

Maple Syrup Urine Disease

Complete Primary Structure of the E₁β Subunit of Human Branched Chain α-Ketoacid Dehydrogenase Complex Deduced from the Nucleotide Sequence and a Gene Analysis of Patients with This Disease

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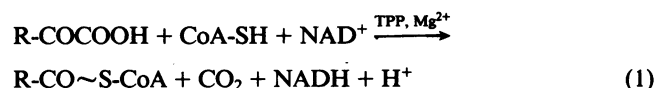
Abstract

A defect in the E₁β subunit of the branched chain α-ketoacid dehydrogenase (BCKDH) complex is one cause of maple syrup urine disease (MSUD). In an attempt to elucidate the molecular basis of MSUD, we isolated and characterized a 1.35 kbp cDNA clone encoding the entire precursor of the E₁β subunit of BCKDH complex from a human placental cDNA library. Nucleotide sequence analysis revealed that the isolated cDNA clone (λhBE₁β-1) contained a 5'-untranslated sequence of four nucleotides, the translated sequence of 1,176 nucleotides and the 3'-untranslated sequence of 169 nucleotides. Comparison of the amino acid sequence predicted from the nucleotide sequence of the cDNA insert of the clone with the NH₂-terminal amino acid sequence of the purified mature bovine BCKDH-E₁β subunit showed that the cDNA insert encodes for a 342-amino acid subunit with a *M_r* = 37,585. The subunit is synthesized as the precursor with a leader sequence of 50 amino acids and is processed at the NH₂ terminus. A search for protein homology revealed that the primary structure of human BCKDH-E₁β was similar to the bovine BCKDH-E₁β and to the E₁β subunit of human pyruvate dehydrogenase complex, in all regions. The structures and functions of mammalian α-ketoacid dehydrogenase complexes are apparently highly conserved. Genomic DNA from lymphoblastoid cell lines derived from normal and five MSUD patients, in whom E₁β was not detected by immunoblot analysis, gave the same restriction maps on Southern blot analysis. The gene has at least 80 kbp. (*J. Clin. Invest.* 1990. 86:242-247.) Key words: maple syrup urine disease • branched chain α-ketoacid dehydrogenase • complementary DNA • cloning • gene analysis

Introduction

Mammalian branched chain α-ketoacid dehydrogenase (BCKDH)¹ (EC 1.2.4.4) is a mitochondrial multienzyme complex catalyzing the oxidative decarboxylation of branched

chain α-ketoacids derived from amino acids such as valine, leucine, and isoleucine (reaction [1]).



The BCKDH complex consists of three catalytic components: branched chain α-ketoacid decarboxylase (E₁), dihydrolipoyl transacylase (E₂), and dihydrolipoamide dehydrogenase (E₃). E₁ is further composed of two subunits, E₁α and E₁β (1-3). E₁ and E₂ components are specific to BCKDH. On the other hand, the E₃ component is common among the three ketoacid dehydrogenase complexes, BCKDH, pyruvate dehydrogenase (PDH), and α-ketoglutarate dehydrogenase (4, 5). The BCKDH complex also contains two specific regulatory enzymes, a kinase (6-8) and a phosphatase (9, 10), responsible for regulation of the catalytic activity through phosphorylation and dephosphorylation.

E₁α is the catalytic subunit phosphorylated at two serine residues responsible for regulation of the catalytic activity by covalent modification (11-13). The function of E₁β is unknown (5). E₂ catalyzes the transfer of the acyl group from the lipoyl moiety to coenzyme A and forms the structural core of the enzyme complex. To this E₁, E₃, kinase, and phosphatase are bound through noncovalent interactions (1, 10, 14).

Lack of BCKDH activity leads to maple syrup urine disease (MSUD), an autosomal recessive inborn error of metabolism (4). Several different phenotypes of MSUD have been elucidated on the basis of clinical features, as follows: classical, intermittent, intermediate, thiamine responsive type, E₁β deficiency, E₂ deficiency, and E₃ deficiency (4). Etiology of MSUD is heterogenous, as mutations in different regions of any of the BCKDH proteins could lead to decreased functions of the entire complex.

We reported that a defect in the BCKDH-E₁β subunit is one cause of MSUD (15, 16). The isolation and characterization of cDNAs encoding all or a part of the human BCKDH-E₁α (17, 18), BCKDH-E₂ component (19-22), and E₃ component (23, 24) have been reported but the primary structure of human BCKDH-E₁β has not and the function of this subunit is not well understood. Molecular cloning of BCKDH-E₁β had not been successful, despite repeated attempts. Most recently, we isolated a cDNA clone corresponding to bovine BCKDH-E₁β (25). In an attempt to elucidate the molecular basis of the disease, we carried out cDNA cloning of the human BCKDH-E₁β. The nucleotide sequence and the primary structure of human BCKDH-E₁β has to be determined to analyze the alterations seen in studies on MSUD patients. We report herein isolation and characterization of a 1.35-kbp cDNA clone that encodes the complete human BCKDH-E₁β precursor. We also made a Southern blot analysis of the BCKDH-E₁β gene in

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1. Abbreviations used in this paper: BCKDH, branched chain α-ketoacid dehydrogenase; MSUD, maple syrup urine disease; PDH, pyruvate dehydrogenase.

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Epstein-Barr virus transformed lymphoblastoid cell lines derived from five nonrelated MSUD patients. BCKDH-E₁β was not detected by immunoblot analysis.

Methods

Materials. Restriction enzymes, pUC18 vector DNAs, 7-DEAZA Sequencing Kits, and random primer labeling kits were purchased from Takara Shuzo Co. (Kyoto, Japan). Nitrocellulose hybridization membranes were from Schleicher & Schuell, Inc. (Kassel, Federal Republic of Germany). [α -³²P]dCTP (specific activity, 3,000 Ci/mmol) were from Amersham Corp. (Arlington Heights, IL).

Isolation of cDNA. The human placental cDNA library constructed in λ gt11 (26) was kindly provided by Dr. J. E. Sadler (Howard Hughes Medical Institute, Washington University School of Medicine). The 1.7-kbp cDNA clone (λ BE₁β-2) for bovine BCKDH-E₁β was isolated using the mixture of synthetic oligonucleotides (17 mer, 24 mixture) as a probe for a bovine liver cDNA library constructed in λ gt11 (25). Approximately 6×10^5 recombinant phage plaques were screened from the human placental cDNA library using the 1.7-kbp cDNA clone (λ BE₁β-2) as a probe. The insert was labeled with [α -³²P] dCTP (3,000 Ci/mmol) using the random primer labeling kit. Prehybridization, hybridization, and washing of nitrocellulose filters were as described (27). Hybridizing plaques detected by autoradiography were picked up from the mother agar plate. Successive screenings were carried out, using fewer and fewer plaques at each step until well-isolated phage plaques had been cloned.

Restriction endonuclease map and nucleotide sequence analysis. Recombinant phage DNA was prepared as described (28). Eco RI-excised cDNA inserts were subcloned into plasmid vector pUC18 and characterized by restriction endonuclease mapping. Restriction fragments were subcloned into pUC18 for sequencing. In addition, ordered serial deletions from the 5' → 3' end of both strands of the pUC18 insert were produced with exonuclease III/mung bean nuclease for sequencing (29). DNA sequencing was performed by the dideoxy chain termination method (30) using an alkali-denatured plasmid as the template (31).

Protein data base search. Homologous amino acid sequences were sought in the GenBank (Release 59.0)/EMBL (Release 18.0) protein data base on a VAX computer using the Wordsearch program (32) (Version 6.0, April 1989). The Segments program was used for the alignment procedure.

Cell lines and cell culture. Lymphoblastoid cell lines derived from disease-free control male, and MSUD patients were established by Epstein-Barr virus-infected transformation of peripheral blood B lymphocytes (33). Kinetic studies on BCKDH activities and immunoblot analysis of BCKDH proteins of these cell lines from MSUD patients (K.Y., Y.T., E.K., T.Ho., Y.O.) have been reported (16). Lymphoblastoid cells were grown in RPMI 1640 medium containing penicillin (100 IU/ml) and streptomycin (100 μ g/ml) supplemented with 10% FCS in an incubator at 37°C. A subculture and a harvest were performed as described (15).

Southern blot analysis of genomic DNA. Total human genomic DNA was prepared from the lymphoblastoid cell lines, as described (34). Southern blotting was performed with 5.0–7.5 μ g of total genomic DNA. DNA was cut by restriction enzymes Bam HI, Eco RI, and Hind III, and subjected to electrophoresis on an 0.8% agarose gel for 14–20 h at 40 V. Southern blot hybridization was principally carried out according to the description of Southern (35). The cDNA insert (λ hBE₁β-1) was radiolabeled using a random primer labeling kit and [α -³²P] dCTP (3,000 Ci/mmol). The filters were prehybridized for 3 h in 50% Formamide, 5× SSC, 100 μ g/ml salmon testis DNA, 50 mM sodium phosphate (pH 6.5), 0.1% SDS, and 10× Denhardt's solution (1× Denhardt's = 0.02% polyvinylpyrrolidone, 0.02% BSA, 0.02% Ficoll). Hybridization was for 24 h in prehybridization buffer containing the labeled cDNA insert. The filters were washed for 1 h at 56°C in 0.1× SSC and 0.1% SDS with two to three changes. Nitrocellulose

membrane filters were exposed to film with intensifying screens at –76°C for 3–5 d.

Results and Discussion

To isolate the human BCKDH-E₁β cDNA clone, we initially screened $\sim 1 \times 10^6$ recombinant phage plaques of a human placental cDNA library constructed in λ gt11 (26), with a specific rabbit antibody raised against bovine BCKDH-E₁β, and obtained five positive clones. All were found to be false positive by nucleotide sequencing.

We then isolated and characterized a cDNA clone coding for bovine BCKDH-E₁β from a bovine liver cDNA library constructed in λ gt11 by screening with a mixture of synthetic oligonucleotide probes corresponding to the COOH-terminal 5-residue sequence of the bovine BCKDH-E₁β (25). Using this 1.7-kbp Eco RI fragment of bovine BCKDH-E₁β cDNA insert (λ BE₁β-2) as a probe, $\sim 6 \times 10^5$ plaque-forming units were screened from a human placental cDNA library. Only one positive clone (λ hBE₁β-1) was plaque purified to homogeneity through five successive rounds of screening, and the cDNA inserts were subcloned into the Eco RI site of pUC18 for further characterization. This recombinant phage clone insert had 1.35 kbp.

The restriction endonuclease map of a cDNA insert from the phage clone λ hBE₁β-1 and sequencing strategy for the insert are shown in Fig. 1. The nucleotide sequence and deduced amino acid sequence are shown in Fig. 2. The λ hBE₁β-1 insert is composed of 1,349 bp consisting of a 4-bp 5'-untranslated sequence, a 1,176-bp-long open reading frame, and a 169-bp 3'-untranslated sequence. The nucleotide sequence surrounding the putative initiator codon, GGGGAUGG, is rather different from the consensus sequence of CC₃CCAUGG (36). A polyadenylation signal of the type AATAAT (37) is found 7 bp upstream of a poly (A) tail.

The open reading frame could be translated into a 392-amino acid residue protein. Comparison of the amino acid sequence predicted from the nucleotide sequence of the clone cDNA insert with the NH₂-terminal amino acid sequence of purified bovine BCKDH-E₁β determined by Edman degradation (25) revealed that the NH₂-terminal 50-amino acid residues of the putative precursor protein are missing the mature E₁β. BCKDH-E₁β is a nuclear encoded mitochondrial protein, the precursor of which seems to contain a leader sequence of 50 amino acid residues. Comparison of the putative E₁β leader sequence (negatively numbered amino acid residues in Fig. 2) with those of other mitochondrial proteins revealed a number of common features. The putative E₁β leader sequence con-

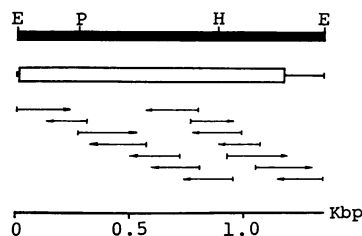


Figure 1. Restriction map and sequencing strategy for human BCKDH-E₁β cDNA. The open box and the line depict coding and noncoding regions, respectively. Restriction sites are indicated above the λ hBE₁β-1 insert (1,349 bp) at the top of the figure,

with restriction enzymes used: Eco RI (E), Pst I (P), Hind III (H). Solid horizontal arrows indicate orientation and region of sequencing.

ATGGCGGTTGTAGCGGCGGCTGCCGGCTGGCTACTCAGGCTCAGGGCGGCAGGGGCTGAGGGGCACTGGCGTCGGCTTCTGGCGGGG MetAlaValValAlaAlaAlaAlaGlyTrpLeuLeuArgLeuArgAlaAlaGlyAlaGlyHisTrpArgArgLeuProGlyAlaGly -50 -40 -30	90
CTGGCGCGGGGCTTTTTCACCCCGCCGCGACTGTCGAGGATGCGGCCAGAGGCGGCAGGTGGCTCATTCTTTTCCAGCCAGATCCG LeuAlaArgGlyPheLeuHisProAlaAlaThrValGluAspAlaAlaGlnArgArgGlnValAlaHisPheThrPheGlnProAspPro -20 -10 1 10	180
GAGCCCCGGGAGTACGGGCAAACTCAGAAAATGAATCTTTTCCAGTCTGTAAACAAGTGCCTTGGATAACTCATTGGCCAAAGATCCTACT GluProArgGluTyrGlyGlnThrGlnLysMetAsnLeuPheGlnSerValThrSerAlaLeuAspAsnSerLeuAlaLysAspProThr 20 30 40	270
GCAGTAATATTTGGTGAAGATGTTGCCTTTGGTGGAGTCTTTAGATGCACTGTTGGCTTGGGAGACAAATATGGAAAAGATAGAGTTTTT AlaValIlePheGlyGluAspValAlaPheGlyGlyValPheArgCysThrValGlyLeuArgAspLysTyrGlyLysAspArgValPhe 50 60 70	360
AATACCCCATTTGTGTGAACAAGGAATTGTTGGATTGGAATCGGAATTGCGGTCACTGGAGCTACTGCCATTGCGGAAATTCAGTTTGCA AsnThrProLeuCysGluGlnGlyIleValGlyPheGlyIleGlyIleAlaValThrGlyAlaThrAlaIleAlaGluIleGlnPheAla 80 90 100	450
GATTATATTTTCCCTGCATTTGATCAGATTGTTAATGAAGCTGCCAAGTATCGCTATCGCTCTGGGGATCTTTTAACTGTGAAGCCTC AspTyrIlePheProAlaPheAspGlnIleValAsnGluAlaAlaLysTyrArgTyrArgSerGlyAspLeuPheAsnCysGlySerLeu 110 120 130	540
ACTATCCGGTCCCCTTGGGGCTGTGTTGGTCATGGGGCTCTCTATCATTCTCAGAGTCTGAAGCATTTTTGGCCATTGCCAGGAATC ThrIleArgSerProTrpGlyCysValGlyHisGlyAlaLeuTyrHisSerGlnSerProGluAlaPhePheAlaHisCysProGlyIle 140 150 160	630
AAGTGTTTATACCCAGAAGCCCTTCCAGGCCAAAGGACTTCTTTGTATGCATAGAGGATAAAAAATCCTGTATATTTTTTGAACCT LysValValIleProArgSerProPheGlnAlaLysGlyLeuLeuLeuSerCysIleGluAspLysAsnProCysIlePhePheGluPro 170 180 190	720
AAAATACTTTACAGGGCAGCAGCGGAAGAAGTCCCTATAGAACCATAACAATCCCACTGTCCCAGGCCGAAGTCATACAGGAAGGGAGT LysIleLeuTyrArgAlaAlaAlaGluGluValProIleGluProTyrAsnIleProLeuSerGlnAlaGluValIleGlnGluGlySer 200 210 220	810
GATGTTACTCTAGTTGCCTGGGGCACTCAGGTTTCATGTGATCCGAGAGGTAGCTTCCATGGCAAAAGAAAAGCTTGGAGTGCTTTGTGAA AspValThrLeuValAlaTrpGlyThrGlnValHisValIleArgGluValAlaSerMetAlaLysGluLysLeuGlyValSerCysGlu 230 240 250	900
GTCATTGATCTGAGGACTATAATACCTTGGGATGTGGACACAATTTGTAAGTCTGTGATCAAAACAGGGCGACTGCTAATCAGTCACGAG ValIleAspLeuArgThrIleIleProTrpAspValAspThrIleCysLysSerValIleLysThrGlyArgLeuLeuIleSerHisGlu 260 270 280	990
GCTCCCTTGACAGGCGGCTTTGCATCGGAAATCAGCTCTACAGTTCAGGAGGAATGTTTCTTGAACCTAGAGGCTCCTATATCAAGAGTA AlaProLeuThrGlyGlyPheAlaSerGluIleSerSerThrValGlnGluGluCysPheLeuAsnLeuGluAlaProIleSerArgVal 290 300 310	1080
TGTGGTTATGACACACCATTTCCTCACATTTTGAACCATTCTACATCCCAGACAAATGGAAGTGTATGATGCCCTTCGAAAAATGATC CysGlyTyrAspThrProPheProHisIlePheGluProPheTyrIleProAspLysTrpLysCysTyrAspAlaLeuArgLysMetIle 320 330 340	1170
AACTATTGACCATATAGGTAGGTATGCATCTTGAGAAAGCTACTATGTGCCCTGACATTAACGTACTGTTAACCAAGACACAGCAATCA AsnTyr***	1260
TCAGTGTTTTGATGGTAACAACTTTGATGGTAAAGTTGATAAAAGGCAACTTTCAGAAGAAATAATGTGCTTTAAAAA	1345

Figure 2. Nucleotide sequence of the λ hBE $_{1\beta}$ -1 insert and deduced amino acid sequence of the human BCKDH-E $_{1\beta}$ precursor. Numbers on the far right correspond to ordinate of the last nucleotide in each row. Nucleotides are numbered in the 5' \rightarrow 3' direction, beginning with the first residue of the ATG triplet encoding the putative initiator methionine. Numbers below the amino acid sequence refer to residues beginning with the NH $_2$ terminus of the mature protein deduced from the purified bovine BCKDH-E $_{1\beta}$ determined by Edman degradation (25). There is a double underline at the polydenylation signal of the type AATAAT (37).

tains periodically spaced basic amino acids rich in Leu and Arg and has few acidic residues (only one Asp at residue -7). These findings are compatible with those proposed for the leader sequence of mitochondrial targeting enzymes (38, 39). On the basis of these findings, the molecular mass of the E $_{1\beta}$ precursor is estimated to be 43,130 and that of the mature E $_{1\beta}$ is 37,585, in good agreement with the 37,000 estimated by immunoblot analysis (15, 16).

A protein homology search revealed that the primary structure of human BCKDH-E $_{1\beta}$ is similar to the human PDH-E $_{1\beta}$ (40), in all regions. Fig. 3 depicts the alignment of homologous regions of human BCKDH-E $_{1\beta}$, bovine BCKDH-E $_{1\beta}$, and human PDH-E $_{1\beta}$. 98% of the amino acid residues of human BCKDH-E $_{1\beta}$ are identical to bovine BCKDH-E $_{1\beta}$ and 33% of the amino acid residues of human BCKDH-E $_{1\beta}$ are identical to the corresponding residues of

Bovine	BCKDH	1	VAHFTFQPDPEPVEYGQTQKMNLFQAVTSALDNSLAKDPTAVIFGEDVA-FGGVFRCTVG	59
Human	BCKDH	1	VAHFTFQPDPEPREYEGQTQKMNLFQSVTSALDNSLAKDPTAVIFGEDVA-FGGVFRCTVG	59
Human	PDH	24	--HWI--APAAVQ-----VTVRDAINQGMDEFLERDEKVFLLGEEVAQYDGAYKVSRG	72
Bovine	BCKDH	60	LRDKYGKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFADYIFPAFDQIVNEAAKYR	119
Human	BCKDH	60	LRDKYGKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFADYIFPAFDQIVNEAAKYR	119
Human	PDH	73	LWKYGDKRRIIDTPISEMCFAGTAVGAAAGLRPIQEFMTFNFSMOATDQVINSAAKTYV	132
Bovine	BCKDH	120	RSGDLFNCGSLTIRSPWGCVGHGALYHSQSPQAFFAHCPGIKVVVPRSPFQAKGLLLSCI	179
Human	BCKDH	120	RSGDLFNCGSLTIRSPWGCVGHGALYHSQSPQAFFAHCPGIKVVVPRSPFQAKGLLLSCI	179
Human	PDH	133	MSGGL-QPVPIVFRGNGCASAGVAAQHSQCFAAWYGHCPGLKVVSPWNSEDAKGLTKSAL	191
Bovine	BCKDH	180	EDKNPCIFFEPKILYRAAVE--QVFEVPEYNIPLSQAEVIOEGSDVTLVANGTQV-HVIR	235
Human	BCKDH	180	EDKNPCIFFEPKILYRAAAE--EVFIEPYNIPLSQAEVIOEGSDVTLVANGTQV-HVIR	235
Human	PDH	192	RKNNPVVVLENELMVGVPFEFLRKLKSKILLIPFGKAKIEROQTHTITVSHSRHVGHGLE	251
Bovine	BCKDH	236	EVDAMAQEKLGVSCEVIDLRTILPWDVDTVCKSVIKTGRLLSHEAPLTG-GFASEISST	294
Human	BCKDH	236	EVDAMAQEKLGVSCEVIDLRTIIPWDVDTICKSVIKTGRLLSHEAPLTG-GFASEISST	294
Human	PDH	252	AAAVLSKE--GVECEVINMRTIRPMDMETIFASVMKTNH-LVTVEGGWPQFGVGAEICAR	308
Bovine	BCKDH	295	VQEECFNLN-LEAPISRVCGYDTFPFH--IFEPFYIPDKWKCYDALRKMINY	342
Human	BCKDH	295	VQEECFNLN-LEAPISRVCGYDTFPFH--IFEPFYIPDKWKCYDALRKMINY	342
Human	PDH	309	INGSPAFNFDAPAVRVYTGADVEMFYAKTIDEDNSIPQVKDIIFATKNTNT	359

Figure 3. Comparison of amino acid sequences of human BCKDH-E₁β (present study), bovine BCKDH-E₁β (25), and human PDH-E₁β (40).

PDH-E₁β; this similarity increased to 82% if conservative amino acid substitutions are taken into account. It has been demonstrated that mammalian α -ketoacid dehydrogenase complexes such as PDH, BCKDH, and α -ketoglutarate dehydrogenase are functionally and structurally similar (4, 5). The

amino acid sequence of the mammalian BCKDH-E₁α is highly homologous to that of mammalian PDH-E₁α (17); the same is true of BCKDH-E₂ (19–21). The present study showed that human BCKDH-E₁β is also similarly homologous to human PDH-E₁β. Extensive homologies between BCKDH-

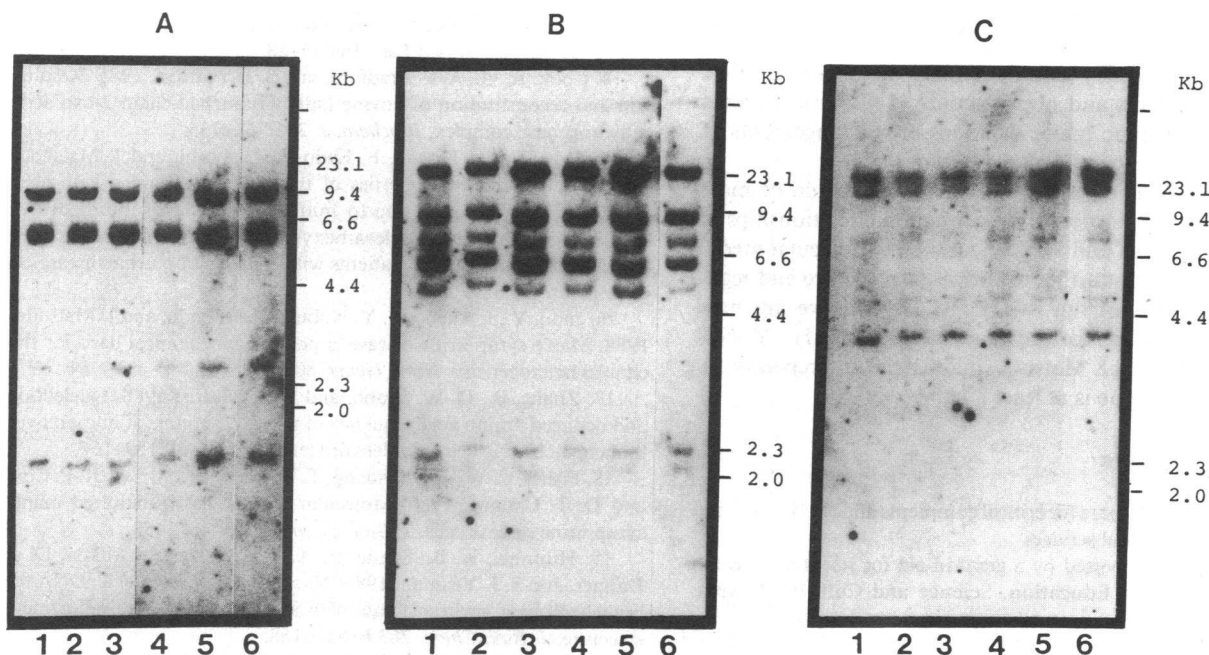


Figure 4. Southern blot analysis of genomic DNA from the MSUD patient in whom CRM for BCKDH-E₁β are absent. (A) Eco RI-digested genomic DNA. Lane 1, disease-free control cell line; lanes 2–6, cell lines from MSUD patients (K.Y., Y.T., E.K., T.H., and Y.O.). Filters were probed with labeled human BCKDH-E₁β cDNA (λhBE₁β-1). (B) Hind III-digested DNA from individuals as in A, hybridized with labeled human BCKDH-E₁β cDNA (λhBE₁β-1). (C) Bam HI-digested DNA from individuals as in A, hybridized with labeled human BCKDH-E₁β cDNA (λhBE₁β-1). The BCKDH-E₁β gene is estimated to be at least 80 kbp long as based on data obtained by cloning of the genomic DNA.

$E_1\beta$ and PDH- $E_1\beta$ throughout the primary structure suggest that the secondary structure, tertiary structure, and function are also similar. Furthermore BCKDH- $E_1\beta$ and PDH- $E_1\beta$ may possibly arise from a common ancestral gene, although the function of $E_1\beta$ has yet to be determined (5). A highly conserved structure of the $E_1\beta$ -subunit of 2-oxo acid dehydrogenases of mammals suggests that the $E_1\beta$ -subunit of these enzymes no doubt plays important roles in enzyme activities.

A defect in the BCKDH complex results in MSUD (4). The etiology of this disease is heterogenous as mutations in different regions of any of the BCKDH proteins could lead to decreased functions of the entire complex. Recently, a defect of E_2 (15, 16, 18, 41, 42), a defect of $E_1\beta$ (15, 16, 18), mutation of $E_1\alpha$ (43), and loss of $E_1\alpha$ and $E_1\beta$ subunits (18) have been detected in MSUD patients.

We analyzed the biochemical basis for clinical heterogeneity in MSUD and noted a defect in $E_1\beta$ as one cause of the disease. In these cases, immunologically cross-reactive material corresponding to BCKDH- $E_1\beta$ was not detected. $E_1\beta$ is associated with $E_1\alpha$ by noncovalent binding and the E_1 subunit is attached to E_2 . Thus, the absence of $E_1\beta$ theoretically could result from abnormalities in structures of $E_1\alpha$ or E_2 . The absence of $E_1\beta$ might not indicate a genetic abnormality in the $E_1\beta$ gene. A detailed analysis of $E_1\beta$ deficiency suggested that the mutations might be heterogenous (15, 16). The $E_1\beta$ deficiency will have to be analyzed at the gene level.

To elucidate the molecular mechanism of $E_1\beta$ deficiency, we first analyzed the expression of $E_1\beta$ transcript in lymphoblastoid cell lines in which $E_1\beta$ was not detected by immunoblot analysis (15, 16). The $E_1\beta$ transcript was not clearly defined by Northern blot analysis using poly (A)⁺ RNA (10–15 μ g), even in normal control lymphoblastoid cell lines (data not shown). The quantity of the $E_1\beta$ transcript may be low or the transcript may readily degrade, a proposal based on our finding that we could obtain only one clone when screening the cDNA-library using the nucleotide probe (λ B $E_1\beta$ -2), as described above.

We also analyzed by Southern blots the genomic DNA from MSUD patients and normal controls (Fig. 4). It seems likely that there are no major deletions or rearrangements of the BCKDH- $E_1\beta$ gene in these patients.

The cDNA clone of human BCKDH- $E_1\beta$ should be most useful for examining structural and functional relationships of the BCKDH complex and for elucidating the molecular mechanisms of MSUD. To further examine the structure and regulatory mechanisms of the BCKDH- $E_1\beta$ gene, we are now cloning genomic DNA for the gene (Mitsubuchi, H., Y. Nobukuni, F. Endo, and I. Matsuda, manuscript in preparation). The BCKDH- $E_1\beta$ gene is at least 80 kbp long.

Acknowledgments

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