

# A nucleotide change at a splice junction in the human $\beta^0$ -globin gene is associated with $\beta^0$ -thalassemia

(human  $\beta$ -globin/splicing/ $\beta^0$ -thalassemia)

MICHAEL BAIRD\*, CATHERINE DRISCOLL\*, HELEN SCHREINER\*, GIUSEPPINA V. SCIARRATTA†, GENNARO SANSONE‡, GULZAR NIAZI‡, FRANCESCO RAMIREZ§, AND ARTHUR BANK\*

\*Columbia University, College of Physicians and Surgeons, Departments of Medicine, Pediatrics, and Human Genetics and Development, 701 West 168th Street, New York, New York 10032; †Centro della Microcitemia, Ospedali Galliera, Via Volta 8, Genoa, Italy; ‡International Health Resource Center of Hawaii, International Reference and Research Center for Blood Diseases, Kauai Preventive Medicine Program, Lihue, Hawaii, Hawaii; and, §Rutgers University Medical School, Department of Obstetrics and Gynecology, Piscataway, New Jersey

Communicated by Elvin A. Kabat, April 6, 1981

**ABSTRACT**  $\beta^0$ -Thalassemia is a heterogeneous group of disorders associated with absence of  $\beta$ -globin. In a survey of DNAs from patients with  $\beta^0$ -thalassemia of diverse ethnic origins, a change at the splice junction at the 5' end of the large intervening sequence (IVS 2) of the human  $\beta$ -globin gene has been found in one patient of Italian and another two of Iranian ethnic origins. The enzyme *Hph* I recognizes a change at this site and generates a larger-than-normal fragment of DNA, which hybridizes specifically to a  $\beta$ -globin IVS 2 probe. No other changes in  $\beta$ -globin gene DNA structure or organization are detectable by extensive restriction endonuclease analysis. The enzyme *Hinfl* which recognizes a sequence beginning three nucleotides from the 5' end of the IVS 2 splice junction, produces normal fragments and localizes the defect to a G-G-T sequence at the 5'-end IVS 2 splice junction. This sequence is known to be remarkably conserved in all globin genes from many species and in most other genes examined to date. Thus, in at least some  $\beta^0$ -thalassemia patients, the  $\beta^0$ -thalassemia defect is associated with a nucleotide change at a splice junction. These patients provide unique examples of naturally occurring defects in splice junctions of eukaryotic genes associated with absence of specific gene function.

The  $\beta^0$ -thalassemias are a heterogeneous group of disorders all characterized by absent  $\beta$ -globin synthesis (1–3). At the mRNA level, the  $\beta^0$ -thalassemias are characterized by one of the following: (i) the absence of  $\beta$ -globin mRNA; (ii) the presence of  $\beta$ -globin mRNA that is abnormal in structure, usually in reduced amounts; or (iii) an unspecified defect in  $\beta$ -globin mRNA in patients from the Ferrara region of Italy (4–10). Gene mapping studies to date, using many different restriction enzymes, have failed to reveal deletions or other alterations in nucleotide sequence in the majority of  $\beta^0$ -thalassemia patients examined (11–14). Deletion of the 3' end of the  $\beta$ -globin gene has been described in a few patients with  $\beta^0$ -thalassemia of Indian extraction (13, 14). In addition, a nonsense mutation at codon 17 has been reported by analyzing the  $\beta$ -globin cDNA structure of a patient with  $\beta^0$ -thalassemia (15). To specifically evaluate splice junctions in the  $\beta$ -globin gene in patients with  $\beta^+$ - and  $\beta^0$ -thalassemia, we utilized a cloned probe representing the large intervening sequence (IVS 2) of the  $\beta$ -globin gene ( $\beta$ -globin IVS 2 probe). Using this probe, we found three individuals homozygous for  $\beta^0$ -thalassemia who generate a unique fragment of DNA that is 100 base pairs longer than the normal fragment with the enzyme *Hph* I. This enzyme recognizes the 5'-end IVS 2 splice junction in the  $\beta$ -globin gene (16, 17); we further localized the nucleotide change to one of three nucleotides of a

G-G-T sequence at the 5'-end IVS 2 splice junction using *Hinfl*; the G-G-T sequence is completely conserved in all globin genes from all species studied to date and in most other genes (18, 19). We conclude that this change in nucleotide sequence at the 5' end of the  $\beta$ -globin IVS 2 splice junction is most likely the cause of the  $\beta^0$ -thalassemia genotype in these individuals.

## MATERIALS AND METHODS

All three patients with homozygous  $\beta^0$ -thalassemia found to have DNA changes had the clinical features of severe homozygous  $\beta$ -thalassemia and parents with classical high  $A_2$   $\beta$ -thalassemia trait. DNA was prepared from peripheral blood samples as described (20). Restriction endonuclease analysis, transfer of DNA fragments to nitrocellulose filters, hybridization to  $^{32}$ P-labeled DNA probes, and radioautography were performed as described (20). The specific probes used were a 4.4-kilobase (kb) *Pst* I cloned DNA fragment (4.4-kb probe), a 0.92-kb  $\beta$ -globin IVS 2 probe, and a 0.95-kb  $\delta$ -globin IVS 2 probe. Each of these probes were obtained by appropriate cleavage of pBR322 plasmids containing these fragments (21, 22). H $\beta$ 1S was obtained from T. Maniatis; this is the pBR322 plasmid containing the 4.4-kb human  $\beta$ -globin gene cloned fragment. The  $\delta$ - and  $\beta$ -globin IVS 2-containing pBR322 plasmids were prepared in our laboratory by isolation of *EcoRI*-*Bam*HI digestion fragments from the  $\delta$ - and  $\beta$ -globin IVS 2 and subsequent cloning into pBR322 (22). Each of the probes was isolated from pBR322 after growth and labeled by nick translation to specific activities between  $1 \times 10^8$  and  $8 \times 10^8$  cpm/ $\mu$ g (20).

## RESULTS

**Specificity of  $\beta$ - and  $\delta$ -Globin IVS 2 Probes.** Specificity was demonstrated by hybridizing the  $\beta$ - and  $\delta$ -globin IVS 2 probes to *EcoRI*- and *EcoRI/Bam*HI-digested DNA from normal individuals. Studies (1, 11, 20) have indicated that the 5.2-kb *EcoRI* fragment contains the  $\beta$ -globin IVS 2 and the 2.25-kb *EcoRI* fragment contains the  $\delta$ -globin IVS 2 (Fig. 1A); in this study (Fig. 1B), the  $\beta$ -globin IVS 2 probe specifically hybridized to the 5.2-kb fragment, and the  $\delta$ -globin IVS 2 probe hybridized to the 2.25-kb fragment, indicating their specificity. Further, when normal DNA was cleaved with *EcoRI* and *Bam*HI, the appropriately sized IVS 2-containing fragment was hybridized with its specific probe. In the case of the  $\delta$ -globin IVS 2, a 0.95-kb fragment was hybridized, whereas with  $\beta$ -globin IVS 2, a 0.92-kb fragment was hybridized (data not shown). These studies indicate that the  $\beta$ -globin IVS 2 probe only hybridizes with

The publication costs of this article were defrayed in part by page charge payment. This article must therefore be hereby marked "advertisement" in accordance with 18 U. S. C. §1734 solely to indicate this fact.

Abbreviations: IVS, intervening sequence; kb, kilobase.

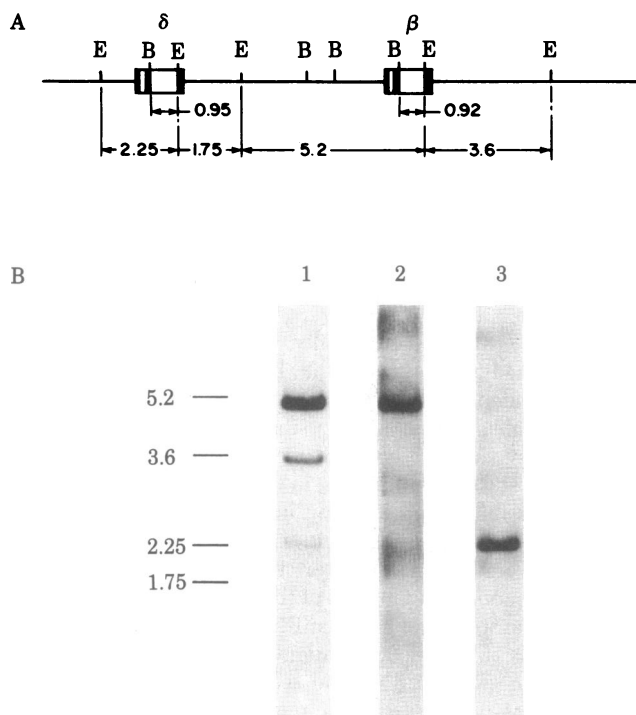


FIG. 1. Specificity of  $\beta$ - and  $\delta$ -globin IVS 2 probe. (A) Restriction map of  $\delta$ - and  $\beta$ -globin genes showing *EcoRI* (E) and *BamHI* (B) sites. The rectangles are the structural genes, in which the dark areas are the coding sequences, and the light areas are the IVSs. The sizes of the *EcoRI* fragments and the *BamHI*-*EcoRI* fragments containing IVS 2 of the  $\delta$ - and  $\beta$ -globin genes are shown in kb. (B) Radioautographs of *EcoRI*-digested normal human DNA, subjected to electrophoresis and hybridization with  $^{32}\text{P}$ -labeled DNA probes. The only difference in the three lanes is the origin of the probe (see text). Lanes: 1, 4.4-kb probe; 2,  $\beta$ -globin IVS 2 probe; 3,  $\delta$ -globin IVS 2 probe. The  $\beta$ -globin IVS 2 hybridizes only to the 5.2-kb fragment, and the  $\delta$ -globin IVS 2 hybridizes to the 2.25-kb fragment alone, indicating their specificity.

fragments of DNA containing the  $\beta$ -globin IVS 2 and not with other DNA fragments containing either  $\beta$ -globin structural genes alone,  $\delta$ - or  $\gamma$ -globin gene sequences, or other unrelated DNA sequences.

**A Change in *Hph* I Cleavage Site in the  $\beta$ -Globin IVS 2 in Three Patients Homozygous for  $\beta^0$ -Thalassemia.** The enzyme *Hph* I is known to cleave at the 5' end of  $\beta$ -globin IVS 2 (17) (Fig. 2A). A single fragment, 0.9-kb in size, was generated from  $\beta$ -globin IVS 2 in normal DNA when this cleavage took place and the  $\beta$ -globin IVS 2 probe was used (Fig. 2). In three patients homozygous for  $\beta^0$ -thalassemia, one of Italian and another two of Iranian ethnic origins, a new fragment, 1.0-kb in size, was found, consistent with the loss of an *Hph* I site at the 5' end of the  $\beta$ -globin IVS 2 (Fig. 2). Loss of an *Hph* I site 3' to IVS 2 would be expected to generate a 1.2-kb fragment (Fig. 2A). When the three  $\beta^0$ -thalassemia DNAs showing the abnormal 1.0-kb *Hph* I fragment were cleaved with both *Hph* I and *BamHI*, a 0.95-kb fragment was generated, confirming that the altered *Hph* I sequence is at the 5' end of the  $\beta$ -globin IVS 2, rather than at the 3' end (data not shown). If the 3'-end *Hph* I site in  $\beta$ -globin IVS 2 had been affected, this double digestion would have resulted in no significant change in the size of the fragments from that with *Hph* I alone (Fig. 2). Five patients with homozygous  $\beta^+$ -thalassemia and 10 other patients homozygous for  $\beta^0$ -thalassemia produced normal-sized 0.9-kb fragments with *Hph* I (Fig. 2).

**Analysis with Other Restriction Enzymes.** Cleavage of the  $\beta^0$ -thalassemia DNAs containing the abnormal *Hph* I pattern

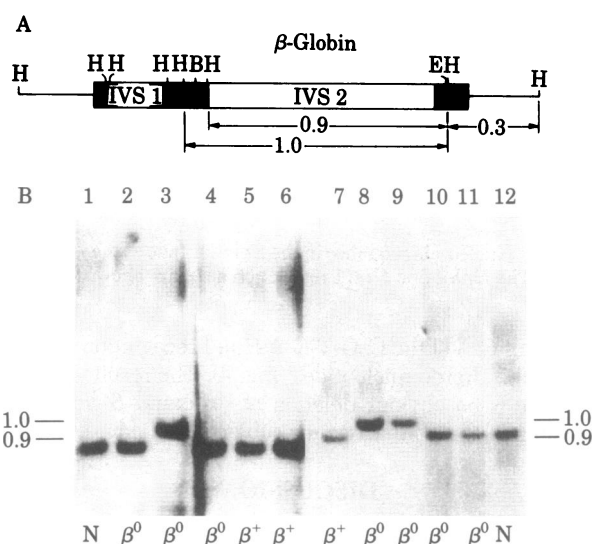


FIG. 2. *Hph* I cleavage of normal and  $\beta$ -thalassemia DNAs. (A) Restriction map of the *Hph* I (H), *BamHI* (B), and *EcoRI* (E) sites in the  $\beta$ -globin gene. The dark areas are the coding regions of the gene. The sizes of *Hph* I fragments are shown in kb. A 0.9-kb fragment is expected with the  $\beta$ -globin IVS 2 probe. (B) Radioautographs of *Hph* I-digested DNAs treated as described and hybridized to a  $^{32}\text{P}$ -labeled  $\beta$ -globin IVS 2 probe. The source of the DNAs used, normal (N) and  $\beta^+$ - and  $\beta^0$ -thalassemia patients, is indicated below. Lane 3 contains the DNA from the  $\beta^0$ -thalassemia patient from Northern Italy described in the text; lanes 8 and 9 are DNAs from two Iranian patients.

with other enzymes, such as *EcoRI* alone, *EcoRI* and *BamHI*, *Pst* I, *Asu* I, *Hae* III, and *Hinf* I, showed no changes from normal (Fig. 3). The presence of a normal *Hinf* I pattern with the  $\beta$ -globin IVS 2 probe was particularly informative because this enzyme recognizes the nucleotides that are three to seven bases away from the 5' end of the IVS 2 (Figs. 3 and 4). Thus, the normal *Hinf* I patterns in the three affected  $\beta^0$ -thalassemia subjects indicate that these nucleotides are intact and eliminate the

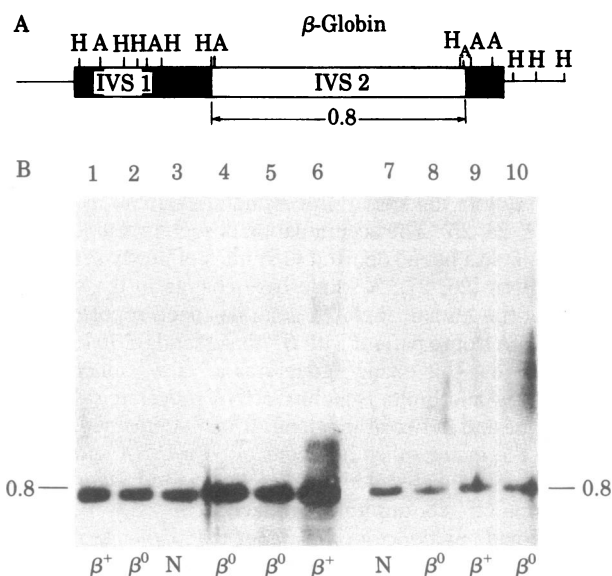


FIG. 3. Restriction analysis of normal (N) and  $\beta^+$ - and  $\beta^0$ -thalassemia DNAs with *Hinf* I (H) and *Asu* I (A). (A) Restriction map of the  $\beta$ -globin gene. The dark areas are the coding regions of the gene. The *Hinf* I and *Asu* I fragments expected in normal DNA with the  $\beta$ -globin IVS 2 probe are 0.8 kb. DNA in lanes 1-6 are cleaved with *Hinf* I and in lanes 7-10 with *Asu* I. Lanes 4 and 8 contain DNA from the  $\beta^0$ -thalassemia patient from Italy with an abnormal *Hph* I fragment.



4. Forget, B. G., Benz, E. J., Skoulchi, A., Baglioni, C. & Housman, D. (1974) *Nature (London)* **247**, 379–385.
5. Ramirez, F., Starkman, D., Bank, A., Kerem, H., Cividalli, G. & Rachmilewitz, E. A. (1977) *Blood* **266**, 231–238.
6. Kan, Y. W., Holland, J. P., Dozy, A. M. & Varmus, H. E. (1975) *Proc. Natl. Acad. Sci. USA* **72**, 5140–5144.
7. Ramirez, F., O'Donnell, J. V., Marks, P. A., Bank, A., Musumeci, S., Schiliro, G., Pizzarelli, G., Russo, G., Luppis, B. & Gambino, R. (1976) *Nature (London)* **263**, 471–480.
8. Ottolenghi, S., Comi, B., Giglioli, B., Williamson, R., Vullo, C., Del Senno, L. & Conconi, F. (1977) *Nature (London)* **266**, 231–240.
9. Old, J. M., Proudfoot, N. J., Wood, W. G., Longley, J. I., Clegg, J. B. & Weatherall, D. J. (1978) *Cell* **14**, 289–298.
10. Benz, E. J., Forget, B. G., Helliman, D. G., Cohen-Solal, M., Pritchard, J., Cavallese, C., Prenskey, W. & Housman, D. (1978) *Cell* **14**, 299–312.
11. Mears, J. G., Ramirez, F., Leibowitz, D. & Bank, A. (1978) *Cell* **15**, 15–23.
12. Bank, A., Mears, J. G., Ramirez, F., Burns, A. L. & Feldenzer, J. (1979) in *Eukaryotic Gene Regulation*, eds. Axel, R., Maniatis, T. & Fox, F. C. (Academic, New York), pp. 355–366.
13. Flavell, R. A., Bernards, R., Kooter, J. M. & deBoer, R. (1979) *Nucleic Acids Res.* **6**, 2749–2760.
14. Orkin, S. H., Old, J. M., Weatherall, D. J. & Nathan, D. G. (1979) *Proc. Natl. Acad. Sci. USA* **76**, 2400–2404.
15. Chang, J. C. & Kan, Y. W. (1979) *Proc. Natl. Acad. Sci. USA* **76**, 2886–2889.
16. Lawn, R. M., Fritsch, E. F., Parker, R. C., Blake, G. & Maniatis, T. (1978) *Cell* **15**, 1157–1174.
17. Lawn, R. M., Efstradiatis, A., O'Connell, C. & Maniatis, T. (1980) *Cell* **21**, 647–651.
18. Breathnach, R., Benoist, C., O'Hare, K., Gannon, F. & Chambon, P. (1978) *Proc. Natl. Acad. Sci. USA* **75**, 4853–4857.
19. Efstradiatis, A., Tosakany, J. W., Maniatis, T., Lawn, R. M., O'Connell, C., Spritz, R. A., DeRiel, J. K., Forget, B. J., Weissman, S. M., Slightom, J. L., Blechl, A. E., Smithies, D., Baralle, F. E., Shoulders, C. C. & Proudfoot, N. J. (1980) *Cell* **21**, 653–668.
20. Mears, J. G., Ramirez, F., Leibowitz, D., Nakamura, F., Bloom, A., Konotey-Ahulu, F. & Bank, A. (1978) *Proc. Natl. Acad. Sci. USA* **75**, 1222–1226.
21. Rodriguez, R. L., Bolivar, F., Goodman, H. M., Boyer, H. W. & Betlach, M. (1976) in *Molecular Mechanisms in the Control of Gene Expression*, eds. Nierlich, D. P., Rutter, W. J. & Fox, C. F. (Academic, New York), pp. 471–478.
22. Burns, A. L., Spence, S., Kosche, K., Ramirez, F., Mears, J. G., Schreiner, H., Miller, C., Baird, M., Leibowitz, D., Giardina, P., Markenson, A. & Bank, A. (1981) *Blood* **57**, 140–146.
23. Wilkinson, T., Chua, C. G., Correll, R. W., Robin, H., Exner, T., Lee, K. M. & Kronenberg, H. (1975) *Biochim. Biophys. Acta* **393**, 195–200.
24. Kacian, D. L., Gambino, R., Dow, L. W., Grossbard, E., Natta, C., Ramirez, F., Spiegelman, S., Marks, P. A. & Bank, A. (1973) *Proc. Natl. Acad. Sci. USA* **70**, 1886–1890.
25. Nienhuis, A. W., Turner, P. & Benz, E. J. (1977) *Proc. Natl. Acad. Sci. USA* **74**, 3960–3964.
26. Kantor, J. A., Turner, P. H. & Nienhuis, A. W. (1980) *Cell* **21**, 149–158.
27. Maquat, L. E., Kinniburgh, A. J., Beach, L. R., Honig, G. R., Lazerson, J., Ershler, W. B. & Ross, J. (1980) *Proc. Natl. Acad. Sci. USA* **77**, 4287–4291.
28. Spritz, R. A., Jagadeeswaran, P., Choudary, P. V., Biro, P. A., Elder, J. T., deRiel, J. K., Manley, J. L., Gefter, M. L., Forget, B. G. & Weissman, S. M. (1981) *Proc. Natl. Acad. Sci. USA* **78**, 2455–2459.
29. Gannon, F., O'Hare, K., Perrin, F., LePenncce, J. P., Benoist, C., Cochet, M., Breathnach, R., Royal, A., Garapin, A., Carri, B. & Chambon, P. (1979) *Nature (London)* **278**, 428–434.
30. Leder, P., Hansen, J. N., Konkel, D., Leder, A., Nishioka, Y. & Talkington, C. (1980) *Science* **209**, 1336–1342.
31. Hamer, D. H. & Leder, P. (1979) *Cell* **18**, 1299–1309.
32. Hamer, D. H. & Leder, P. (1979) *Nature (London)* **281**, 35–42.
33. Mulligan, R., Horward, E. & Berg, P. (1979) *Nature (London)* **277**, 108–112.
34. Shander, M., Van der Woude, S., Proudfoot, N. & Maniatis, T. (1981) *J. Supramol. Struct. Cell. Biochem. Suppl.* **5**, 229.