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A human alcohol dehydrogenase gene (*ADH6*) encoding an additional class of isozyme

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ABSTRACT **The human alcohol dehydrogenase (ADH; alcohol:NAD$^+$ oxidoreductase, EC 1.1.1.1) gene family consists of five known loci (*ADH1–ADH5*), which have been mapped close together on chromosome 4 (4q21–25). ADH isozymes encoded by these genes are grouped in three distinct classes in terms of their enzymological properties. A moderate structural similarity is observed between the members of different classes. We isolated an additional member of the ADH gene family by means of cross-hybridization with the *ADH2* (class I) cDNA probe. cDNA clones corresponding to this gene were derived from PCR-amplified libraries as well. The coding sequence of a 368-amino-acid-long open reading frame was interrupted by introns into eight exons and spanned approximately 17 kilobases on the genome. The gene contains a glucocorticoid response element at the 5′ region. The transcript was detected in the stomach and liver. The deduced amino acid sequence of the open reading frame showed about 60% positional identity with known human ADHs. This extent of homology is comparable to interclass similarity in the human ADH family. Thus, the newly identified gene, which is designated *ADH6*, governs the synthesis of an enzyme that belongs to another class of ADHs presumably with a distinct physiological role.**

Human alcohol dehydrogenases (ADHs; alcohol:NAD$^+$ oxidoreductase, EC 1.1.1.1) are a family of enzymes that catalyze oxidative conversion of various alcohols to the corresponding aldehydes in a reversible fashion. Five kinds of subunits (α, β, γ, π, and χ) governed by five nonallelic genes, *ADH1*, *ADH2*, *ADH3*, *ADH4*, and *ADH5*, respectively, have been identified. These genes were mapped close together on chromosome 4q21–25 (for review, see ref. 1). The expressions of these ADH genes are under the control of tissue-specific and developmental stage-specific mechanisms (for review, see ref. 2).

ADH isozymes of humans and other mammals are grouped in three distinctive "classes" based on their enzymatic characteristics. The isozymes, which exhibit high catalytic activity for oxidation of short-chain aliphatic alcohols, such as ethanol, and are strongly inactivated by pyrazole, are grouped as class I ADH (3). Another type (class II) of ADH isozymes exhibits a high activity for oxidation of long-chain aliphatic alcohols and aromatic alcohols and is less sensitive to pyrazole (4). ADH isozymes, which have virtually no activity for ethanol oxidation but exhibit high activity for oxidation of long-chain alcohols and are completely insensitive to pyrazole, are classified as class III ADH (5). Members within a class show a considerable structural similarity (>85% positional identity) in their amino acid sequences even in distal mammalian species, while a lesser similarity (≈60%) exists between two different classes within the same species (6).

It has been reported that human stomach (7, 8), rat stomach (9), and baboon stomach and eye (10) contain other ADH isozymes that exhibit class II enzymatic characteristics but differ from the liver class II ADH. The structure of the rat stomach ADH was substantially different from that of known rat class I, II, and III ADHs, and thus it was proposed that rat stomach contains another class (class IV) of ADH isozymes (11). The present study demonstrates the existence of an additional human ADH gene, designated *ADH6*, which encodes an additional class of ADHs.†

MATERIALS AND METHODS

Construction of Genomic Library and Isolation and Characterization of Genomic Clones. Human genomic DNA libraries were constructed either with cosmid vector pWE15 or with phage vector λDASH (12). The cosmid library [≈40-kilobase (kb) inserts] was screened with a full-length *ADH2* cDNA probe pUCADHβ14 (13) by the colony hybridization method. The λDASH library (≈15-kb inserts) was screened by the plaque hybridization method with a 0.8-kb-long *Xba* I fragment derived from a cosmid clone cosADH98, which was obtained from the cosmid library (Fig. 1). Restriction mapping analysis, subcloning of the inserts into pBluescript II (Stratagene), and nucleotide sequencing were performed by standard procedures (14, 15).

Construction of cDNA Library and Isolation and Characterization of cDNA Clones. Poly(A)$^+$ RNA was prepared from a Japanese adult male liver by a standard method (14).

An amplified cDNA library corresponding to the 3′ region of the transcript was constructed as described by Frohman *et al.* (16). Briefly, 1 μg of the poly(A)$^+$ RNA was reverse-transcribed using $(dT)_{15}$ adaptor primer [20-mer adaptor GGACTCGAGCTCTAGAAGTT conjugated with poly-$(T)_{15}$]. Unincorporated primer was removed by polyacrylamide gel electrophoresis. One-thousandth of the (−)-strand 3′ cDNA thus produced was used for PCR amplification with a specific 3′ primer (20-mer ATGGTACCAGCAGGTTTACC derived from the sequence of cosADH96 clone) and the adaptor primer described above.

For generation of single (−)-strand 5′ cDNA, 1 μg of the poly(A)$^+$ RNA was reverse-transcribed using a specific reverse transcriptase primer (20-mer CTCTAGAGGAGCGACTGCAT, derived from the sequence of cosADH96 clone). To improve annealing efficiency, the original procedures for construction of a 5′ cDNA library (16) were modified as follows. The single (−)-strand 5′ cDNA was tailed with a deoxycytidine homopolymer, instead of a deoxyadenosine homopolymer, by terminal deoxynucleotide transferase (Pharmacia) (17). pBluescript KS+ vector cleaved by *Sst* II was tailed with a deoxyguanosine homopolymer and used as a primer. The tailed cDNA and the primer were annealed and subjected to the Klenow polymerase reaction. One-twentieth of the reaction product thus produced was used for PCR amplification with a pair of

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Abbreviation: nt, nucleotide.

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†The sequence reported in this paper has been deposited in the GenBank data base (accession no. M68895).

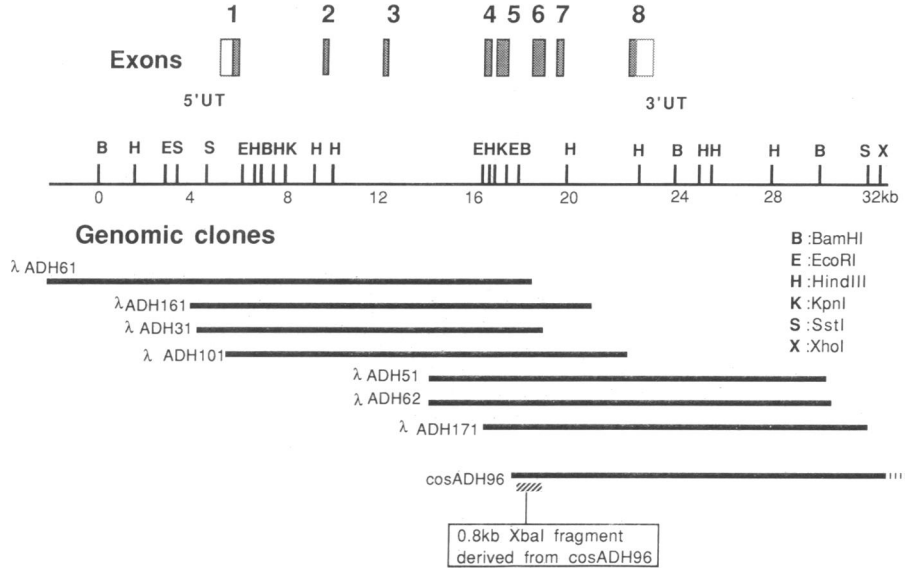

FIG. 1. Restriction map of the *ADH6* gene. Cosmid clone cosADH96 and seven phage clones λADH61, -161, -31, -101, -52, -62, and -171 are shown by horizontal lines. Restriction cleavage sites are indicated by vertical bars. Exons are boxed. Coding regions are shaded, whereas 5′ and 3′ untranslated regions (UT) found in the cDNA clones are in open boxes. A 0.8-kb *Xba* I fragment used for screening the phage library is also indicated.

primers—i.e., a specific 5′ primer (21-mer GCTGGTACCATCAGACATCAG, derived from the sequence of cosADH96 clone) and M13 universal adaptor primer (17-mer GTAAAACGACGGCCAGT).

The products of the PCR were digested with *Sst* I and *Kpn* I and subcloned in pBluescript II KS+ (for 5′ product) or in pBluescript II SK+ (for 3′ product) (Stratagene). Randomly picked clones from the transformed *Escherichia coli* were subjected to analysis by restriction mapping and nucleotide sequencing.

A full-length cDNA was constructed by conjugating the 5′ cDNA clone A8 and the 3′ cDNA clone 1.1, which overlapped at the *Kpn* I site, and cloned in pBluescript SK+ (14). The procedures are schematically outlined in Fig. 2. The nucleotide sequence of the full-length cDNA was established by analysis of both strands.

Detection of mRNA. Total cellular RNA was prepared from a Japanese adult male liver and from a normal part of a surgically removed stomach of a Japanese adult female with adenocarcinoma. RNA preparations with serial 2-fold dilu-

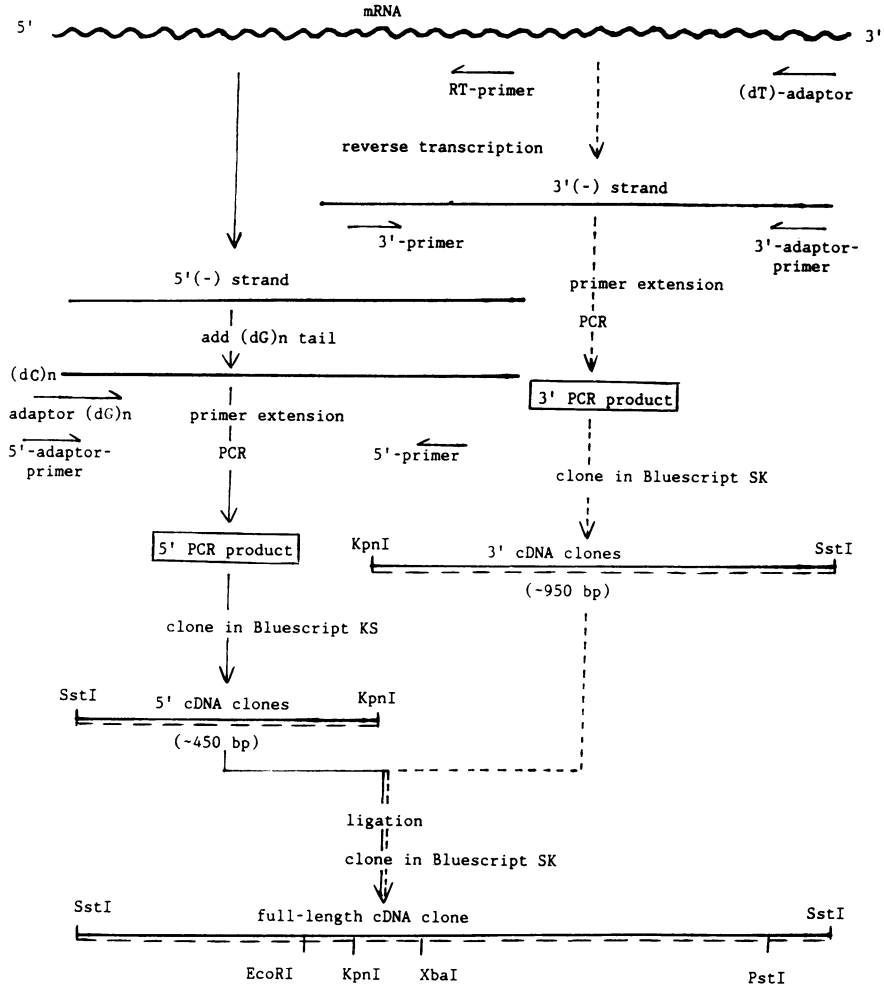

FIG. 2. Strategy for cDNA cloning. Partial restriction map of the full-length cDNA clone is also shown. The structures of reverse transcriptase (RT) primer, specific 5′ primer, 3′ primer, 5′ adaptor primer, and 3′ adaptor primer are described in *Materials and Methods*.

tions (4–0.5 μg per slot) were blotted onto a nitrocellulose filter with a slot blotter (Schleicher & Schuell). The filter was hybridized with the ADH6-specific oligonucleotide probe ACGTCCAGATTTCCAATGGC (16). The filter was deprobed and rehybridized with the ADH2-specific probe GTCATCTGTGCGACAGATTCC.

One microgram of poly(A) RNA prepared from the liver or stomach was used for the PCR amplification by using the two sets of primers—i.e., the ADH6-specific ATGGTACCAGCAGGTTTACC (5′ primer) and ACGTCCAGATTTCCAATGGC (3′ primer), which were expected to produce a 448-base-pair (bp) product from the ADH6 mRNA, and the ADH2-specific GGAATCTGTCACACAGATGAC (5′ primer) and AGCAGTAGTTGCTCTCCGGG (3′ primer), which were expected to produce a 205-bp product from the ADH2 mRNA. One-twentieth of the amplification product was electrophoresed in an agarose gel (1.5%) and blotted onto a nitrocellulose filter. The filter was first hybridized with the ADH6-specific oligonucleotide CAGGATCATTGGAGTGGATG (derived from the coding sequence of *ADH6* shown in Fig. 2), and, after deprobing, the filter was rehybridized with the ADH2-specific probe GGGTCACCAGGTTGCCACTA.

RESULTS

Isolation of Genomic Clones. A genomic clone (cosADH96; insert size, 38 kb) was isolated from the cosmid genomic library by cross-hybridization with the ADH2 cDNA probe (13). Only the 0.8-kb fragment generated by *Xba* I digestion, which was closely located to the end of the insert, gave a positive hybridization signal in Southern blot hybridization with the ADH2 probe. Nucleotide sequencing revealed that a part of this fragment showed a significant homology with exon 6 of the *ADH2* gene (18). The 0.8-kb *Xba* I fragment was used as a probe in turn to obtain seven contiguous genomic clones λADH61, -161, -31, -101, -51, -62, and -171 from the λDASH genomic library (Fig. 1). Southern blot hybridization of these genomic clones with the ADH2 cDNA probe indicated that λADH-61 and λADH-171 overlapped at their 3′ and 5′ regions and together spanned ≈17 kb. Since only exon 5 and exon 6 of this gene were cross-hybridizable with the ADH2 cDNA probe, other exons of the gene were mapped by using its own cDNA as a probe as described below.

Isolation and Characterization of cDNA Clones. Twelve clones were picked from the 5′ PCR-amplified cDNA library, and partial nucleotide sequences of their inserts were determined. Five of them had the nucleotide sequence corresponding to the genomic DNA flanking 5′ primer sequence. The longest two clones (A8 and D7) were analyzed further. Both clones (insert ≈450 bp) contained the initiation codon, the upstream nonsense codon, and 5′ untranslated region of different lengths. Three clones (1.1, 2.10, and 3.2) obtained from the 3′ amplified library had a 0.95-kb insert, which corresponded to the major PCR product. The length of poly(A) stretch at the 3′ end differed in these three clones. A full-length cDNA, which can encode 368 amino acid residues including the initiation methionine, was constructed by conjugating the 5′ A8 and 3′ 1.1 clones.

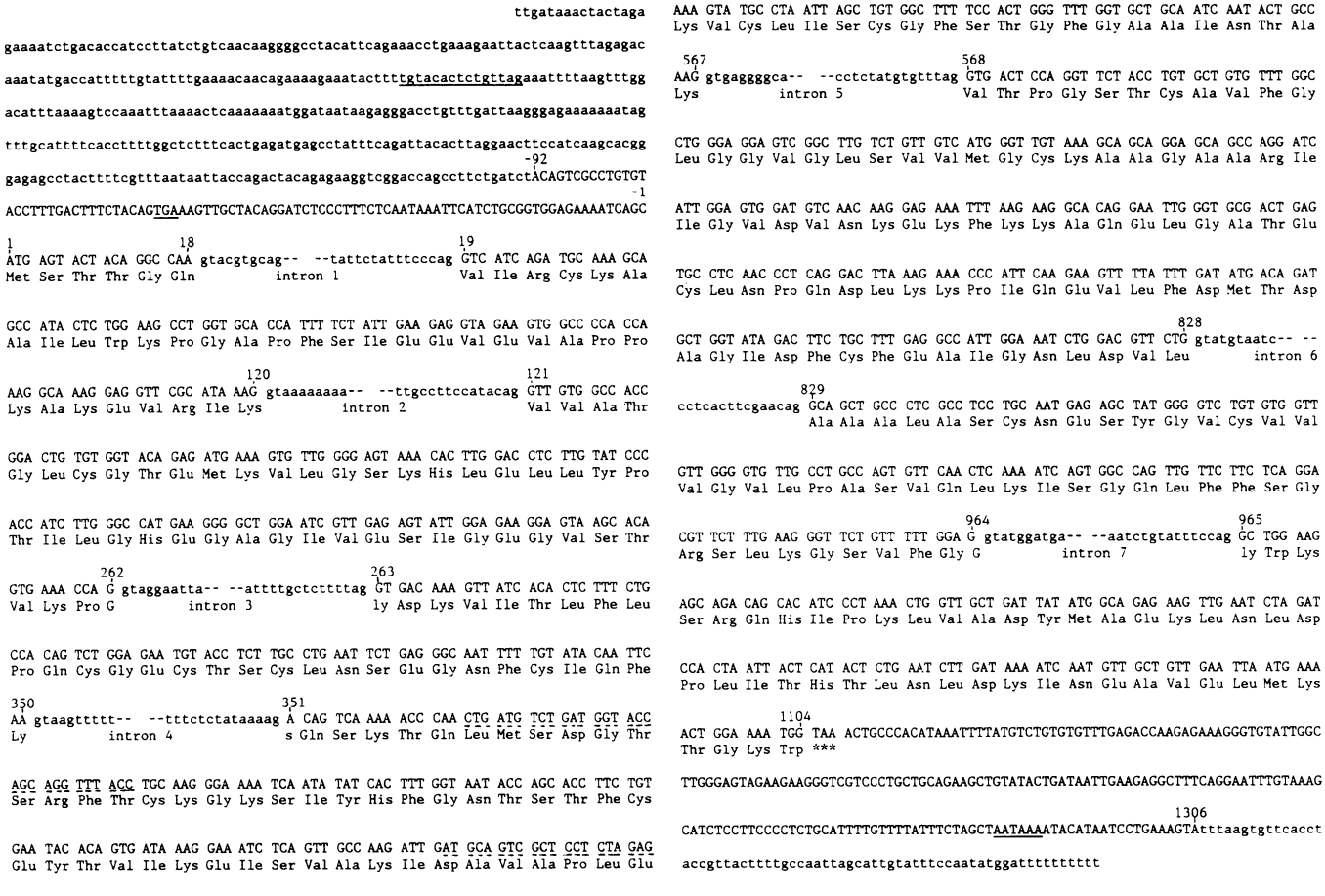

FIG. 3. Nucleotide sequence of the *ADH6* gene and deduced amino acid sequence. Nucleotide residues are numbered on the basis of the cDNA sequence from +1 at the adenine of the initiator codon, and nucleotides in the 5′ untranslated region are indicated by negative numbers. Upstream 5′ in-frame stop codon (TGA) and glucocorticoid response element are underlined. Downstream 3′ polyadenylylation signal (AATAAA) is also underlined. Poly(A) stretch starts from the A at nt 1306. The sequences of reverse transcriptase primer, 5′ primer, and 3′ primer used for construction of the amplified cDNA libraries (Fig. 2) are indicated by dashed lines. cDNA sequence is shown in capital letters, and the 5′ region of the gene and the intron sequences are shown in lowercase letters.

T instead of A at nucleotide (nt) 12, G instead of A at nt 75, T instead of G at nt 223, and T instead of G at nt 714 were found in one of the cDNA clones but not in others and not in the genomic clones and genomic DNA samples obtained from five individuals. Except for G → T at nt 223, which can induce Val → Phe substitution, all nucleotide discrepancies are silent and cannot induce any amino acid substitutions. Since the cDNA clones were derived from PCR amplified libraries, the discrepancies may be attributed to errors that occurred in the PCR. The nucleotide sequence shown in Fig. 3 can be considered to be the authentic normal cDNA structure.

Exon–Intron Organization. Using cDNA clones A8 and 1.1 as probes, the exons were mapped within the genomic regions, which were represented by contiguous phage and cosmid clones. The length of the gene was ≈17 kb (Fig. 1). The nucleotide sequences of exons and exon–intron junctions were determined. All junctions had the consensus GT–AG sequence. The gene consists of eight coding exons interrupted by seven introns and can encode 368 amino acid residues (Fig. 3). The human class I ADH genes (*ADH1*, *ADH2*, and *ADH3*) consist of nine coding exons and encode 375 amino acid residues (13, 18). The newly discovered gene shares common insertion sites with the class I ADH genes (12, 18, 19) from the first through the seventh intron—i.e., the first insertion at positions 5/6, the second at 39/40, the third at 86, the fourth at 115, the fifth at 188/189, the sixth at 275/276, and the seventh at 321. However, the *ADH6* gene lacks exon 9; instead, its exon 8 contains a stop codon

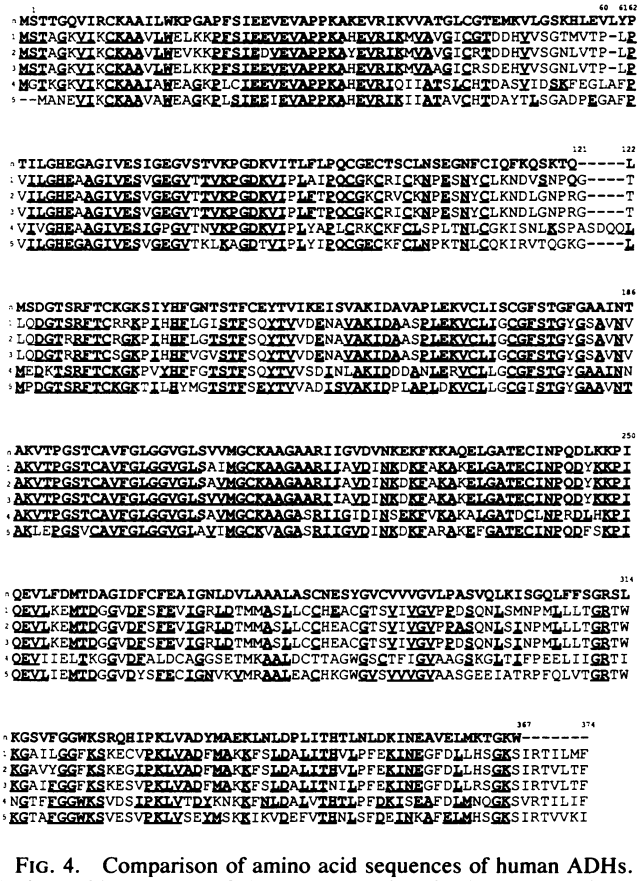

FIG. 4. Comparison of amino acid sequences of human ADHs. Amino acid sequence of the *ADH6* product is shown on *n* lines. Sequences of *ADH1* product (α subunit), *ADH2* (β subunit), *ADH3* (γ subunit), *ADH4* (π subunit), and *ADH5* (χ subunit) are shown on lines 1, 2, 3, 4, and 5, respectively. Identical residues existing in all sequences are indicated by underlined boldface letters. Gaps (–) are inserted to give maximal homology in these sequences. Numbering of amino acid residues is in accordance with that of the class I ADHs. The sequences for α, β, and γ subunits are from ref. 21, that of the π subunit is from ref. 22, and that of the χ subunit is from ref. 23.

followed by a polyadenylylation signal sequence. The cDNA cloned has a poly(A) tail at the expected position. Therefore, the gene cloned is "full," not partial. The possibility of the existence of exon 9 in the *ADH6* gene and formation of mRNA with the extended 3′ coding sequence, which might be produced by alternative splicing, was examined by screening the genomic libraries with the 3′ region of the cloned *ADH6* gene and by amplifying poly(A) RNA using the 3′ sequence of exon 8 as a 3′ primer. The negative results observed suggested the absence of exon 9 in the *ADH6* gene. The gene contains a highly conserved sequence for a glucocorticoid response element (20) at the extended 5′ region (Fig. 3).

Deduced Amino Acid Sequence. A 368-amino-acid-long sequence was deduced from the open reading frame of the gene. The initiation methionine codon was assigned because of the presence of the upstream in-frame stop codon (TGA) (Fig. 3). Compared with the class I ADHs, the deduced amino acid sequence had one insertion between positions 60 and 61, one deletion at position 121, and was shorter by seven residues due to the appearance of a stop codon (TAA) in exon 8 (Figs. 3 and 4). The calculated percentage of positional identity ranged from 56.8% with *ADH4* (class II) to 62.8% with *ADH2* (class I), which is comparable to an interclass similarity (59.5–62.8%) observed in human ADHs (Table 1).

Detection of mRNA. The slot-blot hybridization of cellular RNA with the ADH6-specific oligonucleotide probe and the ADH2-specific probe indicated that both liver and stomach contained the ADH6 mRNA as well as the ADH2 mRNA (data not shown). The analysis of PCR amplification products produced by two sets of primers, one specific for the ADH6 mRNA and the other specific for the ADH2 mRNA, confirmed the above conclusion. A PCR product (448 bp), hybridizable with the ADH6-specific probe, and a PCR product (205 bp), hybridizable with the ADH2-specific probe, were both produced from a stomach poly(A) RNA as well as a liver poly(A) RNA preparation (Fig. 5).

DISCUSSION

Thus far, ADH and other isozymes have been identified through examination of enzymatic characteristics and protein analysis. Since a group of enzymes (i.e., isozymes) have a certain degree of similarity in their coding nucleotide sequences, newly discovered isozymes may be identified and characterized through direct analysis of genomic DNA. The three human class I ADH isozyme subunits are highly similar to each other (≈94% positional identity). A moderate similarity (≈60% positional identity) exists between the human class I, II, and III ADH isozymes (Table 1). Therefore, a gene for a hitherto unknown member of a group of isozymes may be cloned by screening a genomic DNA library with nucleotide probes that contain conserved coding sequences of known isozyme members under a low stringent hybridization condition and/or by selecting weakly positive clones.

In the present study, a cosmid genomic library was screened by a full-length ADH2 cDNA. A genomic clone containing the nucleotide sequence, which was homologous,

Table 1. Similarity of amino acid sequences encoded by the human *ADH* genes

	Class I *ADH1*	Class I *ADH2*	Class I *ADH3*	Class II *ADH4*	Class III *ADH5*
ADH6	62.2	62.8	62.2	56.8	57.4
ADH1	100	93.6	93.1	59.5	59.7
ADH2		100	94.9	59.7	62.5
ADH3			100	59.5	62.8
ADH4				100	61.3

Numbers given are maximum positional identity between the ADH subunits encoded by the genes.

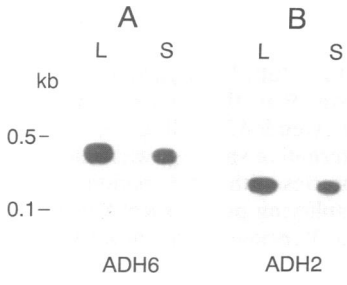

FIG. 5. Detection of ADH6-specific mRNA and ADH2-specific mRNA in the stomach and liver. Poly(A) RNA prepared from the tissues was amplified by using ADH6-specific 5′ and 3′ primers and ADH2-specific 5′ and 3′ primers. Amplified product was electrophoresed and blotted onto nitrocellulose filters. (*A*) Hybridized with ADH6-specific probe. (*B*) Hybridized with ADH2-specific probe. Lanes: L, product from liver poly(A) RNA; S, product from stomach poly(A) RNA.

but not identical, to exon 6 of any one of the known human ADH genes, was obtained. It should be mentioned that exon 6 is highly conserved (88% homology) in all five known human ADH genes. Using this region of the clone as a probe, overlapping genomic clones, which covered an entire gene, were obtained from a λDASH genomic library (Fig. 1). Subsequently, a full-length cDNA was obtained from PCR-amplified cDNA libraries, which were constructed based on the sequence data of the genomic clones (Fig. 2). The method outlined above is useful for the search of additional isozyme members of other enzymes. Another human aldehyde dehydrogenase gene was also cloned and characterized in this laboratory (1, 24).

The general architectural structure of the *ADH6* gene is similar to that of other human *ADH* genes. However, the degree of resemblance between this gene and previously known genes is only ≈60% at the coding nucleotide level and at the deduced amino acid sequence level (Table 1). Since the degree of similarity is much lower than the interisozyme class similarity observed even in different mammalian species (≈85%), the gene must be classified in a different class. Recently, partial amino acid sequence (165 amino acid residues) of rat stomach ADH isozyme was determined, and the sequence was found to be not highly similar to any one of rat class I, II, and III isozymes (11). Thus, the rat stomach ADH was classified in another class, ADH class IV (11). The similarity between the newly discovered human ADH (*ADH6*) and the rat stomach ADH is much lower (62% identity at the amino acid sequence level) than the intraclass similarity of class I, II, and III isozymes between the human and rat (84–95%) (11). Therefore, the human *ADH6* gene cannot be for human class IV isozyme. The isozyme encoded by the *ADH6* gene probably exhibits unique enzymological properties, different from other classes of ADH, and may play a particular physiological role.

The human *ADH6* gene is expressed in the stomach as well as in the liver, as evidenced by cDNA cloning, slot-blot RNA hybridization, and detection of specific mRNA by a PCR method (Fig. 5).

The *ADH6* gene has the glucocorticoid response element, which is highly compatible (12 of 15 nucleotide bases) to the consensus sequence of the element (20) at the 5′ region (Fig. 3), and thus its expression may be under hormonal control. The less homologous response elements existing in the *ADH2* gene were suggested to be functional (25).

The recently reported stomach-specific human ADH isozyme(s) (μ- and/or σ-ADH) appears to correspond to the rat stomach-specific class IV ADH, rather than to the present ADH6 with respect to kinetic properties and tissue specificity (7, 8). However, further studies are required to clarify this point.

A substantial part of orally administered ethanol is metabolized in the stomachs of males, but not of females, and it was reported that the ADH activity of stomach mucus was higher in males than in females (26). It is not yet clear whether or not the stomach ADH (μ or σ) and class I ADH (γ) are involved in the sex difference of ethanol metabolism. The ADH isozyme produced in the stomach by the *ADH6* gene with the hormone response element may play a role in this phenomenon.

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