Monitoring of Caspase-8/FLICE Processing and Activation upon Fas Stimulation with Novel Antibodies Directed against a Cleavage Site for Caspase-8 and Its Substrate, FLICE-Like Inhibitory Protein (FLIP)¹

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We generated and characterized novel antibodies specific for a cleavage site of human **caspase-8/FLICE and its substrate, FLICE-like inhibitory protein (FLIP). The synthetic peptides used as immunogens were CQGDNYQKGIPVETD (#791) and VSEGQLEDSS-LLEVD (#1342), which corresponded to cleaved regions of N-terminal fragments of caspase-8 and FLIP generated by active caspase-8, respectively. Each antibody purified** from rabbit antiserum reacted specifically with the immunogen but not with the peptide **corresponding to the unproteolyzed form, as assessed by ELISA.** *In vitro* **cleavage of GST-FLIP by active caspase-8 generated an N-terminal fragment (GST-p43) and a C-terminal one (pl2). Consistent with other** *in vivo* **data, the FLIP cleavage site follows the Asp residue, LEVD376GPAMKNVEF, identified on N-terminal sequencing of the pl2 fragment. #1342-antibody (#1342-Ab) recognized the GST-p43 fragment but not the uncleaved protein, thus confirming its specificity. When the antibodies were used for immunoblotting, flow cytometry, and confocal laser microscopy, the proteolysis of caspase-8 and FLIP, and the subcellular localization of their digests could be monitored in apoptotic U937 cells. Interestingly, a significant increase in the percentage of cells exhibiting caspase-8 and FLIP cleavage was observed upon Fas stimulation in interferon-7-treated U937 cells, in which the susceptibility to Fas is extremely enhanced. In contrast, U937 cells treated with vitamin D3 or** *all-trans* **retinoic acid showed Fas-resistance, and caspase-8 processing and FLIP cleavage were strongly inhibited. In conclusion, we established a system based on the cleavage site-directed antibodies to monitor the dynamics of caspase-8 processing and activation during apoptosis. Using this system, we found that Fas-susceptibility changes during U937 differentiation occur upstream of caspase-8 processing/activation.**

Key words: caspase-8, cleavage site-directed antibody, differentiation, Fas, FLIP.

lational modifications of proteins. It is essential for the acti-

Limited proteolysis is one of the most important post-trans-
lational modifications of proteins. It is essential for the acti-
initiation of protein degradation (1, 2). Apoptosis, which plays an essential role in development, homeostasis, and defense in multicellular organisms (3), involves the sequen-*This* work was supported in part by grants from the Ministry of tial activation of cysteine proteases known as caspases (4, Education, Culture, Sports, Science and Technology of Japan. 5). Caspases are expressed as inactive proenzymes in living Present address: Department of Molecular Neurobiology, 10kyo cells and become activated on proteolytic cleavage at sites
Institute of Psychiatry, 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo cells and become activated on proteol The institute of Tsychiatry, 2-1-6 naturalizawa, belagaya-au, tokyo following specific aspartate residues. The limited proteoly- $\frac{37}{10}$ whom correspondence should be addressed. Tel/Fax: +81-3. sis results in the generation of an active enzyme lacking an 5449-5311, E-mail: ohmi@ims.u-tokyo.ac.jp N-terminal prodomain and comprising p18 and p10 polypeptides, which form a dimeric $(p10/p18)$, complex (6) . Of aldehyde; CBB, Coomassie Brilliant Blue; DD, death domain; DED, the 14 members of the mammalian caspase family, caspasedeath effector domain; DISC, death-inducing signaling complex; 8 (FLICE/MACH/Mcl6) (7, 8) and caspase-10 (Mch4/ ELISA, enzyme-linked immunosorbent assay; FADD, Fas-associ-
etad, doeth domain, pertain, EITC, duamenting, iacthierupestes. FLICE2 (9, 10) function as initiators of the apoptotic sig-FLICE, Fas-associated death domain protein interleukin-1β-con-
FLICE, Fas-associated death domain protein interleukin-1β-conated at the death domain protein; GST, glu-

ated D. Stimulation of Fas by its cognate ligand or a spetathione S-transferase; IFN, interferon-y; PARP, poly(ADP-ribose) cific agonistic antibody enables recruiting of adapter molepolymerase; PBMC, peripheral blood monocyte; PI, propidium cule Fas-associated death domain protein (FADD) (11, 12), tather S-transferance S-transferance acid; TNF, tumor necrosis factor; and of caspase-8 $(7, 8)$ to Fas via homophilic death domain **POLUARE:** POLYMERALL, PNF-related apoptosis inducing ligand; VD_3 , $1,25\alpha(OH)_2$ (DD) and death effector domain (DED) interactions, respectively tively. Recruitment of caspase-8 to the death-inducing sig*domaing complex (DISC)* accelerates its proteolytic activation $\frac{1}{20002}$ by The Japanese Biochemical Society
eading to the release-of the active complex (p10/p18), into α causing to the release of the active complex $($ *profiles* $)$ and

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Abbreviations: Ab, antibody; Ac-IETD-CHO, acetyl-Ile-Glu-Thr-Aspated death domain protein; FITC, fluorescein isothiocyanate; vitamin D₂; z-VAD-FMK, carbobenzoxy-Val-Ala-Asp-fluoromethyl-
vitamin D₂; z-VAD-FMK, carbobenzoxy-Val-Ala-Asp-fluoromethyl- T_{maxmax} T_{max} T_{max} and T_{max} are ligand; T_{max} (T_{max}) (T_{max}) (T_{max}) α _D, α ₂, α

the cytosol. They process and activate downstream effector caspases (caspases-3 and -7), which in turn results in the specific cleavage of a number of death substrates that ultimately leads to apoptosis *(13).*

To date, eight proteins have been identified as targets of caspase-8: caspase-3 (IETD₁₇₅) (4), caspase-7 (IQAD₁₉₈) (4), caspase-8 (VETD₃₇₄) (4), caspase-13 (LEED₂₈₉) (14), BID (LQTD₅₉)</sub> (15, 16), RIP (LQLD₃₂₄) (17), plectin (ILRD₂₃₉₈) (18) , and FLIP $(LEVD_{376})$ $(19-21)$. FLIP was identified by different groups and independently called FLIP (19), Casper *(20),* FLAME-1 *(21),* CASH *(22),* CLARP *(23),* I-FLICE *(24),* MRIT *(25),* and Usurpin *(26).* At the mRNA level, FLIP exists as multiple spliced variants, but at the protein level only two endogenous forms, $FLIP_{long}$ ($FLIP_{L}$) and $FLIP_{short}$ (FLIP_s), could be detected (19). FLIP_L, which is structurally similar to caspase-8, contains two DEDs and a caspase-like domain. This domain lacks residues that are important for its catalysis, most notably a cysteine residue within the active site. $FLIP_S$ also contains two DEDs but lacks a caspase-like domain. In some cases, FLIP induces apoptosis when overexpressed, but typically it acts as a competitive inhibitor by preventing the processing of initiator caspases required for their activation *(27, 28).* Many researchers have reported enhancement of FLIP expression in Fas-resistant cells *(29-35).* A previous study in our laboratory showed that human monoblastic U937 cells differentiate into CD11b-positive monocyte/macrophage-like cells upon treatment with interferon- γ (IFN), 1,25 α (OH)₂ vitamin D₃ (VD₃), and all-*trans* retinoic acid (RA), and that their susceptibility to Fas- and tumor necrosis factor (TNF) receptor-mediated apoptosis changes: IFN-treated cells become highly susceptible, whereas VD_{3} - and RA-treated cells become Fas-resistant (36). In this pathway, caspase-8 processing/activation is an essential step for the initiation of death signaling. Previously, we could not accurately study caspase processing/activation because there was no system for specifically detecting proteolyzed proteins. This difficulty may be circumvented by the use of antibodies that specifically recognize the cleavage sites of proteolyzed fragments. We have studied proteolysis by using the cleavage site-directed antibodies for protein kinase C_{aloha} and calpain *(37-39).*

In this report, we described a novel system based on cleavage site-directed antibodies for monitoring caspase-8 processing and activation during apoptosis. Using this system we found that changes in Fas-susceptibility occur upstream of caspase-8 processing/activation during U937 differentiation.

EXPERIMENTAL PROCEDURES

Materials—The agonistic anti-Fas/CD95 mAb (clone CH-11, IgM) was purchased from MBL and was used at 50 ng/ ml throughout this study. Carbobenzoxy-Val-Ala-Asp-fluoromethylketone (z-VAD-FMK) and acetyl-Ile-Glu-Thr-Aspaldehyde (Ac-IETD-CHO) were obtained from Bachem and the Peptide Institute, respectively. The differentiation agents, and $1,25\alpha$ (OH)₂ vitamin D_3 (VD₃) and all-*trans* retinoic acid (RA) were purchased from Chugai and Sigma, respectively. Recombinant human IFN- γ (IFN) was kindly provided by Shionogi Pharmaceuticals.

Peptide Synthesis and Antibody Preparation—Peptides were synthesized by the solid phase method with an Applied Biosystems Model 430A peptide synthesizer and purified by reverse-phase high performance liquid chromatography on a C18 column. The following antibodies were generated in rabbits using synthetic peptides, as haptens, conjugated with keyhole lympet hemocyamin (KLH), and purified from antisera by affinity chromatography on the immobilized antigen peptides: anti-human FLIP $(\alpha$ -FLIP) against residues 158-191 (HRIDLKTKIQKYKQSVQGA-GTSYRNVLQAAIQK), anti-cleaved FLIP (#1342-Ab) against residues 357-371 (VSEGQLEDSSLLEVD), anticleaved caspase-8 (#791-Ab) against residues 360-374 (CQGDNYQKGIPVETD), anti-cleaved PARP (#709-Ab) against residues 215-220 (GVDEVA), and anti-PARP (#634-Ab) against residues 215-224 (GVDEVAKKKS).

ELISA—Peptides were immobilized on 96-well plates $(MaxiSorpTM, Nunc AS)$ at a concentration of 1 nmol/50 μ V well. Each antibody $(10 \text{ ng}/100 \text{ \mu}$ *J*/well) was added to plates that had been blocked by pre-incubation for 2 h in 5% bovine serum albumin (BSA)/phosphate-buffered saline (PBS) at room temperature. After a wash, the plates were further incubated with peroxidase-conjugated goat antirabbit IgG. Color was developed with o-phenylenediamine dihydrochloride (OPD) and measured with a Biomek™1000 (BECKMAN) at an absorbance of 490 nm.

Recombinant Proteins—His-tagged caspase-8 lacking the N-terminal prodomain (referred to as His-p30) and GST-FLIP were expressed and purified from *Escherichia coli* strain JM109. In brief, bacteria carrying the expression plasmid (pQE vector, QIAGEN, and pGEX vector, Amersham Pharmacia Biotech AB) were cultured in Luria-Bertani (LB) media containing 50 μ g/ml ampicillin at room temperature to the middle log phase, and then treated with 0.1 mM isopropyl-thio-galactopyranoside (IPTG) for 3 h. The cells were collected by centrifugation, disrupted by sonication in TNG buffer (20 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 10% glycerol) containing 1% Triton X-100, and then centrifuged. Recombinant proteins in the supernatant were affinity-purified with the use of Ni-NTA Agarose (QIAGEN) or Glutathion-Sepharose™4B (Amersham Pharmacia Biotech AB). Protein concentrations were determined by the Bradford method with serially diluted BSA samples as controls.

*In Vitro Cleavage of FLIP—*GST-FLIP (1 nmol) immobilized on glutathione-beads was incubated with a similar ratio of His-p30 for 12 h at 37°C. After centrifugation, the precipitate was washed with TNG buffer, and then bound proteins were solubilized with sodium dodecyl sulfate (SDS)-sample buffer containing 2.3% (w/v) SDS, 10% (w/v) glycerol, 5% (v/v) 2-mercaptoethanol (2-ME), and 10 μ g/ml Bromophenol Blue in 125 mM Tris-HCl, pH 6.8. Unbound proteins were precipitated with 10% (w/v) trichloroacetic acid (TCA). After centrifugation, the precipitates were solubilized with SDS-sample buffer. Each sample was heatdenatured and then subjected to SDS-PAGE, followed by Coomassie Brilliant Blue (CBB) staining or immunoblotting.

Amino-Terminal Sequencing—After the digests had been subjected to SDS-PAGE, they were transferred to a poly- (vinylidene difluoride) (PVDF) membrane (Immobilon, Millipore), using a semi-dry blotting apparatus (Model BE-300, Bio-Craft), and then CBB stained. The bands were excised and analyzed with a Beckman LF3000 protein sequencer.

Immunoblotting-Cells $(1 \times 10^6$ per sample) were washed

with PBS and then treated with 10% (w/v) TCA. After centrifugation, the precipitates were sonicated in 100μ of SDS-sample buffer and then heat-denatured. Samples (corresponding to 1×10^5 cells) were subjected to SDS-PAGE and then transferred onto a PVDF membrane. The membrane was soaked in tris-buffered saline (TBS) containing 20 mg/ml BSA for 1 h at room temperature and then incubated with antibodies overnight at 4°C. After being washed to remove excess antibody, the membrane was incubated with anti-rabbit or anti-mouse IgG conjugated to alkaline

Fig. **1. Antibodies specific for the cleavage site of caspase-8 (#791-Ab) and FLIP (#1342-Ab).** (A) Schematic representation of human caspase-8/FLICE and FLICE-like inhibitory protein (FLIP). Below the structure of each molecule, the three species of synthetic peptides used in this study are shown. The amino acid sequence of each peptide is indicated in one-letter abbreviations. The arrow fol-

lowing the Asp (D) residue within the box indicates the cleavage site generated by active caspase-8. (B) Specificity of the antibodies for a series of synthetic peptides. The affinity for each peptide is expressed as relative intensity in comparison with the immunogen peptide intensity (100%).

Fig. 2. *In vitro* **cleavage of recombinant FLIP by active caspase-8.** (A) GST-FLIP immobilized on glutathione-beads was incubated with purified caspase-8 (His-p30) expressed in *E. coli* or inactive caspase-8 obtained by prior incubation in the presence of a pancaspase inhibitor, z-VAD-FMK, as described under "EXPERIMEN-TAL PROCEDURES." The digests were subjected to SDS-PAGE and visualized by CBB staining. (B-D) Specificity of the antibodies

against FLIP and caspase-8 fragments. Immunoblot staining was performed with (B) α -FLIP, (C) #1342-Ab, and (D) #791-Ab. Lane 1, GST-FLIP alone; lane 2, GST-FLIP treated with His-p30; lane 3, GST-FLIP treated with His-p30 in the presence of caspase inhibitor zVAD; and lane 4, His-p30 alone. The positions of molecular mass standards (in kDa) are shown.

phosphatase (Promega). Antigens were visualized by means of the enzymatic reaction of alkaline phosphatase with 5-bromo-4-chloro-3-indolylphosphate (BCIP) and nitro blue tetrazolium (NBT).

monoblastic U937 cells and human T lymphoblastoid Jurkat cells (provided by the Japanese Cancer Research Resources Bank) were maintained in RPMI-1640 media supplemented with 10% (v/v) fetal calf serum, 2 mM L-glu-

tamine, 100 U/ml penicillin G, and 200 μ g/ml streptomycin at 37°C under a humidified atmosphere of 5% (v/v) $CO₂$. For U937 differentiation, cells (less than 2×10^5 cells/ml) were treated with IFN- γ (100 U/ml), VD₃ (10 nM), or RA (1 μ M) for 3 days, except where indicated. Differentiation was assessed as CD11b expression by flow cytometric analysis with anti-CDllb mAb (DAKO A/S).

Flow Cytometry and Confocal Laser Microscopy—Cells (5 \times 10⁵) were washed with PBS and then fixed with 2% (w/v)

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teins. Fas-stimulated Jurkat cells were harvested at the indicated times (0 to 12 h). #791- and #1342-Abs adsorbed with His-p30 or GST-FLIP/GST-p43 were used. X denotes proteins cross-reacting with #1342-Ab. The positions of molecular mass standards (in kDa) are shown.

paraformaldehyde for 30 min at room temperature. They were then washed twice with PBS and permeabilized with PBS containing 0.2% (w/v) Triton X-100. Samples were centrifuged, and the precipitates were resuspended in 100μ l of PBS containing 0.1% (w/v) Triton X-100 and 3% (w/v) human 7-globulin (Jackson ImmunoResearch Laboratories), and then incubated for 10 min on ice. After centrifugation, the precipitates were incubated with rabbit antibodies for 2 h on ice and then labeled with FITC-conjugated goat antirabbit IgG (TAGO, Inc.) for 1 h on ice. After being washed with PBS, samples were suspended in PBS containing 30 μ g/ml propidium iodide (PI) and then analyzed with a FAC-Scan flow cytometer (Becton Dickinson). The results were calculated with CELLQuest software (Becton Dickinson). The percentage of stained cells was calculated as follows: $100\times$ [fluorescent-positive cells /(fluorescent-positive cells + negative cells)]. The remaining samples were placed on coverslips, and analyzed by confocal laser microscopy (Bio-Rad).

RESULTS

Characterization of Cleavage Site-Directed Antibodies— To investigate proteolysis in apoptotic cells, we developed a system based on the ability of antibodies to recognize a pro-

Fig. **4. U937 cells differentiation caused by interferon^y (IFN),** $1,25\alpha(OH)$ ² vitamin D₃ (VD₃), and all-*trans* retinoic acid (RA). (A) Induction of CDllb on the cell surface during U937 cell differentiation. U937 cells treated with IFN (100 U/ml), $VD₃$ (10 nM), or RA $(1 \mu M)$ were probed with anti-CD11b mAb followed by FITC-conjugated anti-mouse IgG, and then analyzed with a FACScan as described under "EXPERIMENTAL PROCEDURES." (B) Changes in the Fas death pathway in differentiated U937 cells. Differentiated U937 cells were stimulated with agonistic anti-Fas antibodies (CH-11, 50 ng/ml) and then harvested at different times (0 to 12 h). Cleavage of PARP was used as a biochemical hallmark of apoptosis. Whole PARP (116 kDa) and its cleaved fragment (85 kDa) were stained with anti-PARP Ab, which exhibits higher affinity for the 85 kDa fragment than for the whole molecule.

teolyzed site on caspases and their substrates. Here, we generated_antibodies for human caspase^8/FLICE and its substrate, FLIP. Figure 1A presents their structures. Antibodies were purified from rabbit antiserum, and their specificity was determined by ELISA. The synthetic peptides used were as follows: #1613, #791, and #1614, corresponding to uncleaved caspase-8, the cleaved caspase-8 fragment and the N-terminal half of the cleaved fragment, respectively. Similarly, #1615, #1342, and #1616 were designed for FLIP. The affinity of the antibodies for each peptide was expressed as relative intensity compared with that in the case of the immunogen (100%). As shown in Fig. IB, #791 antibody (#791-Ab) exhibited high affinity for the immunogen #791 peptide but hardly reacted with the #1613 and #1614 peptides (25 and 18%, respectively). Similar results were obtained with #1342-Ab, which showed strong specificity for the #1342 peptide but not for the #1615 and #1616 peptides (7 and 14%, respectively). Of note was that both antibodies did not cross-react with the other's immunogen peptide. These data indicate that both antibodies exhibit high specificity for their immunogen peptides.

In Vitro Cleavage of FLIP—For further characterization of the antibodies, we examined their reactivity toward caspase-8 and FLIP cleaved *in vitro.* Active caspase-8 was expressed in *E. coli* because the caspase zymogen possesses intrinsic proteolytic activity, which allows for auto-processing and activation *in situ.* Almost all His-p30 caspase-8 constructs, which lack the N-terminal prodomain, were converted into 18- and 10-kDa fragments, corresponding to the active form (Fig. 2A, lane 4). Immunoblot analysis showed that #791-Ab reacted specifically with a 18-kDa fragment, indicating that #791-Ab not only recognizes the immunogen peptide but also the processed intact caspase-8 (Fig. 2D). Alternatively, recombinant FLIP was expressed as a GST fusion protein and migrated as an 80-kDa band on SDS-PAGE (Fig. 2A, lane 1). Treatment with active caspase-8 resulted in the breakdown of more than 90% of the GST-FLIP constructs into a 68-kDa fragment that corresponded to the GST-p43 fragment of FLIP (Fig. 2A, lane 2). Both the 80- and 68-kDa proteins were detected by α -

Fig. 5. Enhanced or suppressed caspase-8 activation upon Ris stimulation in differentiated U937 cells. Cleavage fragments of caspase-8, FLIP, and PARP were detected with antibodies specific for the cleavage site on each molecule (#791-, #1342-, and #709-Abs, respectively). The samples here are the same as those in Fig. 4B.

A

FLIP, which recognizes the N-terminal DED that is present in all reported isoforms (Fig. 2B). The GST-p43 fragment, but not GST-FLIP, was recognized specifically by #1342-Ab, thus confirming the antibody's specificity (Fig. 2C). As shown in Fig. 2A, lanes 2 and 3, the appearance of the 12 kDa fragment coincided with down-regulation of GST-FLIP, which was effectively suppressed by z-VAD-FMK, a broad spectrum caspase inhibitor. A FLIP cleavage site has been proposed from the following findings: (i) the molecular masses of the cleavage products, p43 N-terminal and pl2 C-terminal fragments; (ii) the existence of $(V/L/IC/L)$ $Q)XD_{376}$, a preferred sequence for caspase-8, within the equivalent region of the caspase-8 cleavage site; and (iii) prevention of FLIP cleavage on substitution of Asp_{376} with Ala. In our study, the N-terminal sequence of the fragment was determined to be GPAMKNVEF, directly indicating that the cleavage site of FLIP is situated after the Asp residue, LEVD376GPAMKNVEF (data not shown). Taken together these data support previous immunoblot results obtained with #1342-Ab. Interestingly, the pl2 fragment coprecipitated with the GST-p43 immobilized on glutathionebeads, showing that the pl2 fragment binds to the N-terminal fragment of FLIP. Furthermore, 10% of the input caspase-8 co-precipitated with the GST-p43/pl2 complex, as determined by CBB staining and immunoblotting. These results are consistent with the previous finding that the caspase-like domain alone is sufficient for interaction with full length caspase-8 *(27, 29, 31).* This raises the possibility that FLIP regulates caspase-8 activity by forming a heterogeneous complex.

Detection of Caspase-8 Processing and Activation in Apoptotic Cells—To monitor caspase-8 activation in apoptotic

cells, a time-course study was performed (Fig. 3). Human monoblastic U937 and Jurkat T cells treated with agonistic anti-Fas mAb (CH-11, 50 ng/ml) were harvested at different time points. Cleavage of caspase-8 and FLIP was detected by using #791- and #1342-Ab, respectively. The predominant expression of the long form of FLIP was confirmed with α -FLIP (data not shown). Upon Fas triggering, the release of the 44- and 26-kDa products of caspase-8 was first detectable by 3-6 h of stimulation in both types of cell (Fig. 3A, left). The 44-kDa band represents a caspase-8 missing a C-terminal plO fragment. The 26-kDa product was presumably derived from the 44-kDa fragment upon further proteolytic cleavage. Unexpectedly, the pl8 fragment of caspase-8 was not detected in either type of cell. This suggests that partially proteolyzed p44 and p26 are sufficient to initiate the apoptotic signaling cascade, although rapid degradation of pl8 may also be responsible for this effect. Alternatively, the 27-/28- and 18-kDa bands appeared with #1342-Ab, but the 43-kDa band was occasionally detected for Jurkat T cells (Fig. 3A, right). These data do not agree with the results on *in vitro* experiments showing the 43-kDa fragment was a major product. However, the unexpected species detected with #1342-Ab disappeared with the use of polyclonal antibodies adsorbed with recombinant FLIP cleaved by caspase-8 but not the uncleaved form, demonstrating that pl8, p27, and p28 were cleavage products of FLIP (Fig. 3B). In the presence of Ac-IETD-CHO, a caspase-8 tropic inhibitor, processing of caspase-8 was inhibited completely, thus preventing FLIP cleavage. These findings show that FLIP is a good substrate for caspase-8 *in vivo* as well as *in vitro.* Therefore, caspase-8 activation may be understood by studying FLIP

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Fig. 6. **Quantitative analysis of the cleavage of caspase-8, FLIP, and PAKP in differentiated U937 cells.** (A) Cells were treated with CH-11 (50 ng/ml) for 9 h, followed by staining with (a) #791-Ab, (b) #1342-Ab, or (c) #709-Ab. Ten thousand cells were analyzed with a FACScan flow cytometry instrument with CELL-Quest software. (B) The percentage of antibodyreactive cells was calculated as described under "EXPERIMENTAL PROCEDURES." The data represent the averages of three independent experiments.

cleavage with the use of #1342-Ab.

Changes to-the Fas Death Pathway in Differentiated U937 Cells—We previously reported that IFN, VD₃, and RA cause the differentiation of U937 cells into CD11b-positive monocyte/macrophage-like cells, and change their susceptibility to Fas-mediated apoptosis *(36).* Figure 4A shows the percentage of CD11b-positive cells detected during U937 differentiation with these reagents. Cells treated with IFN (100 U/ml), VD₃ (10 nM), or RA (1 μ M) were probed with anti-CDllb mAb and then analyzed with a FACScan flow cytometer. IFN increased the percentage of CD11b-positive cells after day 1 of treatment, there being 27% CD11b-positive cells on day 6 . On the other hand, $VD₃$ and RA treatment induced CDllb expression after day 3, there being 51 and 61% CD11b-positive cells on day 6, respectively. For further analysis, we studied differentiated cells on day 3 because they showed more typical features of differentiated cells. Moreover, prolonged incubation in the presence of RA induces terminal differentiation followed by apoptotic cell death (data not shown). Figure 4B shows PARP cleavage in response to Fas triggering in differentiated cells. Upon Fas stimulation, the 85-kDa cleavage product of PARP appeared in normal and IFN-U937 cells, but was not detected in $VD₃$ - and RA-U937 cells. Interestingly, down-regulation

of PARP was accelerated in IFN-U937 cells. These findings are consistent with our previous data as to apoptotic morphology changes *(36).*

Abrogation of Caspase-8 Activation in VD3- and RA-U937 Cells—To understand the changes in Fas-sensitivity that occur during U937 differentiation, we examined whether or not engagement of Fas was followed by the processing and activation of caspase-8. The zymogen form of caspase-8 was constitutively expressed in each differentiated cell type and the processed form was not detected before Fas stimulation (data not shown). In normal and IFN-U937 cells the processed products, p44 and p26, appeared in response to Fas triggering (Fig. 5, upper). Interestingly, caspase-8 processing was accelerated in IFN-U937 cells compared with in normal cells, thus indicating high susceptibility to Fasmediated apoptosis in this treatment group. In parallel, a significant increase in FLIP cleavage was observed in IFN-U937 cells (Fig. 5, middle). In contrast, neither caspase-8 processing nor FLIP cleavage was detected in Fas-resistant VD3- and RA-U937 cells, indicating that the Fas-susceptibility is regulated upstream of caspase-8 processing/activation.

To monitor caspase-8 activation *in situ,* Fas-stimulated cells were analyzed by FACScan flow cytometry (Fig. 6, A and B). Cells showing reactivity to #791-, #1342-, and #709- Abs were present among normal and differentiated U937 cells. Unexpectedly, AFITC (the difference in fluorescence intensity between antibody-reactive and non-reactive cells) did not differ between normal and differentiated cells, irrespective of any difference in Fas-susceptibility. Cleavage of caspase-8, FLIP, and PARP after 9 h of stimulation was observed in a large population of IFN-U937 cells (66, 18, and 45%, respectively) in comparison with in normal cells (13, 9, and 12%). However, cleavage of the three was only observed in a small population of $VD₃$ -U937 cells (4, 2, and 4%, respectively) and RA-U937 cells (4, 2, and 5%, respectively). Therefore, the accelerated apoptosis observed in IFN-U937 cells is attributable to an increase in the population of caspase-activating cells but not to enhancement of proteolysis in a cell.

Subcellular Localization of Proteolyzed Caspase-8 and FLIP—The limited proteolysis of caspases and their death substrates may occur anywhere in a cell *(e.g.* membrane, cytosol, cytoskeleton, nucleus, and several organelles). However, changes in the localization of these fragments affect death signaling. It is necessary to monitor digests to understand the functions of the signaling molecules involved in proteolysis. We monitored the fate of the proteolytic fragments of caspase-8 and FLIP in normal and differentiated U937 cells after Fas triggering. Figure 7 shows the subcellular distribution of the cleavage products of caspase-8 and FLIP under a confocal laser microscope. Signals generated with #791- and #1342-Abs were absent in cells prior to Fas triggering (data not shown). After 6 h of stimulation, there was positive #791-Ab reactivity throughout the cytoplasm of apoptotic U937 cells, in which nuclear fragmentation also appeared (Fig. 7a). Thus, the p44 and p26 fragments observed on immunoblot analysis are released from DISC and may activate downstream caspases to transmit extracellular signals to the cytosol along an orchestrated proteolysis pathway. In this process, the digests of FLIP, p27/28 and pl8 appeared throughout the cytosol in response to Fas stimulation, but whether the

Fig. 7. **Subcellular distribution of the cleavage fragments of caspase-8 and FLIP** Samples after 6 h of culture (shown in Fig. 6) were placed on coverslips, and then the immunofluorescent signals (green) with #791- and #1342-Abs were examined under a confocal microscope PI (red) stained the nucleus.

cleavage of FLIP occurs within DISC or the cytosol in apoptotic U937 cells remains unknown (Fig. 7e). The cytoplasmic localization of caspase-8 and FLIP digests was observed in a large population of IFN-U937 cells stimulated with Fas antigen (Fig. 7, b and f), but was not detected in $VD₃$ - and RA-U937 cells (Fig. 7, c and g, and d and h, respectively). These data are consistent with those obtained on immunoblot and FACScan analysis.

DISCUSSION

A cleavage site-directed antibody is defined as an antibody specific to the terminal region of a digest generated from the precursor or native protein by limited proteolysis. Most importantly, the antibody does not recognize the same sequence within the unproteolyzed form. Our study consisted of three parts: (i) production of cleavage site-directed antibodies, (ii) verification of antibody reactivity, and (iii) application of the antibodies to *in situ* analysis.

The quality of a cleavage site-directed antibody depends on the length of the peptide used as the immunogen. Presumably, a difference in the ternary structure between short and long peptides is responsible. When long peptides are used, the antibody recognizes both proteolyzed and unproteolyzed forms because of the existence of two epitopes within the immunogen, the cleavage site and proximal region. Both the #791- and #1342-peptides are 15 amino acids long, with 4 and 5 charged residues (Lys, Asp, or Glu), respectively. Antibodies against these peptides exhibited tight specificity for the cleavage site but not for its proximal sequence. In addition, they recognized intact fragments cleaved by caspase-8 *in vivo* and *in vitro.* Importantly, both #791- and #1342-Ab did not cross-react with the other's immunogen peptide. Although FLIP exhibits strong similarity to caspase-8 in amino acids, the sequences around a cleavage site within caspase-8 and FLIP are quite different, indicating a subsequent difference in the ternary structure around their cleavage sites. Therefore, the ternary structure may dictate the specificity of antibodies for the cleaved regions of their respective immunogens.

Several independent reports have shown that overexpression of FLIP in certain cell lines results in the appearance of p43, a fragment generated on cleavage after Asp_{376} . However, the major cleavage products of FLIP are p27/28 and pl8 in U937 and Jurkat cells. This should be true for other cells because ectopic FLIP is usually expressed as a Flag-tag protein and is detected by anti-Flag Ab. Therefore, p26/27 and pl8 fragments lacking the Flag-tag would be undetectable. Another report noted that endogenous and ectopically expressed FLIP is recruited into DISC in response to Fas triggering, where p43 is the only fragment of FLIP detected *(27).* This finding is explained by the fact that p43 possesses two functional DEDs to interact with DISC components, whereas p27/28 and pl8 lack one or both DEDs. In fact, p27/28 and pl8 fragments were observed in the cytoplasm but not on the cell surface of apoptotic U937 cells.

Contrary to *in vivo* results, only the p43 fragment of FLIP was observed *in vitro,* and neither pl8/27/28 fragments nor non-specifically cleaved fragments were detected, even upon the addition of a large amount of active caspase-8. However, in a cytosolic extract of untreated U937 cells, endogenous FLIP was completely cleaved into a pl8 fragment after the addition of dATP and cytochrome c (unpublished data). These results indicate that active caspase-8 recognizes $LEVD_{376}$ within FLIP and that additional factor(s) existing in the cytosol are required for complete cleavage of FLIP. Our present *in vitro* and *in vivo* experiments suggest that FLIP cleavage by caspase-8 with unknown factors results in the removal of an N-terminal

prodomain, and the generation of pl8 and pl2 fragments, which are topologically equivalent to the p18 and p10 fragments of active caspase-8. They form heterogeneous complexes *in vitro,* as shown in Fig. 2, and perhaps *in vivo,* but whether this process is responsible for caspase-8 inhibition is unclear.

Our previous paper was the first to report the relation between phagocyte differentiation and apoptosis resistance (36). In support of our findings, other researchers have since reported Fas-resistance in peripheral blood monocyte (PBMC)-derived macrophages *(M<\$>) (29),* dendritic cells (DC) (30), and natural killer cells (NK) *(31).* Moreover, cytotoxic and helper T lymphocytes *(32, 40),* B lymphocytes *(33),* and mast cells *(34),* which play an essential role in cell-mediated and humoral immune responses, have been reported to acquire Fas-resistance through cell activation. In most cases, FLIP is believed to be a key molecule for Fas-resistance because enhanced expression of $FLIP_L$ or $FLIP_s$ in response to differentiation or activation coincides with protection from Fas-induced cell death. In U937 cells, the expression of $FLIP_L$ is strongly up-regulated in response to differentiation stimulation by RA, which is consistent with PBMC-derived *M§* (unpublished data). However, no FLIP cleavage was observed in RA-U937 cells, indicating that FLIP does not function as a dominant negative for caspase-8 in these cells.

RA and VD_3 are known to induce $p21^{CiplWAF1}$, which inhibits cell-cycle progression by binding to $G₁$ cyclin/CDK complexes and proliferating cell nuclear antigen (PCNA) through its N- and C-terminal domains, respectively. Interestingly, overexpression of the CDK-inhibitory domain but not the PCAN-binding domain of p21 blocks TNF-related apoptosis inducing ligand (TRAIL)-mediated apoptosis, in which the processing of caspase-8 is completely inhibited *(41).* Furthermore, cytoplasmic p21 interacts with caspase-3 to prevent Fas-mediated apoptosis *(42).* The findings mentioned above are consistent with our finding of G_{q}/G_{q} arrest in Fas-resistant $VD₃$ - and RA-U937 cells, but Fashypersensitivity in prolific IFN-U937 cells. Therefore, we should address the relation between the cell cycle, differentiation and apoptosis resistance in detail.

Our antibodies proved to be powerful tools for investigating caspase-8 activation *in situ.* The results obtained on flow cytometry and confocal laser microscopy provide us with plenty of quantitative and locative information of high quality. Potential applications of these techniques include analysis of embryos and surgical specimens to reveal novel functions of caspase-8 or FLIP in development and disease. The preparation of a series of characteristic antibodies against other caspases and substrates is under way in our laboratories.

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