Filipino $\beta^0$ thalassaemia: a high Hb A$_2$ $\beta^0$ thalassaemia resulting from a large deletion of the 5' $\beta$ globin gene region

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Abstract

A large novel deletional $\beta$ thalassaemia mutation associated with unusually high levels of haemoglobin (Hb) A$_2$ in heterozygotes is described in two unrelated subjects of Filipino background. The deletion was characterised by DNA mapping including pulsed field gel electrophoresis. Filipino $\beta$ thalassaemia extends for approximately 45 kb beginning approximately 1.5 kb 3' to the $\delta$ globin gene. It is the largest deletion to date which gives rise to the $\beta$ thalassaemia phenotype. This mutation, similar to previously described deletional $\beta$ thalassaemias associated with high Hb A$_2$, removes sequences 5' to the $\beta$ globin gene promoter and emphasises the functional importance of the 5' $\beta$ globin region in eliciting the unusually high level of Hb A$_2$. This example also suggests that it is the 3' sequences which are transposed rather than the actual deletion size which are significant in the raised fetal haemoglobin (Hb F) found with some of the thalassaemias.

Materials and methods

Patients

Whole blood samples were collected with heparin or EDTA as anticoagulants from a 35 year old female (NP) detected on a routine screen and a 30 year old female (LD) as part of routine antenatal tests. Both subjects were Filipino immigrants.

Haemoglobin analyses

Hematological data were obtained from freshly collected blood samples using an automated cell counter. Hb electrophoresis was performed at pH 8.9 on cellulose acetate strips in a Tris-EDTA-borate buffer. Hb A$_2$ was quantitated by elution after electrophoresis on cellulose acetate at pH 8.9. Hb F was quantitated by a modified Betke method.

DNA analysis

Genomic DNA was prepared from peripheral blood buffy coats by phenol-chloroform extraction, digested with restriction endonucleases, separated by electrophoresis through 0.8% agarose gels, and transferred by Southern blotting. DNA probes were labelled with $^{32}$P dCTP. Membranes were hybridised overnight at 65°C with $10^6$ cpm/ml $^{32}$P labelled probe and washed at 65°C to a stringency of 0.1 × SSC and 0.1% SDS for one hour, followed by autoradiography. Three probes from the $\beta$ globin gene cluster were used: (1) 2.3 kb PstI 5; (2) 4.4 kb PstI 5; (3) 2 kb BglII/XbaI fragment of the $\psi$ beta gene. DNA probes from 3' to the $\beta$ globin gene cluster used included: (1) pKRR29, a 1.2 kb EcoRI fragment approximately 18 kb 3' to $\beta^0$; (2) the 3D probe, a 1.0 kb BamHI/EcoRI genomic fragment from the 3' end of Negro HPFH-1; (3) the H500 probe, a 0.5 kb HindIII unique fragment approximately 25 kb 3' to the 3' end of Negro HPFH type 1 obtained from the 5' end of the deletion (~45 kb) was estimated by pulsed field gel electrophoresis. Previous deletions of similar size are associated with increased fetal haemoglobin (Hb F) and are found in (Hb) thalassaemia or hereditary persistence of fetal haemoglobin (HPFH). However, in the current deletion the Hb F levels were not remarkably raised. These data show that DNA sequences surrounding this deletion breakpoint have more relevance to the Hb F phenotype than the actual deletion size and confirm the association between loss of the 5' $\beta$ globin gene specific promoter region and a very high level of Hb A$_2$. 

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from the p3`N10R; (4) the 3' IH probe, a 0.75 kb HindIII-EcoRI fragment from a plasmid containing a 1.1 kb BamHI-BglII genomic fragment obtained from the 3' end of an Indian HPFH deletion, approximately 30 kb 3' to the $\beta$ globin gene; and the 3' VH probe, a 873 bp SacI-BamHI fragment from the 3' breakpoint of Vietnamese HPFH (Motum et al, in preparation). The positions of these probes are illustrated in fig 1B.

**PULSED FIELD GEL ELECTROPHORESIS**

DNA for pulsed field gel electrophoresis was prepared from fresh lymphoblastoid cells from a Filipino $\beta$ thalassaemia heterozygote (NP) and a normal subject. DNA was isolated in agarose blocks and digested with the restriction enzyme SfiI. Specimens were then electrophoresed on the Biorad CHEF-DRII system (Biorad, Richmond CA) for 24 hours at 200 V with pulse times ranging from 20 to 50 seconds. DNA was transferred onto nylon filters (Hybond, Amersham) and hybridised with the PslI $\delta$, PslI $\beta$, and the 3' VH probes labelled by the random hexamer primer method.

**Results**

**HAEMATOLOGY**

Both subjects had a microcytic hypochromic anaemia and haematological parameters consistent with $\beta$ thalassaemia trait but had unusually high levels of Hb A, of 7-7 and 7-5% (table 1). The Hb F level was normal in LD and raised in NP at 4-0%. The latter is only slightly higher than that normally seen in heterozygous $\beta$ thalassaemia.

**RESTRICTION ENDONUCLEASE ANALYSIS**

DNA from NP and LD was digested with various restriction enzymes and hybridised to the $\psi\beta$, PslI $\delta$, and PslI $\beta$ probes from the $\beta$ globin gene cluster to define the 5' breakpoint of the deletion. Subsequently these digests were hybridised to the pRK29, 3' VH, 3' IH, H500, and 3D probes to characterise the 3' breakpoint. In addition to the normal bands, restriction fragments of abnormal size were also present with PslI $\delta$ probe (table 2, fig 2). Since NP and LD are heterozygotes, the normal bands are derived from the wild type $\beta$ globin allele, while the abnormal fragments are from the mutant allele. Hybridisation with the $\psi\beta$ and PslI $\beta$ probes did not show any abnormal bands although the intensity of hybridisation for PD with the PslI $\beta$ probe was significantly reduced. Normal bands were detected with all the 3' globin cluster probes. Reduced intensity of hybridisation was shown with the pRK29, 3' VH, and 3IH probes. Hybridisation with the H500 and 3D probes was entirely normal. Using this information the 5' breakpoint was localised between the AccI site (present) and its nearby 3' EcoRI site (deleted) downstream of the $\delta$ globin gene (fig 2). The 3' breakpoint could not be mapped precisely on restriction enzyme analysis using the probes available. However, it extended beyond the 3' IH probe which was deleted but did not

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**Table 1** Haematological parameters in heterozygous Filipino $\beta$ thalassaemia.

<table>
<thead>
<tr>
<th>Subject</th>
<th>Sex/age</th>
<th>Hb (g/dl) (12.5–16.5)</th>
<th>MCV (f) (76–96)</th>
<th>MCH (pg) (27–31)</th>
<th>Hb $A_2$ (%) (15–37)</th>
<th>Hb F (%) (&lt;1.0)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NP</td>
<td>F/35</td>
<td>12.7</td>
<td>72</td>
<td>22</td>
<td>7.7</td>
<td>4.0</td>
</tr>
<tr>
<td>LD</td>
<td>F/30</td>
<td>10.8</td>
<td>67</td>
<td>23</td>
<td>7.5</td>
<td>1.0</td>
</tr>
</tbody>
</table>

The normal ranges are indicated below the parameter in parentheses.

**Table 2** Comparison of restriction fragment lengths in normal subjects and heterozygous Filipino $\beta$ thalassaemia.

<table>
<thead>
<tr>
<th>Probe</th>
<th>Enzyme</th>
<th>Normal DNA (kb)</th>
<th>NP &amp; LD DNA* (kb)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PslI</td>
<td>Accl</td>
<td>3.5, 2.4</td>
<td>3.5, 2.4</td>
</tr>
<tr>
<td></td>
<td>AccI</td>
<td>4.4, 4.0</td>
<td>4.4, 4.0</td>
</tr>
<tr>
<td></td>
<td>BamHI</td>
<td>15.4, 17</td>
<td>15.4, 17, 9.8</td>
</tr>
<tr>
<td></td>
<td>BglI</td>
<td>&gt;30</td>
<td>&gt;30, 16.5</td>
</tr>
<tr>
<td></td>
<td>BglII</td>
<td>8.2, 5.0</td>
<td>8.2, 5.0</td>
</tr>
<tr>
<td></td>
<td>EcoRI</td>
<td>2.3, 1.8</td>
<td>2.3, 1.8, 6.6</td>
</tr>
<tr>
<td></td>
<td>EcoRV</td>
<td>15.5</td>
<td>15.5, 8.3</td>
</tr>
<tr>
<td></td>
<td>HpaI</td>
<td>7.5, 2.0, 1.5</td>
<td>7.5, 2.0, 1.5</td>
</tr>
<tr>
<td></td>
<td>HindIII</td>
<td>17.5, 7.8, 6.0</td>
<td>17.5, 7.8, 6.0</td>
</tr>
<tr>
<td></td>
<td>NcoI</td>
<td>&gt;8.4</td>
<td>8.4, 4.0</td>
</tr>
<tr>
<td></td>
<td>PswI</td>
<td>12.8</td>
<td>12.8, 16.0</td>
</tr>
<tr>
<td></td>
<td>SacI</td>
<td>16.4</td>
<td>16.4, 18.0</td>
</tr>
<tr>
<td></td>
<td>XbaI</td>
<td>11.1</td>
<td>11.1, 12.3</td>
</tr>
</tbody>
</table>

* Abnormal bands in the probes are underlined.
following digestion probes. Restriction subject (N) XbaI (Bgl) BglII; (H) HindIII; (Bgl) BglI; (E) EcoRI; (Pv) PvuII; (A) AccI. The normal restriction map was derived from the GenBank databank. In the Filipino thalassaemia allele the AccI site at 57450 was present and the EcoRI site at 58035 was absent (both detected with the PstI δ probe).

The approximately 600 bp region of uncertainty is indicated by the hatched area. The restriction sites 3' to the breakpoint in the new DNA are indicated (*). (C) Autoradiograph showing the bands detected with the PstI δ probe in a normal subject (N) and the subjects heterozygous for Filipino β thalassaemia (NP and LD) following digestion with the restriction enzymes EcoRI and AccI.

Figure 2. Restriction map of the normal (A) and abnormal (B) chromosomes surrounding the 5' breakpoint of Filipino β thalassaemia using the PstI δ and PstI β probes. Restriction enzyme sites are: (N) NcoI; (B) BamHI; (X) XmnI; (Xb) XbaI; (Bgl) BglII; (H) HindIII; (Bgl) BglI; (E) EcoRI; (S) SstI; (V) EcoRV; (Pv) PvuII; (A) AccI. The normal restriction map was derived from the GenBank databank. In the Filipino β thalassaemia allele the AccI site at 57450 was present and the EcoRI site at 58035 was absent (both detected with the PstI δ probe). The approximately 600 bp region of uncertainty is indicated by the hatched area. The restriction sites 3' to the breakpoint in the new DNA are indicated (*). (C) Autoradiograph showing the bands detected with the PstI δ probe in a normal subject (N) and the subjects heterozygous for Filipino β thalassaemia (NP and LD) following digestion with the restriction enzymes EcoRI and AccI.

Figure 3. Summary of the β thalassaemia deletions with the corresponding levels of Hb A2 and Hb F in heterozygotes. The numbers correspond to the GenBank coordinates and the sizes of the deletions are in kilobases (kb).

Figure 4. Size of the deletion on PFGE DNA from NP was digested with SfiI and hybridised consecutively with probes PstI δ, PstI β, and 3'VH. In addition to the normal ~140 kb band there was a new 95 kb band detected with the PstI δ probe (fig 1). There were no abnormal bands detected with the PstI β or 3'VH probes consistent with deletion of these loci. These data indicate that the deletion is ~45 kb in size.

Discussion
There are currently over 100 mutations associated with β thalassaemia. The majority involve single base substitutions producing transcription, RNA modification, and translation mutants. There are only eight deletional forms of β thalassaemia. These range from 290 bp to 12-6 kb in size, and are rare except for the Asian Indian deletion type 2 (fig 3). In this study we have defined a new Filipino type β thalassaemia deletion of approximately 45 kb extending from a region 1-1 to 1-7 kb 3' to the δ globin gene. The 3' breakpoint of the Filipino type β thalassaemia could not be precisely defined owing to the limited restriction map and sequence data 3' to the δ globin gene. However, the deletion is the largest described to date which still retains the phenotype of β thalassaemia.

The Filipino β thalassaemia defect joins a discrete groups of thalassaemias which have large deletions of 30 to 50 kb in size. Other members of this group include German Gy(Ay6I)β thalassaemia, Belgian Gy(Ay6I)β thalassaemia, Turkish Gy(Ay6I)β thalassaemia, Black Gy(Ay6I)β thalassaemia, Indian HPFH (HPFH-3), Italian HPFH (HPFH-4), and Vietnamese HPFH (Motum et al, in preparation). All except the Filipino β thalassaemia are characterised by significantly raised Hb F levels. Although some increase in Hb F was observed in one of the two affected subjects, it was only a modest rise (4-0%) and lower than those usually found in heterozygotes with deletion HPFH and Gy(Ay6I)β thalassaemia (ranges in Hb F of 10 to 30% and 4 to 19% respectively). These observations would suggest that the functional nature of the sequences transposed to the β globin gene cluster rather than deletion size is an important determinant of Hb F phenotype.

β thalassaemia heterozygotes with Filipino β thalassaemia have unusually high levels of Hb A2 (mean 7-6%) similar to other examples of deletional β thalassaemia which remove the 5' β globin gene and its associated promoter sequences (fig 3). Family studies in heterozygotes for β thalassaemia and a δ chain variant have shown that the increased Hb A2 in β thalassaemia is derived from δ chains in cis and trans to the β thalassaemia gene. However, a more recent study has shown that the excess Hb A2 is derived from the δ gene in cis to the deletional β thalassaemia allele. The common

Involving the H500 probe which was present (fig 1).

The size and nature of the deletions involved determine the level of Hb A2 and Hb F which are usually very high. The deletions often cause excess synthesis of δ chains which co-migrate with Hb A2 and F in electrophoresis. These deletions are usually due to large deletions in the β-globin locus.

A summary of the deletions observed is given in fig 3. The deletions range from 21 to 124 kb in size and all are derived from the β-globin locus.

The largest deletion observed was a 95 kb deletion which extended from a region 1-1 to 1-7 kb 3' to the δ globin gene. The 3' breakpoint of the Filipino type β thalassaemia could not be precisely defined and is indicated by the hatched area.

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molecular feature of the high Hb A1 producing deletions is their 5' breakpoint regions which lie upstream from the β mRNA cap site.

Thus the β globin gene promoter TATA, CCAAT, and CACCC boxes which are involved in regulation of transcription are deleted.37 The mechanism(s) by which sequences in the 5' β globin gene might influence the δ and γ globin gene expression have not been fully elucidated. Deletions removing the β globin gene promoter regulatory sequences could alter competition for limiting transcription factors and make the latter more available to the δ globin promoter to increase transcription of the δ globin gene. If this were the mechanism for the raised Hb A1 it should affect both the δ gene in cis and in trans to the β thalassaemia allele.

Alternatively it has been suggested that the transcription of the δ globin gene promoter could be influenced by loss of the 5' β promoter, if both are affected by the same 3' enhancer.38 Enhancers have been identified downstream from the Αγ39 and β globin genes40 and on either side of the β globin gene cluster.41 In the latter may be found the locus control regions (LCRs) which consist of five DNase I hypersensitive sites 5' to the α globin gene and one site 21-3 kb (HBS VI) 3' to the β globin gene. Transgenic and transfection experiments have confirmed the critical role played by the LCR in globin gene regulation.40,41 The LCR is thought to represent one mechanism by which deletions of the β globin cluster can have cis acting effects over consider-able distances.41 In the deletional β thalassaemias the absence of a functional β globin gene promoter might permit an enhancer such as the LCR to interact with the δ globin gene in cis. Thus the 3' breakpoint in itself does not appear to play a role in the generation of the high Hb A1 β thalassaemia phenotype, but it may influence the degree of γ chain compensation.

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