Hereditary Hemolytic Anemia Caused by Diverse Point Mutations of Pyruvate Kinase Gene Found in Japan and Hong Kong

By Hitoshi Kanno, David C. Wei, L.C. Chan, Hideaki Mizoguchi, Masahiko Ando, Tatsutoshi Nakahata, Kuniaki Narisawa, Hisaichi Fujii, and Shiro Miwa

We identified four distinct point mutations in homozygous pyruvate kinase (PK) variants in Japanese and Chinese patients with chronic nonspherocytic hemolytic anemia. All gene abnormalities were missense mutations that caused single amino acid substitutions. 1261A (Q421K) and 1436A (R436H), which were identified in PK Sendai and PK Shinshu, had been found in unrelated Japanese and Amish PK variants, respectively. The clinical severity and extremely low residual erythrocyte PK activity of PK Shinshu as well as of the Amish PK might be caused partly by aberrant splicing, because the 1436A mutation changes a nucleotide at the last nucleotide in the exon 10. Recently, we diagnosed a 42-year-old Japanese woman with chronic nonspherocytic hemolytic anemia as having a homozygous PK deficiency, DNA sequencing of the variant PK gene showed a homozygous missense mutation at 1403GCT -> GTT, resulting in a single amino acid substitution from 468Ala -> Val. The gene mutation is likely to impair the allostericity of this enzyme, speculated from the tertiary structure. A homozygous missense mutation in PK Hong Kong, a boy of a non-Han southern Chinese minority group, was identified in exon 7 of the human L-PK gene, 941ATT -> ACT, resulting in a single amino acid substitution from 314lele -> Thr. The R-PK activity is expected to be severely affected, because the mutated amino acid residue is located between the 313 Lys and the 315 Glu, which are very important for acid-base catalysis and magnesium binding, respectively. Both the R- and M2-type PK were shown by polyacrylamide gel electrophoresis of the PK Hong Kong erythrocyte lysate, and this is the first report of a homozygous individual whose erythrocytes contain the immature (M2)-type isozyme.

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Table 1. PCR Primers Used in This Study

<table>
<thead>
<tr>
<th>Primer Code</th>
<th>Primer Sequence</th>
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<tbody>
<tr>
<td>PK-1A</td>
<td>5'-ACTAAGCCGTGATCCCAGCAGT-3'</td>
</tr>
<tr>
<td>PK-2A</td>
<td>5'-AGGCGTGGAGGACCTGCAGT-3'</td>
</tr>
<tr>
<td>PK-2B</td>
<td>5'-CCAGGAAACCTCTCTGCTG-3'</td>
</tr>
<tr>
<td>PK-3A</td>
<td>5'-TACCAAGCCGCGCGCAAGGAG-3'</td>
</tr>
<tr>
<td>PK-3B</td>
<td>5'-TAGTCCTCAAGACAGCTG-3'</td>
</tr>
<tr>
<td>PK-4A</td>
<td>5'-CAGGAGTCATCGGAACATCC-3'</td>
</tr>
<tr>
<td>PK-4B</td>
<td>5'-CCCCGGAGAGGAGGCGAGCTG-3'</td>
</tr>
<tr>
<td>PK-5A</td>
<td>5'-GGTGCAAGCAATGACTGCTG-3'</td>
</tr>
<tr>
<td>PK-5B</td>
<td>5'-GAGGGGCTTGAACTTGCTG-3'</td>
</tr>
<tr>
<td>PK-6A</td>
<td>5'-CAGGCTCGTGTCCTCTCCG-3'</td>
</tr>
<tr>
<td>PK-6B</td>
<td>5'-GTGACGGTGGGAGCAGG-3'</td>
</tr>
</tbody>
</table>

Table 2. Strategy for the Detection of the PK Gene Mutations

<table>
<thead>
<tr>
<th>Mutation</th>
<th>PCR-Primers</th>
<th>DNA Length</th>
<th>Restriction Enzyme</th>
<th>Normal Allele</th>
<th>Mutant Allele</th>
</tr>
</thead>
<tbody>
<tr>
<td>1403T</td>
<td>PK-1A/PB</td>
<td>88 bp</td>
<td>Fnu4HI</td>
<td>49, 21, 16 bp</td>
<td>49, 39 bp</td>
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<tr>
<td>941C</td>
<td>PK-2A/2B</td>
<td>351 bp</td>
<td>Dde I</td>
<td>259, 92 bp</td>
<td>143, 116, 92 bp</td>
</tr>
<tr>
<td>1261A</td>
<td>PK-3A/3B</td>
<td>285 bp</td>
<td>Fnu4HI</td>
<td>130, 122, 33 bp</td>
<td>262, 33 bp</td>
</tr>
<tr>
<td>1436A</td>
<td>PK-4A/4B</td>
<td>201 bp</td>
<td>Hpa II</td>
<td>132, 39, 27, 3 bp</td>
<td>171, 27, 3 bp</td>
</tr>
</tbody>
</table>
PK DEFICIENCY IN JAPAN AND HONG KONG

Fig 1. A pedigree of the PK Hong Kong family and PCR-restriction fragment length polymorphism of the 941T–C mutation. The PCR products flanking the exon 7 of human PK gene were tested to determine whether a new DdeI site is created by the mutation. The samples were applied to a 3% NuSieve-1% HGT agarose gel and were stained with ethidium bromide. M, pBR322 digested with MspI; 1, the father; 2, the mother; 3, the proband; 4, the sister; 5, the sister; and C, normal control.

tical with those in the unrelated variants, PK Fukushima, PK Maebashi, or the Amish PK deficiency, respectively.\(^5,\(^6\) In addition to a change of the encoded amino acid, the 1436A mutation altered the last nucleotide of exon 10, resulting in an alteration of the 5′ splice site consensus sequence, C/AAGgta/gagtcg to C/AAAgagtcgagtcg.\(^17\) To test whether splicing of the PK gene transcript had been impaired, we performed reverse transcription-PCR of the R-type PK mRNA in reticulocytes. Using primers PK-SA and -5B (Table 1) that flank the exon-7 through exon-11 region, only normal 745-bp fragments were shown by ethidium bromide staining of agarose gel, meaning either that the 1436A mutation did not affect the splicing efficiency or that the aberrant transcripts could not be amplified in this system (data not shown).

Identical PK gene mutations with or without same nucleotide polymorphism. To investigate the origin of the identical PK gene mutations in an unrelated Japanese family or distinct ethnic group, we checked the 1705 A/C polymorphism\(^6\) of the PK variants. As shown in Table 3, all PK variants with the 1261A were homozygous with cytosine at no. 1705. In contrast, PK Shinshu (1705 A/A) and the Amish PK variant (1705 C/C) had different polymorphisms.

DISCUSSION

Since the first report of PK deficiency, over 300 PK-deficient hemolytic anemia cases have been described. The degree of anemia varied from a mild compensated anemia to a severe anemia that can be life-threatening during the neonatal or infantile periods. Various gene mutations associated with PK-deficient hemolytic anemia have been reported.\(^6,\(^15,\(^16,\(^18,\(^24\) Progress in understanding the structure-function relationship of this enzyme has allowed this inherited disorder to be diagnosed at the gene level. To date, 21 missense, 1 nonsense, and 2 splicing mutations and 2 insertions and 3 deletions have been documented. Accumulated knowledge of PK gene mutations have provided useful information for both the diagnosis and prognosis of PK-deficient hemolytic anemia.

The missense mutation found in PK Shinshu was identical to that of the Amish PK variant.\(^16\) Although there were some discrepancies in the enzymatic characteristics between PK Shinshu and the Amish variant,\(^2\) it should be emphasized that both variant enzymes showed a lower response to the allosteric activator, fructose-1,6-diphosphate, and normal (increased in the Amish variant) affinity for the substrate, phosphoenolpyruvate. This was accounted for by the occurrence of the amino acid substitution in the C domain of PK, as previously discussed.\(^10\) Clinical records describing PK-deficient patients with a 1436A mutation show that both variants were severely affected during the neonatal or infantile period.\(^10,\(^20\) Although the aberrant transcripts could not be detected in reticulocytes of PK Shinshu, splicing might be disturbed by the 1436A mutation because of the following. First, statistical analysis of the 5′ splice sequences for 97 donor sites of human genes\(^22\) and 542 donor sites of primate genes\(^28\) has shown that 100% (human) or 78% (primates) of the nucleotides at the −1 location of the 5′ splice site (last nucleotide in the preceding exon) were guanine. Second, there are several reports that the G-to-A transition at this position causes exon-skipping or cryptic site utilization,\(^29,\(^35\) and in most cases aberrant mRNAs were produced.

Fig 2. Polyacrylamide gel electrophoresis for detecting PK activity. C, normal control; P, PK Hong Kong. M2 and R show the position of M2- and R-type PK, respectively. In the proband erythrocyte lysate, both R- and M2-type PK were identified.
by skipping the preceding exon, and those were very unstable in vivo. Taken together, it is most likely that the extremely low residual erythrocyte PK activity of the Amish PK (3.9% of normal) and PK Shinshu (11.5%) might be caused by both decreased levels of PK transcripts and an amino acid change of the enzyme.

Table 3 summarizes the structure-function relationship learned from molecular studies of homozygous PK deficiency. As shown in the table, the structural changes near the active site that was constituted by the A domain showed low substrate affinity. PK Hong Kong (941C), PK Tokyo/PK Nagasaki (1151T), PK Fukushima/PK Maebashi/PK Sendai (1261A), and PK Sapporo (1277A) were included in this category. However, the structural alterations in the C domain impaired allosteric activation. PK Hadano (1403T) and PK Shinshu/Amish PK (1436A) were categorized in this group, and these variants seemed to be more severe in the degree of anemia. Among the total of 21 missense mutations including those in the present report, we and other investigators identified that there are 3 mutations in exon 5, 1 in exon 7, 5 in exon 8, 2 in exon 9, 5 in exon 10, and 5 in exon 11 of the human PK gene.

During genetic diagnosis of PK deficiency, we identified 1151T and 1436A mutations in unrelated families of different ethnic origins. Although PK Shinshu and Amish PK had an identical missense mutation at 1436A, they had a distinct DNA polymorphism at no. 1705. These results indicated that the mutation had occurred independently at the same nucleotide. On the other hand, 1261A might have originated from a common ancestor, because the families of PK Fukushima, PK Maebashi, and PK Sendai were derived from the northern part of the main island of Japan, and they shared the same 1705 C/C. Although the 1529A (R510Q) mutation is prevalent in the PK variants of the United States and Europe, we were unable to find this mutation in Japanese PK variants. Although the 1261A and 1151T seemed to be dominant in the Japanese homozygous PK variants, preliminary results provided by the restriction endonuclease digestion of PCR products showed that those missense mutations found in homozygotes were not necessarily common in compound heterozygotes. Therefore, we considered that an efficient screening system for detecting the PK gene mutation is required to clarify the genetic basis of PK deficiency.

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Hereditary hemolytic anemia caused by diverse point mutations of pyruvate kinase gene found in Japan and Hong Kong

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