

Original Research Communication

Molecular Cloning and Expression of Human xCT, the Light Chain of Amino Acid Transport System x_c^-

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ABSTRACT

Transport of system x_c^- is an exchange agency with high specificity for anionic form of cystine and glutamate. The protein mediating this transport is a disulfide-linked heterodimer of a light chain named xCT and a heavy chain previously known as 4F2hc. We have isolated two cDNAs encoding xCT from the human cDNA library. One clone coded for a protein of 501 amino acids with 12 putative transmembrane domains. When functionally expressed in *Xenopus* oocytes together with the human 4F2hc, human xCT induced the transport activity whose characteristics are similar to those of system x_c^- . Another clone seemed to contain a partial human xCT and a long 3' untranslated region. The human xCT gene was localized at chromosome 4q28–31. Analysis of the 5'-flanking region of the human xCT gene revealed several sites for potentially binding of transcriptional factors, including NF-E2 and AP-1. Transport of cystine via system x_c^- has been known as a regulatory factor for the intracellular glutathione level, and its transport activity is induced in response to the oxygen tension in culture. Northern blot analysis demonstrated that the expression of both xCT and 4F2hc was significantly enhanced by oxygen. The results suggest that oxygen regulates the activity of system x_c^- by modulating the expression of both xCT and 4F2hc mRNAs. *Antiox. Redox Signal.* 2, 665–671.

INTRODUCTION

PLASMA MEMBRANE TRANSPORT of amino acids is mediated by several transport systems (Christensen, 1990), and recent studies have shown that some transport systems require two components for expressing their activities (Mastroberardino *et al.*, 1998; Torrents *et al.*, 1998; Pineda *et al.*, 1999; Segawa *et al.*, 1999). The heavy chain of 4F2 cell-surface antigen (4F2hc) has been shown to be the common component of these transporters. We have described in cultured mammalian cells a Na^+ -independent anionic amino acid transport sys-

tem highly specific for cystine and glutamate (Bannai, 1986). Cystine taken up via this system, designated system x_c^- , is rapidly reduced to cysteine, which is used for the synthesis of proteins and glutathione (Bannai and Tateishi, 1986). Because cysteine is a rate-limiting precursor for glutathione synthesis, the intracellular glutathione is regulated by the system x_c^- activity. The activity of system x_c^- is induced by electrophilic agents and oxidative stress (Bannai, 1984; Bannai *et al.*, 1991). In mouse peritoneal macrophages, bacterial lipopolysaccharide drastically induces this activity (Sato *et al.*, 1995). In human fibroblast IMR-90 cells,

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in the presence of 2.2 M formaldehyde, transferred to a Hybond-N⁺ membrane (Amersham Pharmacia Biotech), and hybridized in a solution containing 50% formamide for 16 hr at 42°C. The membranes were washed twice for 15 min at room temperature with 1 × SSC, 0.1% sodium dodecyl sulfate (SDS) and then washed twice for 15 min at 68°C with 0.1 × SSC, 0.1% SDS.

Chromosome mapping

Chromosome mapping was performed by Research Genetics, Inc. using the Genebridge 4 Radiation Hybrid Mapping panel. PCR screening was done using primers 5'-CTCTCCCTATGATATGTTGCTGGAGG-3' and 5'-CGTGAAATGGCATTACAATGGCAGGG-3', which are located at the 3'-untranslated region of the cDNA, clone 2.

Rapid amplification of cDNA ends (5' RACE)

Total RNA was isolated from WI26Va₄ cells, and 5' RACE was performed using the 5' RACE system for rapid amplification of cDNA ends, version 2.0 (Life Technologies), following the manufacturer's protocol.

RESULTS

A cDNA library was constructed from WI26Va₄ cells that had been treated with diethyl maleate for 8 hr to augment the activity of system x_c⁻. This library was screened using mouse xCT cDNA as a probe, and two clones were isolated. The insert of one clone (clone 1) was composed of 1,861 bp and contained a single open reading frame that encoded a putative protein. We decided the transcription initiation site by 5' RACE and found that the predicted transcription initiation site existed at 43 bp 5' upstream of clone 1. Another clone (clone 2) was composed of 5,626 bp and contained a single open reading frame. As shown in Fig. 1, the 5'-terminal sequence of this clone was identical with the sequence of 918 to 1,842 of clone 1, indicating that the 5' region of clone 2 was partially deleted. However, clone 2 contained a long 3'-untranslated region. We have performed Northern blot analysis of total RNA

isolated from human fibroblasts using clone 1 or the 3'-untranslated region of clone 2 as probes. Those probes recognized the same transcript, which was approximately 12 kb (data not shown). Clone 1 cDNA encoded a putative protein of 501 amino acids (Fig. 2). Comparison of the sequence of this protein against protein data bases revealed that this protein has 89% homology to mouse xCT and probably a human homologue, *i.e.*, human xCT. Analysis of the amino acid sequence according to the algorithm of Kyte and Doolittle (1982) predicts

A

hxCT	MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLRKRVTLRLGVSSIIIGTIIGA	60
mxCT	MVRKPVVATISKGGYLQGNMNGRLPSMGDQEPGQEKVVLKKITLLRGVSSIIIGTVIGS	60
hxCT	GIFISPKGVLQNTGSVGMSLTIWTVCGVLSLFGALSYAELGTTIKKSGGHYTYILEVFGP	120
mxCT	GIFISPKGILQNTGSVGMSLVFWACVLSLFGALSYAELGTSIKKSGGHYTYILEVFGP	120
hxCT	LPAFVRVVELLIIRPAATAVISLAFGRYILEPFFIQCEIPELAIKLITAVGITVVMVLN	180
mxCT	LLAFVRVVELLIIRPGATAVISLAFGRYILEPFFIQCEIPELAIKLVAVGITVVMVLN	180
hxCT	SMSVSWARIQIFLTFCKLTAILIIIVPGVQLIKGQTQNFDAFSGROSSITRLPLAFY	240
mxCT	STSVSWARIQIFLTFCKLTAILIIIVPGVQLIKGQTHHFKDAFSGROTSIMGLPLAFY	240
hxCT	YGMAYAGWFLNFVTEEEVENPEKTIPLAICISMAIVTIGVLTNVAYFTTINAEELLIS	300
mxCT	YGMAYAGWFLNFITEEVONPEKTIPLAICISMAITVGVLTNVAYFTTISAEELLQS	300
hxCT	NAVAVTFSERLNGFSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV	360
mxCT	SAVAVTFSERLNGKSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV	360
hxCT	RKHTPLPAVIVLHPLTMIMLFSGLDLSLLNLSFARWLFGLAVAGLIYLRKCPDMHRP	420
mxCT	HKHTPLPAVIVLHPLTMVLMFSGLDLSLLNLSFARWLFGLAVAGLIYLRKCPDMHRP	420
hxCT	FKVPLFIPALFSFTCLFMVALSLYSDPFSTGIGFVITLTGPVAYYLFIVWKKPKWFRIM	480
mxCT	FKVPLFIPALFSFTCLFMVVLVSLYSDPFSTGVGLITLTGPVAYYLFIVWKKPKWFRRL	480
hxCT	SEKITRTLQIILEVVPEDKEL	501
mxCT	SDRITRTLQIILEVVPEDSKEL	502

B

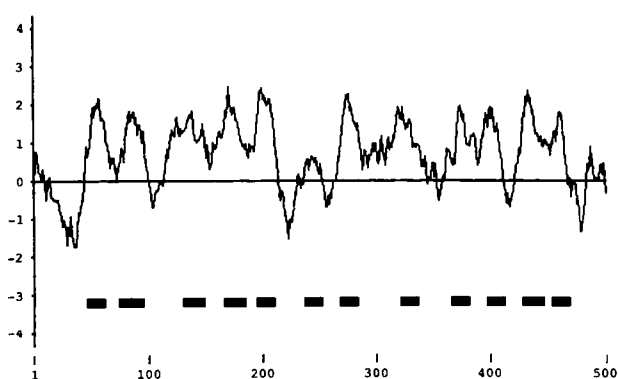


FIG. 2. (A) Sequence alignment of xCT. The deduced amino acid sequences of human xCT (hxCT) and mouse xCT (mxCT) were aligned. Identical and homologous amino acids are indicated by an asterisk and a dot, respectively. (B) Hydropathy plot of human xCT. Kyte-Doolittle hydropathy analysis was done using a window of 17 amino acids. The abscissa indicates the amino acid number. The solid bars indicate the putative transmembrane domains.

an extremely hydrophobic protein that may contain as many as 12 membrane-spanning domains.

When the cRNA from clone 1 was injected into *Xenopus* oocytes in combination with the cRNA of human 4F2hc, the uptake of cystine by the oocytes significantly increased (Fig. 3A). The cystine uptake did not increase with the injection of the cRNA of clone 1 or 4F2hc alone. The increased cystine uptake was inhibited by glutamate, but not by aspartate, arginine, serine, or leucine (Fig. 3B). The results confirm that

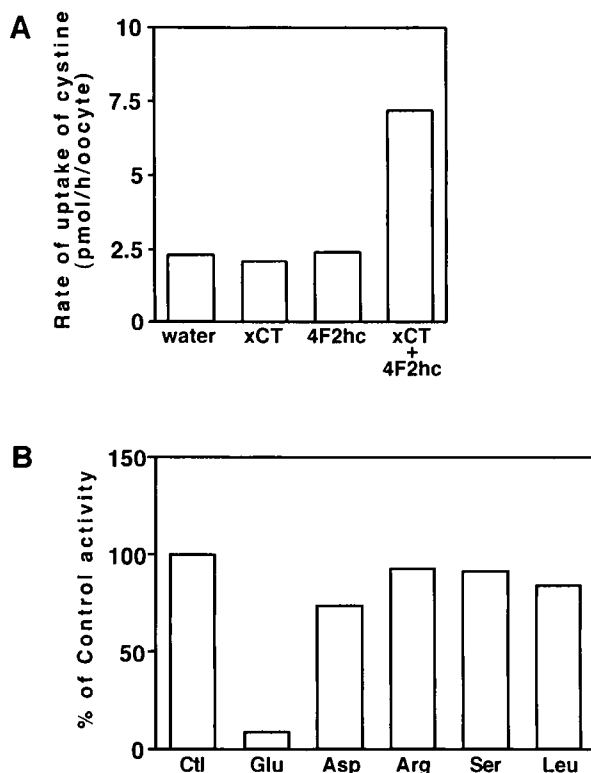


FIG. 3. (A) The rate of uptake of L-cystine in *Xenopus* oocytes. Oocytes were injected with water, 5 ng each of xCT cRNA (labeled as xCT), 4F2hc cRNA (labeled as 4F2hc), or both (labeled as xCT + 4F2hc), and 2 days after injection the rates of uptake of 20 μ M L-[14 C]cystine were measured. Data represent the means of duplicate determinations from one experiment typical of three. (B) Comparison of the inhibitory potential of various amino acids on the uptake of L-cystine. Oocytes were injected with 5 ng each of xCT cRNA and 4F2hc cRNA, and 2 days after injection the rates of uptake of 20 μ M L-[14 C]cystine were measured in the absence (Ctl) or presence of the various L-amino acids (2 mM) indicated. Each data point was calculated by subtracting the uptake value obtained in water-injected oocytes from those in cRNA-injected oocytes, and the uptake value in the absence of inhibitors is designated as 100%. Data represent the means of duplicate determinations from one experiment typical of three.

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-1120  tcactgaatccaaaccacatgtaactatagccaaaatgatctaggattcttttct
-1060  ttccatattgtttttttcttgacacttggtgagaaggtagaagggttaaaatgttt
-1000  tgcctttttgactattgcaaaagtaaatattttatattagcttacatttttaatgcatttt
-940  aaatttataataataacaatagttttatataatgtggaaaaagtcatacataatcatt
-880  actttctataactaccattctgttttctttacaggttttgcctatatacatattttat
-820  gtaattgtaattgtgtaatttgaacttagaatttttttggtaattcaaggaacaac
-760  atgacaatgaaggatattgtatcttttccatagttcaaaaatcacctagtgctaatgag
-700  aatcagaaaatgactattttctggagtcattggaattttgtattagtcacactcgatg
-640  gtgatttaaaatgctgttttatatgagtagtaagaataattttatcttttaattgtga
-580  ggaaggcttatagttgtgtgtatgtgacagaggtataaagtgtagaattcttaatttgt
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-340  cttaaaatgaagtaactatttctgtttcattttgttgaacagcttttgtgtcacta
-280  cgagtgcttttaaatctctgggaaggtctgttctcgaatttactacttctggattggtaa
-220  aatctcttttaagtggtgtctttgttctctaaaaagcttaggtcagttgagcaacaagct
-160  cctctgttttttttttttttaaaaaaaagctgagtaattctggaggtcttctcatgt
-100  ggctgatgcaaacctggagaatttgcattcatcttagctgtagtaagttggtgtgacag
-40  gcaggcgcttaaatcaagcccatgaggaaagctgagctgg+1TTGTAATGATAGGGCGCA
+21  GCAGCAGCAGCAGCAGCAGTGGTGGAAACGAGGAGTGGAGAATTGAGAGCACGATGATA

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FIG. 4. Sequence of 5'-flanking region of human xCT gene. The predicted transcription initiation site is indicated by +1. The potential AP-1 binding sites are shown by underline and the potential NF-E2 binding site is boxed. The TATA-like box is shown by double underline.

the increased uptake is mediated by system x_c⁻ and that the protein encoded by clone 1 cDNA is human xCT.

We have performed database searches (BLAST programs, NCBI) using the sequence of clone 1 and found that three bacterial artificial chromosome (BAC) clones contained at least a part of clone 1 sequence. Two of these BAC clones were obtained and their sequences were analyzed. One BAC clone (CIT-HSP-2283E8.TF) contained the first exon and the 5'-flanking region of human xCT. Another BAC clone (RPC111-60B17.TJ) contained the downstream of 761 of clone 1. A search of the 5'-flanking region, using MatInspector V2.2 based on TRANSFAC 4.0 (Quandt *et al.*, 1995), revealed the presence of one potential binding site of NF-E2 and 12 sequences that are homologous to the consensus AP-1-binding sequence (Fig. 4).

The human xCT gene was chromosome mapped by using a radiation hybrid panel (Genebridge 4 panel) with primers corresponding to the 3'-untranslated region of clone 2 (Fig. 1). The PCR reaction with these primers generated a single product of 355 nucleotides using the BAC clone (RPC111-60B17.TJ) or the

genome DNA derived from human placenta as the templates. Chromosome mapping data demonstrated that the xCT gene was linked to a distance of 0.1 cR (27 kb) from the marker WI-5179 located at chromosome 4q28–31.

We previously demonstrated that oxygen induced the activity of system x_c^- in human fibroblast, IMR-90 cells (Bannai *et al.*, 1989). To investigate the effect of oxygen on the expression of xCT and 4F2hc mRNAs, the cells were cultured at 2, 20, or 80% O_2 for 3 days, and total RNA was isolated. Northern blot analysis of these RNAs showed that the expression of xCT was significantly increased in an O_2 concentration-dependent manner (Fig. 5). It is noteworthy that the expression of 4F2hc was also induced by oxygen. IMR-90 cells, which had been cultured at 2% O_2 for 3 days, were transferred to the atmospheric oxygen and after 8 hr total RNA was isolated. Northern blot analysis of these RNAs revealed that both xCT and 4F2hc mRNAs were significantly induced by the change of oxygen tension (Fig. 6).

DISCUSSION

In the present study, we isolated two cDNA clones for human xCT. Clone 1 contained a

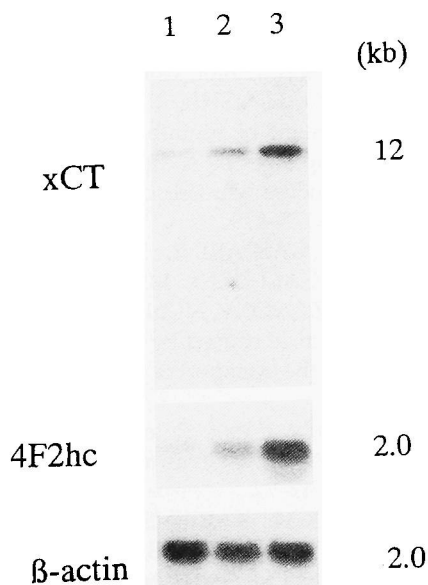


FIG. 5. Effect of oxygen on the expression of xCT mRNA in human fibroblasts. Total RNA was isolated from human fibroblast IMR-90 cells cultured at 2% (lane 1), 20% (lane 2), or 80% (lane 3) O_2 for 3 days. Fifteen micrograms each of total RNA was loaded per lane. The hybridization was performed as described in Materials and Methods.

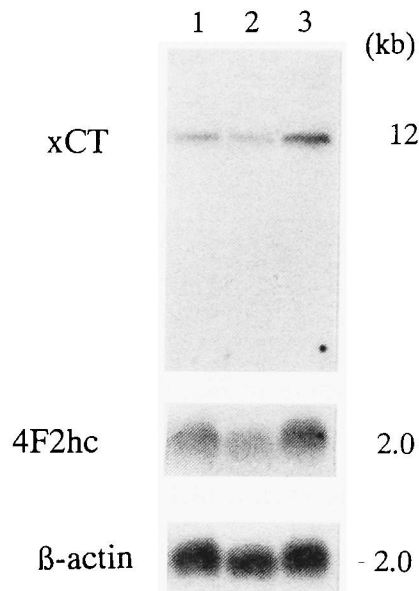


FIG. 6. Induction of xCT mRNA by oxygen. IMR-90 cells were cultured for 3 days at 2% O_2 and total RNA was isolated (lane 1). Then the cells were further cultured at 2% O_2 (lane 2) or 20% O_2 (lane 3) for 8 hr, and total RNA was isolated. Fifteen micrograms each of total RNA was loaded per lane. The hybridization was performed as described in Materials and Methods.

complete reading frame encoding a protein of 501 amino acids. Clone 2 encodes a part of human xCT and has a long 3'-untranslated region. Northern blot analysis of total RNA isolated from human fibroblasts revealed that the major band that hybridized with the probe of human xCT cDNA was approximately 12 kb (Figs. 5 and 6). In Northern blot analysis of total RNA isolated from the mouse peritoneal macrophages, the band of similar size is detected with the probe of mouse xCT cDNA, although some bands of smaller sizes were also detected by the probe (Sato *et al.*, 1999). These results suggest that mRNAs for xCT have 3'-untranslated regions of different lengths, which probably represents alternative splicing, alternative polyadenylation sites, or a combination of both. It is not clear whether the major band mRNA (12 kb) functions as a mature mRNA for translation of xCT in the cell. Recently, mRNA for the cationic amino acid transporter-1, which has a long 3'-untranslated region, is post-transcriptionally modulated, and the 3'-untranslated region plays an important role to stabilize the mRNA (Aulak *et al.*, 1999). It is likely that 3'-untranslated region of xCT mRNA is in-

volved in regulating the expression of xCT post-transcriptionally.

The activity of system x_c^- is induced by electrophilic agents such as diethyl maleate in various mammalian cultured cells (Bannai, 1984; Bannai *et al.*, 1991). This induction is probably mediated by the transcription factor NF-E2 and the electrophile response element (Wasserman and Fahl, 1997), which exists in the 5'-flanking region of human xCT gene (Fig. 4). As shown in Fig. 5, the expression of xCT and 4F2hc mRNAs significantly depended on the O₂ concentration in culture. In the 5'-flanking region of human 4F2hc, there are several AP-1 binding sites (Gottesdiener *et al.*, 1988). Similar sites exist in the 5'-flanking region of the human xCT gene (Fig. 4). AP-1 is a heterodimer of the protein products of individual members of the Fos and Jun immediate-early response gene families, or a homodimer of Jun proteins. AP-1 is activated by various stimuli, including superoxide anion and H₂O₂. This transcription factor may be involved in the regulation of the expression of xCT and 4F2hc by oxygen through these potential AP-1 binding sites.

The gene for human xCT was assigned by linkage analysis to 4q28–31. There are some disorders that are linked in the similar region. However, the link between those disorders and xCT is unknown. Recently, it has been shown that the mutations in the genes for the components of amino acid transporters, rBAT (also named NBAT, D2, or NAA-Tr) and γ^+ LAT-1, cause disorders, cystinuria (Calonge *et al.*, 1994), and lysinuric protein intolerance (Torrrens *et al.*, 1999), respectively. Isolation of human xCT cDNA will enable us to investigate further the genetic disorders and the mutation of xCT gene.

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The nucleotide sequences reported in this paper have been submitted to the GenBank™/EBI

Data Bank with accession number AB026891 and AB042201.

ABBREVIATIONS

BAC, bacterial artificial chromosome; DMEM, Dulbecco's modified Eagle medium; 4F2hc, 4F2 heavy chain; FBS, fetal bovine serum; kb, kilobase(s); 5' RACE, rapid amplification of cDNA ends; SDS, sodium dodecyl sulfate.

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