	抗原賦活法	温度	pH	反応時間
1	加熱	125 度	pH9	Over night
2	加熱	95 度	pH6	30 分
3	加熱	95 度	pH9	30 分
4	Protease	室温		30 分

明瞭な細胞内極性（細胞膜、細胞質、角膜、核内、細胞外マトリックス）を有したシグナルを示すものを陽性と評価した。同一コア内で、陽性細胞と陰性細胞が混在しないものは、非特異的染色と評価した。

＜倫理的配慮＞
個人情報は非連結可能匿名化を行っている。本研究のプロトコルは富山大学倫理委員会の承認を受けている。（認１９－１２）

C: 研究成果

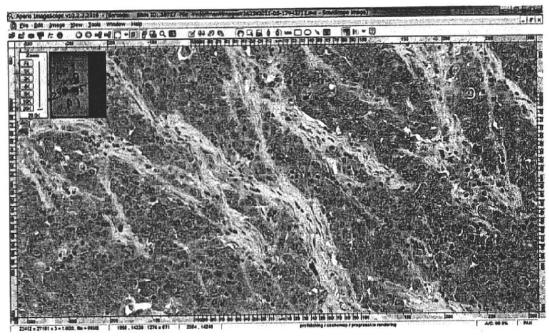
SST-REX 法にホルマリン固定を加えた変法にて研究代表者の北村らが作製した抗体のうち、培養上清抗体として、8 クローン、7 分子の検討を行った。検討した抗体は、EPHA2 (clone ACT140-65 1CBE6-3 と ACT234-07 6B10) 、 Clorf56 (clone ACT230-15 2A1), FSZTL1 (clone ACT41-385), IGFBP1 (clone ACT230-84), GPNMB (clone ACT36-149), MPZL1 (clone ACT208-18), GPR56 (clone ACT88-84)

これらの中で、Clorf56 (clone ACT230-15 2A1), FSZTL1 (clone ACT41-385)の 2 クローンにおいて、特異的染色結果を観察することが出来た。

＜Clorf56 の染色結果＞

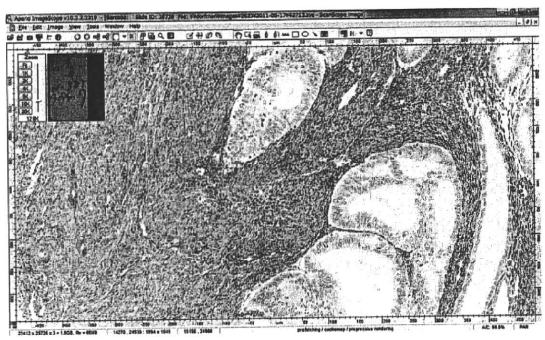
染色性は、上皮細胞特にがん細胞の細胞質に観察された（図２)。

図２： Clorf56 の免疫染色



FSZZTL1 においては、腫瘍性間質の紡錘形細胞において、diffuse な染色性が確認された（図３)。非腫瘍性の間質においては、陽性細胞はほとんど観察されなかった。

図３：FSZTL1 の免疫染色



脳腫瘍（グリオーマ）を標的にして作製された抗体 ACT00140-0044 (clone 4H12G5)にて、染色条件の検討を行ったが、明瞭な特異的陽性像は認められなかった。

Clorf56 (ACT230-0015 2A1)、FSZTL1 (ACT41-385 9C8H7)については、今年度に精製抗体を検討することは出来ず、高集積組織アレイにおける発現の解析は、平成

２３年度に行う。

D. 考察

SST クローン免疫法によるモノクローナル抗体作製は順調に進んでいるが、ホルマリン固定、パラフィン包埋された組織における染色に使用できるモノクローナル抗体の作製は困難であり、初年度には作製抗体において特異的な発現を観察することが出来なかった。今年度、ホルマリンにて固定化した細胞を免疫源として作製したモノクローナル抗体により評価を行ったところ、組織染色に使用できるモノクローナル抗体を８クローン中において２クローン得ることが出来た。ホルマリン固定による抗原の修飾を考慮した変法が有効であると考えられた。本年は、２クローンの培養上清において癌に染色性を有するものを得ることが出来た。今後、精製抗体において染色性を検討し、高集積組織アレイへの応用を行って抗原の病的意義、機能を検討する。

また各分子の各種がん細胞における発現プロファイルを調べる予定である。FSZTL1 については、腫瘍性間質における染色性が強く観察された。このことは、腫瘍の EMT (epithelial mesenchymal transition)との関連性を示唆するものと考えた。更なる検証が必要である。

E. 結論

本年度は SST-REX 法により効率良く SST クローンを樹立したが、これらの SST クローンをホルマリン固定化してマウスに免疫することにより、効率良くパラフィン包埋組織への染色に応用可能なモノクローナル抗体を作製することができた。

さらに、高集積組織アレイを使用して、分子の病的意義と機能を腫瘍横断的に解析する。

F. 研究発表

1. 論文

1. 1. Farris, A.B. III, Demicco, E.G., Le, L.P., Finberg, K.E., Miller, J., Mandal, R., Fukuoka, J., Cohen, C., Gaissert, H.A., Zukerberg, L.R., Lauwers, G.Y., Iafrate. A.J., and Knudson, M.M. (2011) Clinicopathologic and Molecular Profiles of Microsatellite Unstable Barrett Esophagus-associated. **Am J Surg Pathol,** in press
2. Demicco, E.G., Farris, A.B., Baba, Y., Etang, B.A., Bergethno1, K., Mandal, D., Daives, D., Fukuoka, J., Shimizu, M., Santagata, D.D., Ogino, S., Iafrate, A.J., Gaissert, H.A., and Knudson. M.M. (2011) The dichotomy in carcinogenesis of the distal esophagus and esophagogastric junction: Intestinal type vs. cardiac-Type mucosa associated adenocarcinoma. **Modern Pathol.**, in press.
3. 岡澤成祐，河岸由紀男，猪又峰彦，山田 徹，三輪敏郎，林 龍二，松井祥子，菓子井達彦，土岐善紀，長田啓史，福岡順也，戸邉一之 (2011) 肺過誤腫を合併した若年発症肺癌の１例 **日呼吸会誌** 印刷中

4. Kubo, A., Koh, Y., Kawaguchi, T., Isa, S., Okamoto, I., Fukuoka, J., Kusunoki, Y., Kitaichi, M., Takada, M., and Nakagawa, K. (2011) Malignant pleural effusion from lung adenocarcinoma treated by gefitinib **Internal Medicine**, in press.

2. 学会発表

1. 福岡順也.「Inter-observer Agreement - Lung Cancer and IIPs -」大阪呼吸器談話会 2010, 7, 大阪
2. 福岡順也.「Inter-observer agreement — Lung Cancer と IIPs-.」 Shiga Chest Disease Conference, 2010, 7, 滋賀.
3. 福岡順也.「NSCLC の治療を考慮した病理診断の標準化について.」 NSCLC Treatment Forum, 2010, 9, 福岡
4. 福岡順也. 「肺がん治療における病理組織診断の重要性と標準化について. 」第 69 回日本癌学会学術総会ランチョンセミナー, 2010, 9, 大阪
5. 福岡順也. 「肺がんの組織分類と一致率および治療への影響 」 臨床細胞学会広島県支部会 2010, 11, 広島

G. 知的財産権の出願・登録状況

なし

研究成果の刊行に関する一覧表

書籍

著者氏名	論文タイトル名	書籍全体の編集者名	書　籍　名	出版社名	出版地	出版年	ページ
該当なし							

雑誌

発表者氏名	論文タイトル名	発表誌名	巻号	ページ	出版年
美濃部こころ	Expression of ADAMTS4 in Ewing's sarcoma.	Int. J. of Oncol.	37	569-581.	2010
山西　吉典	TIM1 is an endogenous ligand for LMIR5/CD300b and LMIR5 deficiency ameliorates mouse kidney ischemia/reperfusion injury.	J. Exp. Med.	207	1501-1511.	2010
榎本　豊	Characterization of leukocyte mono-Ig receptor 7 (LMIR7)/CLM3 as an activating receptor: Its similarities to and differences from LMIR4/CLM5.	J. Biol. Chem.	285	35274-35283.	2010

Expression of ADAMTS4 in Ewing's sarcoma

K. MINOBE[1,2], R. ONO[1*], A. MATSUMINE[3*], F. SHIBATA-MINOSHIMA[2], K. IZAWA[2], T. OKI[2], J. KITAURA[2], T. IINO[3], J. TAKITA[4], S. IWAMOTO[5], H. HORI[5], Y. KOMADA[5], A. UCHIDA[3], Y. HAYASHI[6], T. KITAMURA[2] and T. NOSAKA[1]

[1]Department of Microbiology and Molecular Genetics, Mie University Graduate School of Medicine, Tsu; [2]Division of Cellular Therapy, The Institute of Medical Science, The University of Tokyo, Tokyo; [3]Department of Orthopaedic Surgery, Mie University Graduate School of Medicine, Tsu; [4]Department of Cell Therapy and Transplantation Medicine, Graduate School of Medicine, The University of Tokyo, Tokyo; [5]Department of Pediatrics and Developmental Science, Mie University Graduate School of Medicine, Tsu; [6]Gunma Children's Medical Center, Gunma, Japan

Received March 29, 2010; Accepted May 18, 2010

DOI: 10.3892/ijo_00000706

Abstract. Ewing's sarcoma (EWS) is a malignant bone tumor that frequently occurs in teenagers. Genetic mutations which cause EWS have been investigated, and the most frequent one proved to be a fusion gene between *EWS* gene of chromosome 22 and the *FLI1* gene of chromosome 11. However, a limited numbers of useful biological markers for diagnosis of EWS are available. In this study, we identified ADAMTS4 (a disintegrin and metalloproteinase with thrombospondin motifs) as a possible tumor marker for EWS using the retrovirus-mediated signal sequence trap method. ADAMTS4 is a secreted protein of 837 amino acids with a predicted molecular mass of 98-100 kDa. It is a member of metalloprotease family, is expressed mainly in cartilage and brain, and regulates the degradation of aggrecans. ADAMTS4 has been suggested to be involved in arthritic diseases and gliomas. Herein, we show that *ADAMTS4* mRNA was expressed in all primary EWS samples and all EWS-derived cell lines examined, while its expression was detected only in small subpopulations of other solid tumors. Furthermore, *ADAMTS4* expression was found to be regulated by *EWS-FLI1* fusion gene-dependent manner. We also demonstrated that ADAMTS4 protein was highly expressed in tumor samples of the patients with EWS by using immunohistochemistry. These results suggest that ADAMTS4 is a novel tumor marker for EWS.

Correspondence to: Dr T. Nosaka, Department of Microbiology and Molecular Genetics, Mie University Graduate School of Medicine, 2-174, Edobashi, Tsu 514-8507, Japan
E-mail: nosaka@doc.medic.mie-u.ac.jp

*Contributed equally

Key words: EWS-FLI1, tumor marker, signal sequence trap, retrovirus

Introduction

Ewing's sarcoma (EWS) is the second most frequent primary bone tumor of childhood and adolescence with aggressive clinical course and poor prognosis. It is recognized that EWS is a part of Ewing's sarcoma family of tumors (ESFTs) which also include the peripheral primitive neuroectodermal tumor (PNET) (1,2), Askin's tumor and extraosseous EWS. Biologically, ESFTs are characterized by common chromosomal translocation between the 5' portion of the *EWS* gene (22q12) and the 3' portion of the members of the *ETS* family genes (3). More than 85% of the cases have the fusion gene *EWS-FLI1* due to t(11;22)(q24;q12) (4,5). Five to 10% of the cases pocess *EWS-ERG* due to t(21;22)(q22;q12) (6). The other rare cases are *EWS-ETV1*, *EWS-E1AF* and *EWS-FEV*, each resulting from t(7;22)(p22;q12), t(17;22) (q12;q12) and t(2;22)(q33;q12), respectively (3,7,8). The EWS-ETS chimeric proteins behave as aberrant transcriptional regulators and are believed to play a crucial role in the onset and progression of the ESFTs (9,10).

Currently, diagnosis of EWS is determined mainly by CD99 immunohistochemistry (11-13), and by genetic aberration. However, CD99 expression is also reported to be positive in some T cell acute lymphoblastic leukemia (T-ALL), acute myelogenous leukemia (AML), ependymoma, synovial sarcoma and pancreatic endocrine tumors (14-16). Besides, not all EWSs have this specific chromosomal translocation. Thus, there is no specific biomarker for differentiating EWS from other soft tissue sarcomas. Among the patients with localized tumor at diagnosis, 20% relapse within 4 years and die of the disease. In contrast, 5-year survival rate is ~20-30% in cases with metastasis. This study was performed to find a useful tumor marker for EWS.

The signal sequence trap (SST) is a strategy to identify complementary DNAs (cDNAs) containing signal sequence that encode secreted and type I membrane proteins (17). To date, various important molecules have been detected including *SDF-1*, a member of the tumor necrosis factor receptor superfamily *TROY*, *Xenopus-Tsukushi*, *Vasorin* and leukocyte mono-Ig-like receptor (*LMIR*) by the SST method

(18-23). In this study, we identified a secreted molecule *ADAMTS4* (a disintegrin and metalloproteinase with thrombospondin motifs) from EWS cell lines by using the SST system based on retrovirus-mediated expression screening (SST-REX) (24,25).

ADAMTS is a family of proteinases which was first described in 1997 (26). Today, 19 different members of the *ADAMTS* family have been identified, but the functions, mechanisms of activation, and substrates of most members remain incompletely understood (27). Members of the *ADAMTS* family are closely related to the *ADAM* (a disintegrin and metalloproteinase) family, but unlike *ADAMs*, the *ADAMTSs* are secreted molecules, some of which bind to the extracellular matrix. *ADAMTS4* was originally purified from chondrocytes and synovial cells stimulated with interleukin-1 (28). The structure of ADAMTS4 consists of six domains, a prodomain, a metalloproteinase domain, a disintegrin domain, a thrombospondin type I motif, a cysteine-rich domain and a spacer domain. It has been demonstrated to cleave the aggrecan at Glu^{373}-Ala^{374}, and therefore is also named as *aggrecanase1* (29-32). The aggrecanase activity of ADAMTS4 is inhibited by TIMP-3 (tissue inhibitor of metalloproteinase-3) (33), which was originally identified as an inhibitor of matrix metalloproteinases. Yamanishi *et al* demonstrated that *ADAMTS4* was overexpressed in synovial cells and chondrocytes in the patients with osteoarthritis (OA) and rheumatoid arthritis (RA) (34). Thus, *ADAMTS4* is considered to play an important role in the aggrecan degradation of articular cartilage in OA and RA. Recent studies reported that ADAMTS4 cleaves not only aggrecan but also brevican, versican and α2-macroglobulin (35).

In this study, we have disclosed that *ADAMTS4* mRNA was expressed in all tissue samples of EWS patients and all EWS cell lines examined, and the mRNA level of *ADAMTS4* was regulated by *EWS-FLI1* in the cell line. We have also demonstrated the ADAMTS4 protein expression by immunostaining of the patients' samples and the cell lines. Thus, we propose that ADAMTS4 is a possible tumor marker of EWS.

Materials and methods

Cell lines. Osteosarcoma cell lines (MG63, HOS, KHOS/NP, SaOS2 and U2OS), neuroblastoma cell lines (KPNSI-FA, LAN-1 and NB69), a lung cancer cell line H460, a liver cancer cell line PLC/PRF/5, a cholangiocarcinoma cell line HuCCT1, a colon cancer cell line SW-48, T-ALL cell lines (Jurkat, PEER, CEM and HPB-ALL), B-ALL cell lines (NALM16, NALM24 and IM9), AML cell lines (MOLM13 and ML1), an acute myelomonocytic leukemia cell line U937, EWS cell lines (SJES-2, SJES-3, SJES-5, SJES-6, SJES-7 and SJES-8), rhabdomyosarcoma cell lines (RMS and SJRH-30), pancreatic cancer cell lines (AsPC-1, BxPC-3 and Capan-1), glioblastoma cell lines (U87MG, U251 and T98G), and gastric cancer cell lines (HGC-27, MKN45, GCIY and KATO-III) were cultured in RPMI-1640 medium (Sigma-Aldrich, St. Louis, MO, USA) containing 10% heat-inactivated fetal bovine serum (FBS) (Sigma-Aldrich). A murine pro-B cell line Ba/F3 was maintained in RPMI-1640 containing 10% FBS and 1 ng/ml murine interleukin-3 (IL-3) (R&D Systems, Minneapolis, MN, USA). A retrovirus packaging cell line Plat-E (36) and NIH3T3 were cultured in Dulbecco's modified Eagle's medium (DMEM) (Sigma-Aldrich) containing 10% FBS. Human mesenchymal stem/progenitor cells (hMSCs) were purchased from Sanko Junyaku (Tokyo, Japan).

Patient samples and normal controls. Samples from 7 patients with EWS, 13 osteosarcoma, 4 chondrosarcoma, 4 synovial sarcoma, and 3 rhabdomyosarcoma, which were obtained at initial surgery at the department of orthopaedic surgery at Mie University Hospital, were examined by reverse transcription (RT)-PCR. Schwannoma, desmoid and lipoma samples were used as controls. Tissue samples for immunohistochemical staining were obtained from 25 EWS patients who underwent an open biopsy or a surgical resection. For enzyme-linked immunosorbent assay (ELISA), we used serum samples of 3 osteosarcomas, 1 osteofibrous dysplasia, 1 chondrosarcoma, 1 synovial sarcoma, 6 EWS and 4 healthy volunteers. Basically sera were isolated before the chemotherapy except for few cases. Informed consent was obtained from each patient or parent and volunteer. This study was approved by the ethics committee at Mie University.

Antibodies and other reagents. A rabbit polyclonal anti-ADAMTS4 antibody which was raised against amino acids 764-837 of human ADAMTS4 (Santa Cruz Biotechnology, Santa Cruz, CA, USA) and a horseradish peroxidase (HRP)-conjugated goat anti-rabbit IgG secondary antibody (Bio-Rad Laboratories, Hercules, CA, USA) were used for immunoprecipitation (IP)-Western blot analysis. Immunostaining was performed by using the following antibodies: the same anti-ADAMTS4 antibody as used for IP-Western analysis, an N-universal rabbit IgG (Dako, Kyoto, Japan), an HRP-conjugated anti-rabbit IgG antibody (Nichirei Biosciences, Tokyo, Japan) for immunohistochemistry, and an Alexa488-conjugated anti-rabbit IgG antibody (Invitrogen, Carlsbad, CA, USA) for immunofluorescence microscopy. For ELISA, a monoclonal anti-ADAMTS4 antibody raised against amino acids 213-685 of the recombinant human ADAMTS4 (R&D Systems), a biotinylated goat anti-ADAMTS4 antibody raised against amino acids 213-685 of the recombinant human ADAMTS4 and an Avidin-HRP (eBioscience, San Diego, CA, USA) were used.

Screening of EWS cDNA library by SST. A human EWS cDNA library was screened by SST-REX as previously described (24,25). Briefly, poly(A)$^+$ RNA was prepared from EWS cell lines using the FastTrack2.0 Kit (Invitrogen). The cDNA was synthesized from the mixture of poly(A)$^+$ RNAs of 6 EWS cell lines with random hexamers, using the SuperScript Choice System (Invitrogen) according to the manufacturer's instructions. The synthesized cDNA was size-separated by electrophoresis on an agarose gel. Fractions greater than 500 bp were collected and inserted into *Bst*XI sites of pMX-SST (25) using *Bst*XI adaptors (Invitrogen). Ba/F3 cells were infected with the retroviruses expressing the EWS-derived cDNA library and selected for growth in the absence of IL-3. Genomic DNAs extracted from IL-3-independent clones were subjected to PCR to recover the

Table I. Primer sequences used in RT-PCR analyses in murine tissues.

Gene	Sense	Antisense
DKFZP56400823	5'-CCATTGCCTGTCTCTCTCATGACA-3'	5'-GAGCTGTGCTCTTCTGTTGGTGA-3'
ADAMTS4	5'-GAGCTGTGCTCTTCTGTTGGTGA-3'	5'-CAGAGAAGCGAAGCGCTTGGTT-3'
DNER	5'-GACATAATCCTGCCCCGCTCT-3'	5'-CTCTGATGGCTTCGTGGCACAT-3'
NGFR	5'-CGTGTTCTCCTGCCAGGACAA-3'	5'-GCTGTGCAGTTTCTCTCCCTCT-3'
LRRN6A	5'-GTCTTCACCGGCCTCAGCAA-3'	5'-CCCTCGATTGTACCGATTGGGTT-3'
ECSM2	5'-GACAACTCAGACCTCGCAGGAA-3'	5'-CATTGGCTGTGGAGCAGCTTTCA-3'
LGALS3BP	5'-CAGGACTACTGTGGACGGCTT-3'	5'-CTACTCCAGGTGGAAGAGGTGTA-3'
PTPRF	5'-GCTGGCCCAGGAGAAGAGTT-3'	5'-GCTCTGCCCATTGTACAGGATCTT-3'
FCGRT	5'-GCTGTGAACTGGCCTCGGATA-3'	5'-CCAGCAATGACCATGCGTGGAA-3'
LAMP2	5'-CGCTGTCTCTTGGGCTGTGAAT-3'	5'-GGCACCTTCTCCTCAGTGATGTT-3'
RCN1	5'-CTAAGCCCGGACGAGAGCAA-3'	5'-GGCCATTGTCCTCGTGGGAA-3'
MMP14	5'-CATGAGTTGGGGCATGCCCTA-3'	5'-CGGCCAAGCTCCTTAATGTGCTT-3'
SDC2	5'-CTCCATTGAGGAAGCTTCAGGAGT-3'	5'-CTTCTGGTAAGCTGCGCTGGAT-3'
DAG1	5'-GGAAGCCCACGGTCACCATT-3'	5'-GCTTGAGCTTGTCGGTAGTGGTA-3'
EPCR	5'-GGCAACGCCTCTCTGGGAAAA-3'	5'-CGGCCACACCAGCGATTATGAA-3'
CD97	5'-CTGGAACAAAGCCTTCGGACCTT-3'	5'-GTCGGTGTCCCAGTACCCATT-3'
CD99L2	5'-GTCCAGAGAGGATATGGAGACACA-3'	5'-GGTTCTGCAGACTGCGTTTCTTG-3'
IGFBP5	5'-GCGACGAGAAAGCTCTGTCCAT-3'	5'-GCCTTGTTCGGATTCCTGTCTCA-3'
CLU	5'-GAAGGCATTCCCGGAAGTGTGTA-3'	5'-GCTGGACATCCATGGCCTGTT-3'
LSAMP	5'-GCTCTGGAATACAGCCTCCGAA-3'	5'-GTGTCATCCCGGTACCACTCAA-3'
NPTN	5'-GTAACCTCACTTCCAGCTCTCACA-3'	5'-GGAGGCAGAGCCAATGGAGTT-3'
EFNA5	5'-GCAGCAACCCCAGATTCCAGA-3'	5'-GATGGCTCGGCTGACTCATGTA-3'
PODXL	5'-CCTTCACCAGTAGCAGTGGACAA-3'	5'-CCACTGTAGACGCCATAGACTGT-3'
TMEM123	5'-CCACTCAGTGCTGACCTCCAA-3'	5'-GTTCGTCAATGCTTCGGTACCGAA-3'
GAPDH	5'-CAGTATGACTCCACTCACGGCAA-3'	5'-CAGATCCACGACGGACACATTG-3'

integrated cDNAs using vector primers. The resulting PCR fragments were sequenced and analyzed.

RT-PCR analysis. RT-PCR was carried out to detect *ADAMTS4* transcript in tumor cell lines, murine tissues and patients' samples. Total RNA was isolated with acid guanidium-phenol-chloroform method, and then 5 μg RNA was reverse-transcribed to cDNA in a total volume of 33 μl with random hexamers by using the Ready-To-Go You-Prime First-Strand Beads (GE Healthcare UK, Buckinghamshire, UK). RT-PCR was performed with the programmable cyclic reactor under the following conditions: denaturation at 94°C for 3 min followed by 30 cycles of amplification (94°C for 30 sec, 60°C for 30 sec, and 72°C for 45 sec). PCR product was separated by 1-2% agarose gel electrophoresis and visualized by ethidium bromide staining. The primers used for RT-PCR was described in Tables I and II.

Cloning of the full-length cDNA encoding ADAMTS4. Full-length *ADAMTS4* was generated as follows. The first half of *ADAMTS4* (1-1194 bp) was isolated from pMX-SST vector by digestion with *Bam*HI. Based on the sequence data, the last half (1195-2514 bp) were amplified by PCR from cDNAs of the EWS cell line SJES-5, and digested with *Bam*HI and *Not*I. The fragment was subcloned into a pMXs-puro retroviral vector (37). The resultant vector was digested with *Bam*HI, and then ligated with the *Bam*HI fragment of the first half of *ADAMTS4*. The primers used for amplification are as follows: SST5', 5'-GGGGGTGGACCATCCTCTA-3'; SST3', 5'-CGCGCAGCTGTAAACGGTAG-3'; ADAMTS4-FL-S, 5'-GAAAGAATTCGCTGCAGTACCAGTGCCATG-3'; ADAMTS4-FL-S2, 5'-GAGCACCTCTCGCCATGTCA-3'; ADAMTS4-FL-AS, 5'-GAAAGAGAATTCGCGGCC GCTTATTTCCTGCCCGCCCAGG-3'; ADAMTS4-AS2, 5'-CTTTGGATCCACATGAGCCATCACAGGGGCCA TGACATGGCGAGAGGTGCTCAAAGGCCCATTCAAA CTGATGCATG-3'.

Transfection and infection. Retroviral transfection was done as described previously (36,37). Briefly, retroviruses were generated by transient transfection of Plat-E packaging cells (36) with FuGENE 6 (Roche Diagnostics, Basel, Switzerland). Ba/F3 and NIH3T3 cells were infected with the retroviruses in the presence of 10 μg/ml polybrene. Selection with G418 or puromycin was started 48 h after infection.

Small interfering (si)RNA design and transfection experiments. EWS-FLI1-specific siRNA (siEF1) for SJES-5 cell line was designed as previously described (38). As a negative control, siGFP was employed (Hayashi-Kasei, Osaka, Japan).

Table II. Primer sequences used in RT-PCR analyses in human cancer cell lines.

Gene	Sense	Antisense
DKFZP56400823	5'-CCATCTGGACTAGCTCTCCACA-3'	5'-GTGCTGGTCACAGTGGAGCTA-3'
ADAMTS4	5'-GTGGAGTCTCCACTTGCGACA-3'	5'-CCAGGGCGAGTGTTTGGTCT-3'
DNER	5'-GTGGTGAAGGTCAGCACCTGT-3'	5'-GGCTGAGGGCACAGAAGTCAA-3'
NGFR	5'-GTTCTCCTGCCAGGACAAGCA-3'	5'-GTCCACGGAGATGCCACTGT-3'
LRRN6A	5'-GTACAACCTCAAGTCACTGGAGGT-3'	5'-CATTGAGCACGCGCAGGTAGTT-3'
ECSM2	5'-CAATGACCCAGACCTCTAGCTCT-3'	5'-GCAGCTTTCAGACAGCCCTGA-3'
LGALS3BP	5'-CCCACAGACCTGCTCCAACT-3'	5'-CCGTCTGGACTGATAGACCAGTT-3'
PTPRF	5'-CAGCCCCTACTCGGATGAGAT-3'	5'-GCGATGACATTCGCATAGCGGTT-3'
FCGRT	5'-CTCTCCCTCCTGTACCACCTT-3'	5'-GTGCCCTGCTTGAGGTCGAAAT-3'
LAMP2	5'-GTGCAGTTCGGACCTGGCTT-3'	5'-CAGCTGCCTGTGGAGTGAGTT-3'
RCN1	5'-GACAATGATGGGGATGGCTTTGTCA-3'	5'-CGGAATTCGTTAAACTGCTCCCGTT-3'
MMP14	5'-CAACATTGGAGGAGACACCCACTTT-3'	5'-GTTCCAGGGACGCCTCATCAAA-3'
SDC2	5'-GCTCCATTGAAGAAGCTTCAGGAGT-3'	5'-GCCTTCTGATAAGCAGCACTGGAT-3'
DAG1	5'-CGGAGGCAGATCCATGCTACA-3'	5'-GGCAGTTTCCAATCTGGTGATGGA-3'
EPCR	5'-CTACTTCCGCGACCCCTATCA-3'	5'-GCGAAGTGTAGGAGCGGCTT-3'
CD97	5'-CAAGACAAGCTCAGCCGAGGT-3'	5'-CTCCCCATCGGAGGACTCAA-3'
CD99L2	5'-CAAGAAACCCAGTGCTGGGGAT-3'	5'-GTACGCTGAACAGCTGGCTCT-3'
IGFBP5	5'-CTCAACGAAAAGAGCTACCGCGA-3'	5'-CTGTCGAAGGTGTGGCACTGAA-3'
CLU	5'-CAATGAGACCATGATGGCCCTCT-3'	5'-CCGGGCTATGGAAGTGGATGT-3'
LSAMP	5'-GGACAACATCACCGTGAGGCA-3'	5'-GGAGACCTCGTTGGCAGCTT-3'
NPTN	5'-CCCTGTCACCCTGCAGTGTA-3'	5'-CCAATGGCGTTGGTGGCATTACA-3'
EFNA5	5'-CCAGAGGGGTGACTACCATATTGA-3'	5'-CGGCTGACTCATGTACGGTGT-3'
PODXL	5'-CTCCACAGCCACAGCTAAACCTA-3'	5'-CTGGCAGGGTAGGTGTTCTCAA-3'
TMEM123	5'-CCATGGCGGCATCTGCAAACAT-3'	5'-CGATACCGAATGCCTCTTCTTGAGT-3'
PCOLCE	5'-CGGACGCTTTTGTGGGACCTT-3'	5'-GGCAGCTTGACTTTAGGCTCAGTT-3'
SEZ6L2	5'-GCACCTGCACTTTGAAAGGGTCT-3'	5'-GTCCCCTTCCCGCACATTCAATAT-3'
IGFBP4	5'-GAAGCCCCTGCACACACTGAT-3'	5'-GAAAGCTGTCAGCCAGCTGGT-3'
IGFBP3	5'-GCATCTACACCGAGCGCTGT-3'	5'-GGGACTCAGCACATTGAGGAACTT-3'
LOX	5'-GTCACTGGTTCCAAGCTGGCTA-3'	5'-GGAATATCTTGGTCGGCTGGGTA-3'
CTGF	5'-GCGTGTGCACCGCCAAAGAT-3'	5'-CGGTATGTCTTCATGCTGGTGCA-3'
SPARC	5'-CTGCCAGAACCACCACTGCAA-3'	5'-CTGCCAGTGTACAGGGAAGATGT-3'
QSCN6	5'-GGCTGACCTGGAATCTGCACT-3'	5'-CATTGTGGCAGGCAGAACAAAGTTC-3'
EDIL3	5'-CTGTGAGTGCCCAGGCGAATTTA-3'	5'-GATTTCATACCCAGAGGCTCAGAACA-3'
MXRA8	5'-GTACACCTGCAACCTGCACCAT-3'	5'-GGGACGATGACATTGATGACGTTGT-3'
PRRT3	5'-GCTGACAGTCACAGGAACTCTGA-3'	5'-GCCTCCTGCAAGTGTTCCTCAA-3'
LRP1	5'-CAATGGCCTGACGCTGGACTAT-3'	5'-CGGTGTCACACTTCCACCAGA-3'
ISLR	5'-GCTCGCTGCAACTCAACCACAA-3'	5'-CTCAGCACTGCCCAGCTCATT-3'
COL6A1	5'-GCAGTACAGCCACAGCCAGAT-3'	5'-GTCAAAGTTGTGGCTGCCCAC-3'
TIMP1	5'-GACCTCGTCATCAGGGCCAA-3'	5'-GCAAGGTGACGGGACTGGAA-3'
LAMP1	5'-CACGTTACAGCGTCCAGCTCAT-3'	5'-CCTTGTAGGAAAAACCGGCTAGAAC-3'
SERPINH1	5'-CTGCTGCGCTCACTCAGCAA-3'	5'-CGTGATGGGGCATGAGGATGAT-3'
COL1A1	5'-CACCTCAAGAGAAGGCTCACGAT-3'	5'-CCACGCTGTTCTTGCAGTGGTA-3'
GAPDH	5'-ACCACAGTCCATGCCATCAC-3'	5'-TCCACCACCCTGTTGCTGTA-3'

The RNA sequences used are as follows: siEF1 (sense 5'-GGC AGCAGAACCCUUCUUAdCdG-3', antisense 5'-UAAGA AGGGUUCUGCUGCCdCdG-3'). SJES-5 cells were plated on a 6-well plate and propagated in RPMI-1640 medium supplemented with 10% FBS. Twenty-four hours later, for transfection, 1 μl of 10 pmol siRNA was diluted with 99 μl of Opti-MEM (Invitrogen), and 2 μl of siFECTOR reagent (B-Bridge International, Mountain View, CA, USA) was diluted with 98 μl of Opti-MEM. Both solutions were mixed gently and incubated at room temperature for 5 min. The mixture was diluted with 800 μl of Opti-MEM, and left at room temperature for 15 min. Next, 1 ml of RNA/liposome

Table III. Genes isolated by the retrovirus-mediated signal sequence trap method (SST-REX).

Isolated gene	Accession number[a]	Frequency[b]
Granulin (GRN)	NM_002087	22
Alzheimer disease amyloid ß A4 precursor protein	NM_201414	16
Procollagen-proline, 2-oxoglutarate 4-dioxygenase	NM_000918	14
NODAL modulator 2 (NOMO2)	NM_173614	12
NODAL modulator 1 (NOMO1)	NM_014287	12
NODAL modulator 3 (NOMO3)	NM_001004067	11
Golgi apparatus protein 1 (GLG1)	NM_012201	10
Podocalyxin-like (PODXL)	NM_001018111	6
Lysosomal-associated membrane protein 2 (LAMP2)	NM_013995	6
Insulin-like growth factor binding protein 3 (IGFBP3)	NM_000598	6
Basigin	NM_198589	6
Dystroglycan 1	NM_004393	6
DKFZP56400823 protein	NM_015393	5
Ephrin-A5	NM_001962	4
SPARC	NM_003118	4
CD97	NM_001025160	4
Calreticulin	NM_004343	4
Insulin-like growth factor binding protein 4 (IGFBP4)	NM_001552	4
Poliovirus receptor	NM_006505	3
Syndecan 2	NM_002998	3
Seizure-related 6 homolog like 2	NM_201575	3
CD276	NM_025240	3
TMED7	NM_181836	3
Ribophorin II	NM_002951	3
Niemann-Pick disease, type C1	NM_000271	3
TMEM165	NM_018475	3
MHC class I antigen	NM_005514	3
Colony stimulating factor 2	NM_000758	3
NGFR	NM_002507	2
Ribophorin I	NM_002950	2
Proline-rich transmembrane protein 3	NM_207351	2
Custerin	NM_203339	2
Prosaposin	NM_002778	2
Leucine rich repeat neuronal 6A (LRRN6A)	NM_032808	2
Lysosomal-associated membrane protein 1 (LAMP1)	NM_005561	2
Quiescin Q6	NM_001004128	2
Neuroplastin	NM_017455	2
Reticulocalbin 1	NM_002901	2
Hemicentin 1	NM_031935	2
Matrix metallopeptidase 14 (MMP14)	NM_004995	2
Collagen, type VI, α1	NM_001848	2
MHC class I polypeptide-related sequence A	NM_000247	2
Low density lipoprotein-related protein 1 (LRP1)	NM_002332	2
TMEM123	NM_052932	2
Collagen, type XV, α1	NM_001855	2
Protein kinase C substrate 80K-H	NM_002743	2
EGF-like module containing, mucin-like, hormone receptor-like 2	NM_152920	2
Collagen, type I, α2	NM_000089	2
Lectin, galactoside-binding, soluble, 3 binding protein	NM_005567	2
Collagen, type VII, α1	NM_000094	2

Table III. Continued.

Isolated gene	Accession number[a]	Frequency[b]
Protein tyrosine phosphatase, receptor type, F	NM_130440	1
Connective tissue growth factor	NM_001901	1
Protein disulfide isomerase family A, member 4	NM_004911	1
Immunoglobulin superfamily containing leucine-rich repeat (ISLR)	NM_005545	1
Collagen, type I, α1	NM_000088	1
Procollagen C-endopeptidase enhancer (PCOLCE)	NM_002593	1
Chromosome 1 open reading frame 56	NM_017860	1
TIMP metallopeptidase inhibitor 1 (TIMP1)	NM_003254	1
Insulin-like growth factor binding protein 5 (IGFBP5)	NM_000599	1
Solute carrier family 24 member 6 (SLC24A6)	NM_024959	1
Neural cell adhesion molecule 2 (NCAM2)	NM_004540	1
Collagen, type V, α1	NM_000093	1
CD248	NM_020404	1
Fc fragment of IgG, receptor, transporter, α	NM_004107	1
Nucleobindin 1	NM_006184	1
delta/notch-like EGF-related receptor (DNER)	NM_139072	1
Limbic system-associated membrane protein (LSAMP)	NM_002338	1
Lysyl oxidase (LOX)	NM_002317	1
Endothelial cell-specific molecule 2 (ECSM2)	NM_001077693	1
Isolate Tor36 (ZE657) mitochondrion	AY738975	1
Lectin, mannose-binding, 1	NM_005570	1
CD99 molecule-like 2	NM_031462	1
EGF-like repeats and discoidin I-like domains 3	NM_005711	1
SIL1 homolog, endoplasmic reticulum chaperone	NM_022464	1
ADAM with thrombospondin type 1 motif, 4 (ADAMTS4)	NM_005099	1
Matrix-remodelling associated 8 (MXRA8)	NM_032348	1
Protein C receptor, endothelial	NM_006404	1
Tissue factor pathway inhibitor	NM_001032281	1
Serpin peptidase inhibitor, clade H member 1 (SERPINH1)	NM_001235	1
Protocadherin γ subfamily A.6	NM_032086	1

[a]Accession number in GenBank protein database. [b]Number of the clones isolated by SST-REX.

complex was added to 1 ml of OPTI-MEM supplemented with 20% FBS. Then, the culture medium of the SJES-5 cells was replaced with the 2 ml of the RNA/liposome-containing medium prepared. Twenty-four hours after transfection, culture medium was replaced with the 2 ml of Opti-MEM with 10% FBS, and grown for another 48 h. The cells were harvested and then total RNA was extracted for RT-PCR analysis. The primers used for RT-PCR are as follows: EWS-FLI1-S, 5'-GGGTATGGCACTGGTGCTTATGAT-3'; EWS-FLI1-AS, 5'-GGCTCCAAAGAAGCTGGAGGAA-3'; EWS-S, 5'-GCCCAGCCCACTCAAGGATAT-3'; EWS-AS, 5'-CCC CTGTGCTAGATTGAGGTTGA-3'; FLI1-S, 5'-GCCAACG CCAGCTGTATCA-3'; FLI1-AS, 5'-GTGTGAAGGCACGT GGGTGTT-3'.

IP-Western analysis. IP-Western blot analysis was performed as previously described (39) with some modifications. Briefly, cells were lysed in RIPA buffer [50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1% NP40, 0.5% deoxycholate, 0.1% SDS]. Cell lysates were immunoprecipitated with the rabbit polyclonal anti-ADAMTS4 antibody. SDS-polyacrylamide gel electrophoresis was performed under reducing conditions using 5-20% gradient gel (Wako Pure Chemical Industries, Osaka, Japan). After transfer to a nitrocellulose membrane, the blot was probed with the rabbit polyclonal anti-ADAMTS4 antibody and then with the HRP-conjugated goat anti-rabbit IgG secondary antibody. ADAMTS4 protein was detected with enhanced chemiluminescence (ECL) Western blotting detection reagents (Santa Cruz Biotechnology).

Immunohistochemical staining. Specimens were retrieved from the patients during surgical resection. Archival tumor blocks were fixed with 10% formaldehyde/phosphate-buffered saline (PBS), and embedded in paraffin. The paraffin-embedded tissues, measuring 4 μm in thickness, were placed on glass slides (Matsunami Glass, Osaka, Japan) and deparaf-

Table IV. Comparison of the gene expression levels between human mesenchymal stem cells (hMSCs) and Ewing's sarcoma (EWS) cells.

A.	hMSC		EWS
DKFZP56400823	–		+
ADAMTS4	–		+
DNER	–		+
NGFR	–		+
LRRN6A	–		+
ECSM2	–		+
LGALS3BP	–		+
PTPRF	–		+
FCGRT	–		+
B.	**hMSC**		**EWS**
LAMP2	+	<	++
RCN1	+	<	+
MMP14	+	<	+
SDC2	+	<	+
DAG1	+	<	+
EPCR	+	<	+
CD97	+	<	+
CD99L2	+	<	+
IGFBP5	+	<	+
CLU	+	<	+
LSAMP	+	<	+
NPTN	+	<	+
EFNA5	+	<	+
PODXL	+	<	+
TMEM123	+	<	+
C.	**hMSC**		**EWS**
PCOLCE	+		+
SEZ6L2	+		+
IGFBP4	+		+
IGFBP3	+		+
LOX	+	>	+
CTGF	+	>	+
SPARC	+	>	+
QSCN6	+	>	+
EDIL3	+		+
MXRA8	+		+
PRRT3	+		+
LRP1	+		+
ISLR	+		+
COL6A1	+	>	+
TIMP1	++	>	+
LAMP1	+		+
SERPINH1	+		+
COL1A1	+		+

++, strongly positive; +, modelately positive; –, negative; > or <, >2-fold difference in the expression level.

finized in xylene for hematoxylin and eosin (H&E) and immunohistochemical staining. Antigen retrieval was performed with citrate buffer (pH 6.0) at 97°C for 45 min. After cooling for 60 min and washing in PBS, the rabbit anti-ADAMTS4 antibody (Santa Cruz Biotechnology) diluted 1:50 in antibody diluent buffer (Dako) was reacted. The slides were then washed and incubated with the HRP-conjugated anti-rabbit IgG antibody. The 3-3' diaminobenzidine tetrahydrochloride (DAB) was used for coloration. Hematoxylin was used as the final nuclear counterstaining.

Immunofluorescence staining. The expression of ADAMTS4 protein was analyzed by immunofluorescence. Cells were fixed for 30 min in 4% paraformaldehyde/PBS, and permeabilized for 30 min in 0.1% Triton X/PBS. Fixed cells were rehydrated with Tris-buffered saline, and then incubated with the rabbit polyclonal anti-ADAMTS4 antibody. Immunofluorescence staining was done with the Alexa488-conjugated anti-rabbit IgG antibody. Nucleus was detected with bisbenzimide (Hoechst-33342, Sigma-Aldrich) staining.

ELISA. To evaluate the expression level of secreted ADAMTS4 protein, supernatants of the EWS cell lines and the patient sera were subjected to ELISA. The 96-well plates were coated with the monoclonal anti-human ADAMTS4 antibody at 4°C overnight. After 3 washes with washing buffer (0.05% Tween-20/PBS), the plates were treated with 10% FBS in PBS for 1 h at room temperature. The recombinant human ADAMTS4 (amino acids 213-685) diluted with 10% FBS in PBS, as standard proteins, and the samples were added to each well, and incubated at room temperature for 2 h. After 5 washes with washing buffer, the Avidin-HRP and the biotinylated anti-human ADAMTS4 detection antibody were added to each well, and incubated for 1 h at room temperature. After 7 washes with washing buffer, 100 μl of tetramethylbenzidine buffer as a substrate was added to each well and incubated for 30 min at room temperature in the dark. Color development was stopped by addition of 100 μl of stop solution (1 N H_3PO_4). Optic density of each sample was measured at 450 nm.

Results

Analysis of isolated cDNA clones. In SST-REX screening, we isolated 322 factor-independent Ba/F3 clones (Table III). Sequencing analyses revealed that integrations derived from 256 clones harbored the signal sequence. Among them, 80 different secreted and type I membrane proteins were identified. We used the database of RefEX, PubMed, ONCOMINE and SMART for the analysis, and 42 proteins that might be related to tumor/cancer onset and progression were selected.

Recent studies have suggested that the origin of EWS is derived from hMSC (40,41). To examine the expression levels of these 42 molecules in EWS in comparison with hMSC, we performed RT-PCR analysis (Table IV). They were classified into 3 groups by mRNA expression profiles; the first group with high expression levels only in EWS (Table IVA), the second group with higher expression levels in EWS than in hMSC (Table IVB), and the third group with similar or lower expression levels in EWS compared with

Table V. Gene expression levels in murine tissues by RT-PCR analysis.

	Brain	Heart	Lung	Liver	Kidney	Spl	Stm	S. int	L. int	Mus	Tes	Thy	BM	OC
DKFZP56400823	+	+	+	–	+	+	+	+	+	+	+	+	+	+
ADAMTS4	++	+	–	+	–	–	–	–	–	+	–	–	+	+
DNER	++	–	–	–	–	–	–	–	–	–	+	–	–	+
NGFR	+	+	–	+	+	–	–	–	–	–	–	–	–	–
LRRN6A	++	–	–	–	–	+	–	+	+	+	+	+	+	+
ECSM2	+	+	+	+	+	–	+	–	–	+	+	+	+	+
LGALS3BP	+	+	+	+	+	+	++	++	+	+	++	++	+	+
PTPRF	+	+	+	+	+	–	+	+	+	+	+	+	–	–
FCGRT	+	+	+	+	+	+	+	+	+	+	+	+	+	+
LAMP2	+	++	+	+	++	++	+	+	+	+	+	+	+	+
RCN1	+	+	+	+	+	–	+	–	–	–	+	+	+	+
MMP14	+	+	+	+	+	–	+	–	–	+	+	+	+	+
SDC2	+	+	+	+	+	–	+	+	–	+	+	+	+	+
DAG1	+	+	+	+	+	+	+	+	+	+	+	+	+	+
EPCR	+	+	+	+	+	+	+	–	–	+	+	+	+	++
CD97	+	+	+	+	+	+	+	+	+	+	+	+	+	+
CD99L2	+	+	+	+	+	–	–	–	–	+	+	+	+	+
IGFBP5	+	+	+	+	+	+	+	+	+	+	+	+	+	+
CLU	+	+	+	+	+	+	+	+	–	+	+	+	+	+
LSAMP	++	+	–	+	+	–	+	–	–	–	+	+	+	+
NPTN	+	+	+	+	+	–	+	+	+	+	+	+	+	+
EFNA5	+	+	+	+	+	–	+	+	+	–	+	+	–	–
PODXL	+	+	+	+	+	–	–	–	–	+	–	–	+	–
TMEM123	–	+	–	+	+	–	–	–	–	+	–	–	–	–

Spl, spleen; stm, stomach; s. int, small intestine; l. int, large intestine; mus, muscle; tes, testis; thy, thymus; BM, bone marrow; OC, osteoclast; ++, strongly positive; +, modelately positive; –, negative.

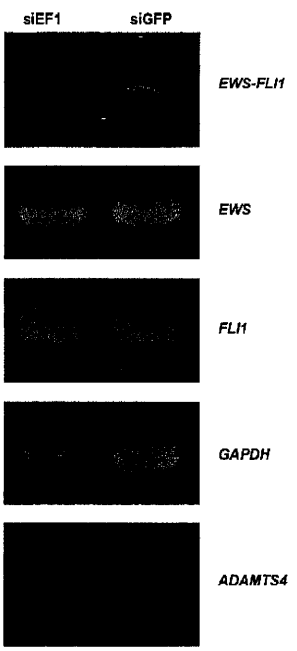


Figure 1. Effects of *EWS-FLI1* suppression on *ADAMTS4* expression. RNA from Ewing's sarcoma cells treated with either siEF1 or siGFP were subjected to RT-PCR experiment. *ADAMTS4* mRNA expression was down-regulated after treatment with *EWS-FLI1*-specific siRNA. *GAPDH* (*glyceraldehyde 3-phosphate dehydrogenase*) was used as an internal control.

hMSC (Table IVC). We picked up 24 molecules from the first and second groups, and examined the expression patterns in murine organs. As shown in Table V, most molecules did not exhibit interesting tissue distribution patterns. However, some of the molecules attracted us by their expression profiles or their novelty as a gene. We focused on 5 molecules: *ADAMTS4*, *DNER* (*delta/notch-like EGF-related receptor*), *NGFR* (*nerve growth factor receptor*), *LRRN6A* (*leucine rich repeat neuronal 6A*) and *ECSM2* (*endothelial cell-specific molecule 2*). We then examined expression levels of these 5 molecules in various solid tumor and hematopoietic cell lines by RT-PCR. As shown in Table VI, expression levels of *ADAMTS4* were higher in EWS, glioblastoma and neuroblastoma in comparison with other cell lines. These results suggested that *ADAMTS4* is one of the first candidate molecules as a marker for EWS among the SST clones.

ADAMTS4 expression is upregulated by EWS-FLI1. Previous studies indicated the expression of the fusion gene, *EWS-FLI1*, was suppressed by using antisense oligonucleotide or siRNA. To decrease the expression level of *EWS-FLI1* in the EWS cell line, we made an siRNA duplex specifically directed against the fusion junction of *EWS-FLI1* transcript. *EWS-FLI1*-specific siRNA (siEF1) was used for SJES-5 cell line. As a control, siGFP was also used. Transfection of siEF1,

Table VI. Gene expression levels of *ADAMTS4, DNER, NGFR, LRRN6A* and *ECSM2* in human cancer cell lines by RT-PCR analysis.

	ADAMTS4	DNER	NGFR	LRRN6A	ECSM2
AsPC-1	–	–	+	–	–
BxPC-3	–	+	–	–	–
Capan-1	–	–	–	–	–
U87MG	+	+	–	–	–
U251	+	++	–	–	–
T98G	–	+	–	–	–
HGC-27	+	–	+	+	–
MKN45	–	+	–	++	–
GCIY	+	+	–	+	–
KATOIII	–	–	–	–	–
MG63	–	+	+	+	+
HOS	+	+	+	+	+
KHOS/NP	–	+	+	+	+
SaOS2	–	+	+	–	–
U2OS	–	+	+	+	–
KPNSI-FA	+	++	+	+	–
LAN-1	+	+	+	+	–
NB69	++	–	+	+	+
H460	+	++	–	+	–
PLC/PRF/5	–	+	+	+	+
HuCCT1	–	++	–	+	+
SW48	–	+	+	–	+
RMS	++	++	+	++	+
SJRH-30	++	+	+	+	+
SJES-2, 3, 5, 6, 7, 8	++	++	+	++	++
MOLM13	–	–	–	–	–
ML1	–	–	–	–	–
U937	–	–	–	–	+
Jurkat	–	–	–	–	+
PEER	–	–	–	–	+
CEM	++	–	–	–	+
HPB-ALL	–	–	–	–	–
NALM24	+	+	–	–	+
NALM16	–	+	+	–	–
IM9	–	–	+	–	+

++, strongly positive; +, moderately positive; –, negative.

but not siGFP, led to significant decrease of the expression level of the *EWS-FLI1* fusion transcript (Fig. 1). In agreement with the specificity of siEF1 against the *EWS-FLI1* fusion gene, the expression level of *EWS* or *FLI1* was not affected. Interestingly, suppression of *EWS-FLI1* expression resulted in decreased expression of *ADAMTS4* transcript. These results suggested that *ADAMTS4* expression was upregulated by EWS-FLI1.

Immunohistochemical analysis on ADAMTS4 protein expression. In order to confirm the expression of ADAMTS4 in EWS at the protein level, we stained 25 tissue samples derived from EWS patients with the anti-ADAMTS4 antibody together with the H&E staining. ADAMTS4 protein was detected in 10 EWS samples, but not in 15 samples where tumors disappeared by chemotherapy (Fig. 2 and data not shown).

Next, to examine the subcellular localization of ADAMTS4, we stained EWS cell lines with the anti-ADAMTS4 antibody. Immunofluorescence microscopy revealed that ADAMTS4 protein was expressed mainly in the cytoplasm of EWS cell lines (Fig. 3C and D) and of the

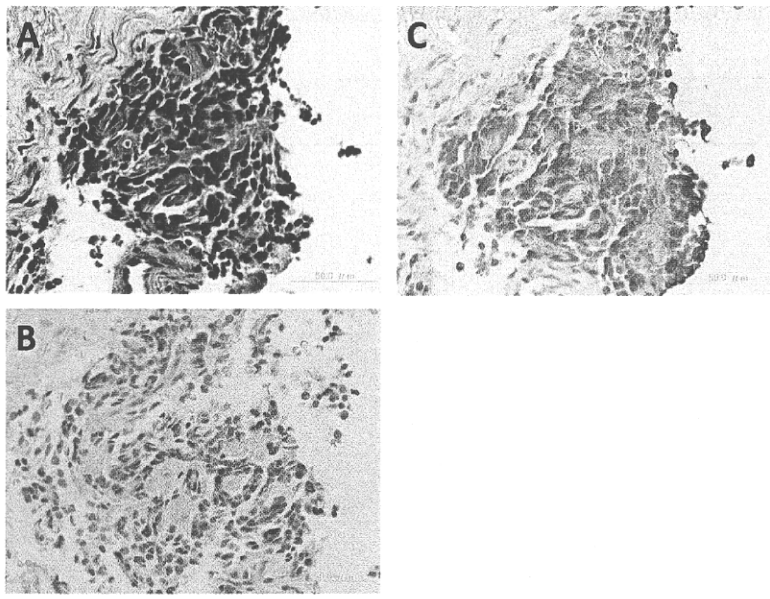


Figure 2. Immunohistochemical analysis of ADAMTS4 protein in the tissue section of the patient with Ewing's sarcoma. (A) Hematoxylin and eosin staining, (B) rabbit IgG, (C) anti-ADAMTS4 antibody.

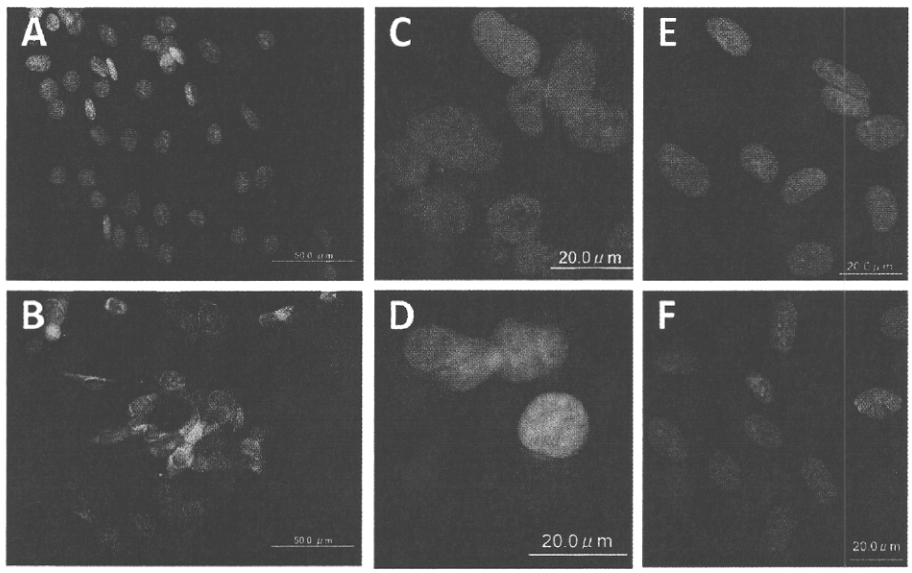


Figure 3. Immunofluorescence staining of ADAMTS4 protein in Ewing's sarcoma cell lines (SJES-2 and SJES-5), osteosarcoma cell lines (MG63 and SaOS2) and NIH3T3 cells expressing ADAMTS4. (A) NIH3T3, (B) ADAMTS4/NIH3T3, (C) SJES-5, (D) SJES-2, (E) MG63, (F) SaOS2.

NIH3T3 cells expressing human ADAMTS4 (Fig. 3B). In contrast, ADAMTS4 was not detected in osteosarcoma cell lines MG63 and SaOS2 (Fig. 3E and F), which did not express *ADAMTS4* at the transcription level (Table VI).

ADAMTS4 is secreted from EWS cells. We next asked whether ADAMTS4 was secreted from EWS cells. First the immunoprecipitates of the cell lysates of EWS cell lines and positive and negative control cells with the anti-ADAMTS4 antibody were electrophoresed, blotted and probed with the same antibody. ADAMTS4 was detcted in EWS cells and the positive control cells as double bands of ~100 kDa (Fig. 4A). We next performed the same experiments using 2 ml each of the supernatants of these cells. Notably, significant levels of expression of ADAMTS4 protein were observed in the supernatants of EWS cells and ADAMTS4/NIH3T3 cells (Fig. 4B). These results suggested that ADAMTS4 was secreted.

Comparative study of ADAMTS4 gene expression in 5 types of sarcomas. We showed that *ADAMTS4* transcripts were expressed in EWS, osteosarcoma and rhabdomyosarcoma cell lines (Table VI). However, whether *ADAMTS4* transcripts are expressed in tumor tissue samples remained unknown. Therefore, we tested if *ADAMTS4* was expressed in soft tissue sarcomas and bone tumors including osteosarcoma, EWS, chondrosarcoma, synovial sarcoma and rhabdomyosarcoma (Fig. 5). Benign tumors including lipoma, desmoid

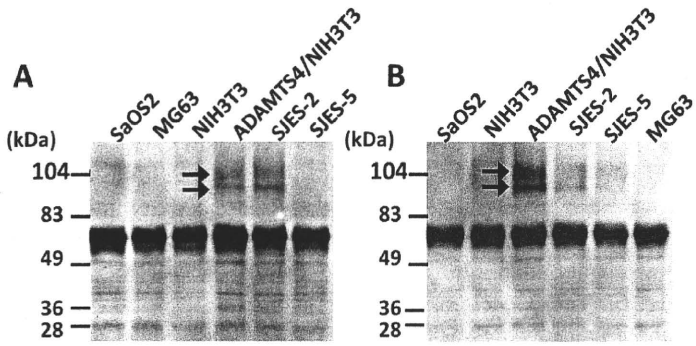


Figure 4. Detection of secreted ADAMTS4 protein. The cell lysates or culture supernatants were immunoprecipitated with the anti-ADAMTS4 antibody, resolved by SDS-PAGE, blotted and probed with the anti-ADAMTS4 antibody. Molecular size markers are shown on the left. Arrows indicate the ADAMTS4 proteins. (A), cell lysates; (B), supernatants.

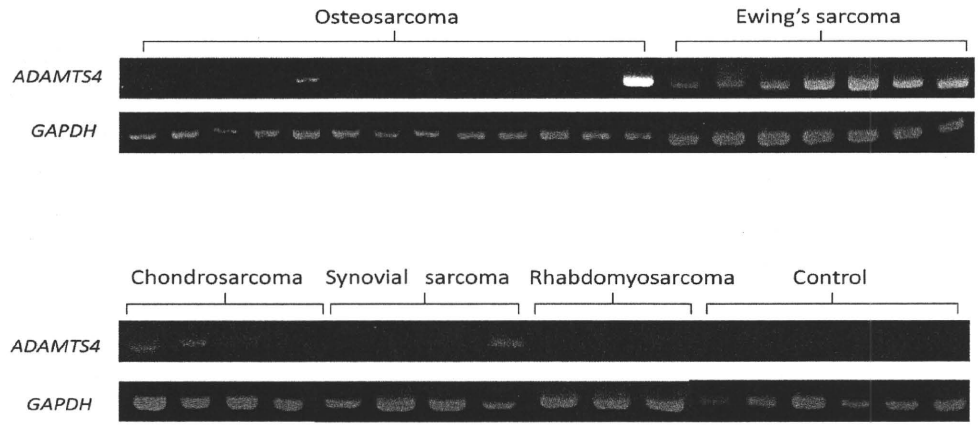


Figure 5. RT-PDR analysis of *ADAMTS4* expression in the patient samples. *GAPDH* expression was used as an internal control.

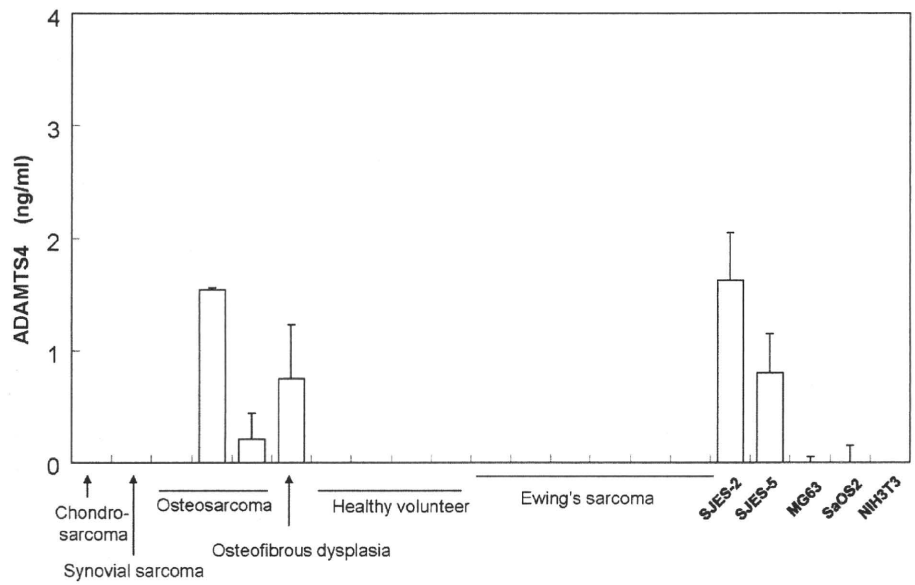


Figure 6. ELISA of ADAMTS4 protein in the patient sera and the supernatants of the cell lines. The error bars represent 1 standard deviation.

and Schwannoma were also examined as controls. In all 7 EWS samples, *ADAMTS4* transcripts were highly expressed. Three out of 4 samples of chondrosarcoma moderately expressed *ADAMTS4*. This result was predictable, since *ADAMTS4* is expressed in normal cartilage cells. Also, 2 out of 13 samples of osteosarcoma and 1 out of 4 samples of synovial sarcoma expressed *ADAMTS4*. *ADAMTS4* transcripts were not detected in the 3 samples of rhabdomyo-

sarcoma, while those were highly expressed in rhabdomyosarcoma cell lines RMS and SJRH-30 (Table VI). Benign tumors examined did not express *ADAMTS4*.

No detection of secreted ADAMTS4 protein in the patient sera. To evaluate the amount of secreted ADAMTS4 protein in the patients, we analyzed ADAMTS4 protein levels in sera by ELISA. In agreement with the results described above, ADAMTS4 was detected in culture supernantants of EWS cell lines SJES-2 and SJES-5 (Fig. 6). The concentration of ADAMTS4 in SJES-2 cells was about twice as high as that in SJES-5 cells. For a positive control, culture supernatant of the NIH3T3/ADAMTS4 cells was also measured (39.9 ng/ml, data not shown). It is noteworthy that ADAMTS4 protein was detected in 2 out of 3 cases of osteosarcoma and in the only case of osteofibrous dysplasia. Consistent with the very high level of *ADAMTS4* transcript shown in the extreme right lane among osteosarcoma samples in Fig. 5, serum from the same patient showed the high level of ADAMTS4 protein in ELISA as shown in Fig. 6 (middle lane among osteosarcoma samples). The other positive samples of osteosarcoma in both figures are not derived from the same patient, because only either serum or RNA was available in these two patients. ADAMTS4 protein was not detected in the 6 EWS patient sera examined. These results indicated that ADAMTS4 is expressed and secreted in EWS cells, but that the ADAMTS4 protein in the serum is not suitable as a marker for EWS.

Discussion

EWS is an aggressive neoplasm with a strong propensity to spread into neighboring tissues. Many patients are diagnosed at advanced stages of EWS. Since EWS has worse prognosis than other soft-tissue sarcomas, it is clinically important to distinguish EWS from other sarcomas. The reason for the poor prognosis in EWS patients is suggested to be that the micro-metastases are formed before clinical symptoms arise and tumors are detected (42). Currently, diagnosis of EWS is determined mainly by CD99 expression or by genetic aberrations that are exemplified by *EWS-FLI1* fusion gene. Since both markers show lack of sensitivity, specificity or feasibility, more useful biomarkers such as surface antigens or secreted proteins are required in clinical areas.

In the present study, we searched for membrane and secreted proteins derived from EWS cell lines using the retrovirus-mediated signal sequence trap method SST-REX, and identified ADAMTS4 as a possible EWS marker. We demonstrated that ADAMTS4 was expressed in EWS cell lines and tissue samples derived from EWS patients. Interestingly, expression of *ADAMTS4* was correlated with expression of *EWS-FLI1*, which is a hallmark of EWS. In addition, we demonstrated that ADAMTS4 was secreted from EWS cells, although we could not detect ADAMTS4 in serum samples derived from EWS patients.

It should be noted that two cases of the osteosarcoma patient samples were found to express high levels of *ADAMTS4*. It is tempting to speculate that a subclass of osteosarcoma with different property may exist.

In conclusion, we identified *ADAMTS4* as a possible marker of EWS by using SST-REX. This is the first report to show the correlation between *ADAMTS4* and EWS. Although ADAMTS4 protein in the serum could not be used as a biomarker for EWS, our study suggested that RNA transcripts of *ADAMTS4* in the tissue sections are useful markers of EWS. Further studies will be required to determine the usefulness of this molecule in differential diagnosis and/or evaluation of the disease activity in clinical settings.

Acknowledgements

We gratefully thank Ms. S. Shoma (The University of Tokyo) for technical support and Dr Y. Murakami (The University of Tokyo) and Dr Y. Fukuchi (Keio University) for helpful comments on this study. This work was supported by a Grant-in-Aid for Cancer Research from the Ministry of Health, Labour and Welfare of Japan.

References

1. Jaffe R, Santamaria M, Yunis EJ, Tannery NH, Agostini RM, Medina J Jr and Goodman M: The neuroectodermal tumor of bone. Am J Surg Pathol 8: 885-898, 1984.
2. Hashimoto H, Enjoji M, Nakajima T, Kiryu H and Daimaru Y: Malignant neuroepithelioma (peripheral neuroblastoma). A clinicopathologic study of 15 cases. Am J Surg Pathol 7: 309-318, 1983.
3. Khoury JD: Ewing sarcoma family of tumors. Adv Anat Pathol 12: 212-220, 2005.
4. Turc-Carel C, Philip I, Berger MP, Philip T and Lenoir G: Chromosomal translocation (11; 22) in cell lines of Ewing's sarcoma. C R Seances Acad Sci III 296: 1101-1103, 1983.
5. Zucman J, Delattre O, Desmaze C, *et al*: Cloning and characterization of the Ewing's sarcoma and peripheral neuroepithelioma t(11;22) translocation breakpoints. Genes Chromosomes Cancer 5: 271-277, 1992.
6. Sorensen PH, Lessnick SL, Lopez-Terrada D, Liu XF, Triche TJ and Denny CT: A second Ewing's sarcoma translocation, t(21;22), fuses the EWS gene to another ETS-family transcription factor, ERG. Nat Genet 6: 146-151, 1994.
7. Jeon IS, Davis JN, Braun BS, Sublett JE, Roussel MF, Denny CT and Shapiro DN: A variant Ewing's sarcoma translocation (7;22) fuses the EWS gene to the ETS gene ETV1. Oncogene 10: 1229-1234, 1995.
8. Arvand A and Denny CT: Biology of EWS/ETS fusions in Ewing's family tumors. Oncogene 20: 5747-5754, 2001.
9. May WA, Gishizky ML, Lessnick SL, Lunsford LB, Lewis BC, Delattre O, Zucman J, Thomas G and Denny CT: Ewing sarcoma 11;22 translocation produces a chimeric transcription factor that requires the DNA-binding domain encoded by FLI1 for transformation. Proc Natl Acad Sci USA 90: 5752-5756, 1993.
10. Ohno T, Rao VN and Reddy ES: EWS/Fli-1 chimeric protein is a transcriptional activator. Cancer Res 53: 5859-5863, 1993.
11. Jambhekar NA, Bagwan IN, Ghule P, Shet TM, Chinoy RF, Agarwal S, Joshi R and Amare Kadam PS: Comparative analysis of routine histology, immunohistochemistry, reverse transcriptase polymerase chain reaction, and fluorescence in situ hybridization in diagnosis of Ewing family of tumors. Arch Pathol Lab Med 130: 1813-1818, 2006.
12. Llombart-Bosch A and Navarro S: Immunohistochemical detection of EWS and FLI-1 proteinss in Ewing sarcoma and primitive neuroectodermal tumors: comparative analysis with CD99 (MIC-2) expression. Appl Immunohistochem Mol Morphol 9: 255-260, 2006.
13. Bernstein M, Kovar H, Paulussen M, Randall RL, Schuck A, Teot LA and Juergens H: Ewing's sarcoma family of tumors: current management. Oncologist 11: 503-519, 2006.
14. Folpe AL, Hill CE, Parham DM, O'Shea PA and Weiss SW: Immunohistochemical detection of FLI-1 protein expression: a study of 132 round cell tumors with emphasis on CD99-positive mimics of Ewing's sarcoma/primitive neuroectodermal tumor. Am J Surg Pathol 24: 1657-1662, 2000.
15. Bernard G, Zoccola D, Deckert M, Breittmayer JP, Aussel C and Bernard A: The E2 molecule (CD99) specifically triggers homotypic aggregation of $CD4^+$ $CD8^+$ thymocytes. J Immunol 154: 26-32, 1995.

16. Zhang PJ, Barcos M, Stewart CC, Block AW, Sait S and Brooks JJ: Immunoreactivity of MIC2 (CD99) in acute myelogenous leukemia and related diseases. Mod Pathol 13: 452-458, 2000.
17. Tashiro K, Tada H, Heilker R, Shirozu M, Nakano T and Honjo T: Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins. Science 261: 600-603, 1993.
18. Shirozu M, Nakano T, Inazawa J, Tashiro K, Tada H, Shinohara T and Honjo T: Structure and chromosomal localization of the human stromal cell-derived factor 1 (SDF1) gene. Genomics 28: 495-500, 1995.
19. Kojima T, Morikawa Y, Copeland NG, Gilbert DJ, Jenkins NA, Senba E and Kitamura T: TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles. J Biol Chem 275: 20742-20747, 2000.
20. Ohta K, Lupo G, Kuriyama S, Keynes R, Holt CE, Harris WA, Tanaka H and Ohnuma S: Tsukushi functions as an organizer inducer by inhibition of BMP activity in cooperation with chordin. Dev Cell 7: 347-358, 2004.
21. Ikeda Y, Imai Y, Kumagai H, Nosaka T, Morikawa Y, Hisaoka T, Manabe I, Maemura K, Nakaoka T, Imamura T, Miyazono K, Komuro I, Nagai R and Kitamura T: Vasorin, a transforming growth factor beta-binding protein expressed in vascular smooth muscle cells, modulates the arterial response to injury in vivo. Proc Natl Acad Sci USA 101: 10732-10737, 2004.
22. Izawa K, Kitaura J, Yamanishi Y, Matsuoka T, Oki T, Shibata F, Kumagai H, Nakajima H, Maeda-Yamamoto M, Hauchins JP, Tybulewicz VL, Takai T and Kitamura T: Functional analysis of activating receptor LMIR4 as a counterpart of inhibitory receptor LMIR3. J Biol Chem 282: 17997-18008, 2007.
23. Ganju RK, Brubaker SA, Meyer J, Dutt P, Yang Y, Qin S, Newman W and Groopman JE: The alpha-chemokine, stromal cell-derived factor-1alpha, binds to the transmembrane G-protein-coupled CXCR-4 receptor and activates multiple signal transduction pathways. J Biol Chem 273: 23169-23175, 1998.
24. Kitamura T, Onishi M, Kinoshita S, Shibuya A, Miyajima A and Nolan GP: Efficient screening of retroviral cDNA expression libraries. Proc Natl Acad Sci USA 92: 9146-9150, 1995.
25. Kojima T and Kitamura T: A signal sequence trap based on a constitutively active cytokine receptor. Nat Biotechnol 17: 487-490, 1999.
26. Kuno K, Kanada N, Nakashima E, Fujiki F, Ichimura F and Matsushima K: Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene. J Biol Chem 272: 556-562, 1997.
27. Porter S, Clark IM, Kevorkian L and Edwards DR: The ADAMTS metalloproteinases. Biochem J 386: 15-27, 2005.
28. Tortorella MD, Burn TC, Pratta MA, *et al*: Purification and cloning of aggrecanase-1: a member of the ADAMTS family of proteins. Science 284: 1664-1666, 1999.
29. Tortorella MD, Malfait AM, Deccico C and Arner E: The role of ADAM-TS4 (aggrecanase-1) and ADAM-TS5 (aggrecanase-2) in a model of cartilage degradation. Osteoarthritis Cartilage 9: 539-552, 2001.
30. Sandy JD, Neame PJ, Boynton RE and Flannery CR: Catabolism of aggrecan in cartilage explants. Identification of a major cleavage site within the interglobular domain. J Biol Chem 266: 8683-8685, 1991.
31. Sandy JD, Flannery CR, Neame PJ and Lohmander LS: The structure of aggrecan fragments in human synovial fluid. Evidence for the involvement in osteoarthritis of a novel proteinase which cleaves the Glu 373-Ala 374 bond of the interglobular domain. J Clin Invest 89: 1512-1516, 1992.
32. Lohmander LS, Neame PJ and Sandy JD: The structure of aggrecan fragments in human synovial fluid. Evidence that aggrecanase mediates cartilage degradation in inflammatory joint disease, joint injury, and osteoarthritis. Arthritis Rheum 36: 1214-1222, 1993.
33. Kashiwagi M, Tortorella M, Nagase H and Brew K: TIMP-3 is a potent inhibitor of aggrecanase 1 (ADAM-TS4) and aggrecanase 2 (ADAM-TS5). J Biol Chem 276: 12501-12504, 2001.
34. Yamanishi Y, Boyle DL, Clark M, Maki RA, Tortorella MD, Arner EC and Firestein GS: Expression and regulation of aggrecanase in arthritis: the role of TGF-beta. J Immunol 168: 1405-1412, 2002.
35. Matthews RT, Gary SC, Zerillo C, Pratta M, Solomon K, Arner EC and Hockfield S: Brain-enriched hyaluronan binding (BEHAB)/brevican cleavage in a glioma cell line is mediated by a disintegrin and metalloproteinase with thrombospondin motifs (ADAMTS) family member. J Biol Chem 275: 22695-22703, 2000.
36. Morita S, Kojima T and Kitamura T: Plat-E: an efficient and stable system for transient packaging of retroviruses. Gene Ther 7: 1063-1066, 2000.
37. Kitamura T, Koshino Y, Shibata F, Oki, T, Nakajima H, Nosaka T and Kumagai H: Retrovirus-mediated gene transfer and expression cloning: powerful tools in functional genomics. Exp Hematol 11: 1007-1014, 2003.
38. Prieur A, Tirode F, Cohen P and Delattre O: EWS/FLI-1 silencing and gene profiling of Ewing cells reveal downstream oncogenic pathways and a crucial role for repression of insulin-like growth factor binding protein 3. Mol Cell Biol 24: 7275-7283, 2004.
39. Nosaka T, Kawashima T, Misawa K, Ikuta K, Mui AL and Kitamura T: STAT5 as a molecular regulator of proliferation, differentiation and apoptosis in hematopoietic cells. EMBO J 18: 4754-4765, 1999.
40. Tirode F, Laud-Duval K, Prieur A, Delorme B, Charbord P and Delattre O: Mesenchymal stem cell features of Ewing tumors. Cancer Cell 11: 421-429, 2007.
41. Riggi N, Cironi L, Provero P, Suva ML, Kaloulis K, Garcia-Echeverria C, Hoffmann F, Trumpp A and Stamenkovic I: Development of Ewing's sarcoma from primary bone marrow-derived mesenchymal progenitor cells. Cancer Res 65: 11459-11468, 2005.
42. Schleiermacher G, Peter M, Oberlin O, Philip T, Rubie H, Mechinaud F, Sommelet-Olive D, Landman-Parker J, Bours D, Michon J and Delattre O: Increased risk of systemic relapses associated with bone marrow micrometastasis and circulating tumor cells in localized Ewing tumor. J Clin Oncol 21: 85-91, 2003.

TIM1 is an endogenous ligand for LMIR5/CD300b: LMIR5 deficiency ameliorates mouse kidney ischemia/reperfusion injury

Yoshinori Yamanishi,[1,3] Jiro Kitaura,[1] Kumi Izawa,[1] Ayako Kaitani,[1] Yukiko Komeno,[1] Masaki Nakamura,[1] Satoshi Yamazaki,[4] Yutaka Enomoto,[1] Toshihiko Oki,[1,2] Hisaya Akiba,[5] Takaya Abe,[6] Tadasuke Komori,[7] Yoshihiro Morikawa,[7] Hiroshi Kiyonari,[6] Toshiyuki Takai,[8] Ko Okumura,[5] and Toshio Kitamura[1,2]

[1]Division of Cellular Therapy and [2]Division of Stem Cell Signaling, The Institute of Medical Science, The University of Tokyo, Minato-ku, Tokyo 108-8639, Japan
[3]Department of Physiological Chemistry and Metabolism, Graduate School of Medicine, The University of Tokyo, Bunkyo-ku, Tokyo 103-0033
[4]Small Animal Model Group, Nakauchi Stem Cell and Organ Regeneration, Japan Science and Technology Agency, Minato-ku, Tokyo 108-8639, Japan
[5]Department of Immunology, Juntendo University School of Medicine, Bunkyo-ku, Tokyo 113-8421, Japan
[6]The Laboratory for Animal Resources and Genetic Engineering, RIKEN Center for Developmental Biology, Kobe 650-0047, Japan
[7]Department of Anatomy and Neurobiology, Wakayama Medical University, Wakayama 641-8509, Japan
[8]Department of Experimental Immunology, Institute of Development, Aging, and Cancer, Tohoku University, Sendai 980-8575, Japan

Leukocyte mono-immunoglobulin (Ig)–like receptor 5 (LMIR5)/CD300b is a DAP12-coupled activating receptor predominantly expressed in myeloid cells. The ligands for LMIR have not been reported. We have identified T cell Ig mucin 1 (TIM1) as a possible ligand for LMIR5 by retrovirus-mediated expression cloning. TIM1 interacted only with LMIR5 among the LMIR family, whereas LMIR5 interacted with TIM4 as well as TIM1. The Ig-like domain of LMIR5 bound to TIM1 in the vicinity of the phosphatidylserine (PS)-binding site within the Ig-like domain of TIM1. Unlike its binding to TIM1 or TIM4, LMIR5 failed to bind to PS. LMIR5 binding did not affect TIM1- or TIM4-mediated phagocytosis of apoptotic cells, and stimulation with TIM1 or TIM4 induced LMIR5-mediated activation of mast cells. Notably, LMIR5 deficiency suppressed TIM1-Fc–induced recruitment of neutrophils in the dorsal air pouch, and LMIR5 deficiency attenuated neutrophil accumulation in a model of ischemia/reperfusion injury in the kidneys in which TIM1 expression is up-regulated. In that model, LMIR5 deficiency resulted in ameliorated tubular necrosis and cast formation in the acute phase. Collectively, our results indicate that TIM1 is an endogenous ligand for LMIR5 and that the TIM1–LMIR5 interaction plays a physiological role in immune regulation by myeloid cells.

CORRESPONDENCE
Toshio Kitamura:
kitamura@ims.u-tokyo.ac.jp

Abbreviations used: BMMC, BM-derived mast cell; CHO, Chinese hamster ovary; ERK, extracellular signal-regulated kinase; FLMC, fetal liver–derived mast cell; IRI, ischemia/reperfusion injury; KIM-1, kidney injury molecule-1; LMIR, leukocyte mono-Ig–like receptor; PS, phosphatidylserine; TIM, T cell Ig mucin.

A growing number of studies have characterized a variety of paired activating and inhibitory receptors (Ravetch and Lanier, 2000; Klesney-Tait et al., 2006; Lanier, 2009). We have previously identified a leukocyte mono-Ig–like receptor (LMIR) mainly expressed in myeloid cells (Kumagai et al., 2003; Izawa et al., 2007; Yamanishi et al., 2008). The mouse LMIR family is also known as the CMRF-35–like molecule/myeloid-associated Ig-like receptor/dendritic cell–derived Ig-like receptor/CD300 family (Luo et al., 2001; Chung et al., 2003; Yotsumoto et al., 2003). LMIR1 and LMIR3 are immunoreceptor tyrosine-based inhibitory motif–containing inhibitory receptors, whereas other members are activating receptors that associate with immunoreceptor tyrosine-based activation motif–containing adaptor proteins (Luo et al., 2001; Chung et al., 2003; Kumagai et al., 2003; Yotsumoto et al., 2003; Izawa et al., 2007; Yamanishi et al., 2008). LMIR5 is a DAP12-coupled activating receptor predominantly expressed in myeloid cells (Yamanishi

The Rockefeller University Press $30.00
J. Exp. Med. Vol. 207 No. 7 1501-1511
www.jem.org/cgi/doi/10.1084/jem.20090581

et al., 2008). However, the ligands for LMIR remained unknown. In this study, we identified T cell Ig mucin 1 (TIM1) as a ligand for LMIR5 by retrovirus-mediated expression cloning (Kitamura et al., 2003).

TIM1–4 are characterized as important regulators of immune responses associated with autoimmunity and allergic diseases (McIntire et al., 2001; Kuchroo et al., 2003, 2008). The TIM molecules are type 1 cell-surface glycoproteins, consisting of an N-terminal IgV domain and a mucin domain. TIM1/hepatitis A virus cellular receptor 1 (Kaplan et al., 1996)/kidney injury molecule–1 (KIM-1; Ichimura et al., 1998) is expressed in activated T cells and delivers a signal that enhances T cell activation and proliferation (Meyers et al., 2005; Umetsu et al., 2005). TIM1 can also interact with itself (Santiago et al., 2007b). In addition, a soluble form of KIM-1/TIM1 is released by shedding (Bailly et al., 2002). On the other hand, TIM4 is expressed in macrophages and dendritic cells and is a natural ligand for TIM1 (Meyers et al., 2005). Interestingly, TIM1 and TIM4 recognize phosphatidylserine (PS) and are critical for the efficient clearance of apoptotic cells (Kobayashi et al., 2007; Miyanishi et al., 2007; Santiago et al., 2007a; Ichimura et al., 2008). Recent reports have demonstrated that the narrow cavity built by the CC' and FG loops of the Ig-like domain is a binding site for PS (Kobayashi et al., 2007; Santiago et al., 2007a,b). In addition, TIM1/KIM-1 expression is strongly induced in the injured kidney epithelial cells (Ichimura et al., 1998, 2008; Waanders et al., 2010), and confers a phagocytic phenotype on epithelial cells (Ichimura et al., 2008). TIM1 is also a marker for renal tubular damage (Waanders et al. 2010).

In the present study, using biological and biochemical analysis, we demonstrate that TIM1 and TIM4 are endogenous ligands for LMIR5. In addition, we generated LMIR5$^{-/-}$ mice and delineated the physiological significance of the LMIR5–TIM1 interaction by using an acute kidney injury model.

RESULTS

Cloning of the ligand for LMIR5

To identify the LMIR5 ligand, we generated an Fc fusion protein containing the extracellular domain of LMIR5 (LMIR5-Fc). Several hematopoietic cell lines were incubated with LMIR5-Fc, which stained A20 cells but not Ba/F3 cells, as determined by flow cytometric analysis, suggesting the expression of LMIR5 ligand in A20 cells (Fig. 1 A). To identify the surface protein bound by LMIR5-Fc, we used retrovirus-mediated expression cloning (Kitamura et al., 2003). A retrovirus cDNA library constructed from A20 cells was transduced via infection to Ba/F3 cells that were not stained by LMIR5-Fc (Fig. 1 A). The transfectants stained by LMIR5-Fc were sorted and expanded in culture. This cycle of sorting and expansion was repeated three times until LMIR5-Fc stained most cells (Fig. S1 A). After we obtained single-cell clones that were stained with LMIR5-Fc, we isolated TIM1 cDNA from most of these clones by PCR (Fig. S1 B and not depicted). We confirmed that a cell-surface glycoprotein TIM1 was expressed in A20 cells but not in Ba/F3 cells by using anti-TIM1 antibody (Fig. 1 A, bottom). When TIM1 was expressed in Ba/F3 cells, LMIR5-Fc strongly stained TIM1-transduced Ba/F3 but not parental Ba/F3 cells. In addition, LMIR5-Fc–staining levels were correlated with TIM1 expression at both surface protein and mRNA levels (Fig. 1, A and B). Collectively, these results indicated that LMIR5-Fc bound to TIM1. In accordance, pretreatment of LMIR5-Fc with 10 μg/ml anti-LMIR5 antibody, but not control antibody, abolished the binding of LMIR5-Fc to TIM1-expressing Ba/F3 cells (Fig. 1 C, left). Similarly, the preincubation of TIM1-expressing Ba/F3 cells with 100 μg/ml anti-TIM1 antibody (222414) suppressed this binding (Fig. 1 D, left). The binding of LMIR5-Fc to TIM1-expressing Ba/F3 cells was dose-dependently inhibited by anti-LMIR5 or anti-TIM1 antibody (Fig. 1, C and D, right). These observations strongly suggested that LMIR5 interacts directly with TIM1. Then, Fc fusion proteins containing the extracellular domains of LMIR1, 2, 3, and 4 (LMIR1/2/3/4-Fc) were generated. TIM1-expressing Ba/F3 cells were bound only by LMIR5-Fc among the LMIR-Fc fusion proteins (Fig. 1 E). When Ba/F3 cells transduced with Flag-tagged TIM1, 2, 3, and 4 were incubated with LMIR5-Fc, LMIR5-Fc bound to those cells transduced with TIM4 as well as TIM1 among the TIM family (Fig. 1 F). In support of this, coimmunoprecipitation experiments illustrated the physical interaction of LMIR5 with both TIM1 and TIM4 (Fig. 1 G). After generating Fc fusion proteins containing the extracellular domains of TIM1 or 4 (TIM1/4-Fc), we incubated LMIR5- or mock-transduced Ba/F3 cells with TIM1-Fc or TIM4-Fc, which stained LMIR5-transduced Ba/F3 cells more strongly as compared with parental Ba/F3 cells (Fig. S1 C), indicating that TIM1 or TIM4 bound to surface-expressed LMIR5. On the other hand, the fact that TIM1-Fc or TIM4-Fc stained parental Ba/F3 cells at significant levels suggested that ligands for TIM1 or TIM4 other than LMIR5 were expressed in Ba/F3 cells. Our results suggested that TIM1 and TIM4 are possible ligands for LMIR5.

The Ig-like domain of LMIR5 binds to that of TIM1 in the vicinity of the PS-binding site

To determine which region of LMIR5 was required for the interaction with TIM1, we generated LMIR5 deletion mutants (LMIR5 del1/2/3/4/5–Fc; Fig. 2, A and B). Notably, like LMIR5-Fc, LMIR5 del1/2/3–Fc bound to TIM1-expressing Ba/F3 cells, whereas LMIR5 del4/5–Fc lacking the C terminus of the Ig-like domains did not bind at all (Fig. 2 C). These results suggested that the intact Ig-like domain of LMIR5 is indispensable for the LMIR5–TIM1 interaction.

According to recent reports, TIM1 and TIM4 bind to PS through the highly conserved binding cleft (FG–CC' cleft) of the Ig-like domains (Kobayashi et al., 2007; Miyanishi et al., 2007; Santiago et al., 2007a,b; Ichimura et al., 2008). To clarify the involvement of this region in LMIR5–TIM1 binding, we generated the TIM1 mutants W115A/F116A (WF/AA) or N117A/D118A (ND/AA), because these mutations in the metal ion–dependent ligand-binding site were reported

to dampen TIM1–PS binding (Kobayashi et al., 2007; Santiago et al., 2007a). Interestingly, these substitutions completely abolished the binding of LMIR5-Fc to TIM1-expressing Ba/F3 cells (Fig. 2 D). Collectively, these findings indicated that LMIR5 bound to TIM1, presumably through the interaction of the Ig-like domain of LMIR5 with the structural

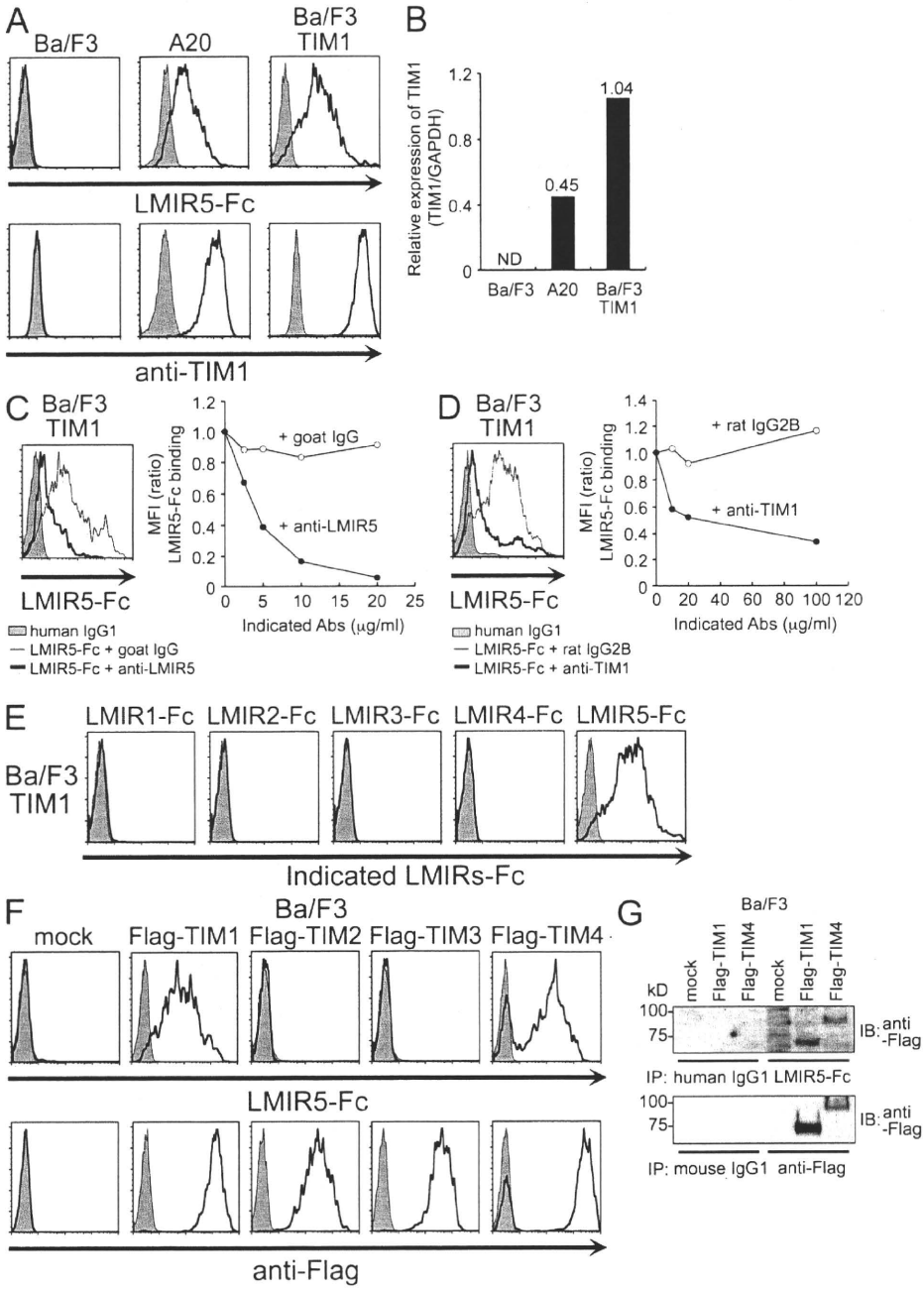


Figure 1. Specific binding of LMIR5-Fc to TIM1-expressing cells. (A) The indicated cells or TIM1-transduced Ba/F3 cells were stained with LMIR5-Fc (top) or with anti-TIM1 antibody (RMT1-4; bottom). (B) Relative gene expression levels of TIM1 were estimated by using real-time PCR. (C) LMIR5-Fc was pretreated with the indicated concentrations (left, 10 μg/ml) of anti-LMIR5 antibody or goat IgG. (D) TIM1-transduced Ba/F3 cells were preincubated with the indicated concentrations (left, 100 μg/ml) of anti-TIM1 antibody (222414) or rat IgG2b. TIM1-transduced Ba/F3 cells were then stained with LMIR5-Fc. The mean fluorescent intensity (MFI) of LMIR5-Fc staining is shown (C and D, right). (E) TIM1-transduced Ba/F3 cells were stained with LMIR1/2/3/4/5-Fc (continuous line histograms). Control staining with human IgG1 is shown (shaded histograms). (F) Ba/F3 cells transduced with Flag-tagged TIM1/2/3/4 or mock transduced were stained with LMIR5-Fc (top, continuous line histograms) or with anti-Flag antibody (bottom, continuous line histograms). Control staining with human (top, shaded histograms) and mouse IgG1 (bottom, shaded histograms) is shown. (G) TIM1 and TIM4 proteins were detected by immunoblotting (IB) with anti-Flag antibody in the immunoprecipitates (IP) of lysates derived from Flag-tagged TIM1-, TIM4-, or mock-transduced Ba/F3 cells incubated with LMIR5-Fc (top) or anti-Flag antibody (bottom). All data are representative of three independent experiments. ND, not detected.