

# BST-1, a surface molecule of bone marrow stromal cell lines that facilitates pre-B-cell growth

(CD38/rheumatoid arthritis)

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Communicated by Tadimitsu Kishimoto, January 31, 1994

**ABSTRACT** Bone marrow stromal cells are essential for B-lymphocyte development. However, how stromal cells regulate B lymphopoiesis is not clear. In this paper, we report the molecular cloning of a stromal cell line-derived glycosylphosphatidylinositol-anchored molecule, BST-1, that facilitates pre-B-cell growth. The deduced amino acid sequence of BST-1 exhibited 33% identity with CD38. BST-1 was expressed in a wide range of tissues and in umbilical vein endothelial cells, whereas it was scarcely expressed in a variety of hematopoietic cell lines. The gene for BST-1 was assigned to chromosome 14q32.3, where immunoglobulin heavy-chain genes are clustered. BST-1 expression was enhanced in rheumatoid arthritis patient-derived bone marrow stromal cell lines that were previously shown to have an enhanced ability to support the growth of a pre-B-cell line as compared with stromal cell lines derived from healthy donors.

The growth and development of B-lineage cells are regulated by close associations between hematopoietic cells and the bone marrow (BM) microenvironment (1–4). BM-derived stromal cells not only produce soluble factors but also express surface molecules that are key molecules acting on B-lineage cells. For example, interleukin 7 (IL-7) is a stromal cell-derived factor that stimulates B-lineage cell growth (5). Stem-cell factor (SCF) is also involved in B lymphopoiesis, since it shows B-cell growth-stimulatory activity in synergy with IL-7 (6–8). In addition to these factors, other adhesion molecules on stromal cells are crucial for B lymphopoiesis. CD44 and VCAM-1 are involved in *in vitro* interaction between stromal cells and lymphocytes (9, 10). Surrogate immunoglobulin light-chain complexes on B-cell progenitors that can transduce activating signals are essential for normal B lymphopoiesis (11), suggesting the presence of ligand for the surrogate light-chain complexes in the BM microenvironments. Further, it has been suspected that yet unknown stromal cell molecules may be involved in B-lineage cell growth and development (12, 13). We have found that BM stromal cell lines derived from rheumatoid arthritis (RA) patients may provide such unidentified cell surface molecules (14).

To identify these unknown molecules, we prepared monoclonal antibodies (mAbs), RF3 and SG2, against RA-derived BM stromal cell lines and cloned a cell surface molecule, designated as BM stromal cell antigen 1 (BST-1), that facilitates pre-B-cell growth.<sup>§</sup>

## MATERIALS AND METHODS

**Cell Lines.** All BM stromal cell lines and synovial cell lines were previously established by transfecting the plasmid pACT-SVT (a gift from Y. Kaneda, Osaka University), which

encodes the simian virus 40 large tumor (T) antigen into cultured BM stromal cells or synovial cells derived from RA and multiple myeloma (MM) patients and healthy donors (14, 15). Human umbilical vein endothelial cells (HUVECs) were isolated from umbilical cords by collagenase treatment. The cells were cultured in medium T199 supplemented with 20% fetal bovine serum and endothelial mitogen (50 µg/ml; Funakoshi, Tokyo) on 0.1% gelatin-coated dishes.

**mAb Generation.** BALB/c mice were immunized with a representative clone of a RA-derived BM stromal cell line, RASV5-5 (14), or a RA-derived synovial cell line, SynSV6-14. Spleen cells from immunized mice were fused with the murine plasmacytoma cell line XAg653 as described (16).

**cDNA Cloning.** Poly(A)<sup>+</sup> RNA was isolated from the RA-derived synovial cell line SynSV1-4 by a FastTrack mRNA-isolation kit (Invitrogen). Double-stranded cDNA was synthesized with a TimeSaver cDNA synthesis kit (Pharmacia), ligated with *Bst*XI adapters, and cloned into the expression vector pEF-BOS, kindly provided by S. Nagata (Osaka Bioscience Institute) (17). Plasmid DNAs were transfected into 293T cells (kindly provided by T. Fujita, Rockefeller University, New York) by calcium phosphate precipitation. A positive pool was identified by the ability to confer reactivity for RF3 as assessed by flow cytometry on a FACScan (Becton Dickinson). The DNA sequence was determined by the dideoxy method on an A.L.F. DNA sequencer (Pharmacia).

**Preparation of Soluble Form of BST-1.** pΔ63-BOS, an expression plasmid encoding a predicted soluble form of BST-1, was prepared by introducing a termination codon at Thr<sup>298</sup> in the insert cDNA of p63-BOS. The culture supernatants of 293T cells transfected with pΔ63-BOS DNA were used for experiments.

**Northern Blot Analysis.** Poly(A)<sup>+</sup> RNAs were isolated from SynSV6-14, RASV5-5, and NFSV1-1 cell lines. Poly(A)<sup>+</sup> RNA (1 µg per lane) was electrophoresed through a 1% agarose/formaldehyde gel and transferred to a nylon membrane. Human multiple tissue Northern blots were purchased from Clontech. A 948-bp *Pst* I–*Pst* I fragment was labeled with [ $\alpha$ -<sup>32</sup>P]dCTP by a multiprime labeling kit (Amersham).

**Phosphatidylinositol-Specific Phospholipase C Treatment of Cells.** Cells were washed with phosphate-buffered saline and incubated at 37°C for 1–2 hr with gentle shaking in phosphate-buffered saline containing 1% fetal bovine serum and phosphatidylinositol-specific phospholipase C (2 units/ml; Funakoshi).

Abbreviations: BM, bone marrow; RA, rheumatoid arthritis; mAb, monoclonal antibody; MM, multiple myeloma; GPI, glycosylphosphatidylinositol; HUVEC, human umbilical vein endothelial cell; IL, interleukin.

<sup>§</sup>The sequence presented in this paper has been deposited in the GenBank data base (accession no. D21878).

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**Flow Cytofluorometry.** A variety of cell lines or cells were stained with RF3 and analyzed by FACScan as described (14). Fluorescein isothiocyanate labeled goat anti-mouse immunoglobulin was used as second antibody.

**Fluorescence *in Situ* Hybridization of the Human BST-1 Gene.** Fluorescence *in situ* hybridization was performed (18, 19) with a 1.4-kb BST-1 cDNA probe labeled with biotin-16-dUTP (Boehringer Mannheim) by nick-translation.

**Establishment of BALB 3T3 Transfectants Expressing Human BST-1.** Twenty micrograms of *Sca* I-cut p63-BOS and 2  $\mu$ g of *Bam*HI-cut pSV2neo (a gift from T. Taniguchi, Osaka University) were transfected into a mouse fibroblast cell line, BALB 3T3, by a GenePulser (Bio-Rad). Two days later, the neomycin analogue G418 (Sigma) was added to the medium at 2 mg/ml and resistant clones were isolated.

***In Vitro* Analysis of DW34 Pre-B Cells by Coculture with Stromal Cells.** BST-1-positive BALB 3T3 transfectants were examined for their ability to support the growth of a mouse pre-B-cell line, DW34 (20) (kindly provided by S.-I. Nishikawa, Kyoto University). Stromal cell lines were plated at  $10^5$  cells per well on 24-well plates and irradiated at 30 Gy after 24 hr. Two thousand DW34 cells per well were inoculated onto the irradiated cell monolayers and cultured for 4 days. DW34 cells were harvested from each well and the viable cells were counted by trypan blue dye exclusion. The number of recovered cells was <2000 per well without stromal cells.

## RESULTS

**Establishment of mAbs RF3 and SG2.** Since RA-derived cell lines RASV5-5 and SynSV6-14 had a high ability to support the growth of a pre-B-cell line, DW34 (ref. 14 and data not shown), we first prepared murine mAbs against these cell lines to identify the stromal cell surface molecules involved in pre-B-cell growth. We selected two mAbs, RF3 (IgG2a) and SG2 (IgG2a), that were reactive with RASV5-5 and SynSV6-14, but not with a healthy donor-derived nonsupportive cell line, NFSV1-1 (data not shown). RF3 inhibited the reactivity of SG2 for RASV5-5 and vice versa, suggesting that these two antibodies recognize closely located epitopes on the same molecule (data not shown). The molecule recognized by RF3 and SG2 was termed BST-1.

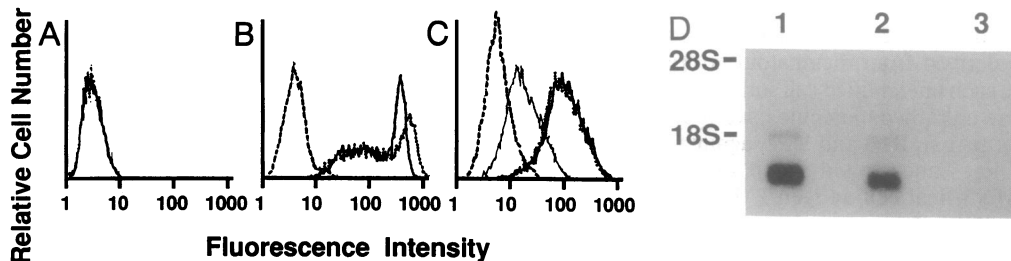
**Molecular Cloning of BST-1.** To characterize the molecular nature of BST-1, we cloned the cDNA, p63-BOS, by expression cloning. This clone conferred on transfected 293T cells reactivity with both RF3 and SG2 (Fig. 1A and B), confirming that the two mAbs recognize the same molecule. Further, the reactivity with RF3 was inhibited by culture supernatants of 293T cells transfected with p $\Delta$ 63-BOS (Fig. 1C), which encodes a soluble form of BST-1, suggesting that the insert cDNA of p63-BOS encodes BST-1 itself, but not the molecule

that induced the expression of BST-1. Northern blot analysis of mRNA from SynSV6-14, RASV5-5, and NFSV1-1 cells revealed a major band of  $\approx$ 1.4 kb (Fig. 1D), a size roughly equivalent to that of the cloned cDNA. The insert cDNA of p63-BOS contains a single open reading frame (Fig. 2). In this frame, the initiator ATG is followed by 317 codons before the termination triplet TAA. Since hydrophobic amino acids are abundant in residues 1–28, this region appears to be a typical signal peptide, suggesting that the mature protein probably consists of 290 amino acids.

**Amino Acid Homology of BST-1 with CD38 and ADP-Ribosyl Cyclase.** The nucleotide sequence of the insert cDNA was compared with other DNAs in the GenBank (release 76) and EMBL (release 34) data bases by GENEWORKS 2.2.1 (IntelliGenetics); no significant similarity with any known DNA sequences was found. However, comparison of the deduced amino acid sequence of BST-1 with the Swiss-Prot (release 25) protein data base revealed that BST-1 showed 33% amino acid identity with human lymphocyte antigen CD38 (Fig. 3) (21, 22), which exhibited a 29% identity with *Aplysia* ADP-ribosyl cyclase (23). BST-1 itself showed less but significant (26%) identity with the cyclase. The positions of nine cysteine residues in the extracellular region of BST-1 were completely conserved among CD38 and the cyclase, suggesting that these molecules may be distantly related.

**BST-1 Is a Glycosyl-Phosphatidylinositol (GPI)-Anchored Membrane Protein.** In addition to a signal peptide, BST-1 contains a short C-terminal hydrophobic region without an intracytoplasmic region, suggesting that BST-1 is a GPI-anchored membrane protein. Treatment with phosphatidylinositol-specific phospholipase C decreased the BST-1 surface expression of a BALB 3T3 cell line transfected with p63-BOS by 49% but did not decrease that of a type I membrane protein, R25 antigen (16). The same treatment decreased the surface expression of another GPI-anchored molecule, Thy-1, on EL4 mouse lymphoma cells by 73%. Further, the surface expression of BST-1 on RASV5-5 decreased by 47% after treatment with phospholipase C, but CD29 (VLA $\beta$ 1) did not. These results suggest that BST-1 may be anchored to the cell membrane by a GPI linkage.

**Distribution of BST-1 on Human Cell Lines and Tissues.** Surface expression of BST-1 on a variety of cell lines and cells was investigated by flow cytofluorometry (Table 1). BST-1 expression was observed on unstimulated HUVECs. IL-1, which induced the expression of the adhesion molecules VCAM-1 and ELAM-1 (refs. 24 and 25; data not shown), had no significant effect on BST-1 expression of HUVECs. In general, hematopoietic cell lines tested had little expression of BST-1, although Jurkat and U-937 showed significant expression. Tissue distribution of BST-1 was



**FIG. 1.** (A and B) Insert cDNA of p63-BOS encodes BST-1. Transformed human embryonic kidney cells (293T cell line) were transfected with pEF-BOS (A) or p63-BOS (B) and incubated with RF3 (solid lines) or SG2 (dotted lines) followed by fluorescein-labeled goat anti-mouse immunoglobulin. In A, all flow cytometry profiles were almost identical. (C) Inhibition of RF3 reactivity of RASV5-5 by the presence of a soluble form of BST-1. RASV5-5 cells were incubated with RF3 (2  $\mu$ g/ml) as first antibody in the absence (thick solid line) or presence (thin solid line) of 293T cell supernatants containing soluble BST-1 or in the presence of control supernatant (dotted line). The control supernatant did not affect the flow cytometry profile of cells incubated with RF3 alone. In A–C, control data of cells stained with second antibody alone are represented as dashed lines. (D) BST-1 mRNA expression in RA synovium-derived cell line SynSV6-14 (lane 1), RA BM stromal cell line RASV5-5 (lane 2), and healthy donor BM stromal cell line NFSV1-1 (lane 3). One microgram of poly(A)<sup>+</sup> RNA was fractionated per lane in an agarose/formaldehyde gel. A *Pst* I–*Pst* I fragment derived from p63-BOS was used as probe. Positions of 28S and 18S rRNAs are indicated.

5' CCGGAACCGCAACA 16  
 127  
 ATG GCG GCC CAG GGG TGC GCG GCA TCG CGG CTG CTC CAG CTG CTG CTG CAG CTT CTG CTT CTA CTG TTG CTG CTG GCG GCG GGC 211  
 Met Ala Ala Gln Gly Cys Ala Ala Ser Arg Leu Leu Gln Leu Leu Leu Leu Leu Ala Ala Gly 28  
 GGG GCG GCG GCG GGG TGG GCG GCG GAG ACC AGC GCA CAC TTG CCG GAC ATC TTC CTG GGC CQC TGC GCC GAG TAC GCG GCA 295  
 Gly Ala Arg Ala Arg Trp Arg Ala Glu Gly Thr Ser Ala His Leu Arg Asp Ile Phe Leu Gly Arg Cys Ala Glu Tyr Arg Ala 56  
 CTG CTG AGT CCC GAG CAG CGG AAC AAG AAC TGC ACA GCC ATC TGG GAA GCC TTT AAA GTG GCG CTG GAC AAG GAT CCC TGC TCC 379  
 Leu Leu Ser Pro Glu Gln Arg Asn Lys Asn Cys Thr Ala Ile Trp Glu Ala Phe Lys Val Ala Leu Asp Lys Asp Pro Cys Ser 84  
 GTG CTG CCC TCA GAC TAT GAC CTT TTT ATT AAC TTG TCC AGG CAC TCT ATT CCC AGA GAT AAG TCC CTG TTC TGG GAA AAT AGC 463  
 Val Leu Pro Ser Asp Trp Asp Leu Phe Ile Asn Leu Ser Arg His Ser Ile CCC Arg Asp Lys Ser Leu Phe Trp Glu Asn Ser 112  
 CAC CTC CTT GTT AAC AGC TTT GCA GAC AAC ACC CGT CGT TTT ATG CCC CTG AGC GAT GTT CTG TAT GGC AGG GTT GCA GAT TTC 547  
 His Leu Leu Val Asn Ser Phe Ala Asp Asn Thr Arg Arg Phe Met Pro Leu Ser Asp Val Leu Tyr Gly Arg Val Ala Asp Phe 140  
 TTG AGC TGG TGT CGA CAG AAA AAT GAC TCT GGA CTC GAT TAC CAA TCC TGC CCT ACA TCA GAA GAC TGT GAA AAT AAT CCT GTG 631  
 Leu Ser Trp Cys Arg Gln Lys Asn Asp Ser Gly Leu Asp Tyr Gln Ser Cys Pro Thr Ser Glu Asp Cys Glu Asn Asn Pro Val 168  
 GAT TCC TTT TGG AAA AGG GCA TCC ATC CAG TAT TCC AAG GAT AGT TCT GGG GTG ATC CAC GTC ATG CTG AAT GGT TCA GAG CCA 715  
 Asp Ser Phe Trp Lys Arg Ala Ser Ile Gln Tyr Ser Lys Asp Ser Ser Gly Val Ile His Val Met Leu Asn Gly Ser Glu Pro 196  
 ACA GGA GCC TAT CCC ATC AAA GGT TTT TTT GCA GAT TAT GAA ATT CCA AAC CTC CAG AAG GAA AAA ATT ACA CGA ATC GAG ATC 799  
 Thr Gly Ala Tyr Pro Ile Lys Gly Phe Phe Ala Asp Tyr Glu Ile Pro Asn Leu Gln Lys Glu Lys Ile Thr Arg Ile Glu Ile 224  
 TGG GTT ATG CAT GAA ATT GGG GGA CCC AAT GTG GAA TCC TGC GGG GAA GGC AGC ATG AAA GTC CTG GAA AAG AGG CTG AAG GAC 883  
 Trp Val Met His Glu Ile Gly Pro Asn Val Glu Ser Cys Gly Glu Gly Ser Met Lys Val Leu Glu Lys Arg Leu Lys Asp 252  
 ATG GGG TTC CAG TAC AGC TGT ATT AAT GAT TAC CGA CCA GTG AAG CTC TTA CAG TGC GTG GAC CAC AGC ACC CAT CCT GAC TGT 967  
 Tyr Ser Cys Ile Asn Asp Tyr Arg Pro Val Lys Leu Leu Gln Cys Val Asp His Ser Thr His Pro Asp Cys Ala Leu Lys Ser 280  
 GCC TTA AAG TCG GCA GCA GCC GCT ACT CAA AGA AAA GCC CCA AGT CTT TAT ACA GAA CAA AGG GCG GGT CTT ATC ATT CCC CTC 1051  
 Met Gly Phe Gln Ala Ala Ala Thr Gln Arg Lys Ala Thr Ser Leu Tyr Thr Thr Gln Arg Ala Gly Leu Ile Ile Pro Leu 308  
 TTT CTG GTG CTG GCT TCC CGG ACT CAA CTG TAA CTGGAACCTGTGTTGCTAACCCTCCCTCCAGCCCTGCAGCCCTCCCTTCAGCTCATCATTCGGT 1151  
 Phe Leu Val Leu Ala Ser Arg Thr Gln Leu ... 318  
 CTGCTATACCAAAAGATTCTGTTATCTAAGAAGCTTTTTCGCGGGAACCGATGCTCTGAAATGTTATTCAATGAGGCATATGTTACGATTTCAGAAACAAAGAA 1262  
 TAGTCTATTAGCAGGTTAAAAAATGCTGCTAGTAATAAACAAGTATTTCCTATTGTTATATGACCAAAAGCATTGGAAGTCAGACTCTGTTATATATCAAA 1373  
 CATTAAAGAAATCTAATAAAGCTGTATTTTACATC 3' 1411

FIG. 2. Nucleotide and deduced amino acid sequence of the open reading frame encoding human BST-1. The putative signal peptide and the C-terminal hydrophobic region are indicated by the dashed and solid lines, respectively. Four potential N-linked glycosylation sites are indicated with asterisks.

examined by Northern blot analysis (Fig. 4). Expression of BST-1 mRNA was detected in various tissues, including placenta, lung, liver, and kidney.

**Chromosomal Mapping of the Human BST-1 Gene.** Fluorescence *in situ* hybridization showed that the human BST-1 gene was located on chromosome 14 at q32.3 (Fig. 5), where immunoglobulin heavy-chain genes are clustered.

BST-1 MA-----AAG-----CAASRLLOL-L-LLLELLLLLAAG 28  
 CD38 MANCEPSPVSGDKPCCRLSRRADLCIGVSILVILLVVLAIV 42  
 Cyclase M-----SPV-AIIA-C-----VC-----LAVLTSISPSA 24  
 BST-1 GARRR-VRANGTSAHLNDIFLGRCAEYRALSPFRNKNIT 68  
 CD38 VRRNQTSGSGHTTKRFPETVLARCVRYTE-IEPEARHVDC 83  
 Cyclase IVPTR--ELENVFLGRCKDYETIR--YLDID-PRVR-SDCS 59  
 BST-1 AIWEAFKVAL-DRDPCSVLPSDYDLEINLSRHSIFRDRSLFW 109  
 CD38 SVWDAFKGAFISKPEPCNITEEDYDPLMKLGTQIVPCNKILLW 125  
 Cyclase ALWKDFPKAFSFKNECDLDELGSYKDFFTSAQQOLEKRVMEFW 101  
 BST-1 ENSHLLVNSFADNTRFRMPELSDVLYGRVADFLSWCRQKNDG 151  
 CD38 SRKIDLARQFTQVQDMFTLEDTLGLYLDLILWCGEFTNISK 167  
 Cyclase SGVYDEADYANTGKRYITLEDLTLGYMLNSLWCGQRANFG 143  
 BST-1 LDYQSCP-SDCENNPVDSFWKRSIQYSKDSGVEIVMLN 192  
 CD38 INYQSCPDKWRCENNPVDFWKTVSRRAEACDVEIVMLN 208  
 Cyclase FNERVCPDF-KTCPVQARESPWGMASSTVAHSAGEVITVMVD 184  
 BST-1 GSEPTGA--VPIKGFADYELINLQEKIRTRIRIVVMEIGG 132  
 CD38 GSRSR-I--FDKNSIFGSEVHNLQEKVQTLGAVIHHGGRE 248  
 Cyclase GSNPK-VPAVTRPDSFFGKYLENL-TNKVTRVKVITVLERLGE 224  
 BST-1 PNVEFCGEGSMVLEKRIEDMGFQYSCHINDYRPNKLLQCVDE 274  
 CD38 DSRDLQDPTIKLELSIISKRNIDFSCKNITRDKFLQCVKN 290  
 Cyclase KIEKCGAGSLDLEKLVKAKHFAFDQVENPNAIFLQSDN 266  
 BST-1 STHPDCNLRSAAAATQRKAPSLYTEQRAGLIPLFLVLSRT 316  
 CD38 FEDSSCTSEI 300  
 Cyclase ENARECNLAKRFYRIA 282  
 BST-1 QL 318  
 CD38  
 Cyclase

FIG. 3. Homology of BST-1 with human CD38 antigen and *Aplysia* ADP-ribosyl cyclase. The deduced amino acid sequences of the above proteins were aligned by using the new protein alignment program (GENEWORKS 2.2.1) and by inspection. Two or more identical amino acids are boxed. Gaps are indicated as hyphens. Amino acids are numbered at the right of each line. Conserved cysteines are marked by asterisks.

Table 1. Expression of BST-1 in a variety of cells

Name	Origin	MFI	
		Control	RF3
Nalm6	Pre B	2.8	2.8
Daudi	B	5.2	6.8
CL4	B	2.8	2.8
Ramos	B	3.2	3.2
U-266	Myeloma	3.5	3.5
MOLT-4	T	3.8	3.8
Jurkat	T	4.8	9.2
U-937	Histiocyte	2.1	38.0
K562	Erythroblast	3.2	3.2
HL-60	Promyelocyte	4.1	5.9
HUVECs*	Endothelium		
- IL-1		6.2	42.0
+ IL-1		6.2	42.0
Flow6000	Fibroblast	7.5	10.0
FL	Amnion	4.8	4.8
HepG2	Hepatoma	2.8	2.8
T24	Bladder carcinoma	2.7	2.7
SKMG4	Glioblastoma	6.7	6.7
HeLa	Cervical carcinoma	3.2	3.2
RASV5-5	RA BM stroma	6.5	90.0
SynSV6-14	RA synovium	8.7	78.0
NFSV1-1	Normal BM stroma	6.7	8.7

Cells were incubated without (control) or with RF3 and were washed before addition of fluorescein-labeled goat anti-mouse Ig. Results are expressed as mean fluorescence intensity (MFI) of stained cells.

\*HUVECs were unstimulated or were stimulated with IL-1 (100 units/ml) for 4 hr.

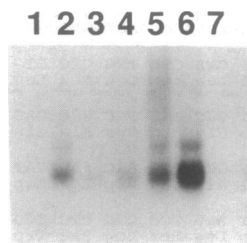


FIG. 4. Expression of BST-1 mRNA in a variety of tissues. A *Pst* I-*Pst* I fragment derived from p63-BOS was used as a probe. Lanes: 1, pancreas; 2, kidney; 3, skeletal muscle; 4, liver; 5, lung; 6, placenta; 7, brain.

**Effect of BST-1 on DW34 Cell Growth.** To examine whether BST-1 was involved in pre-B-cell growth, we transfected p63-BOS into a murine fibroblast cell line, BALB 3T3, and obtained several stable transfectants expressing human BST-1. These transfectants were cocultured with a stromal

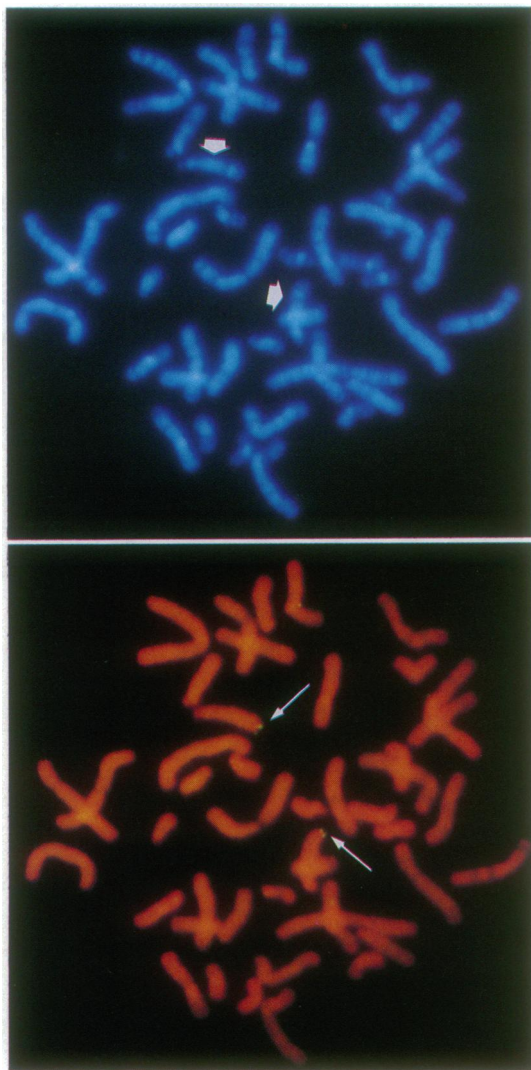


FIG. 5. Localization of the human BST-1 gene by fluorescence *in situ* hybridization. (Upper) G-banding pattern of same chromosomes through a UV-2A filter (Nikon). (Lower) Propidium iodide-stained metaphase chromosomes (the same chromosomes as in Upper) showing the fluorescein signals (arrows) through a B-2A filter (Nikon). Sixty-eight metaphase cells were examined. Of these, 7 cells exhibited double spots on both homologous 14q32.3 chromosome segments and other 23 cells had double spots on one 14q32.3 and a single spot on the other 14q32.3.

cell-dependent mouse pre-B-cell line, DW34 (20). The mean number of DW34 cells recovered from the cocultures [ $(2.3 \pm 0.4) \times 10^5$ , mean  $\pm$  SEM,  $n = 6$ ] was about twice that from cocultures with BST-1-negative clones [ $(1.3 \pm 0.3) \times 10^5$ ,  $n = 5$ ;  $P = 0.0001$ , unpaired *t* test where  $P < 0.01$  was considered significant].

**Enhanced Expression of BST-1 on RA BM-Derived Stromal Cell Lines.** Surface expression of BST-1 on panels of RA, MM, and healthy donor-derived BM stromal cell lines was investigated by flow cytometry (Fig. 6). The results are represented as subtracted mean fluorescence intensity (SMFI) of 13 BM stromal cell lines derived from six RA patients, 11 lines from four MM patients, and 12 lines from four healthy donors. SMFI was calculated by subtracting the mean fluorescence intensity of cell lines stained with second antibody alone. All of the RA-derived lines expressed BST-1, whereas only 7 out of 11 of MM-derived lines and 7 out of 12 of healthy donor-derived lines did. Furthermore, BST-1 expression in the RA-derived clones was significantly higher than in the healthy donor-derived clones (SMFI =  $53.1 \pm 9.3$  vs.  $18.5 \pm 5.2$ ,  $P = 0.004$ ). BST-1 expression of the MM-derived clones was not significantly different from that of the healthy donor-derived clones (SMFI =  $17.5 \pm 4.8$  vs.  $18.5 \pm 5.2$ ,  $P = 0.884$ ). The data suggest that both the frequency of BST-1-positive cells and the frequency of the cells with an enhanced expression of BST-1 increase in RA-derived BM stromal cell lines.

## DISCUSSION

We have cloned a surface molecule, BST-1, from BM stromal cell lines. BST-1 is a GPI-linked membrane protein showing a significant similarity with CD38 and facilitates the stromal cell-dependent growth of a mouse pre-B-cell line.

BST-1 is considered to be one of the cell surface molecules expressed on BM stromal cells that play roles in B lymphopoiesis, although we have not examined whether BST-1 is indeed expressed in the BM microenvironment. (i) Enhanced expression of BST-1 was observed in RA-derived BM stromal cell lines that showed an enhanced ability to support the growth of the mouse pre-B-cell line DW34 as compared with those derived from healthy donors. (ii) Stable transfectants of BALB 3T3 cells expressing human BST-1 facilitated pre-B-cell growth better than BST-1-negative BALB 3T3 cells. Human BST-1-negative BALB 3T3 transfectants or

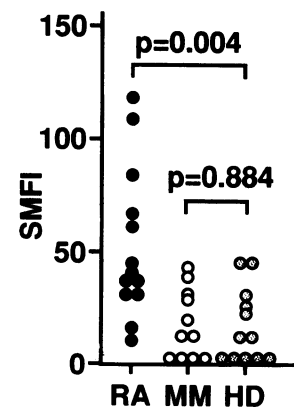


FIG. 6. Surface expression of BST-1 on BM stromal cell lines. BST-1 surface expression was evaluated by flow cytometry with RF3 and fluorescein-labeled goat anti-mouse immunoglobulin as first and second antibodies, respectively. Results are represented as subtracted mean fluorescence intensity (SMFI; see text) on the vertical axis. An unpaired *t* test was performed to compare the SMFI of stromal cell lines derived from three groups, RA and MM patients and healthy donors (HD). Values of  $P < 0.01$  were considered to be significant.



parental BALB 3T3 cells significantly supported DW34 cell growth, suggesting that BST-1 may not be essential for DW34 cell growth. However, it is possible that the mouse BST-1 homologue is expressed on BALB 3T3 cells.

Although BST-1 is a GPI-linked membrane protein, whereas CD38 is a type II integral membrane protein, they showed a similar overall amino acid structure, suggesting that BST-1 may have a function similar to that of CD38. Anti-CD38 induces an increase of intracellular  $Ca^{2+}$  and an immunoglobulin-independent activation and proliferation of B cells (26). This activation is suggested to be mediated by the ADP-ribosyl cyclase activity of CD38 that catalyzes the synthesis of cyclic ADP-ribose from nicotinamide adenine dinucleotide (27). Cyclic ADP-ribose is a potent mediator to induce  $Ca^{2+}$  release independently of the inositol 1,4,5-trisphosphate receptor (28, 29). However, it is unknown how CD38 plays a role in B-cell activation as a cell surface enzyme.

Human CD38 is expressed on immature lymphocytes and has been suggested to be involved in lymphocyte development (21, 22). On the other hand, BST-1 is expressed on stromal cell lines and umbilical vein endothelial cells and is distributed in a wide range of tissues, suggesting that BST-1 may have a function different from that of CD38. BST-1 may act as a ligand for CD38 through like-like interaction; this possibility should be examined. Ubiquitous expression of BST-1 suggests that BST-1 may have multiple functions in addition to its role in B-cell growth. Further characterization of BST-1-positive cell lineages in normal tissues should be useful in elucidating the physiological role(s) of BST-1.

RA is a systemic autoimmune disease of unknown etiology and primarily affects joint synovial tissues. We previously showed that RA-derived BM stromal cell lines had an enhanced ability to support pre-B cell growth (14). Further, the expression of BST-1 was enhanced in RA-derived BM stromal cell lines compared with healthy donor-derived ones, suggesting the presence of abnormalities in the BM microenvironment in RA patients. This hypothesis may be supported by the fact that BM transplantation resulted in a complete remission of RA or psoriatic arthritis in certain cases (30, 31). Although it remains to be clarified how BST-1 functions *in vivo*, we assume that polyclonal B-cell abnormalities in RA may be, at least in part, attributed to BST-1 overexpression on the stromal cell population. The molecular mechanism(s) that induces such abnormal expression of multiple genes, including those encoding BST-1 and IL-6, may lead to better understanding of the etiology of RA (32, 33).

We thank Drs. S. Nagata and S.-I. Nishikawa for providing the plasmid and cell lines; Drs. K. Boru, E. Barsoumian, and Y. S. Choi for critical reading of the manuscript; and Ms. R. Masuda and M. Tsuda for secretarial assistance. This work was supported in part by Grants-in-Aid for Scientific Research from the Ministry of Education, Science, and Culture and by grants from the Ministry of Welfare and Health and The Mitsubishi Foundation in Japan.

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