A Unique Gene Encodes Spliceoforms of the B-Cell Adhesion Molecule Cell Surface Glycoprotein of Epithelial Cancer and of the Lutheran Blood Group Glycoprotein

By Cecile Rahuel, Caroline Le Van Kim, Marie Genevieve Mattei, Jean Pierre Cartron, and Yves Colin

Two new members of the Ig superfamily, the Lutheran (Lu) blood group glycoprotein and the B-cell adhesion molecule (B-CAM) epithelial cancer antigen, have been recently cloned from human placenta and colon cancer HT29 cell line, respectively. Although amino acid sequences deduced from cDNA analysis suggested that B-CAM should represent an abridged form of the Lu glycoprotein lacking the last 40 amino acids of the putative cytoplasmic tail, the relationship between the genes encoding these polypeptides has not been determined. In the present report, we showed by Southern blot analysis that the Lu and B-CAM cDNAs derived from a unique LU gene which exhibited an HindIII RFLP associated with the Lu\textsuperscript{7}/Lu\textsuperscript{8} blood group polymorphism. Accordingly, in situ hybridization of the Lu cDNA probe confirmed the localization of the Lutheran blood group locus to chromosome 19 q13.2-13.3, as previously shown for a B-CAM DNA probe. Sequence comparison between cDNA and genomic PCR fragments indicated that the Lu and B-CAM transcripts previously isolated are generated through the alternative use of internal splice donor and acceptor sites within an exon located at the 3' end of the LU gene. These spliceoforms corresponded to 2.5 kb and 4.0 kb mRNA species detectable by Northern blot in all tissues and cell lines in which the LU gene is expressed; their primary structures are consistent with the presence of both the Lu and B-CAM antigens on two glycoprotein isoforms. However, the 4.0 kb transcript was very poorly expressed as compared to the 2.5 kb species except in the colon carcinoma HT29 cell line, suggesting a differential regulation of the Lu/B-CAM messenger RNA in some tumor tissues.

The Lutheran (Lu) blood group antigens were originally shown to be carried by low abundance erythrocyte membrane glycoproteins of apparent molecular mass 85 (major species) and 78 kD (minor species) on immunobLOTS.\textsuperscript{4,5} Further studies indicated that these glycoproteins (gp), or related molecules, although restricted to erythroid cells in peripheral blood,\textsuperscript{4,5} are expressed in a broad range of human cells and tissues and may represent developmentally regulated molecules in human liver.\textsuperscript{6,7} Recently, the primary structure of the 85 kD Lu gp was deduced from the nucleotide sequence of a human placenta cDNA clone.\textsuperscript{8} Hydrophathy plot analysis indicated that the predicted mature protein is a type I membrane polypeptide of 597 amino acids composed of a large extracellular domain of 518 residues with five potential N-glycosylation sites, followed by a single transmembrane domain and a cytoplasmic tail of 59 amino-acids. Immunological studies with antibodies against the extracellular\textsuperscript{9-11} and the cytoplasmic and/or transmembrane\textsuperscript{12,13} domains of erythrocyte Lu gp suggested that the 85 kD and 78 kD gp species differ only by the length of the cytoplasmic tail, which contains a consensus binding site for proteins carrying a Src homology 3 domain.\textsuperscript{14} Most interestingly, comparison of the predicted amino acid sequence of Lu gp with protein data bases revealed significant homology with numerous members of the Ig superfamily (IgSF). The extracellular part of Lu gp consists of five IgSF-like domains, two variable-(V)-region and three constant-region (C2) set domains.\textsuperscript{5}

In independent and previous studies, the human basal cell adhesion molecule (B-CAM), a cell surface antigen of epithelial cancer, has been cloned and shown to be also a new IgSF member with the V-V-C2-C2-C2 arrangement of immunoglobulin domains.\textsuperscript{6} cDNA sequence comparison provided the first indication of a relationship between B-CAM and Lu and indicated that the predicted amino acid sequence of B-CAM differed from that of the 85 kD Lu gp only by the lack of the last 40 amino acids of the cytoplasmic tail.\textsuperscript{5} However, available nucleotide sequence on the 3' untranslated region of the two cDNAs exhibited no homology.

The B-CAM antigen was first identified by monoclonal antibodies (MoAbs) raised against human tumor cells and was shown to be overexpressed in ovarian carcinomas in vivo and upregulated following malignant transformation in some cell types.\textsuperscript{19} In addition, B-CAM was expressed in a variety of normal human tissues and cells but not on hematopoietic cells.\textsuperscript{10,11,12,13,14}

The role of Lu and B-CAM antigens is yet to be clarified, but their structural homology with the MUC18 human cell surface antigen of invasive melanoma\textsuperscript{11,12} and the SCI chicken neural adhesion molecule,\textsuperscript{13} two other IgSF members with the V-V-C2-C2-C2 domain structures known as cellular adhesion molecules, suggested that they may share similar functions. In this context, it has already been observed that substrate-adherent growth of some cell types might be correlated with B-CAM expression.\textsuperscript{8,14}

In this report, we show that the previously isolated Lu and B-CAM cDNA clones\textsuperscript{5,16,17} represent alternatively spliced transcripts of a unique gene on chromosome 19q13.2-13.3. The structure and tissue distribution of these mRNA spliceoforms are consistent with the immunocharacterization of two Lu and B-CAM active glycoproteins in various cells.

MATERIALS AND METHODS

Materials. Oligonucleotides and primers came from Genset (Paris, France). Restriction enzymes and pUC vectors came from

From INSERM U76, GIP-Institut National de la Transfusion Sanguine, Paris; and INSERM U406, Marseille, France.

Submitted March 7, 1996; accepted April 19, 1996.

Address reprint requests to Yves Colin, PhD, Unité INSERM U76, GIP-Institut National de la Transfusion Sanguine, 6, rue Alexandre Cabanel, 75015 Paris, France.

The publication costs of this article were defrayed in part by page charge payment. This article must therefore be hereby marked "advertisement" in accordance with 18 U.S.C. section 1734 solely to indicate this fact.

© 1996 by The American Society of Hematology.

0006-4971/96/8805-0036$3.00/0
Appligene (Strasbourg, France). T4 DNA ligase and polynucleotide kinase were from Biolabs (Northbrook, IL) and radiolabeled nucleotides from Amersham (Bucks, UK). Thermus aquaticus polymerase (Taq Polymerase) was purchased from Life Technologies (Gaithersburg, CA). The random priming labelling kit came from Boehringer (Mannheim, Germany). T7 cycling sequencing kit was obtained from Pharmacia (Uppsala, Sweden).

DNA probes. Lu and/or B-CAM cDNA probes were made by polymerase chain reaction (PCR) amplification using primers designed from available sequence information's (see Fig 1). The PCR1 probe was amplified between primers LB1 and LB32 (see Table 1 for oligonucleotide sequences) and corresponded to the common sequence of Lu and B-CAM cDNAs between nt +4 to nt +1,761 (+1 taken as the first residue of the initiator AUG). PCR2 was amplified between primers L36 and L37 and corresponded to nt 1,891 to nt 1,982 of the Lu specific 3' noncoding sequence. PCR3 was amplified between primers B1 and B3 and corresponded to nt 1,769 to 1,912 of the B-CAM specific 3' untranslated region.

The 1,039 bp PCR4 probe was made by genomic PCR amplification between primers LB44 and L2 (see Table 1), and was used as specific B-CAM probe (nt +1,744 to 2,782 of the B-CAM transcript). The amplified cDNAs were electrophoresed on agarose gels and labeled by the random priming method (specific activity, 5 x 10^6 cpdpg/mg) to be used as probes.

Southern analysis. Human genomic DNA extracted from peripheral leukocytes was digested with restriction enzymes (10 U/μg DNA), resolved by electrophoresis in 0.8% (wt/vol) agarose gels and transferred as described by Southern on a nylon membrane GT (Bio-Rad, Hercules, CA). Hybridization with cDNA probes (2 x 10^6 cpdpg/mL) was performed for 16 hours at 65°C according to the manufacturer's recommendations, and final washings were done at 65°C in 40 mmol/L Na-phosphate, 0.1% (wt/vol) sodium dodecyl sulfate (SDS) for 20 minutes.

PCR amplification of RNA and genomic sequences. Genomic DNA was used as a template for PCR amplification using primer LB44 as a 5' primer and L2 or B2 as 3' primers (Table 1 and Fig 3). Five micrograms of total cellular RNA from human kidney and human fetal brain (Clontech, Palo Alto, CA) were used for cDNA preparations with a kit from Pharmacia. About 500 ng of the first strand cDNA was used as a template for PCR amplification with various B-CAM and Lutheran primers (50 pmols each), specific of the 3' ends of the cDNAs. Reactions were performed in 50 mmol/L KCl, 10 mmol/L Tris (pH 8.3), 3 mmol/L MgCl2, 0.001% (wt/vol) gelatin, 0.2 mmol/L of the four dNTPs, and 2.5 units of Taq polymerase (Perkin Elmer-Cetus, Norwalk, CT). Thirty cycles of amplification were performed in a Perkin Elmer-Cetus thermal cycler under the following conditions: denaturation for 30 seconds at 94°C, primer annealing for 30 seconds. (see Table 1 for annealing temperatures) and extension at 72°C for 1.5 minutes.

DNA sequencing. cDNA and genomic inserts were subcloned into the pUC18 vector and sequenced on both strands by chain termination method with a Pharmacia T7 sequencing kit, using universal primers or specific oligonucleotides as internal primers.

Northern blot analysis. Northern blots were prepared as described with 15 μg of total RNAs from different human cell lines or 2 μg of poly(A+) RNAs from normal tissues. Multitissue northern (MTN) blots were purchased from Clontech. Hybridization with the PCR1, PCR2, and PCR4 probes were performed at 65°C in 7% (wt/vol) SDS, 300 mmol/L Na-phosphate. Stringent washes were performed at 65°C in 40 mmol/L Na-phosphate, 0.1% (wt/vol) SDS for 20 minutes.

In situ chromosome hybridization. The PCR1 probe was used for chromosome hybridization on metaphasic cells obtained from phytohemagglutinin-stimulated peripheral blood lymphocytes for 72 hours. The conditions for probe labeling, hybridization, washings, and for visualization of hybridization on chromosomes were described.

RESULTS

Comparison of the Lu and B-CAM cDNA sequences. Sequence comparison indicated that the previously isolated Lu and B-CAM cDNAs' were identical from nt -6 to nt +1,764 which encoded a polypeptide chain made of a cleavable signal peptide (31 residues), the NH2 extracellular region (515-518 residues), the transmembrane domain (20-23 residues) and exhibited no homology with the incomplete 3' untranslated regions of the Lu cDNA that extended from nt 1,765 to nt 2,390.

The identity of the B-CAM and Lu cDNA sequences be-
A UNIQUE GENE FOR LU AND B-CAM GLYCOPROTEINS

![Diagram of gene expression](image)

- Boxes represent cDNA sequences coding for the signal peptide (Sp), the extracellular (Ext) and transmembrane (TM) domains and for the first 19 amino acids of the cytoplasmic domain (Cyt) common to the Lu and B-CAM gps, previously cloned from human placenta and HT29 cell line, respectively. Black boxes refer to the sequence coding for 40 additional residues specific of the Lu cytoplasmic tail. Broken and heavy lines refer to the partial B-CAM and complete Lu specific 3' noncoding regions, respectively. Initiation and termination codons are indicated. Localizations of Lu and/or B-CAM specific PCR probes are indicated.

between nucleotides -6 to +1,764 raised the question as to whether these two cDNA species derived from the same gene or from two highly related genes. To resolve this problem, 3 primer sets were designed (see Materials and Methods and Fig 1), to construct DNA probes specific of the 3' end of Lu and B-CAM cDNAs (PCR2 and PCR3, respectively) and for nucleotide sequence encoding the common extracellular and intramembranous domains of Lu and B-CAM gps (PCR1).

In situ chromosome hybridization of the Lu/B-CAM cDNA probe. When the Lu/B-CAM PCR1 probe was used for in situ hybridization to human metaphasic chromosomes, a unique signal was detected on chromosome 19. In the 100 metaphases examined, 29.8% of the silver grains associated to chromosome 19 and 79.8% of them mapped to the 19q13.2-q13.3 region (not shown).

Southern blot analysis of the human Lutheran and B-CAM loci. As a first approach to investigate the relationship between the gene(s) encoding the Lu and B-CAM gps, Southern blot analysis of genomic DNA from unrelated donors serologically typed as Lu(a+b-) (n = 2), Lu(a-b+) (n = 4), and Lu(a+b+) (n = 7) was performed with the PCR1 probe common to the Lu and B-CAM cDNAs, the PCR2 probe specific of the Lu sequence and the PCR3 probe specific of the B-CAM sequence (see above). On BamHI digests, the Lu/B-CAM PCR1 probe detected three fragments (18 kb, 10 kb, and 0.5 kb), regardless of the Lu/Lu status of the samples (Fig 2A). In contrast, PCR1 revealed on HindIII digests a restriction fragment length polymorphism (RFLP) associated with the expression of the Lu* and Lu* antigens, because either a 22 kb or a 20 kb HindIII fragment was detected in the homozygous Lu*(a-b+) or Lu*(a-b+) samples, respectively. Both fragments were present in the heterozygous Lu*(a+b+) samples. However, this RFLP most likely did not identify the site of the Lu/Lu* antigenic polymorphism but rather represented a linked DNA polymorphism in a non coding region of the Lu gene, since the coding sequence of the published Lu* cDNA2 did not contain any HindIII recognition site and the HindIII genomic fragment carrying the Lu* allele was shown here to be longer than that carrying the Lu allele.

The Lu PCR2 probe revealed the same HindIII patterns as PCR1, but it detected only the 10 kb fragment in the BamHI digest (Fig 2B). Interestingly, the B-CAM PCR3 probe exhibited the same hybridization pattern to that of the PCR2 probe (Fig 2C).

These results, particularly the finding that the B-CAM PCR3 probe revealed the Lu/Lu* associated HindIII RFLP, strongly suggested that the Lu and B-CAM cDNAs derived from a unique Lu gene by a mechanism, which will be further explored below.

**PCR amplification of Lu and for B-CAM cDNAs and genomic DNA sequences.** cDNA sequence comparison indicated that the first nucleotides of B-CAM which differ from the Lu sequence correspond to those of a consensus splice donor site (GTGAG, nt 1,765 to 1,769, see Fig 3). This observation suggested that the downstream sequence of the B-CAM mRNA was transcribed from a region of the Lu gene which was skipped from the Lu mRNA by splicing at an internal splice donor site. Alternative splicing of the sequence, downstream of the junction between Lu and B-CAM cDNAs, was assessed by comparing the PCR products obtained when cDNA (kidney or fetal brain) or genomic DNA were used as templates for amplification between primers surrounding the Lu/B-CAM divergence site (nt 1,765). The same 70 bp PCR product was amplified from cDNA or genomic DNA with the B-CAM specific primer set LB44-B2, whereas the Lu specific primer set LB44-L2 amplified fragments of 61 bp and 1,039 bp from cDNA and genomic DNA templates, respectively (not shown). These results indicate that within the Lu gene region under study, the Lu but not the B-CAM coding region was disrupted by a DNA sequence of 978 bp (Fig 3). Sequence analysis revealed a complete homology between the 5' half of this 978 bp genomic fragment (Fig 4) and the partial 3' untranslated region of the B-CAM cDNA previously published (nt 1,765 to nt 2,390). Southern and/or sequencing analysis of the 765 bp and 556 bp PCR products, obtained after amplification of cDNA templates between primer sets B4-L37 and B9-L45 (see Fig 3), indicated that the uncharacterized 3' end of the B-CAM cDNA correspond to the 3' end of the 978 bp sequence followed by the sequence of the published Lu cDNA from nt 1,764 to the poly(A) addition site. In the course of this study, we also characterized an intron of 92
Southern blot analysis of DNA from donors homozygous or heterozygous for the Lu⁺ and Lu⁻ blood group antigens. DNAs from Lu(a+b⁻), Lu(a-b⁺) and Lu(a+b⁺) individuals were digested with the restriction enzymes BamHI and HindIII and hybridized with Lu and/or B-CAM cDNA probes. Blots were sequentially hybridized with: (A) the PCR1 probe specific of the common 5' sequence of the Lu and B-CAM cDNAs, (B) the PCR2, and (C) PCR3 probes, specific of the 3' noncoding region of the Lu and B-CAM cDNAs, respectively. Only typical results with some donors of each phenotype (see Results) are shown.

Fig 2. Schematic representation (not to scale) of the alternatively spliced 3' region of 4.0 kb and 2.5 kb Lu/B-CAM mRNAs. Open and black boxes are as in Fig 1. The 978 bp sequence (nt 1,765 to 2,741) of the 4.0 kb mRNA is skipped from the 2.5 kb mRNA species by the use of internal splice donor and acceptor sequences (underlined). TGA termination codons are double underlined. Nucleotides 2,742 to 3,357 (noncoding sequences) of the 4.0 kb transcript (thick line) are identical to nt 1,764 to 2,379 (coding and noncoding sequences) of the 2.5 kb mRNA. Roman and italic upper case letters refer to coding and noncoding sequences, respectively, and lower case letters to nontranscribed sequences. Only relevant nucleotides are given. Nucleotides of the 92 bp intron are not taken into account for numbering the 4.0 and 2.5 kb mRNA sequences. Location of the PCR primers are indicated.

Fig 3. Schematic representation (not to scale) of the alternatively spliced 3' region of 4.0 kb and 2.5 kb Lu/B-CAM mRNAs.
A UNIQUE GENE FOR LU AND B-CAM GLYCOPROTEINS

FIG 4. Nucleotide and deduced amino-acid sequences of the alternatively spliced LU 3' region. Significance of upper, lower, and italic letters are as in Fig 4. Bold face letters refer to nucleotide sequences untranslated from the 4.0 kb mRNA but translated from the 2.5 kb transcript. Transcribed sequences are indicated by dashes. ST-gp, short tail glycoprotein; LT-gp, long tail glycoprotein.

bp which disrupted the LU coding sequence just before the last codon, i.e., at a position corresponding to the 3' noncoding region of B-CAM (Figs 3 and 4).

The genomic and cDNA sequence analysis reported here demonstrated that the Lu and B-CAM cDNAs (from nt -6 to the poly(A) addition site) represent RNA spliceforms of the LU gene which differ only by the sequence corresponding to nt 1,765 to 2,741 (Figs 3 and 4). The presence of this DNA region in the B-CAM cDNA resulted in a translation termination signal TGA at the first triplet following the Lu/B-CAM divergence site, whereas its absence in the Lu cDNA resulted in an open reading frame extending until the 41st...
triplet downstream of this position. These results prompted us to analyze the tissue distribution of the two spliceforms by Northern blot analysis.

**Tissue distribution of Lu/B-CAM mRNA spliceforms analyzed by Northern blot.** Whereas the Lu and B-CAM cDNAs were previously shown to recognize a singlesize mRNA species of 2.5 kb or 3.0 kb in several normal human tissues (heart, brain, placenta, lung, liver, skeletal muscle, kidney, and pancreas), we detected two signals at 2.5 kb and 4.0 kb with the Lu/B-CAM PCR1 probe in the same tissues and others of adult and fetal origin, as well as in the cell lines HeLa and HT29 (Fig 5A). Among hematopoietic tissues and cells, the two transcripts were found in human bone marrow and erythroid spleen but neither in leukocytes nor in HEL and K562 erythroleukemic cell lines. The size difference between the two mRNA species was consistent with the size of the alternatively spliced Lu/B-CAM sequence described above. Furthermore, the PCR4 probe corresponding to the 978 bp DNA region spliced from the Lu mRNA revealed only the 4.0 kb transcript in all tissues where the LU gene was expressed (Fig 5B). These results, together with the sequence analysis previously reported, showed that the 2.5 kb and 4.0 kb mRNA species correspond to the previously published Lu and B-CAM cDNAs, respectively. However, it is noteworthy that the level of the 4.0 kb transcripts was very low as compared to that of the 2.5 kb species in all tissues and cell lines, except in the colon carcinoma HT29 cell line (Fig 5).

**DISCUSSION**

We have shown that the Lu and B-CAM cDNA clones encoding the erythrocyte 85 kD Lu blood group active glycoprotein and the B-CAM epithelial cancer antigen, respectively, represent alternatively spliced transcripts of a single **LU** gene. This conclusion is supported by the following results: (1) sequence homology between Lu and B-CAM cDNAs and chromosomal localization of the Lu (5 and present results) and B-CAM probes to chromosome 19q13.2-13.3; (2) PCR probes designed from the 3' untranslated sequences specific to each cDNA clones detected the same single copy gene and revealed the same HindIII RFLP associated with the Lu'/Lu<sup>5</sup> blood group polymorphism; (3) amplification and sequence analysis of the 3' end of the **LU** gene, and of the uncharacterized 3' end of the B-CAM cDNA, indicated that the only difference between the Lu and B-CAM cDNAs was the presence in the latter of an additional 978 bp sequence flanked by consensus splice donor and acceptor motifs. Alternative use of these internal splice sites was deduced from the characterization with relevant probes of the 2.5 kb and 4.0 kb Lu/B-CAM mRNA species on Northern blots.

In previous immunochemical studies, a rabbit antiserum raised against the cytoplasmic and/or transmembrane domains of erythrocyte Lu gp was shown to precipitate the Lu gps of apparent molecular weight 85 but not 78 kD from unsealed membranes, suggesting that these two components may represent protein isoforms, although the 78 kD gp may simply be a proteolytic fragment of the 85 kD gp. Our results suggest that the alternative splicing event previously described (leading to the synthesis of Lu and B-CAM gps cloned from placenta tissue and colon carcinoma HT29 cells, respectively) could account for the presence of 85 and 78 kD Lu active components in erythrocyte membranes. This hypothesis is substantiated by Northern blot analysis showing the presence of the 2.5 and 4.0 kb Lu/B-CAM transcripts isoforms in bone marrow and erythroblast RNA preparations. The difference of 7 kD between the two Lu gp species might be accounted for by the extra 40 amino acids (calcu-
A UNIQUE GENE FOR LU AND B-CAM GLYCOPROTEINS

5.8 kD glycoprotein species. This size difference most likely resulted from a different pattern of glycosylation because Nglycanase treated B-CAM consisted of 75 and 65 kD polypeptides, which are similar in size to the N-glycanase treated erythrocyte Lu antigens (73 and 66 kD, respectively). Altogether, these observations suggest that (1) the B-CAM clone of HT29 might represent the 4.0 kb Lu/B-CAM transcript encoding a short tail gp; (2) the Lu and B-CAM antigens, defined by their respective antibodies, are both carried by long and short tail isoforms of the Lu/B-CAM polypeptides; (3) as shown for other membrane glycoproteins, the Lu/B-CAM gpps are most likely differently glycosylated in erythroid and nonerythroid cells, which would explain why the F8/G253 MoAbs used to define B-CAM did not react with erythroid cells, although these cells express the Lu epitopes.

Other independent immunocytochemical studies performed with anti-Lu or anti-B-CAM MoAbs strongly suggest that the tissue distributions of the Lu and B-CAM antigens are similar. However, further investigations will be necessary to determine whether, in nonerythroid cells and tissues, which, like HT29, express both B-CAM and Lu antigens, defined by their respective antibodies, both carried by long and short tail isoforms of the Lu/B-CAM polypeptides. Northern blot analysis performed in the course of this study confirmed that the LU gene was widely expressed in normal tissues and upregulated in fetal versus adult stages (at least in lung, liver, and kidney) and suggests that the long tail Lu/B-CAM gp (encoded by the 2.5 kb transcript) was predominantly expressed as compared to the short tail isoform (encoded by the 4.0 kb transcript), except in the colon carcinoma cell line HT29. The Lu/B-CAM gp carrying a long cytoplasmic tail contained a consensus binding site for SH3 motifs, which was absent from the short cytoplasmic tail isoform. Because molecules carrying SH3 elements are involved in intracellular signaling pathways, it can be speculated that alternative splicing of the cytoplasmic domain may affect the potential function of the LU encoded proteins. Similarly, it has been proposed that alternative splicing of the cytoplasmic tail of CD44 glycoproteins, which exhibited potential sites for protein kinases A and C, might be related to the potential role of the CD44 variants in T-cell activation by modulating intracellular signaling.

Further investigations should determine whether differential regulation of the alternative splicing of the Lu/B-CAM messenger leading to overexpression of the short tail isoform, might be associated with malignant transformation and to the nonpolarized expression of B-CAM observed in epithelial ovary cancers.

ACKNOWLEDGMENT

We are grateful to Dr Parice Codogno (INSERM U410, Hopital Xavier Bichat, Paris) for the generous gift of HT29 cells and RNAs and to Dr Veronique Van Huffel (GIP-INTS, Paris) for the gift of Lu-typed genomic DNAs.

REFERENCES

1. Parsons SF, Mallison G, Judson PA, Anstee DJ, Tanner MJA, Daniels GL: Evidence that the Lu b blood group is located on red cell membrane glycoproteins of 85 and 78 kD. Transfusion 27:61, 1987


5. Parsons SF, Mallison G, Holmes CH, Houlihan JM, Simpson KL, Mawby, WJ, Spurr NK, Sanne D, Barclay AN, Anstee DJ: The Lutheran blood group glycoprotein, another member of the immunoglobulin superfamily, is widely expressed in human tissues and is developmentally regulated in human liver. Proc Natl Acad Sci USA 92:5490, 1995


14. Rettig WJ, Spengler BA, Garin-Chesa P, Old LJ, Biedelder JL: Coordinate changes in neuronal phenotype and surface antigen

www.bloodjournal.orgFrom www.bloodjournal.org by guest on September 24, 2017. For personal use only.


A unique gene encodes spliceoforms of the B-cell adhesion molecule cell surface glycoprotein of epithelial cancer and of the Lutheran blood group glycoprotein

C Rahuel, C Le Van Kim, MG Mattei, JP Cartron and Y Colin