Medical Journal of the
Islamic Republic of Iran

Volume 8
Number 2
Summer 1373
August 1994

Basic Science In Medicine

MOLECULAR STUDIES ON THE DISTRIBUTION OF β - THALASSEMIA IN IRAN: THE BASIS FOR PRENATAL DIAGNOSIS

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ABSTRACT

By application of modern recombinant DNA technology, especially the polymerase chain reaction (PCR)/dot-blot hybridization techniques, we have investigated the molecular basis of β-thalassemia from four different regions of Iran: central, south-east, south and north. In this study, the DNA samples were isolated from patients and for the identification of the mutations, the 6 oligonucleotide probes for the mutations of IVS.1/nt. 110, IVS.1/nt.6, IVS.1/nt.1, nonsense codon 39, frameshift codon 8 and IVS.2/nt.1 were selected with respect to their relative frequency in the neighbouring country, Turkey. Four mutations accounted for 76.2% and of these, the most frequent was the nonsense codon 39 mutation, which accounts for 60.3% of the β-thalassemia alleles tested. The remainder, in decreasing order of frequency, were frameshift codon 8(9.5%), IVS.1/nt.6 (4.8%) and IVS.1/nt.110(1.6%). No hybridization was observed with the probes corresponding to the mutations of IVS.1/nt.1(G/A) and IVS.2/nt.1(G/A). These results also revealed that the distributions of different types of mutations were different in the four regions. This information and the introduction to the methodology used in this study will facilitate the prenatal diagnosis of the disease in Iran.

MJIRI, Vol. 8, No. 2, 101-107, 1994.

Keywords: β-Thalassemia, β-Globin gene mutations, Polymerase chain reaction, Molecular hybridization,Regional distribution.

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INTRODUCTION

Worldwide, β-thalassemia is one of the most common hereditary autosomal recessive disorders, primarily in regions of the world endemic for malaria, including the Mediterranean basin, West Africa, India, wide parts of Asia and south China.[1-16] This heterogenous genetic disease has mutations that is ethnically specific because of malaria-positive selective pressure.[7]

It has been estimated that 3% of the world population, or 150 million people, carry a β-thalassemia gene.[2,5] The disease is characterized by a deficiency or absence of β-globin production by different mechanisms, resulting in dependence on blood transfusion to sustain life. Indeed, most homozygous patients present with a most severe transfusion-dependent anemia within the first 2 years of life and later suffer from the long-term consequences of iron overload (thalassemia major).

Heterozygous subjects are usually asymptomatic. Their hematology is characterized by a slight to moderate anemia with a marked hypochromia and microcytosis (thalassemia minor).[2]

Even with chelation therapy to remove excess iron stores, the life expectancy in classic β-thalassemia major is shortened to 25 to 30 years on average.[5]

β-Thalassemia defects in Mediterraneans (Italians, Greeks and Turks) living in the United States were among the first to be identified[12,17,18] and the results of these studies were later confirmed by others. The mutations described in the first studies have been found to be common in many Mediterranean countries. In 1978, the β-globin gene was one of the first human genes to be cloned in bacteria.[19] It was fortunate that the gene was unusually small and simple for a human gene: it is 1.6 kb in size occurring only once in the haploid human genome (single copy). It is arranged together with the other β-like globin genes (ε,G_γ and A_γ and δ) in a 60 kb gene complex on the short arm of chromosome 11(11p15).[5,7] The coding information of all globin genes is contained on three exons which are divided by two introns of largely unknown function.[20,21]

Regarding the pathology of β-thalassemia, the expression of the β-globin gene can be inactivated at any step on its way from DNA to protein (transcription, RNA processing, translation) by more than 100 known mutations resulting in β-thalassemia. Although the degree to which these processes are affected frequently varies with the type of mutation, the identification of these mutations, the determination of the severity of each mutation, and the search for other factors that could modify the clinical presentation of the disease (haplotype, α-thal., high HbF determinants) is one of the prerequisites of a comprehensive prenatal diagnosis program.[12]

Advances in recombinant DNA technology, especially the polymerase chain reaction (PCR)/dot blot hybridization techniques, have led to the elucidation of the molecular etiology of many types of β-thalassemia.[22-28] To date, there are more than 100 known different β-thalassemia mutations.[5,7,17,29-40] However, in spite of this heterogeneity in the molecular genesis of this disease, a much more limited number accounts for the inactivation of most β-globin genes in many affected populations. In general, each population tends to have a different group of mutations consisting of a few that are very common and a variable number of rare ones,[8,15,17-18,41-55] although exceptions could be found and some mutations were present in several populations.[43]

Regarding the spectrum of mutations which differs considerably between different ethnic groups, many examples could be mentioned. For example, in Sardinia, the codon 39(C/T) nonsense mutation can be found in about 95% of the β-thalassemia genes.[56] In other populations, the genetics are not quite as homogeneous but 10 mutations or less account for more than 90% of all β-thalassemia genes in most ethnic groups. 10 mutations have been described in Asia Indians, of which five have been found to be the most common.[8,25,31,41,43] Also, five mutations appear to be prevalent in Mediterraneans: IVS-I-110(G→A), codon 39 (C→T), IVS-I-6(T→C), IVS-I-1(G→A) and IVS-II-745 (C→G).[6,9,17,34,36,41,48,50,51,53,56-57] In addition, the screening of large numbers of Mediterranean β-thal. patients during the last several years has resulted in the detection of many other mutations which occur at intermediate and low frequencies.[5,58-62] Since the spectrum of mutations differ in each population, it might be expected that different ameliorating factors would predominate in each group and in general, this appears to be the case. This relative simplicity of the population genetics facilitates the practical approach to genetic screening and to prenatal diagnosis programs.

Mutational data maps prepared on a country and, if possible, regional basis, could facilitate the diagnostic procedure by indicating the screening sequence according to the incidence of each mutation. Country scale frequencies of β-thalassemia mutations have been already determined for several, mainly Mediterranean, countries[10,12,55,63-64] and also for Turkey.[57,65-67] However, in Iran, molecular diagnosis as well as mutational data maps at a regional basis are presently still unavailable. The present study which has been initiated as a first attempt in this direction has allocated the underlying mutation types in 63 β-thalassemia cases in four main regions of Iran, among which most of the study cases are obtained from Queshm Island, because this island is one of the biggest islands in the Persian Gulf, with a total population of 70,000 and a high rate of consanguineous marriages. Hence it is worth studying the presence of various kinds of mutations and molecular diagnosis of this genetic disorder among these people. In general, β-thalassemia is one of the major public health problems in Iran, where a total of 15000 β-thalassemic patients are living in different regions of the country. Yearly influx of population

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growth increases this figure by 1500 patients, which means the growth of β-thalassemia patients is one every 6 hrs. in Iran. The highest number of patients are living in Gilan, Mazandaran and Hormozgan province. In this study, for the first time, national screening for point mutations was initiated. In order to diagnose the type and frequency of β-thalassemia mutations in a large number of patients, considering the fact that these patients were chosen at random and some of them are related, this disuribution is expected to reflect the unbiased frequency of β-thalassemia mutations among the Iranian population. For the time being we are doing an extensive, national large scale screening and the results will be published in the near future.

MATERIALS AND METHODS

Blood samples

The blood samples (n= 319) were collected from the thalassemic patients and their families for β-thalassemia combination cases. Some of the samples were related. The localities of the origin of these individuals were determined through careful inquiries.

DNA isolation

DNA was isolated from each blood sample using the method described by Poncz et al.[68]

PCR primers and mutation specific probes

All primers for the PCR amplification and the mutation specific oligonucleotide probes used in the hybridizations[55,57] were synthesized with an LKB/Pharmacia Gene Assembler Plus DNA synthesizer.

Polymerase chain reaction (PCR)

PCR was carried out principally according to the method of Saiki et al.[27] Each amplification tube contained 50 mM KCl, 10 mM Tris-HCl (pH=8.3), 1.5 mM $MgCl_2$, 2 μM each primer, 0.2 mM each dNTP, 0.1μg of template DNA and 1.0 units of Taq Polymerase (Boehringer Mannheim) in a total volume of 50 μl. The PCR cycles were done either manually or by means of a Coy thermocycler. The cycles comprised incubations of 1 min. at 95°C, 1 min. at 60°C and 3 min. at 72°C. In total, 25-30 cycles were performed.

Dot blotting

Aliquots of the amplified product(5-8μ l) were adjusted to 0.4 M-NaOH/25 mM EDTA in a volume of 100μl and applied onto nylon membranes (Nytran-13). DNA was fed to the membrane by UV light (254 nm) for 2 min.

Mutation analysis by probe hybridizations and ARMS procedure

The oligonucleotide probes was labeled at the 5-end with ^{32}P, using [^{32}P] ATP (7000 Ci/mmol) (Dupont-NEN) and polynucleotide kinase. The membranes were prehybridized in a solution of 5×SSPE/5× Denhardt's/0.5% SDS for 30 min. at the hybridization temperature determined for each probe. Hybridization temperatures were determined according to the T_m values of each probe calculated by the relationship of T_m(°C)=4 (G+C)+2 (A+T). Thereafter, the radioactively labeled probe was added to the fresh hybridization solution and hybridization was conducted for 1 hr. at a hybridization temperature. The membrane was washed twice with 2×SSPE containing 0.1% SDS at room temperature, and once with 5×SSPE containing 0.1% SDS at washing temperature for 10 min. Membranes dried at room temperature were exposed to Kodak X-Omat AR film for 1-12 hr. at -70°C.[28]

RESULTS AND DISCUSSION

The development of new methodologies has facilitated the identification of β-thal. mutations, the most important being the polymerase chain reaction (PCR) procedure,[22,27] which has expedited the processes of screening for β-thal. defects[69] and sequencing of DNA.[24-25]

The results of the hybridizations of β-thalassemia chromosomes (i.e. the number of the dots hybridizing with at least one control probe from 319 β-thalassemia patients, out of which 63 random samples were chosen) with 6 different oligonucleotide probes corresponding to the mutations of IVS. 1/nt. 110 (G/A), IVS.1/nt. 6(T/C), IVS.1/nt.1 (G/A), nonsense codon 39, frameshift codon 8(-AA) and IVS.2/nt.1(G/A), are represented in Table I. Four mutations accounted for 76.2%, and the most frequent of these was the nonsense codon 39 mutation, which accounts for 60.3% of the β-thalassemia chromosomes tested. The remainder in decreasing order of frequency were frameshift codon 8(9.5%), IVS.1/nt.6 (4.8%) and IVS.1/nt. 110(1.6%). No hybridization was observed with the probes corresponding to the mutations of IVS.1/nt.1(G/A) and IVS.2/nt.1(G/A).

TABLE I. Frequencies of 6 β-thalassemic mutations in Iran

Mutation Type	No. of mutations	Frequency of mutations (%)
Nonsense Codon 39(C/T)	38	60.3
Frameshift Codon 8(-AA)	6	9.5
IVS.1/nt. 6(T/C)	3	4.8
IVS.1/nt. 110(G/A)	1	1.6
IVS.1/nt. 1(G/A)	-	0
IVS.2/nt. 1(G/A)	-	0

The distribution of the mutation types in heterozygotes, compound heterozygotes and homozygous cases are shown

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in Table II. The nonsense codon 39 mutation is present in all 5 compound heterozygous cases, in 75% of the homozygous cases and finally 90% of the heterozygous cases.

TABLE II. The distribution of the mutation types in homozygous, compound heterozygous and heterozygous cases.

Mutation Type	No. of samples
Fsc.8/Nonsense codon.39	3
IVS.1/nt.6/Nonsense codon.39	1
IVS.1/nt. 110/Nonsense codon.39	1
IVS.1/nt.6 homozygote	1
Nonsense codon.39 homozygote	3
Nonsense codon.39 heterozygote	27

Table III shows the distribution of β-thalassemic mutations among the DNA samples from Iran.

TABLE III. Distribution of β-thalassemic mutations among DNA samples from Iran.

DNA Sample Number	Mutation Type	Molecular Diagnosis
3	Fsc.8/Codon.39	Double Heterozygote
1	IVS.1-nt.110/Codon.39	Double Heterozygote
1	IVS.1-nt.6/Codon.39	Double Heterozygote
3	Codon.39	Homozygote
1	IVS.1-nt.6	Homozygote
3	Fsc.8	Heterozygote
27	Codon.39	Heterozygote

In this study, the DNA samples were isolated from patients from four different regions of Iran, and for the identification of the mutations, the 6 oligonucleotide probes for the mutations of IVS.1/nt.110, IVS.1/nt.6, IVS.1/nt.1. nonsense codon 39, frameshift codon 8 and IVS.2/nt.1. were selected with respect to their relative frequency in the neighbouring country, Turkey.[16] The nonsense condon 39(C/T) mutation which was the most frequent mutation in this study, is in agreement with previous studies in Sardinia,[50,56] Spain,[53] France[48] and Tunisia,[52] corresponding to a rather Western Mediterranean prototype.

Although these results appear to display some degree of heterogeneity, only a few mutations appear to be prevalent. Nearly 76% of β-thalassemia mutations have been identified with 4 probes in general, consistant with the findings of several other research groups,[50,53] and support the general observation that in most populations a few mutations (five or less) are prevalent and account for most of the β-thal. alleles. Nonsense codon 39 was found to be the most frequent mutation in Iran. On the other hand, unlike findings of other research groups[16,57,65-67] in which IVS.1/nt.110 (G/A) and IVS.1/nt.6(T/C) were found as the most frequent mutations in Turkey and a few other countries, these two mutations accounted for only 1.6% and 4.8% respectively in Iran. However, the frequency of IVS.1/nt.6(T/C) is relatively near the frequency of this mutation in Greece,[12] Lebanon[34] and France.[48] Likewise, the frequency of IVS.1/nt.110 (G/A) in Iran is roughly in agreement with that reported in other investigations[50] in the Sardinian population, but shows great differences with Cyprus (Turkish)[9], Lebanon,[34] Greece[12] and Turkey.[69]

Frameshift codon 8 (-AA) which accounts for 9.5% of our β-thal. alleles tested, is not among the few common β-thal. mutations in several Mediterranean countries.[5,9,12,34,41,48,50,52,53,56,58,69]

The results of the remaining two probes corresponding to the mutations of IVS.1/nt.1(G/A) and IVS.2/nt.1(G/A) which show no hybridizations in our tested samples, are consistent with the findings of other research groups in the Sardinian[50] population, whereas the former is also in agreement with results obtained from Lebanon[34] and the latter is consistent with reports from Sicily[70], Tunisia[52] and Spain.[53] Meanwhile, they are present among β-thal. mutations in Greece and Italy,[12,41,56] Yugoslavia,[63] and Turkey[58,69] populations in different frequencies.

TABLE IV. Regional distribution of β-thalassemic mutations in Iran

Region	Nc39 (θ)	Fsc8 (Ω)	IVS.1 nt.6	IVS.1 nt.110	IVS.1 nt.1	IVS.2 nt.1
A	9	2	3	1	-	-
B	27	3	-	-	-	-
C	1	-	-	-	-	-
D	2	1	-	-	-	-
Total	39	6	3	1	0	0

A, Central part of Iran (Tehran, Ghom, Saveh)
B, South-east (Queshm Island)
C, South (Shiraz)
D, North (Ramsar, Tonekabon)
(θ) Nonsense codon 39
(Ω) Frameshift codon 8(-AA)



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Of the six β-thalassemic mutations detected, the nonsense codon 39 (C/T) mutation appeared to be the most frequent on a regional basis (Table IV). The obtained samples from four Iranian regions comprises the following cities: Tehran, Ghom, Saveh, Shiraz, Ramsar, Tonekabon and Queshm Island.

Prevention of β-thalassemia by genetic counselling and prenatal diagnosis is an important health issue. Techniques for prenatal diagnosis of monogenic disorders by DNA analysis have progressed such that today, following DNA amplification by PCR, prenatal diagnosis by direct detection of relevant mutations is possible in most cases in the first trimester of pregnancy. The technique of allele-specific priming of the PCR used for carrier screening in this study has also been successfully used for over 100 cases of prenatal diagnosis.[71] As it detects the mutations directly, this method overcomes the labour -intensive process of studying the DNA polymorphisms in family members.

The results of this first attempt have potential important implications and may suggest that in Iran, as in many other countries (such as Greece)[12], it will be possible to perform prenatal diagnosis in most patients, especially in regions like Queshm Island by searching for a few mutations (although countries such as Tunisia[52] and Turkey[16,69] do not appear to follow this rule).

An extensive evaluation of the data with respect to possible region-dependent mutational differences will contribute to a better understanding of these mechanisms. Further studies including detailed family histories from patients and their relatives can possibly help to trace the precise geographical origins of the various alleles identified in this study. Also, further and more extensive large scale studies of regional distributions of β-thal. mutations, along with different types of this disease in Iran and their incidence, will undoubtedly contribute great insight to a more rational application for the planning of programs of β-thalassemia prevention.

ACKNOWLEDGEMENTS

We would like to express our gratitude to Mr. Karimi, Queshm Island Hospital, Mr. Tavakoli, Ms. Farivar and Ms. Karimi of NRCGEB, and Ms. Zoroofchi from the Childrens' Medical Center, Tehran University of Medical Sciences, for their helpful assistance. This work was supported by a grant from the National Research Centre for Genetic Engineering and Biotechnology (NRCGEB), Islamic Republic of Iran.

REFERENCES

1. Aksoy M, Dincol G, Erdem S: Survey on hemoglobin variants, β-thalassemia, G6PD deficiency and haptoglobin types in Turkish people living in Manavgat, Serik and Boztepe (Antalya). Hum Hered 1980, 30: 3-6.
2. Weatherall DJ, Clegg JB: The Thalassemia Syndromes. 3rd ed. Blackwell Scientific Publications, Oxford. 1981.
3. Yuregir GT, Aksungur P, Burgut R, Solakoglu A, Atalay EO, Aksoy M: A survey of high HbA_2 β- thalassemia hemoglobin variants, G6PD deficiency and iron-deficiency anemia in Karatas (Cukurova, Southern Turkey). Tr J Med Sci 1989; 13: 203-210.
4. Cavdar AO, Arcasoy A: The incidence of β-thalassemia and abnormal hemoglobins in Turkey. Acta Hematol 1971: 45: 312-318.
5. Kazazian HH, Boehm C: Molecular basis and prenatal diagnosis of β-thalassemia. Blood 1988, 72: 1107-1116.
6. Cao A, Gossens M, Pirastu M: β-thalassemia mutations in Mediterranean populations. Br J Hematol 1989, 71: 309-312.
7. Bunn HF, Forget BG: Hemoglobin: molecular, genetic and clinical aspects. WB Saunders, Philadelphia, 1986.
8. Thein SL, Hesketh C, Wallace RB, Weatherall DJ: The molecular basis of thalassemia major and thalassemia intermedia in Asian Indians: application to prenatal diagnosis. Br J Haematol 1988, 70.225-231.
9. Sozuoz A, Berkalp A, Figus A, Loi A, Pirastu M, Cao A: β-thalassemia mutations in Turkish Cypriots. J Med Genet 1988, 25: 766-768.
10. Schnee J, Eigel A, Horst J: Direct mutation analysis of β-thalassemia genes in families of various ethnic origins residing in Germany. Blut 1989, 59: 237-239.
11. Huang S, Zhou X, Zhu H, Ren Z, Zeng Y: Detection of β-thalassemia mutations in the Chinese using amplified DNA from dried blood specimens. Hum Genet 1990, 84: 129-131.
12. Kattamis C, Hu H, Cheng G, Reese AL, Gonzales Redondo JM, Kutlar A, Kutlar F, Huisman THJ: Molecular characterization of β-thalassemia in 174 Greek patients with thalassemia major. Br J Hematol 1990; 74: 342-346.
13. Lin LI, Links Lin KH, Chang HC: The spectrum of β-thalassemia mutations in Taiwan: identification of a novel frameshift mutation. Am J Hum Genet 1991, 48: 809-812.
14. Varawalls NY, Old JM, Sarkar Venkatesan R, Weatheral DJ: The spectrum of β-thalassaemia mutations on the Indian subcontinent: the basis for prenatal diagnosis. B J Haematol 1991, 78: 242-247.
15. Kulozik AE: β-thalassaemia: molecular pathogenesis and clinical variability. Eur J Pediatr 1992, 151: 78-84.
16. Atalay EO, Cirakoglu B, Dincolc G, Atalay A, Kilinc Y, Aytekin H, Yuregir GT, Arpaci A, Bermek E, and Aksoy M: Regional distributions of β-thalassaemia mutations in Turkey. Internat J Hematol 1993, 57, 207-211.
17. Orkin SH, Kazazian HH Jr, Antonarakis SE, Goff SC, Boehm CD, Sexton JP, Waber PG, Giardina PJV: Linkage of β-thalassaemia mutations and β-globin gene polymorphisms with DNA polymorphisms in human β-globin gene cluster. Nature 1982, 296, 627-631.
18. Kazazian HH Jr; Orkin SH, Markham AF, Chapman CR, Youssoufian H, Waber PG: Quantification of the close association between DNA haplotypes and specific β-thalassaemia mutations in Mediterraneans. Nature 1989, 310: 152-154.

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19. Lawn RM, Fritsch EF, Parker RC, Blake G, Maniatis T: The isolation and characterization of linked Y-and β-globin genes from a cloned library of human DNA. Cell 1978, 15: 1157.
20. Myers RM, Tilly K, Maniatis T: Fine structure genetic analysis of a β-globin promoter. Science 1986, 232: 613-618.
21. Kulozik AE, Bellan-Koch A, Bail S, Kohne F, Kleibauer E: Thalassemia intermedia: moderate reduction of β-globin gene transcriptional activity by a novel mutation of the proximal CACCC promoter element. Blood 1991, 77: 2054-2058.
22. Saiki RK, Scharf S, Faloona F, Mullis KB, Horn Gt, Erlich HA, Arnheim N: Enzymatic amplification of β-globin genomic sequences and restriction site analysis for diagnosis of sickle cell anemia. Science 1985, 230: 1350.
23. Mullis KB, Faloona F: Specific synthesis of DNA in vitro via a polymerase-catalyzed chain reaction. Methods Enzymol 1987, 155: 335.
24. Wrischnik LA, Higuchi RG, Stoneking M, Erlich HA, Arnheim N, Wilson AC: Length mutations in human mitochondrial DNA: direct sequencing of enzymatically amplified DNA. Nucleic Acids Res 1987, 15: 529.
25. Wong C, Dowling CE, Saiki RK, Higuchi RG, Erlich HA Kazazian HH: Characterization of β-thalassaemia mutations using direct genomic sequencing of amplified single copy DNA. Nature 1987, 330: 384-386.
26. Engeke DR, Hcener PA, Collins FS: Direct sequencing of enzymatically amplified human genomic DNA. Proc Natl Acad Sci USA 1988, 85: 544.
27. Saiki RK, Gelfand DH, Stoffel S, Scharf SJ, Higuchi R, Horn CT, Mullis KB, Enhrlich HA: Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. Science 1988, 239: 487-494.
28. Newton CR, Graham A, Heptinstall CE, Powell SJ, Summers C, Karlsheker N, Smith JC, Markham AF: Analysis of any point mutation in DNA: the amplification-refractory mutation system (ARMS). Nucl Acids 1989, 17: 2503-2516.
29. Orkin SH, Kazazian HH Jr: The mutation and polymorphism of the human β-globin genes and its surrounding DNA. Annu Rev Genet 1984, 18: 131-137.
30. Chen TC, Orkin SH, Antonarakis SE, et al: β-thalassaemia in China: use of in vivo RNA analysis and oligonucleotide hybridization in systematic characterization of molecular defects. Proc Natl Acad Sci USA 1984, 81: 2821-2825.
31. Kazazian HH, Orkin SH, Antonarakis SE, et al: Molecular characterization of seven β-thalassaemia mutations in Asian Indians. EMRO J 1984b, 3: 593-596.
32. Antonarakis SE, Orkin SH, Cheng TC, Scott AF, Sexton JP, Trusko SP, Charache S, Kazazian HH Jr: β-thalassemia in American Blacks: novel mutations in the 'TATA' box and an acceptor splice site. Proc Nat Acad Sci USA 1984, 81: 1154-1158.
33. Thein SL, Old JM, Fiorelli G, Wainscoat JS, Sampietro M, Wallace RB, Weatherall DJ: Feasibility of prenatal diagnosis of β-thalassaemia with synthetic DNA probes in two Mediterranean populations. Lancet, ii, 1985, 345-347.
34. Chehab FF, Der Kaloustian V, Khouri EP, Deeb SS, Kan YW: The molecular basis of β-thalassemia in Lebanon: application to prenatal diagnosis. Blood 1987, 69: 1141-1145.
35. Atweh GF, Wong C, Reed R, et al: A new mutation in IVS-1 of the human β-globin gene causing β-thalassamia due to abnormal splicing. Blood 1987, 1: 147-51.
36. Wainscoat JS, Old JM, Weatherall DJ, Orkin SH: Themolecular basis for the clinical diversity of β-thalassemia in Cypriotes. Lancet. 1983, i, 1235-1237.
37. Zhang J, Cai S, He X, Lin H, Huang Z: Molecular basis of β-thalassemia in South China: strategy for DNA analysis. Hum Genet 1988, 78: 37-40.
38. Novelletto A, Hafez M, Deidda G, Di Rienzo A, Felicetti L, EL-Tahan H, Morsi Z, El-Ziny M, AL-Tonbary Y, Sittien A, Terrenato L: Molecular characterization of β-thalassemia mutations in Egypt. Hum Genet 1990, 85: 272-274.
39. Lindeman R, Hu SP, Volepato F, Trent RJ: Polymerase chain reaction (PCR) mutagenesis enabling rapid non-radioactive detection of common β-thalassaemia mutations in Mediterraneans. Br J Haematol. 1991, 78: 100-104.
40 Varawalla NY, Old JM, Sarkar R, Venkatesan R, Weatherall DJ: The spectrum of β-thalassaemia mutations on the Indian subcontinent: the basis for prenatal diagnosis. Br J Haematol, 1991, 78: 242-247.
41. Kazazian HH Jr, Orkin SH, Antonarakis SE, Sexton JP, Boehm CD, GoffSC, Waber PG: Molecular characterization of seven β-thalassaemia mutations in Asian Indians. EMRO Journal, 1984a, 3: 593-596.
42. Antonarakis SE, Kazazian Jr HH, Orkin SH: DNA polymorphisms and molecular pathology of the human globin cluster. Hum Genet 1985, 96: 1-14.
43. Wong C, Antonarakis SE, Goff SC, Orkin SH, Boehm CD, Kazazian, HH: On the origin and spread of β-thalassemia: recurrent observation of four mutations in different ethnic groups. Proc Nat Acad Sci USA 1986, 83: 6529-6532.
44. Kazazian HH Jr, Dowling CE, Waber PG, Huang S, Lo WHY: The spectrum of β-thalassemia genes in China and South-east Asia. Blood. 1986, 68: 964-966.
45. Loi A, Pirastu M, Cao A, Ulbridh R, Hansmann L: Prenatal diagnosis of most common Mediterranean β-thalassaemia mutants. Lancet 1986, i: 274.
46. Chan V, Chan TK, Chebab FF, Todd D: Distribution of β-thalassemia mutations in South China and their association with haplotypes. Am J Hum Genet. 1987, 41: 678-685.
47. Wong C, Dowling CE, Saiki RK, Higuchi RG, Erlich H, Kazazian HH Jr: Characterization of β-thalassemia mutations using direct genomic sequencing of amplified single copy DNA. Nature 1987, 330: 384-386.
48. Milland M, Berge-Lefranc JL, Lena D, Cartouzou G: Oligonucleotide screening of β-thalassemia mutations in the south-east of France. Hemoglobin 1987, 11: 317-327.
49. Akar N, Cavadar AO, Dessi E, Loi A, Pirastu Cao A: β-thalassaemia mutations in the Turkish population. J Med Genet 1987, 24: 378-379.
50. Rosatelli C, Leoni GB, Tuven T, Scalas MT, Di Tucci A, Cao A: Thalassaemia mutations in Sardinians: implication for prenatal diagnosis. J Med Genet 1987, 24: 97-100.
51. Coutinho GomesMP, Gomes daCostaMG, Braga LB, et al: β-thalassaemia mutations in the Portuguese population. Hum Genet 1988, 78: 13-15.
52. Chibani J, Vidaud M, Duquesnoy P, et al: The peculiar

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spectrum of β-thalassaemia genes in Tunisia. Hum Genet 1988, 78: 190-192.

53. Amselem S, Nunes V, VidaudM, Estivill X, Wong C, d'Auriol L, Vidaud D, et al: Determination of the spectrum of β-thalassaemia in Spain by use of dot-blot analysis of amplified β-globin DNA. Am J Hum Genet 1988, 43: 95-100.
54. Wong C, Antonarakis SE, Goff SC, Orkin SH, Forget BG, Nathan DG, Giardina PJV, Kazazian HHJr: β-thalassemiadue to two novel nucleotide substitutions in consensus acceptor splice sequences of the β-globin gene. Blood 1989, 73: 914-918.
55. Kazazian HH: The thalassemia syndromes: Molecular basis and prenatal diagnosis in 1990. Sem Hematol 1990, 27: 209-228.
56. Pirastu M, Saglio G, Camaschella C, Loi A, Serra A, Bertero T, Gabutti W, Cao A: Delineation of specific β-thalassemia mutations in high-risk areas of Italy: A prerequisite for prenatal diagnosis. Blood 1988, 71: 983-988.
57. Diaz-Chico JC, Yang KG, Stoming TA, Efremov DG, Kutlar A, Kutlar F, Aksoy M, Altay C, Gurgey A, Kilinc Y, Huisman THJ: Mild and severe β-thalassemia among homozygotes from Turkey: identification of the types by hybridization of amplified DNA with synthetic probes. Blood. 1988, 71: 248-251.
58. Fei YJ, Stoming TA, Efremov GD, Efremov DG, Battacharia R, Gonzalez-Redondo JM, Altay C, Gurgey A, Huisman THJ: β-Thalassemia due to a T→A mutation within the ATA box. Biochemical and BiophysicalResearchCommunications 1988, 153: 741-747.
59. Gonzalez-Redondo JM, Kattamis C, Huisman THJ: Characterization of three types of β-thalassemia resulting from a partial deletion of the β-globin gene. Hemoglobin 1989a, 13: 377-392.
60. Gonzalez-Redondo JM, Stoming TA, Kutlar A, Kutlar F, Lanclos KD, Howard EF, Fei YJ, Aksoy M, Altay C, Gurgey A, Basak AN, Efremov GD, Petkov G, Huisman THJ: AC→T substitution at nt-101 in a conserved DNA sequence of the promoter region of the β-globin gene is associated with 'silent' β-thalassemia. Blood 1989b, 73: 1705-1711.
61. Jankovic L, Efremov GD, Petkov G, Kattamis C, George E, Yang KG, Stoming TA, Huisman THJ: Three novel mutations leading to β-thalassemia. (Abstract). Blood 1989, 74(Suppl): 63a.
62. Kollia P, Gonzalez-Redondo JM, Stoming TA, Loukopoulos D, Politis C, Huisman THJ: Frameshift codon 5 [FSC-5(-CT)] thalassemia: a novel mutation detected in a Greek patient. Hemoglobin 1989, 13: 597-604.
63. Dimovski A, Efremov DG, Jankovic L, Juricic D, Zixovski N, Stojnovski N, Nikoloy N, Petkov GT, Reese AL, Stoming TA, Efremov GD, Huisman THJ: β-thalassemia in Yugoslavia. Hemoglobin 1990, 14: 15-24.
64. Petkoy GH, Efremov GD, Efremov DG, Dimorski A, Tschaikorova P, Tschaikorova R, Rogina B, Kutlar A, Kutlar F, Reese AL, Stoming TA, Huisman THJ: β-thalassemia in Bulgaria. Hemoglobin 1990, 14: 25-33.
65. Oner R, Altay C, Gurgey A, Aksoy M, Kilinc Y, Stoming TA, Reese AL, Kutlar A, Kutlar F, Huisman THJ: β-thalassemia in Turkey. Hemoglobin 1990, 14; 1-13.
66. Basak AN, Ozcelik EL, Ozer A, Tolun A, Kirdar B: Molecular characteristics of Turkish patients with β-thalassemia. Tr J Med Sci 1991, 15: 426-434.
67. Basak AN, Ozcelik H, Ozer A, Tolun A, Aksoy M, Agaoglu L, Ridolfi F, Ulukutlu L, Akar N, Gurgey A, Kirdar B: Hum Genet 1992, (in press).
68. Poncz M, Solowiejczky D, Harpel B, Mory Y, Schwartz E, Surrey S: Construction of human gene libraries from small amounts of peripheral blood. Hemoglobin 1982, 6: 27-36.
69. Basak AN, Ozcelik H, Ozer A, Tolun A, Kirdar B, Aksoy M, Agaoglu L, Ulukutlu L, Cavdar A, Gurgey A: β-thalassemia in Turkey: a systematic molecular characterization of point-mutations by gene-amplification and dot-blot hybridization. Abstracts, Third International Conference of Thalassemia and the Hemoglobinopathies, Sardinia, April 1989, P. 16.
70. Di Marzo R, Dowling CE, Wong C, Maggio A, Kazazian HH Jr: The spectrum of β-thalassaemia mutations in Sicily. Br J Haematol. 1988, 69: 393-397.
71. Old JM, Varawalla NY, Weatherall DJ: Rapid detection and prenatal diagnosis of β-thalassaemia: studies in Indian and Cypriot populations in the U.K. Lancet 1990, 336: 834-837.

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