centrifuged at 2000 *g* for 10 min. The supernatant was used as the sample. One hundred microliters of each standard blank or sample (in duplicate) was added to wells coated with MMP-2 antibody. The 96-well plate was then incubated overnight at 4°C. Any MMP-2 present within the samples was bound to the wells and other components were removed by washing. All standards and one well for each sample were activated with aminophenylmercuric acetate (APMA, 0.5 mM) to determine total MMP-2 levels, and the remaining wells were incubated with assay buffer alone to determine endogenous activated MMP-2. The detection reagent was then added to each well and the plate was incubated at 37°C for 4 h. After incubation, the absorbance of each well was read at 405 nm on a microplate reader and the concentrations (nanograms per milliliter) of total MMP-2 and endogenous activated MMP-2 were determined for each sample from a standard curve using Revelation Software (Dynatech, UK). Final tissue values were expressed as nanograms per milligram of protein.

MMP-9 assay

Standards and samples were run in the same manner as described for MMP-2 on a microplate coated with MMP-9 antibody, except that 1 mM APMA was used for activation, and incubation with the detection reagent was done at 37°C for 6 h. The absorbance was read with a microplate reader as described for MMP-2. Final tissue values were expressed as nanograms per milligram of protein.

Results

Measurement of subcutaneous tumor

We measured the major axis of the tumor to examine whether the administration of Kurozu or Kurozu-M could inhibit tumor growth. In the DLD cell–transplanted model, the major axes were 8.1 ± 0.5 mm in the control group, 7.90 ± 0.80 mm in Kurozu group, and 7.8 ± 0.80 mm in the Kurozu-M group. There were no significant differences among the three groups (Fig. 1A). However, in the Lovo cell–transplanted model, the major axes of the tumor were 8.2 ± 0.5 mm in the control group and 7.8 ± 0.8 mm in the Kurozu group, but significantly reduced to 6.0 ± 0.8 mm in the Kurozu-M group ($P < 0.05$ versus control; Fig. 1B).

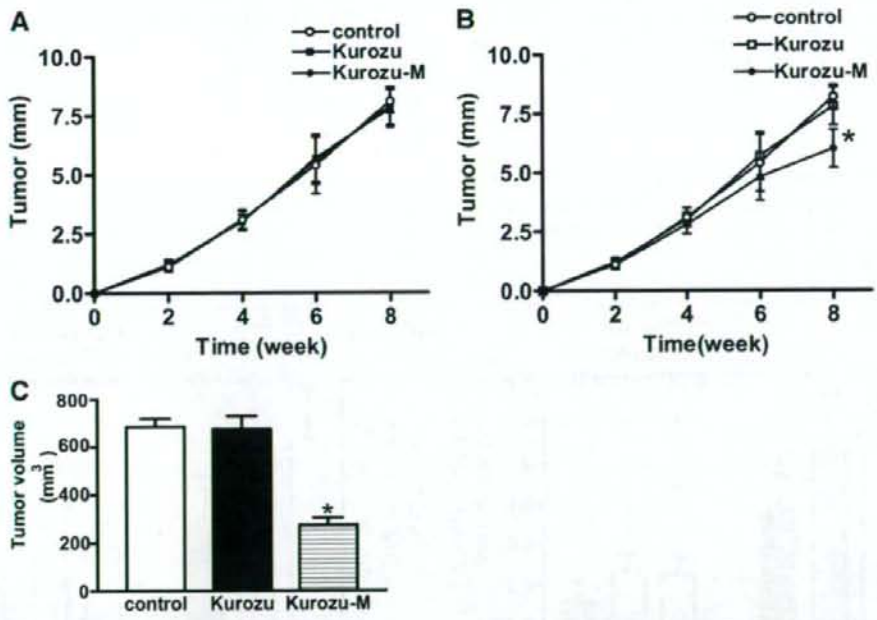

Fig. 1. Antitumor effect of Kurozu and Kurozu moromimatsu. Female nu/nu mice were injected with 1×10^6 Lovo cells or DLD cells into the right flank. (A) Time course of tumor growth in DLD-1 cell–transplanted mice (long diameter). Open circles represent the control group, solid squares the Kurozu-treated group, and solid circles the Kurozu moromimatsu–treated group. (B) Time course of tumor growth in Lovo cell–transplanted mice (long diameter). Open circles indicate the control group, open squares the Kurozu-treated group, and solid circles the Kurozu moromimatsu–treated group. (C) Tumor volume in Lovo cell–transplanted mice. Tumor volume was measured 8 wk after Lovo cell inoculation. The open bar indicates the control group, the solid bar the Kurozu-treated group, and the horizontally lined bar the Kurozu moromimatsu–treated group. Values are means ± SD. *$P < 0.001$ versus other groups.

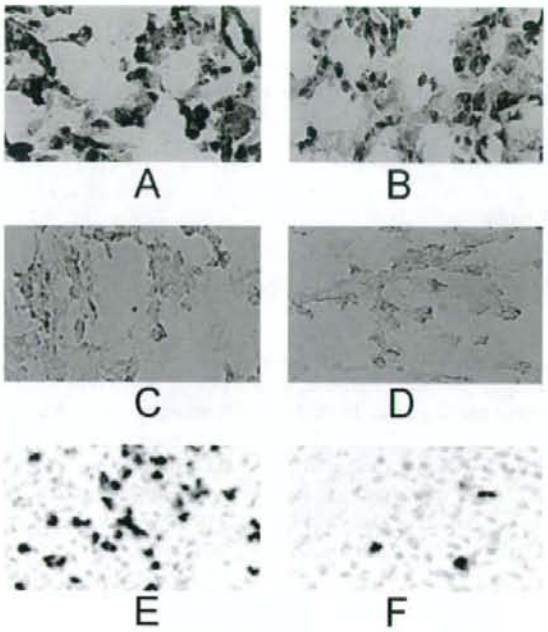

Fig. 2. Histologic examination of cancerous tissue after Lovo cell transplantation. Hematoxylin-eosin staining of tumor from (A) the control group and (B) the Kurozu moromimatsu–treated group. Terminal deoxynucleotidyl transferase-mediated dUTP nick end-labeling staining of tumor from (C) the control group and the (D) Kurozu moromimatsu–treated group. Nitrotyrosine staining of tumor from (E) the control group and (F) the Kurozu moromimatsu–treated group.

In the Lovo cell–transplanted model, the tumor volumes were 684.0 ± 34.0 mm^3 in the control group, 672.0 ± 56.0 mm^3 in the Kurozu group, and 273.0 ± 32.0 mm^3 in the Kurozu-M group ($P < 0.005$ for the Kurozu-M group versus control; Fig. 1C).

The following results refer to the Lovo cell–transplanted model.

HE staining, TUNEL staining, and nitrotyrosine immunostaining

The HE staining showed no accumulation of polymorphonuclear leukocytes, which have been implicated in active oxygen production, in tumor tissue in the control group or the Kurozu-M group (Fig. 2A,B).

The TUNEL staining indicated that apoptosis in the Kurozu-M group was at the same level as that in the control group (Fig. 2C,D).

Because we previously found that nitrotyrosine, generated from peroxynitrite and tyrosine, is produced in human colon cancer [5], we examined whether the administration of Kurozu-M could inhibit nitrotyrosine formation. In the control group, many cells produced nitrotyrosine, whereas in the Kurozu-M group, only a few cells produced nitrotyrosine (Fig. 2E,F).

MMP-2 and MMP-9 assays

To investigate the role of MMPs in the action of Kurozu-M, we examined whether or not Kurozu-M altered the levels and activation of MMPs.

Total MMP-2 amounted to 8.8 ± 2.5 ng/mg of protein in the control group and 8.6 ± 2.8 ng/mg of protein in the Kurozu group. However, it was significantly reduced to 5.6 ± 1.8 ng/mg of protein by administration of Kurozu-M ($P < 0.05$ versus control; Fig. 3A). Activated MMP-2 amounted to 0.25 ± 0.06 ng/mg of protein in the control group, 0.27 ± 0.08 ng/mg of protein in the Kurozu group, and 0.12 ± 0.05 ng/mg of protein in the Kurozu-M group ($P < 0.05$ for the Kurozu-M group versus control; Fig. 3A).

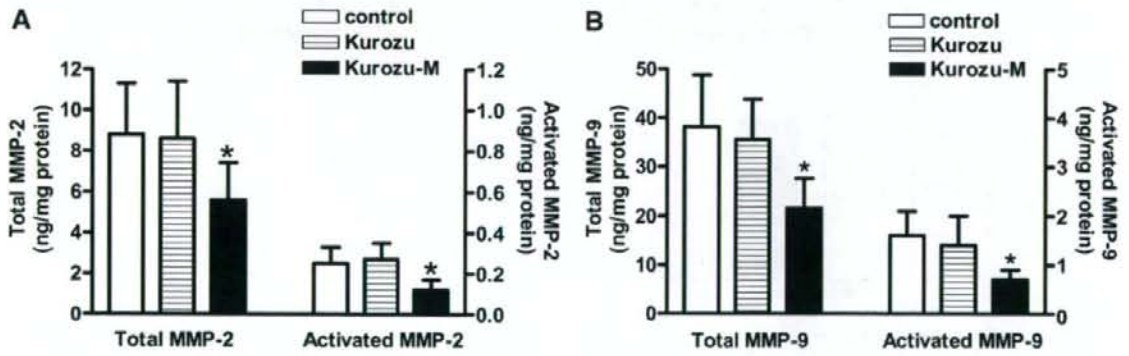

Fig. 3. Anti-metalloproteinase effect of Kurozu and Kurozu moromimatsu. (A) Total and activated metalloproteinase-2 in cancerous tissue after Lovo cell inoculation. The open bar represents the control group, the horizontally lined bar the Kurozu-treated group, and the solid bar the Kurozu moromimatsu-treated group. (B) Levels of total and activated metalloproteinase-9 in cancerous tissue after Lovo cell inoculation. The open bar represents the control group, the horizontally lined bar the Kurozu-treated group, and the solid bar the Kurozu moromimatsu–treated group.Values are means ± SD. $^*P < 0.001$ versus other groups.

Total MMP-9 amounted to 38.2 ± 10.6 ng/mg of protein in the control group and 35.6 ± 8.22 ng/mg of protein in the Kurozu group. However, it was significantly reduced to 21.5 ± 6.1 ng/mg of protein by administration of Kurozu-M ($P < 0.05$ versus control; Fig. 3B). Activated MMP-9 amounted to 1.6 ± 0.5 ng/mg of protein in the control group, 1.4 ± 0.6 ng/mg of protein in the Kurozu group, and 0.7 ± 0.2 ng/mg of protein in the Kurozu-M group ($P < 0.05$ for the Kurozu-M group versus control; Fig. 3B).

Discussion

Our results indicate that the administration of Kurozu-M inhibits the development of colon cancer in human colon cancer cell transplantation model in mice. Further, the administration of Kurozu-M inhibited nitrotyrosine production, decreased total MMP-2 and total MMP-9 levels, and inhibited activation of MMP-2 and MMP-9 in the lesion in this model.

Earlier studies had indicated that extract of Kurozu can inhibit chemical carcinogenesis [3,4,6]. However, in our study, the administration of Kurozu-M inhibited the development of colon cancer in a mouse model, whereas the administration of Kurozu did not prevent tumor growth. The major constituent of Kurozu is acetic acid, whereas the major component of Kurozu-M is a complex mixture of organic materials, including bacterial metabolites. The active components of Kurozu-M remain to be identified.

In this study, we found that administration of Kurozu-M inhibited production of nitrotyrosine in tumor tissue. Nitrotyrosine is generated through two pathways in vivo. One is the peroxynitrite pathway, in which tyrosine reacts with peroxynitrite to afford nitrotyrosine, and the second is the myeloperoxidase pathway, in which tyrosine reacts with myeloperoxidase and nitrite [7,8]. We previously reported that peroxynitrite is produced in human colon cancer tissue [5]. In contrast, myeloperoxidase is localized in polymorphonuclear leukocytes in vivo, but in this study we could not detect any accumulation of polymorphonuclear leukocytes by means of HE staining of cancerous tissue. Therefore, Kurozu-M administration may inhibit the peroxynitrite pathway. Possible mechanisms include inhibition of nitric oxide, superoxide, and/or peroxynitrite production, and scavenging of nitric oxide, superoxide, and/or peroxynitrite. Further work is needed to examine these possibilities.

The administration of Kurozu-M also inhibited MMP-2 and MMP-9 activity in cancerous tissue. These are representative gelatinases that contribute to the distant metastasis of cancer [9], and they are produced by cancer cells or macrophages [10]. A tetradecanoylphorbol acetate-responsive element is present in the promoter region of MMP-9 and is activated by various cytokines, such as interleukin and tumor necrosis factor [11]. In addition, MMP-9 is activated by nuclear factor-κB and MMP-2 [12]. MMP-2 is mainly activated by MT1-MMP, but recently it was shown that peroxynitrite also activates MMP-2 [13,14]. Kurozu-M may have inhibited cancer growth in our model through inhibition of peroxynitrite formation and MMP-2 and MMP-9 activities.

Kurozu moromimatsu was active against Lovo cells in this study, but not against DLD-1 cells. Lovo and DLD-1 cells differ not only in the degree of cellular differentiation but also in the expression of furin, which contributes to MMP activation [15]. The former line originates from well-differentiated adenocarcinoma and expresses furin protein, whereas the latter originates from poorly differentiated adenocarcinoma and does not express furin protein. It would be worth examining whether MMP activity is reduced in the absence of furin.

Conclusion

The administration of Kurozu-M inhibited tumor growth in a Lovo cell–transplanted mouse model and also inhibited nitrotyrosine production and activation of MMP-2 and MMP-9.

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Intravenous injection of phagocytes transfected ex vivo with FGF4 DNA/ biodegradable gelatin complex promotes angiogenesis in a rat myocardial ischemia/reperfusion injury model

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Abstract Conventional gene therapies still present difficulties due to poor tissue-targeting, invasiveness of delivery, method, or the use of viral vectors. To establish the feasibility of using non-virally ex vivo transfected phagocytes to promote angiogenesis in ischemic myocardium, gene-transfection into isolated phagocytes was performed by culture with positively charged gelatin impregnated with plasmid DNA. A high rate of gene transfection was achieved in rat macrophages and human monocytes, but not in mouse fibroblasts. The efficiency was 68 ± 11 % in rat macrophages and 78 ± 8 % in human monocytes. Intravenously injected phagocytes accumulated predominantly in ischemic tissue (13 ± 8 %) and spleen (84 ± 6 %), but negligibly in other organs in rodents. The efficiency of accumulation in the target ischemic tissue reached more than 86 % on direct local tissue injection. In a rat model of myocardial ischemia-reperfusion, intravenous injection of fibroblast growth factor 4 (FGF4)-gene-transfected macrophages significantly increased regional blood flow in the ischemic myocardium (78 ± 7.1 % in terms of flow ratio of ischemic/non-ischemic myocardium) compared with intravenous administration of saline (36 ± 11 %) or non-transfected macrophages (42 ± 12 %), or intramuscular administration of naked DNA encoding FGF4 (75 ± 18 %). Enhanced angiogenesis in the ischemic tissue we confirmed histologically. Similarly, intravenous injection of FGF4-gene-transfected monocytes enhanced regional blood flow in an ischemic hindlimb model in mice (93 ± 22 %), being superior to the three other treatments described above (38 ± 12, 39 ± 15, and 55 ± 12 %, respectively).

Phagocytes transfected ex vivo with FGF4 DNA/gelatin promoted angiogenesis. This approach might have potential for non-viral angiogenic gene therapy.

Key words angiogenesis – cells – gene therapy – growth substances – ischemia

Abbreviations and acronyms

ANOVA = analysis of variance
FGF4 = fibroblast growth factor-4
GFP = green fluorescent protein
pI = isoelectric point

Introduction

Conventional gene therapies still require improvement with regard to transfection efficiency and safety [1, 2], as well as tissue targeting [3], despite recent advances. Achievement of a high transfection rate often requires a viral vector, but the safety of the viruses has not yet been

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established [4–6]. Conventional non-viral vectors seem to be inferior to viral ones in transfection efficiency, except for nucleofection [7, 8]. Conventional gene therapy using a viral vector can induce inflammation in the gene-transduced tissue [9]. Moreover, in vivo gene-delivery to the localized target tissue usually necessitates invasive approaches. For example, direct gene-transfection to cardiomyocytes requires surgical operation [10] or cardiac catheterization [11, 12]. On the other hand, ex vivo gene-transfection is less invasive, but tissue-targeting by intravenous injection is difficult to achieve [3].

Macrophages accumulate in ischemic tissue based on the mechanism of immune response (chemotaxis) [13]. This suggests that intravenous transplantation of macrophages may target the ischemic tissue in vivo. Tabata et al. previously reported that gelatin particles are phagocytized by macrophages [14, 15]. The isoelectric point (pI) of gelatin can be changed by modification of its residues, and positively charged gelatin can be impregnated with negatively charged substances [16] such as nucleic acid [17]. Thus, gelatin may be suitable as a vector for transfecting phagocytes ex vivo.

We describe here a study aimed at examining the feasibility of a new concept for less invasive, cell-based gene therapy, by means of ex vivo gene transfection into isolated phagocytes (macrophages and monocytes) using a non-viral vector, gelatin, followed by intravenous injection of the transfected phagocytes. The present method has significant advantages over conventional cell-based gene delivery [18, 19], in that the intravenously injected cells (phagocytes) not only produce protein from the transfected gene, but have a tissue-targeting ability.

Methods

This study was performed in accordance with the Guideline of Tokai University School of Medicine on Animal Use, which conforms to the NIH Guide for the Care and Use of Laboratory Animals (DHEW publication No. (NIH) 86-23, Revised 1985, Offices of Science and Health Reports, DRR/NIH, Bethesda, MD 20205).

Animals

A total of 121 Fisher rats (male, 10 weeks old, Clea Japan Inc., Tokyo) and 61 nude SCID mice (male, 6 weeks old, Shizuoka Animal Center, Shizuoka, Japan) were used. Rats were anesthetized by inhalation of diethyl ether for harvesting macrophages and with isofluren (1.5–3 %) for thoracotomy, after which they were mechanically ventilated with a mixture of oxygen and nitrous oxide. Mice were anesthetized by intraperitoneal injection of sodium pentobarbital (40 mg/kg).

A model of myocardial ischemia-reperfusion injury was prepared in 41 rats. The remaining 80 rats were used for collecting activated macrophages. The heart was exposed via thoracotomy, and the proximal left anterior descending coronary artery was ligated [20] for 180 min, followed by reperfusion. A model of hindlimb ischemia was prepared in 61 mice. The left femoral artery was ligated and resected [21].

Cells

Macrophages were obtained from 80 rats. Thioglycolate (4 %, 8 ml) was injected into the peritoneal cavity, and after 4 days, peritoneal macrophages were collected [22]. Monocytes were obtained from peripheral blood of healthy volunteers. Leukocyte-rich plasma was obtained by dextran 500 sedimentation and layered onto Nycoprep 1.068 (Nycomed, Birmingham, UK). The monocyte-containing layer was aspirated, washed twice and allowed to adhere to the dish for 90 minutes. Fibroblasts (NIH 3T3, Invitrogen Corporation, Carlsbad, CA) were also used. The cells were resuspended in RPMI 1640 medium (Sigma) containing 5 % heat-inactivated fetal calf serum and cultured for 7–14 days. The cell viability and type were determined by trypan blue exclusion and by immunostaining using anti-macrophage antibody up to 14 days.

Genes and vector

Complementary DNA (cDNA) of green fluorescent protein (GFP), Renilla luciferase or human hst1/FGF4 (FGF4) [17] was inserted into the expression vector pRC/CMV (Invitrogen Corporation, Carlsbad, CA) and the constructs were designated as pRC/CMV-GFP, pRC/CMV-luciferase and pRC/CMV-HST1-10, respectively. Preparation and purification of the plasmid from cultures of pRC/CMV-GFP-, pRC/CMV-luciferase-, or pRC/CMV-HST1-10-transformed *Escherichia coli* were performed by equilibrium centrifugation in cesium chloride-ethidium bromide gradients.

Gelatin was prepared from porcine skin [14]. After swelling in water the gelatin particles used in this study were spheroids with a diameter of approximately 5–30 μm, water content of 95 %, and pI of 11. Gelatin (2 mg) was incubated with 50 μg of the plasmid for 7 days at 4 °C to make a gelatin-DNA complex [14].

Experimental protocols

Ex vivo gene transfection Macrophages, monocytes, and fibroblasts (1×10^6) were cultured with the gelatin-DNA complex (2 mg of gelatin plus 50 μg of DNA) for 14 days on a culture dish (100 mm in diameter). Gene ex-

pression of GFP was evaluated by fluorescence microscopy and fluorescence-activated cell sorting. Luciferase activity in the cell lysate was evaluated with a photon counter system after cell lysis [23].

Organ distribution of phagocytes injected intravenously and directly into ischemic muscle To examine tissue-targeting by intravenous injection of transfected phagocytes, the distribution of the cells into organs was evaluated by immunohistochemistry. In the rat model of myocardial ischemia-reperfusion injury, the GFP-gene-transfected macrophages (1.0×10^6 each) were injected into the superficial dorsal vein of the penis at the initiation of reperfusion (n = 7 and 5, respectively). In the mouse model of hindlimb ischemia, the GFP-gene-transfected monocytes (1.0×10^6) were injected into the caudal vein 14 days after induction of ischemia (n = 5). To examine the tissue-targeting by direct local injection of transfected phagocytes, the distribution of the cells into organs was also evaluated. In the rat model of myocardial ischemia-reperfusion injury (n = 7) and the mouse model of hindlimb ischemia (n = 5), the same numbers of transfected macrophages and monocytes were directly injected into ischemic myocardium and ischemic skeletal muscle, respectively. Tissue samples were obtained 24 hours after cell administration. Each tissue was homogenized and cytospin was performed. Immunohistochemical analysis was done with anti-GFP antibody (CLONTECH, USA. GFP-monoclonal antibody). GFP positive macrophages were counted in each tissue and expressed as a percentage of total GFP-positive cells.

Amelioration of ischemia by intravenous injection of angiogenic gene-transfected phagocytes The angiogenic effect of intravenously injected FGF4-gene-transfected phagocytes on the ischemia models was evaluated. In the rat model of myocardial ischemia-reperfusion injury, FGF4-gene-transfected macrophages (n = 5), non-transfected macrophages (1.0×10^6 each) (n = 5), or saline (n = 5) were injected into the superficial dorsal vein of the penis, or naked FGF4-DNA (50 μg) was injected directly into the ischemic myocardium (n = 5), at the initiation of reperfusion. Fourteen days after the cell administration, blood flows in the ischemic and non-ischemic regions in the heart were evaluated with a non-contact laser Doppler flowmeter (FLO-N1, Omegawave Corporation). Then, tissue samples were obtained and histological analysis was performed. In a mouse model of hindlimb ischemia, just after induction of ischemia, FGF4-gene-transfected monocytes (n = 15), non-transfected monocytes (n = 8) (1.0×10^6 each), or saline (n = 10) were injected into the caudal vein, or naked FGF4-DNA (50 μg) was injected directly into the ischemic muscle (n = 12). Fourteen days after induction of ischemia, blood flows in the limbs were evaluated with the noncontact laser Doppler flowmeter (FLO-N1, Omegawave Corporation).

Histology

Ten micrometer sections were cut from formalin-fixed, paraffin-embedded tissue. Two sections were used for H.E. staining and azan staining, and eight sections were used for immunohistochemical staining. Immunohistochemical staining was performed by an indirect immunoperoxidase method. Anti-GFP antibody, anti-Mac1 antibody (BMA Biomedicals Ag, Switzerland), and anti-CD31 antibody (Serotec, UK) were used as primary antibodies. Mac1-antigen is specific to macrophages/monocytes. Anti-Ig, peroxidase-linked species-specific F(ab')2 fragments (Amersham Pharmacia Biotech UK Ltd., UK), were used as a secondary antibody. Double staining was performed with alkaline staining and peroxidase staining. The vessel density stained with von Willebrand factor-antibody was calculated by morphometric assessment in one 16 randomly selected fields of each heart and expressed as number/mm^2.

Statistical analysis

Data are presented as mean values ± SD. Differences were assessed by using ANOVA (analysis of variance) with the Scheffe's multiple comparisons test. A value of $P < 0.05$ was considered statistically significant.

Results

Ex vivo gene transfection

We studied whether genes could be transfected into isolated rat macrophages, human monocytes, and mouse fibroblasts ex vivo by using gelatin. Transfection of the GFP gene into isolated rat macrophages (Figs. 1A and B) and human monocytes (Figs. 1C and D), but not into mouse fibroblasts (data not shown), was achieved by culture with gelatin-DNA complex for 14 days. The gene transfection efficiency into rat macrophages was 68 ± 11 % (30 experiments, Fig. 2A) and that into human monocytes was 78 ± 8 % (30 experiments) as determined with a fluorescence activated cell sorter. Sequential analysis after luciferase-gene transfection into rat macrophages revealed high expression after 14 days of culture (Fig. 2B).

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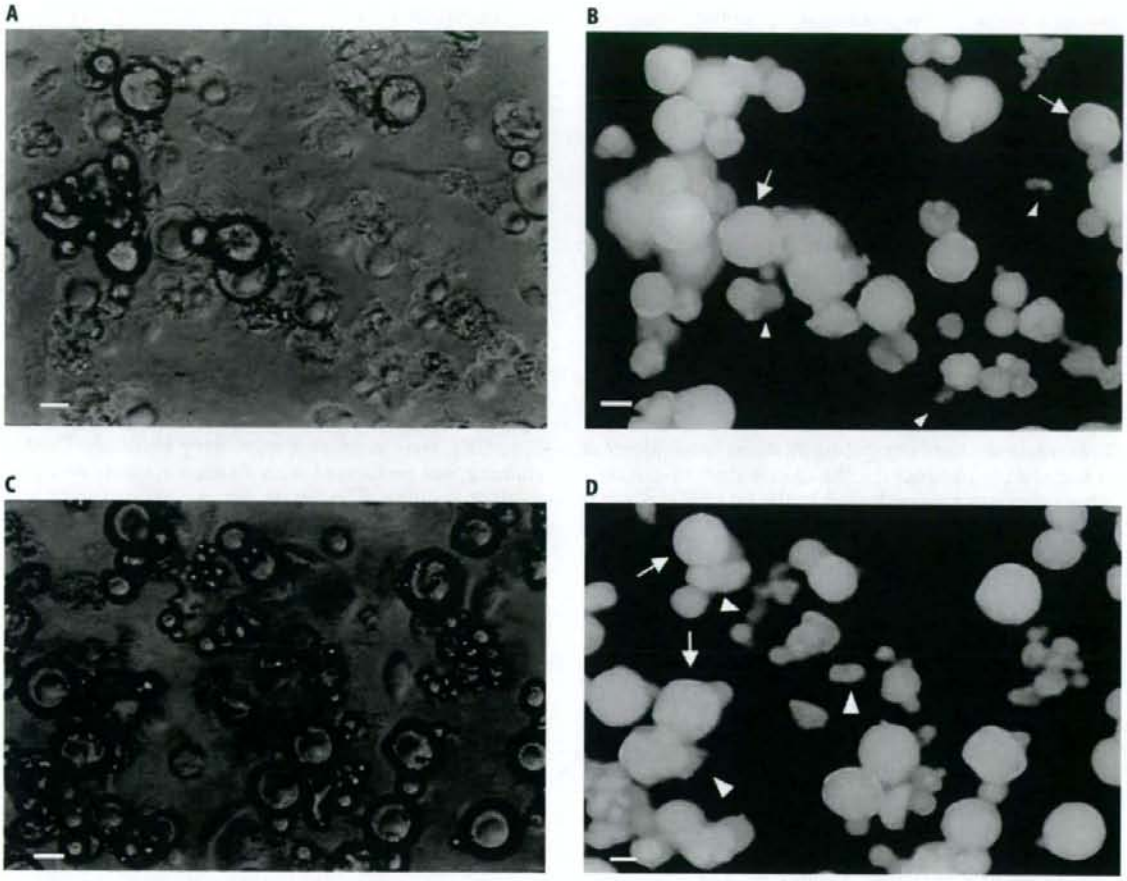

Fig. 1 Fluorescent presentation of ex vivo gene transfection with gelatin-DNA complex in macrophages/monocytes as well as fibroblasts. Rat macrophages (**A** and **B**) and human monocytes (**C** and **D**) were cultured with gelatin-GFP-gene complex for 14 days. Transmittance microscopic images (**A** and **C**) and fluorescence images (**B** and **D**) of the cells are shown. Macrophages (**B**) and monocytes (**D**) show fluorescence due to GFP. Arrowheads indicate GFP-expressing cells. Arrows indicate gelatin particles themselves. Bars = 20 μm

Organ distribution of phagocytes injected intravenously or directly into ischemic muscle

We studied quantitatively whether intravenously injected luciferase-gene-transfected phagocytes could target ischemic tissues (the third and fifth columns from the left in Table 1). In non-ischemic rats, the injected macrophages were recognized almost exclusively in the spleen (98 ± 4 %) (n = 7, the second column in Table 1). In non-ischemic mice, similar results were observed (n = 7, data not shown). In a rat with myocardial ischemia-reperfusion injury, some of the intravenously injected macrophages were incorporated into the heart (the third column in Table 1). The incorporation into the post-ischemic pericardium amounted to 13 ± 6 % (n = 7) (non-ischemic rats 0 ± 0 %, n = 7, Table 1). The incorporated cells expressed GFP (Fig. 3). Fibrosis with inflammatory infiltrates was recognized in the anterior wall of the left ventricle, extending to the interventricular septum (Figs. 3A and B). These infiltrates were mainly polymorphonuclear leukocytes and macrophages (Figs. 3C and D). Approximately 20 % of the macrophages showed GFP-positivity in this area (Figs. 3E and F). Similar tissue-targeting by intravenously injected monocytes was confirmed in a mouse model with hindlimb ischemia (13 ± 7 %, n = 7, the fifth column in Table 1). Furthermore, we studied whether local intramuscular injection increased the degree of tissue targeting (the fourth and sixth columns from the left in Table 1). After direct injection of phagocytes into ischemic muscle, 86 ± 10 % and 88 ± 6 % of the cells remained in the target tissue in the two models. Thirteen and 11 % of phagocytes in-

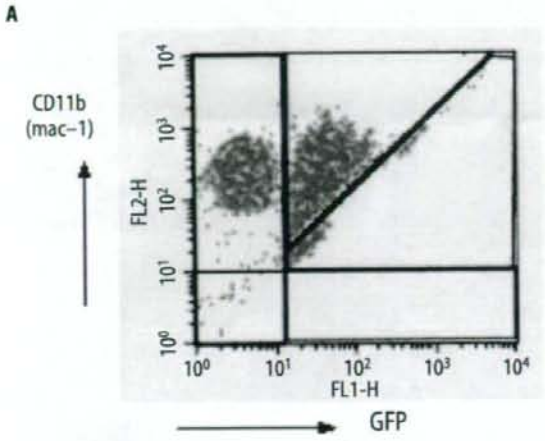

Fig. 2 Quantitative assessment of gene transfection into rat macrophages. (**A**) Fluorescence-activated cell sorting analysis of transfected macrophages done on day 14 of culture with reference to GFP-positive and Mac1-positive cells. (**B**) Sequential changes of luciferase activity in cultured macrophages in the presence of luciferase-gene-gelatin complex. Values are mean ± SD. The number of experiments is shown in parentheses

jected into the cardiac or hindlimb muscle migrated to the spleen. In the other organs, accumulation of phagocytes were negligible.

Amelioration of ischemia by intravenously injected angiogenic-gene-transfected phagocytes

In the rat model with myocardial ischemia-reperfusion injury, we studied the angiogenic effect of intravenously injected macrophages transfected with fibroblast growth factor 4 (FGF4) gene by using gelatin. Intravenous injection of these macrophages (1.0×10^6) significantly increased the regional blood flow in the ischemic myocardium (78 ± 7.1 %, n = 8, in terms of flow ratio of ischemic/non-ischemic myocardium) compared with the other three treatments ($P < 0.05$, ANOVA), that is, intravenous administration of saline (35 ± 10 %, n = 8), intramuscular administration of naked DNA encoding FGF4 (50 μg, direct intramyocardial injection after thoracotomy) (58 ± 5.3 %, n = 8), and intravenous administration of the same number of non-transfected macrophages (42 ± 12 %, n = 8) (Fig. 4A). Histological analyses revealed angiogenesis in the ischemic tissue after the administration of transfected cells (Figs. 4B and C). Similar results were observed in the mouse model with hindlimb ischemia. Intravenous injection of FGF4-gene-transfected monocytes (1.0×10^6) enhanced regional blood flow in the ischemic leg (Fig. 4D). The increase of blood flow in the mice with transfected monocytes (93 ± 22 % in terms of flow ratio of ischemic/non-ischemic leg) was significantly larger than those obtained with the other three treatments described above (38 ± 12, 55 ± 12, and 39 ± 15 %, $P < 0.05$, ANOVA). Neither lymph node swelling in any part of the body nor pathologic change in the spleen or lung, such as angioma or abnormal immune response, was found in any of the animals.

Table 1 Organ distribution of phagocytes injected into the vein and into local tissue

Organ	Normal i.v. (7 rats)	Myocardial injury i.v. (7 rats)	Myocardial injury i.m. (7 rats)	Hindlimb ischemia i.v. (7 mice)	Hindlimb ischemia i.m. (7 mice)
Heart	0 ± 0	13 ± 6	86 ± 10	0 ± 0	0 ± 0
Hindlimb muscle	0 ± 0	0 ± 0	0 ± 0	13 ± 7	88 ± 6
Spleen	98 ± 4	84 ± 6	13 ± 10	84 ± 6	11 ± 6
Lung	1 ± 2	1 ± 1	1 ± 2	1 ± 2	1 ± 1
Liver	1 ± 2	1 ± 1	1 ± 1	1 ± 2	1 ± 1
Brain	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Kidney	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Intestine	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0

Each value shows a distribution ratio (%) into organs of transfected macrophages/monocytes (mean ± SD). *i.v.* intravenous injection into the vein; *i.m.* direct injection into the jeopardized muscle

Discussion

The advantages of the present method are as follows. First, genes can easily be transfected into phagocytes (macrophages/monocytes). In preliminary experiments, we found that genes can also be transfected into endothelial progenitor cells [25]. Compared with other transfection method, the transfection efficiency was high (68 ± 11 %) and it is not necessary to use a potentially hazardous viral vector [2, 26, 32]. Second, the phagocytes can target the pathologic tissues by chemotaxis even after intravenous injection, and higher tar-

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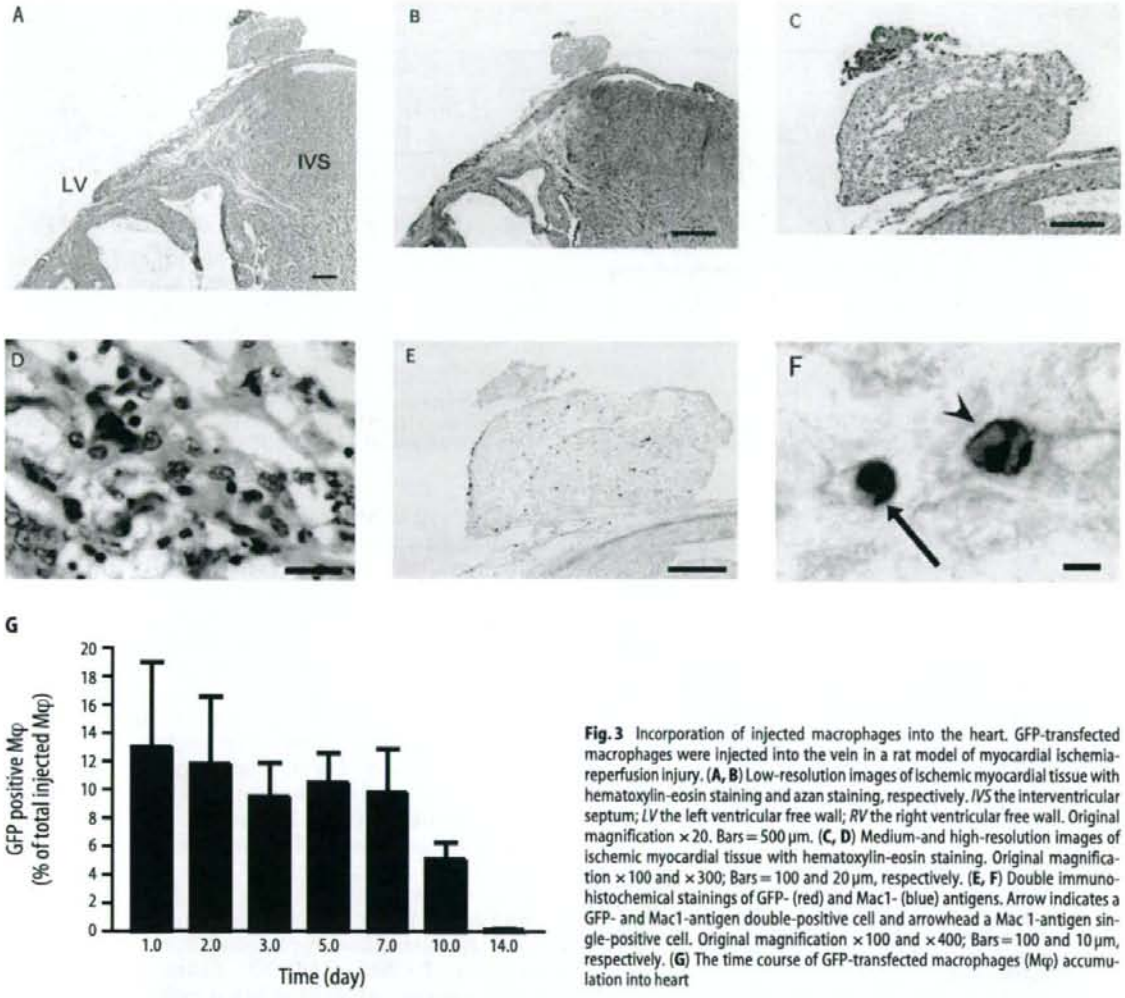

Fig. 3 Incorporation of injected macrophages into the heart. GFP-transfected macrophages were injected into the vein in a rat model of myocardial ischemia-reperfusion injury. (**A, B**) Low-resolution images of ischemic myocardial tissue with hematoxylin-eosin staining and azan staining, respectively. *IVS* the interventricular septum; *LV* the left ventricular free wall; *RV* the right ventricular free wall. Original magnification ×20. Bars = 500 μm. (**C, D**) Medium-and high-resolution images of ischemic myocardial tissue with hematoxylin-eosin staining. Original magnification ×100 and ×300; Bars = 100 and 20 μm, respectively. (**E, F**) Double immunohistochemical stainings of GFP- (red) and Mac1- (blue) antigens. Arrow indicates a GFP- and Mac1-antigen double-positive cell and arrowhead a Mac 1-antigen single-positive cell. Original magnification ×100 and ×400; Bars = 100 and 10 μm, respectively. (**G**) The time course of GFP-transfected macrophages (Mφ) accumulation into heart

geting is available if they are administered locally. The injection is repeatable. We confirmed that the angiogenic gene-transfected phagocytes enhanced angiogenesis after ischemia-reperfusion injury in rat heart and ameliorated ischemia in a mouse hindlimb model.

The injected phagocytes migrated into pathologic tissues, presumably in response to the release of cytokines such as monocyte chemoattractant protein 1 by injured endothelial cells [27]. Adhesion molecules such as P-selectin [28] are probably involved in the recruitment of phagocytes to the vessel wall. The injected phagocytes also migrated to the spleen, but no pathologic change was found in the spleen.

The present method has several advantages over conventional methods of cell-based gene therapy such as fibroblast-based and smooth muscle cell-based approaches [18, 19, 33, 34]. For example, monocytes do not aggregate in vessels, while fibroblasts or smooth muscle cells cannot be injected intravenously because of aggregation. The transfected phagocytes not only synthesize protein from the transfected gene, but also are partially targeted to the impaired tissue. In addition, the transfection rate was better than those of methods such as lipofection, viral vectors and electroporation [26, 29]. The newly developed technique of nucleofection has a transfection efficiency of 40–70 % [30], which is similar to that of our method, but our procedure is easier to use [30, 31]. Further, the therapeutic effect obtained here was superior to that of conventional gene therapy which we reported previously, i.e., intramuscular injection of

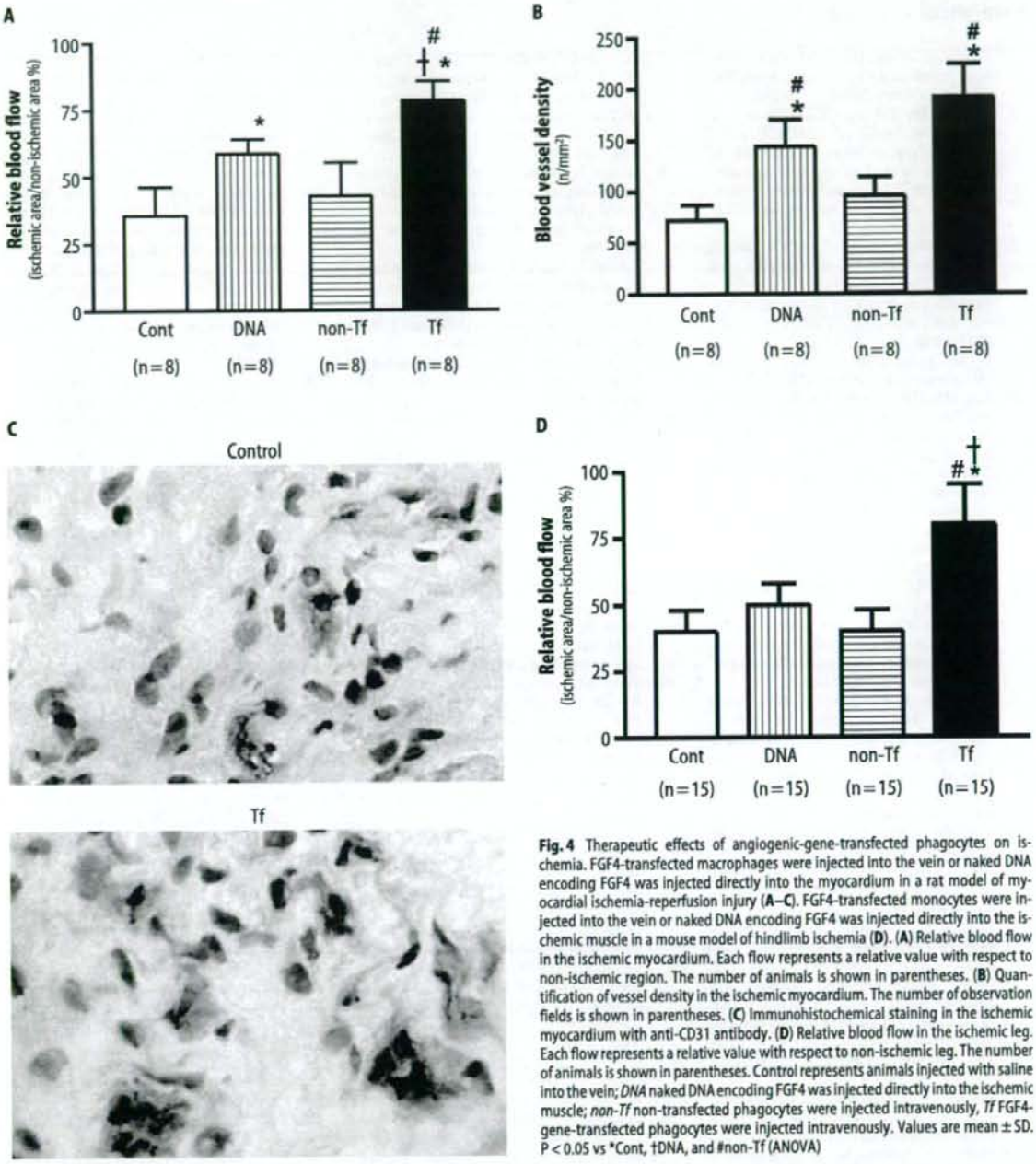

Fig. 4 Therapeutic effects of angiogenic-gene-transfected phagocytes on ischemia. FGF4-transfected macrophages were injected into the vein or naked DNA encoding FGF4 was injected directly into the myocardium in a rat model of myocardial ischemia-reperfusion injury (**A–C**). FGF4-transfected monocytes were injected into the vein or naked DNA encoding FGF4 was injected directly into the ischemic muscle in a mouse model of hindlimb ischemia (**D**). (**A**) Relative blood flow in the ischemic myocardium. Each flow represents a relative value with respect to non-ischemic region. The number of animals is shown in parentheses. (**B**) Quantification of vessel density in the ischemic myocardium. The number of observation fields is shown in parentheses. (**C**) Immunohistochemical staining in the ischemic myocardium with anti-CD31 antibody. (**D**) Relative blood flow in the ischemic leg. Each flow represents a relative value with respect to non-ischemic leg. The number of animals is shown in parentheses. Control represents animals injected with saline into the vein; *DNA* naked DNA encoding FGF4 was injected directly into the ischemic muscle; *non-Tf* non-transfected phagocytes were injected intravenously, *Tf* FGF4-gene-transfected phagocytes were injected intravenously. Values are mean ± SD. $P < 0.05$ vs *Cont, †DNA, and #non-Tf (ANOVA)

naked DNA, in ischemia models of heart and leg [17]. The major disadvantage of our method is the cell preparation time of 2 weeks before therapy can be started, and further work is needed to speed up this process.

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Crystal structures of catrocollastatin/VAP2B reveal a dynamic, modular architecture of ADAM/adamalysin/reprolysin family proteins

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Abstract Catrocollastatin/vascular apoptosis-inducing protein (VAP)2B is a metalloproteinase from *Crotalus atrox* venom, possessing metalloproteinase/disintegrin/cysteine-rich (MDC) domains that bear the typical domain architecture of a disintegrin and metalloproteinase (ADAM)/adamalysin/reprolysin family proteins. Here we describe crystal structures of catrocollastatin/VAP2B in three different crystal forms, representing the first reported crystal structures of a member of the monomeric class of this family of proteins. The overall structures show good agreement with both monomers of atypical homodimeric VAP1. Comparison of the six catrocollastatin/VAP2B monomer structures and the structures of VAP1 reveals a dynamic, modular architecture that may be important for the functions of ADAM/adamalysin/reprolysin family proteins.

Keywords: ADAM; Adamalysin; Reprolysin; MDC protein; Metalloproteinase disintegrin; Apoptotic toxin

1. Introduction

Hemorrhagic snake venoms induce local and systemic hemorrhaging by disrupting the walls of the blood vessels in envenomed patients [1]. In vitro, they induce apoptosis specifically in cultured vascular endothelial cells [2]. Vascular apoptosis-inducing protein (VAP)1 and VAP2 were originally isolated from *Crotalus atrox* venom [3,4], and similar apoptotic toxins have been isolated from other snake venoms [5–7]. VAP1 is a disulfide-bridged homodimeric protein with an apparent molecular weight of 110 kDa, and an isoelectric point of 8.5. VAP2 is a single chain protein with a MW of 55 kDa and an isoelectric point of 4.5 [3,4,8]. VAPs are members of the P-III class of snake venom metalloproteinases (SVMPs), possessing a metalloproteinase/disintegrin/cysteine-rich (MDC) domain architecture typical of a disintegrin and metalloproteinase (ADAM)/adamalysin/reprolysin family proteins [9,10]. VAP-induced apoptosis is dependent on its catalytic activity [8], is inhibited by antibodies to integrins α3, α6, β1 and CD9 [11], and involves activation of specific caspases [12]. However, the physiological targets of VAPs and the underlying mechanism of VAP-induced apoptosis remain elusive.

ADAMs are a family of mammalian membrane-anchored glycoproteins that have been implicated in the processing of cell surface and extracellular matrix proteins [13,14]. The crystal structures of several P-I class SVMPs, which contain only a metalloproteinase (M)-domain, and the isolated M and disintegrin/cysteine-rich (DC) domains of ADAMs have been determined [15–18]. However, structures of ADAM/adamalysin/reprolysin family proteins that include the entire MDC domain have not been determined. The relevance of the multidomain structure to the catalytic and adhesive functions of this family of proteins is an important issue that remains to be elucidated. To better understand the structure–function relationship of ADAM/adamalysin/reprolysin family proteins, and how it relates to the molecular mechanism of VAP-induced apoptosis, we have been engaged in crystallographic studies of VAPs. Recently, we determined the crystal structure of VAP1, revealing the MDC domain architecture for the first time [19]. Although the intrinsic two-fold symmetry of atypical homodimeric VAP1 conferred a great advantage for both its crystallization and structural resolution, the possibility remained that the spatial arrangement of the MDC domains of VAP1 differed from that of monomeric SVMPs and ADAMs, due to crystallographic restraints imposed on the molecule. The majority of ADAMs and SVMPs do not to form VAP1-type dimers, most likely due to the lack of a consensus QDHSK sequence [19] (residues 320–324 in VAP1, in which the Nζ atom of Lys324 is coordinated by the six oxygen atoms of another monomer and plays a pivotal role in dimer formation), and Cys365, which are conserved among the dimeric SVMPs (Supplementary Fig. 1). Therefore, to elucidate the general architecture of proteins of the ADAM/adamalysin/reprolysin family, we crystallized VAP2 and determined its structure. We modeled all of the structures as monomers of VAP2B, which is identical to catrocollastatin, a protein previously isolated as a platelet aggregation inhibitor [20]. Here we describe the structure of catrocollastain/VAP2B, as determined in three different crystal forms. These are the first reported crystal structures of the monomeric class of proteins in ADAM/adamalysin/reprolysin family.

2. Materials and methods

Protein preparation and crystallization were performed as previously described [21]. The diffraction data sets were collected at the

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Abbreviations: ADAM, a disintegrin and metalloproteinase; MDC, Metalloproteinase/disintegrin/cysteine-rich; SVMP, Snake venom metalloproteinase; HVR, Hyper-variable-region; ncs, Non-crystallographic symmetry; VAP, Vascular apoptosis-inducing protein; PEG, Polyethyleneglycol

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SPring-8 beamline BL41XU using the ADSC quantum 315 CCD detector with a wavelength of 1.0 Å at 100 K. Images were reduced using HKL2000 [22] (Table 1). Structures were solved using the molecular replacement (MR) method and the MOLREP program of the CCP4 suite [23], with the structure of VAP1 (2ERO) as a starting model. The M- and C-domains of the VAP1 were used separately as the search models. An MR solution was initially obtained from the Form 2-2 crystal data set, which assumed two M-domains and two C-domains in the asymmetric units. After the model was manually rebuilt using TURBO-FRODO [24], it was subjected to torsional molecular dynamic refinements using CNS [25]. Iterative refinements and manual rebuilding of the model improved the electron-density map and enabled us to model the remaining part of the molecule. The composite omit electron-density maps created by CNS were used to confirm the chain tracing. After the polypeptide chains were modeled, we modeled zinc and calcium ions and the inhibitor GM6001 (3-(*N*-hydroxycarboxamide)-2-isobutyl-propanoyl-Trp-methylamide), then the components of the carbohydrate chain linked to Asn371.

The two monoclinic crystal structures were solved by MR with the domains of the refined Form 2-2 crystal structure as a starting model. In all three crystal forms, the asymmetric unit contained two monomers of catrocollastatin/VAP2B. Refinement statistics are shown in Table 1. During the course of our analysis, we found a point mutation (F203V) in the crystallized specimens. By comparing the structures with that of VAP1, which has a phenylalanine at this position, we determined that this mutation does not introduce a large structural change or affect the flexibility of the molecule. Graphical representations were prepared using the programs TURBO-FRODO [24], MOLSCRIPT [26], RASTER3D [27] and PyMOL [28].

3. Results and discussion

3.1. Structural determination

Purified VAP2 was crystallized in variety of forms [21]. In the current study, we determined the structures of three of these crystal forms. Previously, we observed that the VAP2 preparation is a mixture of two homologous polypeptide chains, VAP2A and VAP2B [29]. To identify the molecules in the crystals as either VAP2A or catrocollastatin/VAP2B, we carefully analyzed the composite omit electron-density maps corresponding to the 11 amino acid residues that are distinct between the two proteins (Supplementary Fig. 1). Based on this assessment, the major component in the three crystals was determined to be catrocollastain/VAP2B. Therefore, in the present study, we modeled all six molecules as catrocollastain/VAP2B. The indole ring of GM6001 provided additional

Table 1
Data collection and refinement statistics

	Form 2-1	Form 2-2	Form 2-5
Data collection			
Space group	$P2_1$	$P2_12_12_1$	$C2$
Cell dimensions			
a, b, c (Å)	56.9, 138.0, 59.2	57.7, 118.2, 138.5	220.7, 79.5, 58.7
α, β, γ (°)	90, 91.5, 90	90, 90, 90	90, 91.7, 90
Resolution (Å) (high resolution shell)	50–2.15(2.23–2.15)	50–2.50(2.59–2.50)	50–2.70(2.80–2.70)
No. of unique reflections	48664(4428)	33288(2925)	26911(2313)
[a]R_{merge}	0.081(0.196)	0.089(0.321)	0.085(0.231)
$I/\sigma(I)$	9.8(4.6)	10.3(3.7)	10.1(5.5)
Completeness (%)	98.1(89.5)	98.6(88.4)	95.9(82.5)
Redundancy	3.3(2.0)	6.5(3.3)	3.4(2.8)
Refinement			
Resolution (Å) (high resolution shell)	50–2.15(2.23–2.15)	50–2.50(2.59–2.50)	50–2.70(2.80–2.70)
No. of reflections	48628(4386)	33099(2922)	26907(2276)
[b]R_{work}	0.175(0.195)	0.227(0.316)	0.199(0.264)
[c]R_{free}	0.228(0.277)	0.286(0.399)	0.260(0.328)
Average B-factors (No. of atoms)			
All atoms	19.9(7292)	38.5(6801)	25.1(6823)
Protein	18.5(6422)	38.1(6438)	24.7(6438)
Main chain atoms	17.2	36.9	23.1
Side chain atoms	19.9	39.5	26.5
Zn^{2+}	13.6(2)	24.9(2)	18.7(2)
Ca^{2+}	14.6(6)	41.4(6)	21.5(6)
Carbohydrate	54.2(139)	81.4(88)	37.4(226)
GM6001	16.2(56)	36.9(56)	0(-)
Water	26.5(668)	31.6(211)	22.2(151)
R.m.s deviations			
Bond lengths (Å)	0.0047	0.0065	0.0045
Bond angles (°)	1.20	1.44	1.14
Ramachandran plot			
Most favored	87.2%	84.3%	82.8%
Additional allowed	12.1%	15.0%	16.4%
Generously allowed	0.4%	0.6%	0.4%
Disallowed	0.1%(R297B)	0.1%(R297B)	0.3%(R297A/R297B)

[a]$R_{merge} = \Sigma_{hkl}\Sigma_i \mid I_i(hkl) - \langle I(hlk)\rangle|/\Sigma_{hkl}\Sigma_i I_i(hkl)$, where $I_i(hkl)$ is the ith intensity measurement of reflection hkl and $\langle I(hlk)\rangle$ is its average.
[b]$R_{work} = \sum||F_{obs}| - |F_{calc}||/\sum|F_{obs}|$.
[c]R_{free} = R-value for a randomly selected subset (5%) of the data that were not used for minimization of the crystallographic residual. A single crystal was used for measurement of each data set.

crystal contacts for the neighboring molecule, resulting in crystals that were distinct from the inhibitor-free form.

3.2. Overall structure

The overall structure of catrocollastatin/VAP2B is presented in Fig. 1. The structure of the M-domain was very similar to the corresponding structures in adamalysin II [15] and ADAM33 [17], with a flat elliptical shape and a core formed by a five-stranded β-sheet and four α-helices. A conserved methionine (Met357, Met-turn) was present downstream of the consensus HEXXHXXGXXHD sequence, which contains three histidines (His333, His337 and His343) that function as ligands of the catalytic zinc atom, and a glutamate residue (Glu334) that functions as the general base (Fig. 2). These structural features are typical of the metzincine family of metalloproteinases [30,31]. A bound calcium ion was identified opposite the active site cleft and close to the crossover point of the N- and C-terminal segments of the M-domain (Ca^{2+}-binding site I), as in the structures of adamalysin II [15] and ADAM33 [17]. The M-domain is followed by the D-domain, which can be sub-divided into "shoulder" (D_s) and "arm" (D_a) segments. D_s protrudes from the M-domain close to Ca^{2+}-binding site I, opposing the catalytic zinc atom. The C-domain is sub-divided into "wrist" (C_w) and "hand" (C_h) segments. Because of its curved structure, with the concave surface toward the M-domain, the distal portion of C_h comes close to and faces the catalytic site, thus the entire molecule adopts a C-shaped conformation. In the D_s and D_a segments, there are Ca^{2+} ions (sites II and III, respectively) that stabilize the structure. Details of the Ca^{2+}-coordinations are shown in Supplementary Fig. 2. The distal portion of the C-shape, spanning residues 561–582 of the C_h domain, is the region in which the amino acid sequence is most divergent and variable in length among ADAM/adamalysin/reprolysin family proteins (Fig. 2 and Supplementary Fig. 1). We designated this region as the hyper-variable-region (HVR), and have proposed that it represents a potential exosite for target recognition [19]. Aside from Cys377, whose side chain is embedded in the hydrophobic core, all 34 cysteinyl residues are involved in disulfide bonding. The number and spacing of cysteinyl residues, and the structures of the Ca^{2+}-binding sites are strictly conserved among ADAM/adamalysin/reprolysin family proteins (Fig. 2 and Supplementary Fig. 1). Fig. 2 shows the sequence alignment of a selected subset of ADAMs and SVMPs; alignment of the full sequences of catrocollastatin/VAP2B and 107 proteins of the ADAM/adamalysin/reprolysin family can be found in Supplementary Fig. 1.

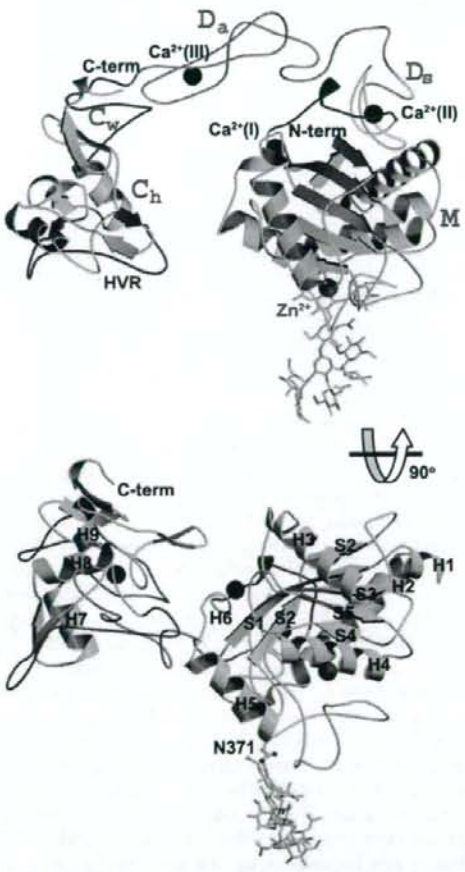

Fig. 1. Ribbon diagrams of catrocollastatin/VAP2B. The M-domain, linker, D_s, D_a, C_w, and C_h segments and the HVRs are shown in red, yellow, grey, cyan, pink, grey, green and blue, respectively. Zinc and calcium ions are represented as red and black spheres, respectively. The carbohydrate moiety linked to Asn371 is shown as a stick representation.

3.3. Flexible modular architecture

The structures of the M-domain (Fig. 3A), D_s (Fig. 3C), and C_w/C_h (Fig. 3B) of the six catrocollastatin/VAP2B molecules were nearly identical (r.m.s.d of 0.33, 0.45 and 0.59 Å, respectively). They were also essentially the same as the corresponding regions of VAP1 (r.m.s.d of 0.78, 0.63 and 1.1 Å, respectively (Fig. 3A–C)). However, the relative orientations of the sub-domains were quite variable. The largest difference was observed when the M domains of the six catrocollastatin/VAP2B molecules are superimposed. The $D_s/D_a/C_w/C_h$ portion should be rotated by approximately 13° relative to the M-domain, bringing about a 15-Å displacement at the distal end of C_h (Fig. 3A). A similar plot of the C_h segments superimposed shows less hinge bending, bringing approximately a 6-Å displacement at the distal portion of D_s (Fig. 3B). This conformed that the hinge motion occurs largely between the M domain and D_s. The bending of the main chain at two residues, Val403 and Gly438, is most prominent (Fig. 3C), however, the entire linker region (which is defined by the segment between two structural Ca^{2+}-binding sites, I and II) also moves in concert with the bending motion of Val403 (Fig. 3D). In this concerted movement of the linker, the side chain of Leu408 in D_s is positioned at a pivotal point (Fig. 3D and E). The main chain carbonyl oxygen atom of Leu408 coordinates the calcium ion at site II, whereas, the side-chain of Leu408 protrudes from D_s and interacts with a small hydrophobic cavity on the surface of the M domain (Fig. 3D). A balky hydrophobic residue (Leu or Phe or Tyr) at this position is highly conserved among ADAM/adamalysin/reprolysin family proteins (Supplementary Fig. 1), and its side chain probably functions as

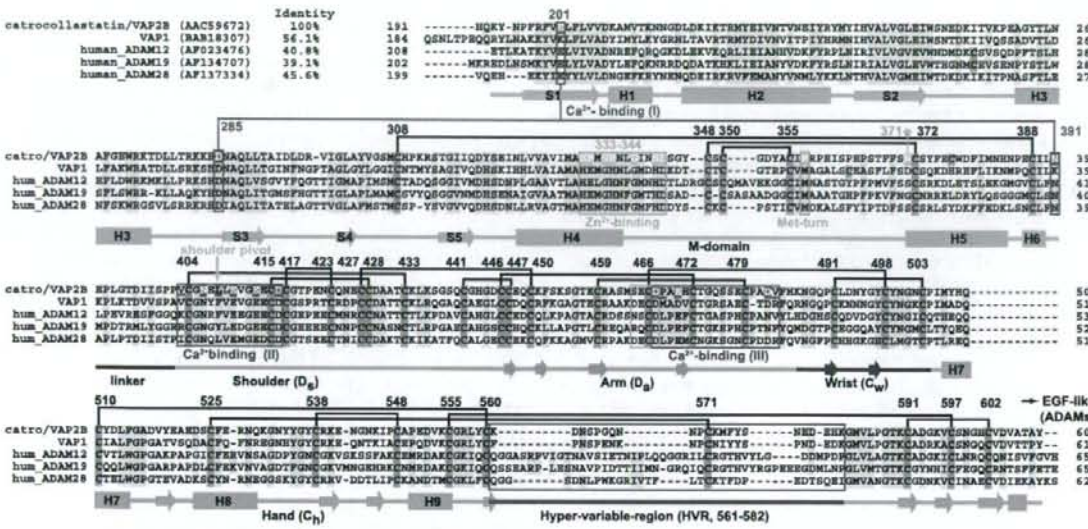

Fig. 2. Sequence alignment of catrocollastatin/VAP2B, VAP1 and human ADAMs. The cysteinyl residues and the conserved residues are shaded in pink and yellow, respectively. Disulfide bridges, secondary structures and domains are drawn schematically. The HVR, Ca^{2+}-binding sites, Zn^{2+}-binding site and disintegrin-loop are boxed in blue, red, green and cyan, respectively. The Ca^{2+}-coordinating residues are shaded in red.

a universal joint (shoulder joint) that allows D_s to adopt various orientations with respect to the M domain. The linker has fewer specific interactions with D_s and has a rather high B-factor (Supplementary Figs. 3 and 4). It is divergent and variable in length (7–12 aa), particularly in human ADAMs (Supplementary Fig. 1), thus may function primarily in connecting D_s to the M domain. The linker may also restrict the mobility of the shoulder joint, and thus determine the preferred orientation of the M domain of each ADAMs relative to the rest of the molecule for distinct targets. The residues forming the hydrophobic cavity with which Leu408 interacts are less conserved and also have relatively high B-factors (Supplementary Figs. 3 and 4). Thus they may also contribute to the flexibility of the shoulder joint.

Previously, we suggested a putative mechanism of HVR-mediated target recognition and catalysis by this family of proteins [19]. The present study allows us to incorporate into the previous model that intrinsic flexibility may be important for fine-tuning substrate recognition, by adjusting the spatial alignment of the catalytic and adhesion sites during the catalytic cycle (Fig. 3F). The structure of the lower half of the D_a segment in catrocollastatin/VAP2B was different from that of VAP1 (Fig. 3B and Supplementary Fig. 3C), most likely due to the substitution of Glu470 (in catrocollastain/VAP2B) with Asp471 (in VAP1), and the insertion of Pro480 (in catrocollastain/VAP2B). All the ADAMs, with the exception of ADAMs 10 and 17, which lack Ca^{2+}-binding site III, and the monomeric P-III and P-IV SVMPs contain Glu470 and Pro480 (see Supplementary Fig. 1). Thus, it is likely that they adopt a more catrocollastatin/VAP2B-like structure. As was observed in VAP1, the disintegrin-loop is packed by C_w, and forms a less flexible D_a/C_w junction, and therefore is unavailable for ligand binding. Differences in the orientation of D_a and C_w among these proteins may be important for proper spatial alignment of the catalytic and adhesion units and for substrate binding specificity. The angle between C_w and C_h in catrocollastatin/VAP2B was nearly invariant. It was essentially the same as that seen in VAP1 (Fig. 3B), but substantially different than that of ADAM10 [18,19]. Whether different ADAM/adamalysin/reprolysin family proteins have distinct C_w/C_h orientations remains to be established.

3.4. Modular architecture and post-translational processing

The disintegrins that are commonly found in Viperid venoms are typically generated by proteolytic processing of larger precursor molecules, the P-II class of SVMPs, which contain an M-domain plus a disintegrin portion [32,33]. The flexible modular structure described above points to a potential mechanism of selection of cleavage sites for this processing event. The cleavage sites of the medium-sized disintegrins (~70 amino acids) are usually within Ca^{2+}-binding site II, whereas, those of the shorter ones (41–51 residues) are at the boundary between D_s and D_a. The longer disintegrins (~84 residues) are processed within the linker between M and D_s (Fig. 4 and Supplementary Fig. 1). Most of the P-II SVMPs have fewer cysteine residues within their D_s segment (3 or 5 cysteine residues, see Supplementary Fig. 1) compared to P-III SVMPs, and thus have fewer disulfide bonds. Additionally, they contain substitutions of the calcium-binding residues at site II, indicating that they have a less stable D_s structure compared to P-III SVMPs. Long disintegrins have the same number of cysteine residues (7 cysteine residues) and Ca^{2+}-binding residues at site II as P-III SVMPs and ADAMs, and thus would be predicted to have a more stable D_s structure, which may account for their cleavage at the linker between M and D_s. A protective role for calcium against auto proteolysis in the linker region has been reported [34], and the linker region is usually removed from P-I SVMPs post-translationally [35]. Collectively, these observations suggest that differential susceptibility to proteolysis in the linker region and D_s, due to variability in the number of disulfide bonds and the presence or absence of bound calcium at site II, may underlie the

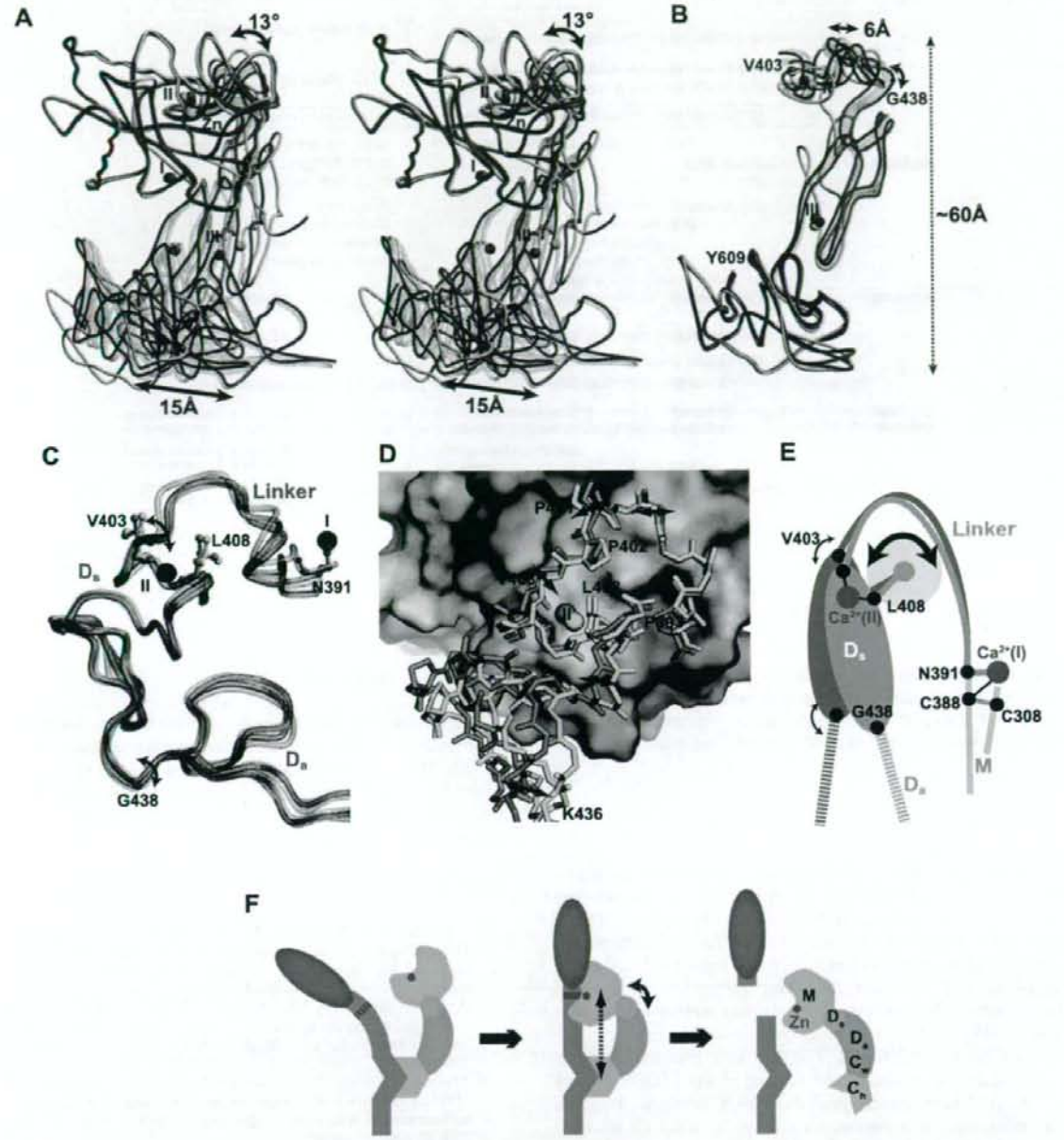

Fig. 3. Mobility of the sub-domains. (A) The M-domains of the six catrocollastatin/VAP2B molecules and the VAP1 monomer were superimposed and are shown in stereo. Two representative catrocollastatin/VAP2B molecules are shown in blue and red, the other four catrocollastatin/VAP2B molecules are in gray, and the VAP1 monomer is in green. The zinc ion is shown as a yellow sphere. The calcium atoms bound to the red and blue catrocollastatin/VAP2B molecule and VAP1 are shown as red, blue and green spheres, respectively. Superimposition of the D_b and C_a segments of the six catrocollastatin/VAP2B molecules and the VAP1 monomer are shown in B and C, respectively. (D) Close-up view of the shoulder joint. The molecular surface of the M-domain is colored according to the electrochemical surface potential (red to blue). The linker and part of the D_a segment of the two representative catrocollastatin/VAP2B molecules are shown as stick representations in pink and cyan, respectively. (E) Schematic diagram of the hinge motion at the shoulder joint. (F) Schematic model of substrate recognition and cleavage by a soluble ADAM/adamalysin/reprolysin protein.

generation of disintegrins with different lengths. Fertilin α (ADAM1) and β (ADAM2) undergo proteolytic processing within Ca^{2+}-binding site III and the linker region, respectively at different stages of sperm maturation (Fig. 4, Supplementary Fig. 1) [36,37]. The current structural data suggests that Ca^{2+}-binding, together with a flexible modular structure, may also

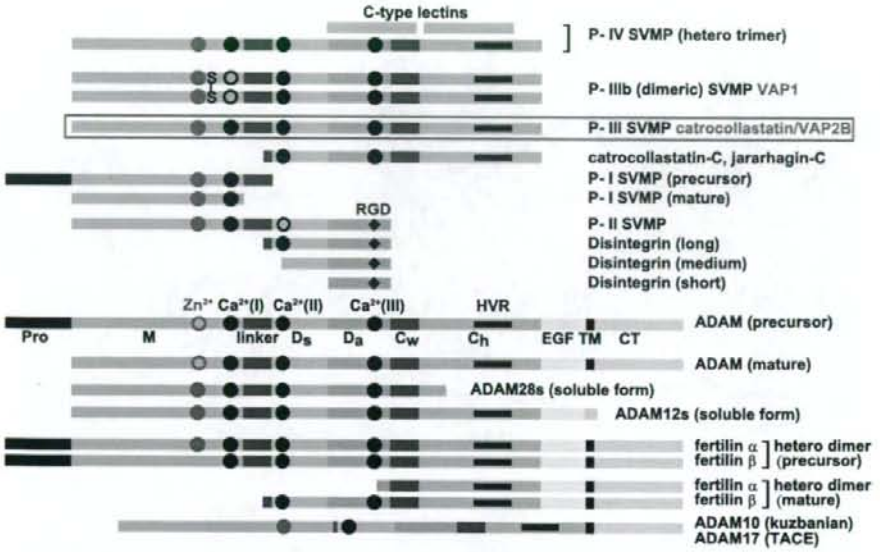

Fig. 4. Schematic representation of the modular architecture of ADAM/adamalysin/reprolysin family proteins. Each sub-domain is colored as for Fig. 1; the pro-domain (Pro), EGF-like domain (EGF), transmembrane region (TM) and cytoplasmic domain (CT) are in black, yellow, black and light salmon, respectively. The RGD sequences in disintegrins and an interchain disulfide bond in VAP1 are indicated. The Zn^{2+} and Ca^{2+} ions are shown as red and black circles, respectively; the closed circles indicate that all the members have a complete metal-binding sequence, whereas, open circles indicate that some members do not have it.

play a role in differential proteolytic processing of precursor proteins, giving rise to the biochemical and functional complexity of Crotalid and Viperid snake venoms, as well as post-translational regulation of ADAMs' functions.

4. Conclusion

ADAMs are widely distributed and constitute major membrane-bound sheddases that proteolytically process cell-surface-proteins for cell–cell communication. As such, they have emerged as potential therapeutic targets for a variety of diseases. SVMPs are key toxins involved in venom-induced pathogenesis, and thus are important targets for antivenom therapeutics. However, the physiological targets of ADAMs and SVMPs, and the molecular mechanism of target recognition are poorly understood. The structures presented here reveal a dynamic, modular architecture of the MDC domains of ADAM/adamalysin/reprolysin family proteins. Intrinsic flexibility may be important for fine-tuning substrate recognition, adjusting the spatial alignment of the catalytic and adhesion sites, and for post-translational regulation of this family of proteins.

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Appendix A. Supplementary data

The atomic coordinates and structure factors have been deposited in the Protein Data Bank under accession codes 2DW0, 2DW1 and 2DW2 for the Form 2-1, Form 2-2 and Form 2-5 crystals, respectively. Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.febslet.2007.04.057.

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Hypothermia reduces ischemia- and stimulation-induced myocardial interstitial norepinephrine and acetylcholine releases

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