Homozygous $\beta^+$ thalassaemia owing to a mutation in the cleavage-polyadenylation sequence of the human $\beta$ globin gene

M Losekoot, R Fodde, C L Harteveld, H van Heeren, P C Giordano, L N Went, L F Bernini

Abstract
A mild, non-transfusion dependent, $\beta$ thalassaemia phenotype is described in a Dutch patient homozygous for a mutation in the cleavage–polyadenylation sequence of the $\beta$ globin gene. The molecular basis of the mutation, AATAGAA$>$AATGAA, was determined using denaturing gradient gel electrophoresis (DGGE) and direct sequencing of genomic DNA amplified by the polymerase chain reaction (PCR). Different fragments of the $\beta$ globin gene were amplified and analysed on DGGE for the presence of mutations. The fragment with an abnormal melting behaviour was reamplified and the base substitution in the polyadenylation sequence was identified by direct sequencing.

In the past 20 years it has become clear that both the phenotype and the molecular basis of $\beta$ thalassaemia show great heterogeneity. More than 90 mutations involving single base substitutions, small deletions, and insertions within the $\beta$ globin gene or its immediately flanking sequences have been characterised to date. These mutations either affect transcription, RNA splicing, RNA modification, or translation, or produce unstable $\beta$ globin chains.

Mutations at the RNA cleavage and polyadenylation sequence AATAAA, located 110 nucleotides 3' from the termination codon of the $\beta$ globin gene, result in the formation of elongated and unstable mRNA molecules. Four of these mutations have been described and they all appear to result in a $\beta^+$ thalassaemia phenotype.

The analysis of the phenotype expressed by a particular mutation can be difficult in compound heterozygotes for two different molecular lesions, and therefore the description of homozygous patients can be of value. In this article we report the haematological and molecular analysis of a Dutch patient homozygous for a mutation at the cleavage-polyadenylation sequence of the $\beta$ globin gene (AATAGAA$>$AATGAA), who displayed a very mild $\beta^+$ thalassaemia phenotype.

Materials and methods
HAEMATOLOGICAL ANALYSIS
Haematological parameters were measured according to standard methods. Globin biosynthetic ratios in reticulocytes were measured by $^3$H-leucine labelling and isoelectric focusing. Identification of haemoglobins in haemolysates was carried out by starch gel electrophoresis.

MOLECULAR ANALYSIS
DNA extraction and haplotype analysis were performed following standard procedures. Amplification by polymerase chain reaction and direct sequencing of amplified material was performed as previously described. The template for the direct sequencing experiment was amplified with amplifiers C and E, while a-D was used as a sequencing primer.

The gel apparatus and electrophoresis conditions for the denaturing gradient gel electrophoresis (DGGE) were as described in Myers et al. In short, one fifth of the amplification product was electrophoresed on a 6% polyacrylamide gel with a linearly increasing gradient of denaturant (100% denaturant = 7 mol/l urea/40% formamide (v/v)). For primers GC.A and pCO4, a–pCO4 and GC.B, and GC.a–B and IVS–2 a gradient from 45 to 75% denaturant was used; for primers C and D, and a–D and E a gradient from 25 to 55% denaturant was applied. The gels were run at 50 V, 30 mA for 16 hours. After electrophoresis the gel was stained with ethidium bromide (0.5 µg/ml) for 30 minutes and examined under UV transillumination. The nucleotide sequence of the amplifiers is given in the legend to fig 1.
Haematological data.

<table>
<thead>
<tr>
<th></th>
<th>Proband</th>
<th>Mother</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex/age</td>
<td>F26</td>
<td>F49</td>
</tr>
<tr>
<td>Hb (g/dl)</td>
<td>9-8</td>
<td>14-1</td>
</tr>
<tr>
<td>RBC (10(^9)/l)</td>
<td>3.77</td>
<td>5.30</td>
</tr>
<tr>
<td>Ret (%)</td>
<td>280</td>
<td>11</td>
</tr>
<tr>
<td>SeFe (mg/l)</td>
<td>1.3</td>
<td></td>
</tr>
<tr>
<td>Bilirubin (mg/l)</td>
<td>1.9</td>
<td></td>
</tr>
<tr>
<td>PCV (%)</td>
<td>0.31</td>
<td>0.44</td>
</tr>
<tr>
<td>MCV (fl)</td>
<td>82</td>
<td>83</td>
</tr>
<tr>
<td>MCHC (g/l)</td>
<td>26.0</td>
<td>26.6</td>
</tr>
<tr>
<td>MCH (pg)</td>
<td>31.6</td>
<td>32.04</td>
</tr>
<tr>
<td>Osmotic fragility</td>
<td>Very decreased</td>
<td>Slight decreased</td>
</tr>
<tr>
<td>Hb A(_2) (%)</td>
<td>4-6</td>
<td>3-7</td>
</tr>
<tr>
<td>Hb F (%)</td>
<td>5-6</td>
<td>0-4</td>
</tr>
<tr>
<td>(\beta/\alpha) ratio</td>
<td>0.26</td>
<td>0.55</td>
</tr>
</tbody>
</table>

The proband showed a hypochromic anaemia with a strong haemolytic component, normal MCV, low MCH, decreased osmotic fragility, unbalanced \(\beta/\alpha\) globin synthesis ratio, and increased levels of Hb \(A_2\) and Hb F. A peripheral blood smear showed anisopoikilocytosis, hypochromia, basophile stippling, target cells, and the presence of schistocytes and erythroblasts (~50% of all nucleated cells). The patient became pregnant at 30 and 32 years of age. The first pregnancy ended with the premature birth of an immature infant who died of sepsis shortly after birth. During the second pregnancy, which resulted in the delivery at term of a healthy baby, the patient was repeatedly transfused in order to keep the Hb levels between 12 and 13 g/dl.

The mother of the proband is an apparently healthy woman whose heterozygosity for \(\beta\) thalassaemia is indicated only by a moderate increase of Hb \(A_2\) and an unbalanced \(\beta/\alpha\) globin synthesis ratio. The same abnormality, an increase of Hb \(A_2\) and slightly decreased osmotic fragility, was found in an aunt and two brothers of the mother. The father and other members of the family were not available for examination; the only important information we could obtain was the existence of consanguinity between the proband's parents.

On the basis of the clinical, haematological, and biochemical data, we concluded that the patient had a very mild form of \(\beta\) thalassaemia caused (considering the consanguinity of the parents) by homozygosity for the same kind of mutation.

Molecular analysis

Various regions of the \(\beta\) globin genes of the proband were amplified with different primer combinations.
Discussion

The highly conserved sequence AATAAA, found 10 to 30 nucleotides upstream of most polyadenylation sites in eukaryotic mRNA, forms a part of the recognition site for endonucleolytic cleavage of primary transcripts.10

In a cloned β thalassaemia gene containing an AATAAA>AACAAA mutation, a fraction of the β globin mRNA extends at least 900 bp 3’ of the normal polyadenylation site. The cleavage and polyadenylation at the normal polyadenylation site is markedly inefficient but not completely extinguished.2 The presence of normally processed RNA probably accounts for the mild phenotype in carriers of a mutation in the cleavage-polyadenylation sequence.2

Elongated RNA transcripts have also been observed in a human α thalassaemia gene containing an AATAAA>AATAAG mutation in the cleavage-polyadenylation sequence of the α2 globin gene.10 11 When this gene is transfected into HeLa cells it not only fails to process the 3’ end, but also fails to terminate transcription.10 The amount of normal α2 mRNA present in the reticulocytes of the homozygous α thalassaemia patient is about 10 to 20% of that found in a normal subject.11

Jankovic et al1 described the AATAAA>AATGAA mutation in the β globin gene of Yugoslavian, Greek, and Bulgarian subjects. Haematological data from these subjects, all heterozygotes or compound heterozygotes, displayed a rather mild β+ thalassaemia phenotype comparable to that of the mother of the proband described in this paper. Since no information was provided by Jankovic et al1 on the haplotype on which the mutation occurs in these subjects, we cannot speculate on the origin of the mutation in the Dutch patient.

Until now four different mutations in the AATAAA sequence of the β globin gene (AACAAA, AATGAA, AATAGA, AATAAG) have been described, causing a mild form of β thalassaemia.1-3 A combination with other more severe types of β thalassaemia might result in a transfusion dependent β thalassaemia major syndrome, while in combination with milder mutations, an intermediate type of thalassaemia, like in the proband, is usually observed.3

We are grateful to Dr J W Werre who brought the patient to our attention.

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