<td>2896</td>
<td>226 (214)</td>
<td>15.9</td>
</tr>
<tr>
<td>14</td>
<td>Male</td>
<td>3242</td>
<td>218 (209)</td>
<td>12.6</td>
</tr>
<tr>
<td>15</td>
<td>Male</td>
<td>3090</td>
<td>223 (206)</td>
<td>13.6</td>
</tr>
<tr>
<td>16</td>
<td>Male</td>
<td>3150</td>
<td>237 (234)</td>
<td>14.5</td>
</tr>
<tr>
<td>17</td>
<td>Male</td>
<td>3624</td>
<td>306 (295)</td>
<td>10.5</td>
</tr>
</tbody>
</table>

Hb indicates hemoglobin; GOT, glutamine oxaloacetate transaminase; GPT, glutamine pyruvate transaminase; ND, not determined.

* Value in parentheses is concentration of indirect acting bilirubin.
anese population (the allele frequency is .16).12 G71R may be the most common UGT1A1 mutation in Asians.20 Recently we revealed the mutation to be a genetic basis of fasting hyperbilirubinemia.21

In our in vitro expression study the G71R form of the enzyme had 32% and 60% of normal activity in the homozygous and heterozygous states, respectively.22 Our recent study of neonatal hyperbilirubinemia showed that heterozygous G71R was a risk factor for elevated serum bilirubin levels in the early neonatal period.12 Indeed, as noted earlier, 16 of the 17 infants in this study had nonphysiologic neonatal hyperbilirubinemia during the first postpartum week.

No specific component or combination of components in breast milk has been demonstrated to be the cause of BMJ, although extensive investigations have been conducted since BMJ was first described. In contrast, bilirubin UGT1A1 activity in early infancy is <1% of the adult activity, which is reached by 3 months of age.23 BMJ is usually observed before 3 months of age and then disappears even if breastfeeding is continued, implying a close relationship between BMJ and enzyme activity. Those facts and our present results suggest that the UGT1A1 mutations detected in this study may be an underlying cause of BMJ and that breast milk component(s) may trigger BMJ in neonates who have those mutations.

We found a mutation of the distal element in the enhancer region (Table 2, case 5) that had been reported previously.16 Although our in vitro expression study demonstrated that the C→A mutation at –1353 of the element decreased transcriptional activity of UGT1A1 to –85% of normal,16 it is uncertain whether the mutation would cause the elevation of serum bilirubin level in this case.

Recently, a homozygous 2-basepair insertion mutation in the TATA box (A(AT)/TAA) has been reported to be a contributory factor for prolonged neonatal jaundice.24 We did not detect that mutation, however, in this study of Japanese infants with prolonged hyperbilirubinemia triggered by breast milk. The G71R polymorphism has only been observed in East Asians,12,20 and our latest study revealed that G71R but not A(TA)/TAA is a risk factor for nonphysiologic neonatal hyperbilirubinemia.12 Furthermore, the frequency of the A(TA)/TAA allele is considerably lower in the Japanese population (.07–.15)12,16 than in the European population (.4).25 Thus, we might not detect homozygous A(TA)/TAA in Japanese infants with BMJ.

Mild BMJ is not a clinically significant problem, and we did not analyze infants with mild jaundice in this study. The analysis of more severe BMJ, however, revealed that 8 of 17 neonates (47%) were homozygous and 7 (41%) were heterozygous for missense mutations of UGT1A1. In our previous study of Japanese cases with Gilbert’s syndrome, most (93%) of the patients with missense mutations were heterozygotes.10 Furthermore, there is a G71R UGT1A1 polymorphism among Japanese.12 These facts suggest that mild BMJ may also be associated with the missense mutation of UGT1A1 and may be an infantile phenotype of Gilbert’s syndrome. Analysis of UGT1A1 in infants with moderate to severe prolonged unconjugated hyperbilirubinemia associated with ingestion of breast milk would help differentiate this condition from Crigler-Najjar syndrome.

**CONCLUSION**

We suggest that an underlying cause of prolonged unconjugated hyperbilirubinemia associated with breast milk is mutations in UGT1A1 and that the hyperbilirubinemia may be an infantile and inducible phenotype of Gilbert’s syndrome. We are following the serum bilirubin concentrations of these cases to further elucidate the relationship between BMJ and Gilbert’s syndrome.

**ACKNOWLEDGMENTS**

This work was supported in part by grants in aid for scientific research (to H.S.) from the Ministry of Education, Science, and Culture of Japan (Grant 11670494) and by the Hepatic Diseases Research Foundation (Shiga, Japan).

We thank R. Nishikawa, A. Sato, and T. Narita at the Department of Pediatrics, Ohmihachiman Municipal Hospital, and H. Hattori and H. Aotani at the Department of Pediatrics, Shiga

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**TABLE 2. UGT1A1 Mutations in Infants With BMJ**

<table>
<thead>
<tr>
<th>Case No.</th>
<th>211G→A</th>
<th>1456T→G</th>
<th>A(TA)/TAA</th>
<th>Other Mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Hetero</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Hetero</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td>Distal element*</td>
</tr>
<tr>
<td>6</td>
<td>Hetero</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>Homo</td>
<td>Hetero</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>Hetero</td>
<td>N</td>
<td>Hetero</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
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<td>Hetero</td>
<td>N</td>
<td>N</td>
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<td>14</td>
<td>N</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>Hetero</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>Hetero</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>Homo</td>
<td>N</td>
<td>N</td>
<td></td>
</tr>
</tbody>
</table>

Homo indicates homozygous mutation; hetero, heterozygous mutation; N, no mutation.

* Distal element*: a heterozygous mutation on the distal element of UGT1A1
University of Medical Science, for their examination and care of the patients.

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