Haemoglobin Lepore in Cyprus

Z. ZACHARIADIS, P. E. NUTE, and G. STAMATOYANNPOULOS

From the Central Laboratory, Nicosia General Hospital, Nicosia, Cyprus, and the Departments of Medicine (Division of Medical Genetics) and Anthropology, and the Regional Primate Research Center, University of Washington, Seattle, Washington 98195, USA

Summary. Structural analysis documented the presence of haemoglobin Lepore_{Washington} (= Lepore_{Boston}) in a Greek Cypriot family and provided further evidence that, of the various types of Lepore mutants, only one is common in the Mediterranean area. Two individuals in this family were heterozygous for both Hb Lepore and β thalassaemia, but they exhibited striking differences in the clinical severity and course of the disease. The data illustrate that additional environmental or genetic factors play roles in determining or modifying the pathophysiological consequences of highly specific molecular defects and, thus, their ultimate clinical phenotypes.

Since the original description of Hb Lepore in persons of Mediterranean descent (Gerald and Diamond, 1958), several studies have shown that the Lepore mutants are not uncommon in southern European and near Eastern populations. The Hb Lepore trait has been detected among Greeks (Fessas et al., 1962; Malmos et al., 1962; Stamatoyanopoulos and Fessas, 1963, 1964; Fraser et al., 1964; Stamatoyanopoulos, unpublished data), Yugoslavians (Fraser et al., 1966; Duma et al., 1968), Italians (Pearson et al., 1959; Silvestroni and Bianco, 1963; Barkham et al., 1964; Labie et al., 1966; Quattrin et al., 1967; Quattrin and Venturato, 1974), Rumanians (Rowley et al., 1969), Turkish Cypriots (Beaven et al., 1964), and Iranians (Rahbar et al., 1974). The data suggest that the Lepore trait is spread throughout the areas in which the β-thalassaemia genes exist at polymorphic frequencies. In this paper we present evidence that the Lepore trait is present in Greek Cypriots. Structural analysis identified the variant observed in Cyprus as Hb Lepore_{Washington} (= Lepore_{Boston}) and supports the view that only one, among several possible Lepore mutants, is common in Mediterranean populations.

Methods

Haematological studies were performed using standard techniques. Haemolysates were examined by starch-gel electrophoresis in a Tris-borate buffer system, pH 8.6 (O. Smithies, cited in Huehns and Shooter, 1965). Levels of Hb F were measured by alkali denaturation (Betke et al., 1959). In addition, the relative proportions of haemoglobin A, A2, F, and the abnormal component were determined following their isolation by chromatography of 2.5 × 44.5 cm columns of DEAE-Sephadex (A-50) (Huisman and Dozy, 1965), employing a gradient formed by mixing 1 litre of 0.05 mol/l Tris-HCl, pH 8.0 (starting buffer) with 1 litre of 0.05 mol/l Tris-HCl, pH 7.3 (limiting buffer). All buffers were 0.002 mol/l in KCN. Isolated haemoglobins were identified and checked for purity by starch-gel electrophoresis as described above.

Following acid-acetone precipitation of haem-free globin from the abnormal chromatographic fraction, α and non-α chains were separated on a 2 × 10 cm column of Whatman CM-52 carboxymethyl-cellulose according to the method of Clegg et al. (1968).

Isolated non-α chains (56 mg) were dialysed free of salts, lyophilized, and aminoethylated as described by Jones (1964), with the exceptions that urea was replaced by an equimolar amount of guanidine-HCl and 2-mercaptopethanol was substituted by 40 mg of dithioerythritol. After digestion by trypsin-TPCK (Worthington Biochemical Co), 2.8 mg of peptides were subjected to paper electrophoresis in a buffer of pyridine, acetic acid, and water (10:0.4:90 by volume), pH 6.4 (Ingram, 1958), followed by descending chromatography in a solvent of pyridine, isoamyl alcohol, and water (35:35:30 by volume) (Baglioni, 1965). Peptides were located by staining with 0.3% buffered ninhydrin in acetone and tryptophan-containing peptides were detected with the Ehrlich reagent (Easley, 1965). A second map was

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prepared using 5.9 mg of the digest. Selected peptides were eluted (Sanger and Tuppy, 1951; Clegg et al, 1966) with 6 mol/l HCl, hydrolysed for 24 h in sealed capillary tubes, and subjected to amino-acid analysis.

The ratio of γ chains containing glycine in position 136 to those with alanine in this position was determined for Hb F from the proposita. Haem-free globulin F was cleaved by cyanogen bromide and the C-terminal γ-chain fragment (γCB-3) was isolated on a 1.8 × 292 cm column of Sephadex G-50 (fine) equilibrated and developed with 1% formic acid (Nute et al, 1973). Following recovery by lyophilization, the γCB-3 fragments were dissolved in 6 mol/l HCl and duplicate hydrolysates were made in vacuo at 108°C for 24 h before amino-acid analysis.

**Family report**

**Proposita.** The proposita (II.1, Fig. 1) was referred for study at the age of 8 because she presented with pallor and her spleen was palpable to 3 cm below the costal margin. Her bodily development was normal. Haematological examination revealed a moderate anaemia (Hb = 7.8 g/dl, PCV = 33, RBC = 4.7 × 10^{12}/l, MCV = 70 fl, MCH = 16.6 pg, and MCHC = 23.7 g/dl). Blood films showed striking abnormalities in erythrocyte morphology, with hypochromia, moderate microcytosis and anisocytosis, poikilocytosis, leptocytosis, mild anisochromia, moderate numbers of target cells, and a few fragmented cells. The reticulocyte count was 2.1% and no normoblasts were observed. Chromatography of the proposita's haemoglobins (Fig. 2) and identification of the various components by starch-gel electrophoresis showed that Hbs F + F1 + A3 constituted 79.5% of the total. Haemoglobins A and A2 were present at levels of 10.5% and 2.9%, respectively; the remaining 7.5% consisted of an abnormal component which resembled the Hbs Lepore both electrophoretically and chromatographically. The proposita had never required transfusions.

**Other family members.** Examination of other members of the family (Fig. 1) revealed that the father had typical β-thalassaemia trait with elevated Hb A2 (5.3%). The mother showed haematological signs of thalassaemia trait (Hb = 12.4 g/dl, PCV = 41, RBC = 5.61

![Fig. 1. Family pedigree.](image)

![Fig. 2. Elution profiles produced by chromatography of haemolysates from the proposita and her mother on DEAE-Sephadex (see text for details).](image)

Results

Peptide maps (Fig. 3) of the non-α chains from the abnormal haemoglobin showed no sign of a peptide corresponding in position to βT3. However, a peptide was present whose position closely
approximated that predicted for δT₃. Moreover, the peptides whose locations roughly approximated those of βT₁₀ and βT₁₂ appeared to have slightly slower chromatographic mobilities than would be expected of normal β-chain peptides, suggesting that the abnormal chain was δ-like through residues 86 or 87. The presence of a peptide corresponding in position to βT₁₂b indicated that the chain was β-like in structure from positions 116 through 146.

Amino-acid analyses (Table I) confirmed the suspected δ-β structure of the abnormal chain, showing it to be δ-like from the N-terminus through position 87 and β-like in positions 116 through the C-terminus. Positions 88 through 115 are identical in both δ and β chains and, hence, could be specified by the corresponding portions of either the β- or δ-chain genes. Analysis of peptides T₂, T₃, T₁₀, T₁₁, T₁₂a, and T₁₂b (constituting residues 83 through 120) produced no evidence of deletion or duplication of any residues, indicating that the crossover which led to the formation of the δ-β gene resulted in the synthesis of a chain with 146 residues. Thus, the structure of the abnormal chain corresponds to that described for the δ-β chain of Hb LeporeWashington (= LeporeBoston) (Baglioni, 1962, 1965; Baglioni and Ventruto, 1968).

The results of γCB-3 analysis indicated that the proportions δγ and γγ chains in the Hb F of the proposita are well within normal limits. The values of 0.41 and 0.40 residues of glycine and 2.63 residues of alanine obtained from the two analyses demonstrate that the ratio of δγ to γγ chains is 2:3, the ratio expected for the Hb F of normal individuals after the first year of life (Schroeder and Huisman, 1970). Apparently, the deletion of portions of the δ- and β-chain genes that occurs with the formation of the δ-β gene of Hb LeporeWashington has no obvious effects on the relative activities of the δγ and γγ genes in the genome.

**Discussion**

The structures of the Lepore haemoglobins as products of unequal crossing over between β and δ

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**TABLE I**

AMINO-ACID COMPOSITIONS OF SELECTED PEPTIDES FROM THE δ-β CHAINS OF HB LEPOREWASHINGTON*

<table>
<thead>
<tr>
<th>Peptide</th>
<th>δ-like</th>
<th>Identical in δ and β</th>
<th>β-like</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>T₂</td>
<td>T₃</td>
<td>T₄</td>
</tr>
<tr>
<td>Asp</td>
<td>0.94 (1)</td>
<td>1.86 (2)</td>
<td>2.88 (3)</td>
</tr>
<tr>
<td>Thr</td>
<td>0.84 (1)</td>
<td>0.97 (1)</td>
<td>1.27 (1)</td>
</tr>
<tr>
<td>Glu</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Pro</td>
<td>1.00 (1)</td>
<td>1.87 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Gly</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Ala</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Val</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Met</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Leu</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Tyr</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Phe</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Lys</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>His</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Arg</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>Trp†</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
<tr>
<td>SAE-Cys</td>
<td>1.00 (1)</td>
<td>1.82 (2)</td>
<td>1.91 (2)</td>
</tr>
</tbody>
</table>

* Those peptides in which β and δ chains are known to differ, plus peptides constituting the region in which the transition from δ- to β-chain structure occurs (residues 88 to 115), were selected for analysis. Numbers in parentheses refer to the compositions of corresponding peptides in normal δ (for the δ-like peptides) and β (for the β-like peptides) chains.
† Detected on maps after staining with the Ehrlich reagent (Easley, 1965).
<table>
<thead>
<tr>
<th>Type</th>
<th>δ-β chain structure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hollandia</td>
<td>$\delta$ 22 50 $\beta$</td>
</tr>
<tr>
<td>Baltimore</td>
<td>$\delta$ 50 $\beta$</td>
</tr>
<tr>
<td>Washington</td>
<td>$\delta$ 86 86 $\beta$</td>
</tr>
</tbody>
</table>

![Image](http://jmg.bmj.com/)

The three structural types of δ-β chains found in the Lepore haemoglobins: Hb Lepore\textit{Hollandia} (Barnabas and Muller, 1962), Hb Lepore\textit{Baltimore} (Oster tag and Smith, 1969), and Hb Lepore\textit{Washington} (Baglioni, 1962; Labie et al, 1966). The broken lines connecting the δ- and β-like sequences represent those segments of the chains that are identical in both δ and β chains.

Genes have been well documented. Of the several theoretical δ-β products of such events (Smithies, 1964; Stamatoyannopoulos et al, 1969), three have been characterized (Fig. 4). Analyses of the Lepore mutants from Italian (Baglioni, 1965; Labie et al, 1966; Baglioni and Venturro, 1968; Quattrini and Venturro, 1974) and Greek (Baglioni and Venturro, 1968) individuals suggest that only one type, Hb Lepore\textit{Washington}, is common among Mediterranean populations. Our study supports this view, as it demonstrates unequivocally that the abnormal haemoglobin in the Cypriot family is identical in structure to Hb Lepore\textit{Washington}. The uniformity of the structural analyses suggests that the Lepore variants in the various Mediterranean populations share a common origin or that the type of crossover giving rise to the δ-β chains of Hb Lepore\textit{Washington} occurs more frequently than do those responsible for other Lepore mutants. Alternatively, if one assumes that all types of Hb Lepore occur as new mutations with nearly equal frequencies, the Hb Lepore\textit{Washington} trait may confer a greater selective advantage on its carriers than either the Lepore\textit{Baltimore} or Lepore\textit{Hollandia} traits, especially in those environments where the thalassaemia trait appears to be favoured by selection.

The discordance in the clinical courses of II.1 and II.3 described in this report is of interest. Both have the Hb Lepore/β-thalassaemia genotype and, presumably, identical defects in β-chain synthesis. The older child has a mild disease which was first detected at the age of 8 years; the clinical course is that of thalassaemia intermedia. The younger child has shown the signs of a severe β-thalassaemia major; typically, she began to receive transfusions at the age of 6 months. This striking difference illustrates that several genetic and/or environmental factors, in addition to the manifestations of the basic molecular lesion, take part in shaping the final clinical presentation of a genetic disease. In the case of these two sibs, differences in the proportion of the erythroid cell population involved in γ-chain synthesis, or differences in the rate of degradation of excess α chains in normoblasts might underlie the discordance in clinical phenotypes.

Ashiotis et al (1973) have shown that 10% of the Cypriot population carry α-thalassaemia-1 or α-thalassaemia-2 genes. Given this high frequency of carriers, it is not unlikely that the least severely affected sib (II.1) bears an α-thalassaemia gene in addition to being heterozygous for both Hb Lepore and β thalassaemia. Association of α thalassaemia with homozygosity for the β-thalassaemia determinant is expected to ameliorate the effects of the latter condition by partially correcting the imbalance between amounts of α and β chains synthesized (Fessas, 1967; Kan and Nathan, 1970). Reduction in the level of excess α chains will lower the extent of ineffective erythropoiesis and produce a more favourable clinical picture (Fessas, 1967). Thus, approximately 1 in 10 Cypriots with homozygous β thalassaemia should present with mild symptoms, owing to the presence of an α-thalassaemia determinant in his genome; this is the approximate proportion of mildly affected β-thalassaemia homozygotes in the patient population of Cyprus and among Cypriots attending paediatric clinics in London (B. Modell, personal communication). It appears likely that the inheritance of an α-thalassaemia gene by II.1 but not by II.3 is the cause of the clinical discordance between the two sibs of identical Hb Lepore/β-thalassaemia genotypes. Unfortunately, we have not yet been able to test this possibility by carrying out studies of haemoglobin synthesis.

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**References**


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