

CLONING OF THE MURINE LYMPHOCYTE FUNCTION-ASSOCIATED MOLECULE-1 α -SUBUNIT AND ITS EXPRESSION IN COS CELLS¹

Yael Kaufmann,² Elaine Tseng, and Timothy A. Springer³

From the Center for Blood Research, and the Department of Pathology, Harvard Medical School, 800 Huntington Ave., Boston, MA 02115

The lymphocyte function-associated molecule 1 (LFA-1, CD11a/CD18) is an integrin that mediates adhesion of immune cells by interaction with two members of the Ig superfamily, ICAM-1 and ICAM-2. LFA-1 consists of an α subunit ($M_r = 180,000$) and a β subunit ($M_r = 95,000$). We report here the isolation and expression of the murine α subunit cDNA (GenBank accession no. M60778). The deduced sequence comprises a 1061 amino acid extracellular domain, a 29 amino acid transmembrane region, and a 50 amino acid cytoplasmic domain. It has a 72% amino acid identity with its human counterpart and 34% identity with the murine Mac-1 α subunit. The murine LFA-1 α subunit could be expressed on the cell surface of a fibroblastoid cell line, COS, by cotransfection with either the human or murine β subunit cDNA.

LFA-1⁴, and the other leukocyte integrins, Mac-1 and p150.95, are involved in leukocyte interactions during inflammation and the immune response. LFA-1, expressed on virtually all leukocytes, is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, CTL-mediated killing, and antibody-dependent killing by granulocytes and monocytes (1). LFA-1 has two counter-receptors, ICAM-1 (2, 3) and ICAM-2 (4), which are both members of the Ig superfamily. Mac-1 and p150.95 are expressed primarily on myeloid cells. Both Mac-1 and p150.95 may be involved in iC3b binding (5, 6) and myeloid cell-endothelial cell interaction (7, 8). The three leukocyte integrins are $\alpha\beta$ heterodimers having distinct α subunits (LFA-1 α or CD11a, Mac-1 α or CD11b, and p150.95 α or CD11c) and a common β subunit, CD18 (9-11). These three molecules constitute a subfamily of the integrin family. The three leukocyte integrin α subunits are more homologous to each other than to other integrin receptors and possess an inserted or I domain of

200 amino acids, which is not found in other integrin α subunits, with the exception of VLA-1 and VLA-2 (12).

LFA-1 was originally identified in the mouse (13, 14) and later in the human system where it has been cloned and sequenced (12, 15). There are species-specific differences, because human LFA-1 will bind to both murine and human ICAM-1, whereas murine LFA-1 will bind to murine and not human ICAM-1. This species specificity resides in the murine α subunit (16). We have been interested in the structural basis for the function of LFA-1 in inflammation and the immune response and in identifying regions on the LFA-1 subunits that are important to their adhesive and signal transduction functions. As a first step toward this end, we have cloned the murine LFA-1 α subunit cDNA, determined its nucleotide and deduced amino acid sequence, and showed that it can be expressed in COS cells in association with either the murine or the human β subunit.

MATERIALS AND METHODS

Library screening and clone isolation and characterization. Procedures for hybridization of human LFA-1 α probe to the cDNA library and clone characterization were as described in Maniatis et al. (17). An *EcoRI-BamHI* fragment corresponding to most of the coding region (nucleotides 1-2955) of the human LFA-1 α cDNA (12) was labeled with ³²P by nick translation, hybridized in 5x SSC, 5x Denhardt's solution, 0.1% SDS, 50% formamide, and 50 μ g/ml denatured herring sperm DNA at 37°C to a murine cDNA library kindly provided by A. Turner and M. Davis, Stanford University, Stanford, CA. The library was constructed from cytoplasmic RNA of B cell lymphoma line BCL1 (American Type Culture Collection, CRL 1669, Bethesda, MD), which had been induced for 19 h with rIL-2 (1000 U/ml), and IL-5 (10% of a COS cell supernatant of a transient transfection with IL-5 clone). The library was constructed in lambda ZAP XHO-MID, a derivative of λ ZAP that had been modified to possess only one *Apal* site in the SK⁻ polylinker. The cloning site was *XhoI*. Filters were washed twice with 2x SSC and 0.1% SDS at 20°C for 15 min and once at 37°C for 30 min and exposed to x-ray film overnight. Clones containing hybridizing sequences were purified and the plasmids containing inserts were excised with the helper phage R408 (Stratagene, La Jolla, CA).

Two clones denoted 23 and 28 were characterized by partial sequence and restriction enzyme mapping. The composite sequence of these clones contains the entire murine LFA-1 α coding region. Five restriction fragments were subcloned from clones 23 and 28 into pBluescript and the two DNA strands were sequenced by the dideoxy chain termination method (18). The ends of the fragments were sequenced with the pBluescript primers and internal regions were sequenced using synthetic primers complementary to the murine LFA-1 α sequence (Fig. 1).

DEAE-dextran transfection of COS cells. The entire coding region of the human LFA-1 α and β subunit cDNA (12, 15) and the murine β subunit cDNA (19) were subcloned into the expression vector Ap^rM8, an ampicillin resistant modification of CDM8 (L. B. Klickstein, unpublished observations). A cDNA clone containing the entire coding sequence of the murine LFA-1 α subunit was prepared by removing the *EcoRI* fragment of clone 28 corresponding to the 3' end of its cDNA and replacing it with the *EcoRI* fragment of clone 23 containing the downstream cDNA portion of 3083 nucleotides (Fig. 1). The proper orientation of the 3' insert was determined by

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² On leave of absence from the Institute of Hematology, Chaim Sheba Medical Center, Tel Hashomer and Sackler School of Medicine, Tel Aviv University, Tel-Aviv, Israel.

³ Address correspondence and reprint requests to Dr. Timothy Springer, Center for Blood Research, 800 Huntington Avenue, Boston, MA 02115.

⁴ Abbreviations used in this paper: LFA-1, lymphocyte function-associated Ag 1; mLFA, murine LFA.

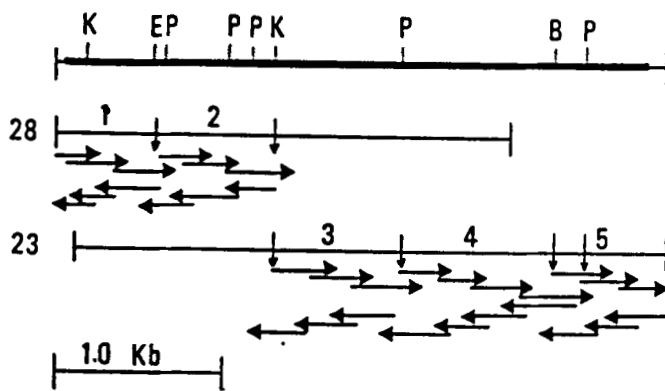


Figure 1. Restriction map of murine LFA-1 α subunit cDNA clones. The open reading frame and untranslated regions are indicated with a thick and thin line, respectively. Numbers 1 to 5 show restriction fragments subcloned for sequencing. Arrows indicate the sequencing strategy. The relevant restriction sites are: *EcoRI* (E), *PstI* (P), *KpnI* (K), and *BamHI* (B).

complete digestion with *HindIII* + *Sall*. The murine LFA-1 α cDNA (3662 nucleotides) and murine β cDNA (2856 nucleotides) were excised from pBluescript by digestion with *XhoI* and *EcoRI*, respectively, ligated with *BstXI* linkers after blunting of the *XhoI* and *EcoRI* sites with Klenow fragment of DNA polymerase I and subcloned into the *BstXI* site in Ap^rM8 (20). The human LFA-1 α and β subunits cDNA (4.5 and 2.7 kb, respectively) were isolated by complete digestion with *HindIII* + *XbaI* and ligated to Ap^rM8. The α and β subunit cDNA were cotransfected into COS cells, a monkey kidney fibroblastoid cell line, using DEAE-dextran (20, 21).

Indirect immunofluorescence and mAb. COS cells were harvested with 5 mM EDTA in HBSS and cell surface expression of LFA-1 α and β subunits were examined by indirect immunofluorescence as detailed previously (21). The mAb used in these experiments include TS1/22 and TS1/18 to the human LFA-1 α and β subunit, respectively (10), and M17/4.2 and M18/2a.8 to the murine LFA-1 α and β subunits, respectively (22, 23). An mAb to horseradish peroxidase, ZPOI (Zymed Laboratories, San Francisco, CA) was used as a negative control. FITC-conjugated goat-anti-mouse Ig (0.1 mg/ml) (Zymed Laboratories), was used as a second antibody.

RESULTS AND DISCUSSION

Identification and characterization of murine LFA-1 α cDNA clones. A lambda ZAP cDNA library constructed from the mouse B cell lymphoma line BCL1 was screened with a probe containing the majority of the coding region of human LFA-1 α subunit cDNA (12). Seven clones were isolated and two, denoted 28 and 23, were characterized in detail. Clone 28 is 2.75-kb long and contains the nucleotide sequence corresponding to the 5' end of the human LFA-1 α subunit open reading frames, including a putative initiation codon (ATG). Clone 23 is 3.5-kb long, it overlaps most of clone 28 except for the 5' 143 nucleotides and extends 0.9-kb further downstream to include the end of the coding sequence (Fig. 1). The composite sequence of clones 28 and 23 of 3662 nucleotides contains the 3489 nucleotide coding sequence, a 5' untranslated region of 59 nucleotides and a 3' untranslated region of 114 nucleotides (Fig. 2).

Nucleotide and deduced amino acid sequence of the mLFA-1 α chain. The sequence of the N-terminal 20 amino acids of the mLFA-1 α subunit previously determined by N-terminal sequencing (24) is in perfect agreement with that deduced from the DNA sequence (underlined in Fig. 2). The mature α subunit is preceded by a 23 residue signal peptide with a consensus peptidase cleavage sequence (Ala-X-Ser/Pro) (25). There is a single

upstream translation initiation codon at nucleotide 60. The mature mLFA-1 α subunit has an extracellular domain of 1061 residues, a single hydrophobic transmembrane region of 29 residues and a cytoplasmic tail of 50 residues (Fig. 2). The mature protein is predicted to be $M_r = 125,400$. Fifteen N-linked glycosylation sites (Asn-X-Thr/Ser) are present in the extracellular domain (Figs. 2 and 4). These values agree with the M_r of the mLFA-1 subunit translated *in vitro* ($M_r = 140,000$) and the mLFA-1 α glycoprotein ($M_r = 180,000$) (26).

The mLFA-1 α subunit contains within the extracellular domain an inserted (I) domain of about 190 amino acids (residues 124-310) (Fig. 3). I domains are found in the three human leukocyte integrin α subunits sequenced to date, murine Mac-1 α , and in VLA-1 and 2 but not other VLA α subunits or the IIbIIIa and vitronectin receptor α subunits. These I domains are homologous with repeated domains in von Willebrand factor, cartilage matrix protein, and a single domain in complement components C2 and factor B (1, 27). Three repeats with a putative divalent cation binding site motif are found at amino acid residues 432-587. Other integrin α subunits contain either three or four putative divalent cation binding motifs (1, 27). Most of the cysteines and N-glycosylation sites are found outside the I region and the putative divalent cation binding motifs (Fig. 3). A paucity of cysteines in this region is found in other leukocyte integrin α subunits as well (12, 28-31), and is consistent with a previous suggestion that this region may undergo conformational changes, important in ligand binding (12, 32).

Comparison of sequence homology between the mLFA-1 α chain and its human counterpart (Figs. 3 and 4) shows overall 72% identity with the highest identity (82%) for the putative divalent cation binding repeats and the lowest identity (55%) for the cytoplasmic domain (Fig. 3). The high conservation of the putative cation binding motif is consistent with an involvement of this region in the functional activity of LFA-1 α . Divalent cations (1 mM Mg^{2+} or 0.1 mM Mg^{2+} and 1 mM Ca^{2+}) are required for cellular interactions that are dependent on LFA-1 (32), for LFA-1-dependent binding of cells to purified ICAM-1 (3), and for binding of purified LFA-1 protein micelles to purified ICAM-1 (33). The low conservation of the cytoplasmic tail is consistent with a recent finding (34) that the human LFA-1 α chain with its cytoplasmic domain truncated so that it contains only the 14 residues adjacent to the membrane, can associate with the β chain and fully supports binding to ICAM-1. Comparison of sequence identity between mouse LFA-1 α and mouse Mac-1 α chains reveals an overall identity of 34% with the highest identity between the first two putative divalent cation binding sites.

Expression of murine LFA-1 α subunit on surface of COS cells. We examined whether the murine α subunit could be expressed in the fibroblastoid COS cell line, and the requirement for coexpression with the murine or human β subunit. COS cells were transiently transfected with α or β subunit cDNA alone or together and surface expression was detected with mouse anti-human or rat anti-mouse first antibody, followed by a second antibody to mouse IgG and flow cytometry (Fig. 5). This second antibody stained rat IgG (somewhat more weakly than mouse IgG) by cross-reaction. Cotransfection of the α and β subunit cDNA yielded efficient expression on the sur-

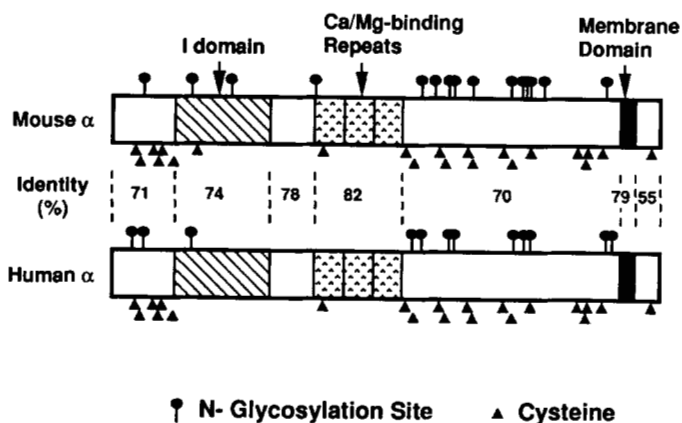


Figure 3. Schematic representation of murine and human LFA-1 α subunits. Black lollipops (above schematic) and triangles (below schematic) indicate potential glycosylation sites and cysteines, respectively. Sequences of the domains were compared using the ALIGN program; the percent identities are indicated.

LFA-1 subunits form interspecies hybrid $\alpha\beta$ complexes. Formation of murine-human $\alpha\beta$ complexes was previously detected in somatic cell hybrids of a murine T cell line with normal human lymphocytes or with β subunit-deficient (LAD patient) lymphocytes (35).

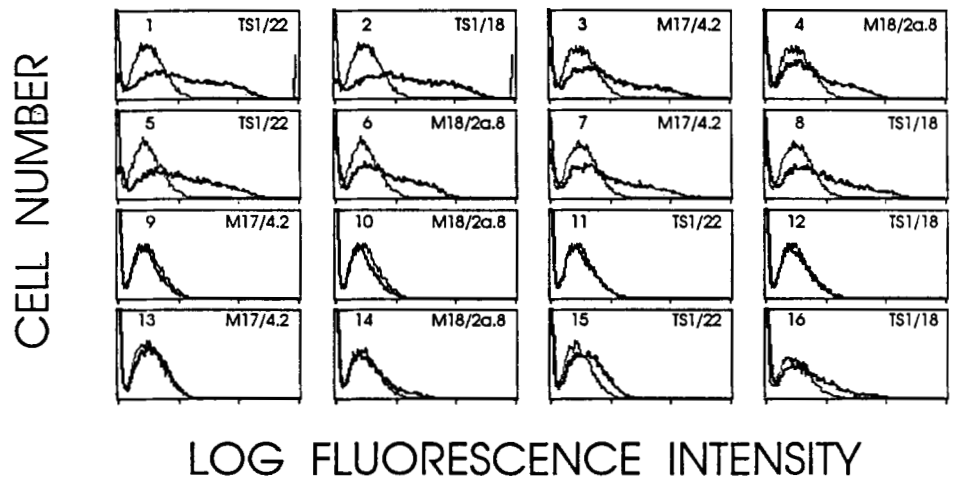
The sequence of the mLFA-1 α subunit determined in this study, which shows high homology with its human counterpart, explains the efficient association of mouse-human $\alpha\beta$ hybrid complexes on the cell surface. The finding that the highest homology between murine and human LFA-1 α subunits (as well as between mLFA-1 and mMac-1 α subunits) is located in the putative cation binding region is compatible with the importance of this region in the function of leukocyte integrins. The relatively low homology (55%) of the murine and human LFA-1 α cytoplasmic domains is of interest. By contrast, the murine and human β subunit cytoplasmic domains are 96% identical (19, 36, 37). These findings suggest that association with the cytoskeleton or regulation of avidity for ICAM-1 by signals from the cytoplasm (33), may be mediated by the β subunit rather than the α subunit. This is in agreement with the observation that truncation of the LFA-1 α subunit cytoplasmic domain has no effect on binding to ICAM-1, whereas binding is markedly diminished by β subunit cytoplasmic domain truncation (34).

We have isolated and sequenced a murine LFA-1 α subunit cDNA and shown that it is competent for expression in COS cells in the presence of a human or murine β subunit cDNA. The regions of the LFA-1 α subunits that are most strongly conserved in evolution have been

mLFA-1	1	YNLDTRPTQSF.LAQAGRHFQYVQLQIEDGVVVGAPGEGDNTGGLYHCRTSSEFCQVPSLHGSNHTSKYLGMTLATDAAK
hLFA-1		V GAR SPPR R VGN I NS S Q QSGTGH L T R Y PTD
	81	GSLACDPGLSRTCDQNTYLSGLCYLFPQSLGPMQNRFPAYQECMKGVLDVFLFDGSSQLDRDFEKILEFMKDVMRK
		I R N Q G GF I N M QPDE Q D K I Domain -->
	161	LSNTSYQFAAVQFSTDCRTEFTFLDYVQKNKPDVLLGSVQPMFLLTNTFRAINVVAHVFKESGARPDATKVLVIITD
		SYK D S .W D A KH KH L G ATE R L I
	241	GEASDKGNISAADITRYIIGIGKHFVSVQKQKTLHFASEPVEEFVKILDTFEKLKDLFTDLQRIYAIEGTNRQDLTS
		T S D K I QTKES E K K AS E K V SK -- I Domain
	321	FMELSSSGISADLSKGHAVVGAVGARDWAGGFLDLREDLQGATFVGGQEPLTSDVRRGGYLGVTVAWMTSRSSRPLLAAGA
		R KA DD I N PE A T LF QKTS S
	401	FRYQHVGVLLFQAPEAGGRWNQTKIEGTQIGSYFGGELCSVDLDQDGEAELLIGAPLFFGEGRGRVFTYQRRQSLF
		M R E QG H S V T H G V T Y I LG Metal Binding Domains -->
	481	EMVSELQGDGPFYPLGRFGAAITALTDINGDRLTDVAVGAPLEEQGAVYIFNGKPGGLSPQPSQRIQGAQVFPGRWFRGS
		E E G V RH E T LS Q
	561	IHGVDKLGDRDLADVVVGAEGRVVLSRPFVVDVTELSFSPEEIPVHEVECSYSAREEQKHGVKLCACFRKPLTPQFQ
		E G A SQMI M LM A TSNRM E NITI Q S Y <-- Metal Binding Domains
	641	GRLLANLSYTLQLDGHRMRSRGLFPDGSHELSGNTSITPKSCLDFHFHPICIQDLISFINVSLNFSLEEGTFRDQK
		V T T R GR RR IAV TSM T S V V W R
	721	.GRAMQFILRPSIHTVTKIEPFKNCGEDKCKEANLTL.SPARSGPLRLMSSASLAVEWLNSNGEDAYVVRDLDDFP
		AQ KDIP L SE W RV F RA TAF S LS LE Q H
	801	RGLSFRKVEMLQPHSRMPVSCCELTEGSSLLTKLKNVSSPFIKAGQEVSLQVMFNTLLNSWEDFVELNGTVHCENEN
		P K QI P ER SRA S HS A M V GS HAN T N D
	881	SSLQEDNSAATHIPVLYPNILTKEQENSTLYISFTPKGPKTQQVQHVYQVRIQPSAYDHNMPTEALVGVVPRPHSEDLI
		D L T I I I IQD D V IH KM IH I V Q P GP
	961	TYTWSVQTDPLVTCHSEDLKRFSSAEQPCLPQGVQFRCPVFRWEILIQVTGTVELSKEIKASSTLSCSSLSVSNSSK
		HQ ME P P Y E L.PD AE AL V Q V I L VG E MF I
	1041	HFHLYGSKASEAQVLVKVDLIHEKEMLVHYVLSGIGGLVLLFLIFLALYKVGFFRNLKERMEADGGVPNGSPFEDTDFL
		N L VM VVY Q YL L L IV GR I A SEQ
	1121	AVPGEETKDMGCLEPSGRVTRTKA
		.S Q AG P K LBEKDESG

Figure 4. Comparison of the murine and human α subunits. The amino acid sequences of the murine and human LFA-1 α subunits were aligned. Only the human LFA-1 α residues different from the mouse are shown. Gaps are marked with a period. Boundaries of domains are marked and are based on homologies to other integrins and the p150.95 α subunit exon structure (38).

Figure 5. Immunofluorescence flow cytometry of COS cells after transfection with murine and human α and β subunit cDNA alone or together. COS cells were transfected with the following LFA-1 cDNA: panels 1 and 2, human (h) α + h β ; panels 3 and 4, murine (m) α + m β ; panels 5 and 6, h α + m β ; panels 7 and 8, m α + h β ; panels 9–12, expression vector with no insert; panel 13, m α ; panel 14, m β ; panel 15, h α ; and panel 16, h β . The mAb used to detect surface proteins are indicated (anti-h α TS1/22, anti-h β TS1/18, anti-m α M17/4.2, and anti-m β M18/2a.8). In all panels the specific mAb staining profile is shown with a dark line and staining with the negative control mAb ZP01 is shown with a light line.



defined. The work reported here should facilitate further studies on the structure and function of the LFA-1 α subunit.

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