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Signal-Transducing Adaptor Protein-2 Modulates Fas-Mediated T Cell Apoptosis by Interacting with Caspase-8

Yuichi Sekine,* Chikako Yamamoto,* Michinori Kakisaka,* Ryuta Muromoto,* Shigeyuki Kon,* Dai Ashitomi,* Natsuko Fujita,† Akihiko Yoshimura,† Kenji Oritani,† and Tadashi Matsuda*

We found that an adaptor protein, signal-transducing adaptor protein (STAP)-2, is a new member of the Fas–death-inducing signaling complex and participates in activation-induced cell death in T cells. STAP-2 enhanced Fas-mediated apoptosis and caspase-8 aggregation and activation in Jurkat T cells. Importantly, STAP-2 directly interacted with caspase-8 and Fas, resulting in enhanced interactions between caspase-8 and FADD in the Fas–death-inducing signaling complex. Moreover, STAP-2 protein has a consensus caspase-8 cleavage sequence, VEAD, in its C-terminal domain, and processing of STAP-2 by caspase-8 was crucial for Fas-induced apoptosis. Physiologic roles of STAP-2 were confirmed by observations that STAP-2–deficient mice displayed impaired activation-induced cell death and superantigen-induced T cell depletion. Therefore, STAP-2 is a novel participant in the regulation of T cell apoptosis after stimulation. The Journal of Immunology, 2012, 188: 6194–6204.

The survival of peripheral lymphocytes is strictly controlled to maintain physiologic levels of T cells and B cells in the immune system (1, 2). In response to infection or immunization, T cells expressing Ag-specific TCRs go into an activated and proliferative phase, and some differentiate into effector cells (3). Activated T cells then produce cytokines, which coordinate the immune response to eliminate pathogens. Clearance of the Ag is accompanied by the shutdown of T cell immune responses and involves apoptosis of a large fraction of Ag-activated T cells; this prevents accumulation of no-longer-needed and potentially dangerous effector cells and thereby precludes immunopathology. Two distinct but ultimately converging pathways control apoptosis initiation, which has been known as activation-induced cell death (AICD) (4). One pathway is the mitochondrial apoptotic pathway, which is triggered by the BH3-only protein Bim (5, 6). Mice lacking Bim accumulate excess lymphocytes and myeloid cells, and their Bim-deficient cells are abnormally resistant to cytokine deprivation, deregulated calcium flux, and ER stress (6, 7). The other pathway is in part mediated through interactions between the death receptor (DR) Fas and its ligand, FasL, expressed on activated T cells (8, 9). Fas oligomerization leads to the formation of the Fas–death-inducing signaling complex (Fas-DISC) that initiates apoptosis. In natural mutant mice for the Fas and FasL genes (10), lymphoproliferation occurs even in germ-free environments and is frequently associated with autoimmunity.

Recently, we cloned signal-transducing adaptor protein (STAP)-2 as a c-fms-interacting protein (11). STAP-2 contains an N-terminal Pleckstrin homology (PH) domain, and central region is distantly related to the SH2 domain. STAP-2 also has a C-terminal proline-rich region and a YXXQ motif. As expected from the structure, we previously found that STAP-2 interacts with a variety of molecules and modifies their functions. The SH2 domain binds to FAK (12), ErB kinases (IKKs) or MyD88 (13), the PH and SH2 domains bind to STAT5 (14) and LMP1 (15), and the YXXQ motif binds to STAT3 (11). It is noteworthy that thymocytes from STAP-2–deficient mice show enhanced IL-2–dependent and TCR-mediated cell growth (14) and exhibit enhanced cell adhesion to fibronectin after PMA treatment (12) and reduced SDF-1α–induced T cell migration (16). Thus, STAP-2 is likely to play an important role in the regulation of mature T cell functions.

In this study, we found that STAP-2 participates in AICD in T cells. In this case, a direct interaction between STAP-2 and caspase-8 seems to augment the Fas-DISC formation, thereby enhancing AICD. With two types of mouse model experiments, we showed that STAP-2 plays a physiologic role in the ability of the immune system to eliminate activated T cells. Taken together, our findings indicate that STAP-2 is a novel participant in the regulation of T cell apoptosis by controlling Fas-mediated caspase-8 activation.

Materials and Methods
Reagents, Abs, and mice
Recombinant human TRAIL, PHA, and dexamethasone (DEX) were obtained from Wako (Osaka, Japan). Recombinant human TNF-α was a gift from Dainippon Sumitomo Pharma (Osaka, Japan). Recombinant murine His-tagged FasL was purchased from R&D Systems (Minneapolis, MN). Propidium iodide, staurosporine, and etoposide were purchased from Sigma-Aldrich (St. Louis, MO). The pan-caspase inhibitor z-VAD-fmk and the caspase-8-specific inhibitor z-IETD-fmk were purchased from Calbiochem (Darmstadt, Germany). Expression vector for Halo-tagged human Fas and HaloLink resin were purchased from Promega (Madison, WI). Expression vectors for HA-tagged caspase-8/Mch5 (17) and FLAG-FADD

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Abbreviations used in this article: AICD, activation-induced cell death; DED, death effector domain; DEX, dexamethasone; DR, death receptor; Fas-DISC, Fas–death-inducing signaling complex; FasL, Fas ligand; FLIP, FLICE-like inhibitory protein; HPK1, hematopoietic progenitor kinase 1; IKK, IκB kinase; KO, knockout; OVA, OVA CFA, 100 mg chicken OVA emulsified in CFA; PH, Pleckstrin homology; SEB, staphylococcal enterotoxin B; sFasL, soluble Fas ligand; siRNA, small interfering RNA; STAP, signal-transducing adaptor protein; WT, wild type.
(18) were provided by T. Miyazaki (Hokkaido University) and S. Akira (Osaka University). Recombinant soluble Fas ligand (sFasL) (19) was provided by S. Nagata (Kyoto University). Epitope-tagged STAP-2, GST-fusion STAP-2 mutants, and Myc-tagged STAP-2 deletion mutants were described previously (14). Myc-tagged STAP-2 D260A (STAP-2 DA), Myc-tagged STAP-2 D260E (STAP-2 DE), and FLAG-tagged-Caspase-8 deletion mutants were generated by PCR methods and sequenced (primer sequences are available on request). Anti-Fas Ab (CH11) was purchased from Bachem (Ulm, Germany). Anti-caspase-3, anti–caspase-7, anti-cleaved caspase-7, anti–caspase–8, anti–PARP, anti-cleaved PARP, and anti-Myc (9B11) Abs were purchased from Cell Signaling Technologies (Beverly, MA). Anti-GST and anti-Fas (M-20) anti-His probe (H-3) Abs were obtained from Sigma-Aldrich (St. Louis, MO). Anti-actin, anti-HA, and anti-Myc (9E10) Abs were from Sigma-Aldrich (St. Louis, MO), anti-FADD (clone 1) Ab was obtained from BioLegend, Inc. Anti-mouse IgM Ab was obtained from Jackson ImmunoResearch Laboratories (West Grove, PA). Anti-human STAP-2 Ab was generated by immunized guinea pig. The generation of STAP-2–deficient mice was described previously (11). STAP-2–deficient mice were backcrossed for >10 generations onto C57Bl/6 or C57/He mice. Mice were housed and bred in the Pharmaceutical Sciences Animal Center of Hokkaido University. All animals were maintained under pathogen-free conditions and in compliance with national and institutional guidelines. All protocols were approved by the Hokkaido University animal ethics committee.

Cell culture, cell purification, and apoptosis detection
Human T cell leukemia cell line, Jurkat was maintained in RPMI 1640 medium supplemented with 10% FCS. Stable Jurkat transformants expressing STAP-2 wild type (WT), STAP-2 ASH2, and STAP-2 DA were established as described previously and maintained in the above medium in the presence of 418 (0.5 mg/ml). Human T cell lymphoma, HUT78, was maintained in RPMI 1640 medium supplemented with 10% (FCS). Human embryonic kidney carcinoma cell line, 293T was maintained in DMEM containing 10% FCS, and the indicated plasmids were transfected with the standard calcium precipitation protocol (14). For isolation of splenocytes and T cells, single-cell suspensions of splenocytes from 6–12–week-old mice were prepared as described previously (16). Splenic T cells were purified (>95% CD3⁺ cells) by negative selection by EasySep Mouse T Cell Enrichment Kit (StemCell Technologies, Vancouver, BC, Canada). Apoptosis was measured by cytometric analysis by staining with propidium iodide and Annexin-V-Fluos (Roche, Penzberg, Germany) or TUNEL staining performed by In Situ Cell Death Detection Kit, TMR Red (Roche Diagnostics) according to the manufacturer’s instructions. Apoptosis was measured using flow cytometry (FACSCanto II, BD Biosciences) and further analyzed using CellQuest software. Murine splenic T cells and DO11.10 transfectants were also cultured without or with the indicated amount of DEX for 72 h. The number of viable cell was analyzed using CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer’s instructions. Cell viability is shown as a ratio of treated sample cells to untreated control cells.

Analysis of cell viability and caspase activity
The number of viable Jurkat T cells with the indicated treatments was measured using a WST-8 assay (Cell Counting Kit-8; Wako Pure Chemical). Cell viability was evaluated as the ratio of the absorbance of the sample to that of the control. Caspase-8, -3, and -7 activities were measured using the Caspase-Glo 8 Assay and Caspase-Glo 3/7 Assay kits essentially according to the manufacturer’s instructions (Promega).

Immunoprecipitation, immunoblotting, Fas-DISC formation, and in vitro caspase-8 digestion assay
The immunoprecipitation and Western blotting assays were performed as described previously (14). Cells were harvested and lysed in a lysis buffer (50 mM Tris-HCl, pH 7.4, 0.15 M NaCl, containing 1% NP-40, 1 mM sodium orthovanadate, 1 mM PMSF). The immunoprecipitates (1 mg) or lysates were resolved on SDS-PAGE and transferred to PVDF transfer membrane (PerkinElmer, Boston, MA). The filters were then immunoblotted with each Ab. Immunoreactive proteins were visualized using an ECL detection system (Millipore, Bedford, MA). Fas-DISC formation analysis was performed as described previously (20). Briefly, 1.5 x 10⁶ cells were treated with 20 ng/ml anti-Fas Ab CH11 and incubated at 37°C for 30 min followed by cross-linking with anti-His probe mAb for 10 min at 37°C as described previously (21). The cells were lysed and immunoprecipitated with anti-Fas Ab. For in vitro caspase-8 digestion assay, 293T cells were transfected with Myc-tagged STAP-2. After 24 h, the cells were lysed and immunoprecipitated with anti-Myc Ab. The immunoprecipitates were incubated with caspase-8 assay buffer (20 mM Pipes, pH 7.2, 0.1 M NaCl, containing 0.1% CHAPS and 10% sucrose, 10 mM DTT, 1 mM EDTA, 1 mM PMSF) and incubated with recombinant active caspase-8 (5 U; MLB, Tokyo, Japan) at 37°C for 4 h. After boiling the SDS sample buffer, samples were subjected to SDS-PAGE, followed by Western blot analysis.

FACS analysis
The following mAbs were used: PE-conjugated anti-B220, FITC-anti-CD4, PE-anti-CD4, PE-anti-CD95, FITC–anti-CD178, FITC–anti-TCR-β, FITC–anti-V β6 and FITC–anti-V β8 Abs (BD Pharmingen). Cell suspensions were incubated for 30 min on ice with an appropriate Ab in 50 μl PBS. The two-color cytofluorometric analysis was performed as described above.

Transfection of small interfering RNA
Silencing of caspase-8 or caspase-3 expression in Jurkat/STAP-2 cell was achieved by their specific small interfering RNAs (siRNAs). Jurkat/STAP-2 cells (5 x 10⁵) were nucleofected with control (Qiagen) or caspase-8 (no. 1: 5'-GAGUCUGGCUCAAACUAATT-3', no. 2: 5'-CAGCAUCAUCAAAGAATTT-3', no. 3: 5'-UGAUG CGAAUAGGCUAG-3') or caspase-3 (no. 1: 5'-CGCCUGAU GGUAACUGAAAGA-3', no. 2: 5'-UCCUGUAAACACCCAUACAUCC-3', no. 3: 5'-UGACUCUCAACGAGUCCCUAC-3') siRNA using the Cell Line Nucleofector Kit V (Amaza Bio-systems, Gaithersburg, MD).

In vivo mouse model for AICD
The mouse model of in vivo AICD was performed as described previously (23). In brief, anti-CD3 Ab (145-2C11) (5 μg) or isotype control Ab (5 μg) was injected i.v. into the tail veins of 9–11–week-old WT or STAP-2 knockout (KO) mice. Then, 20 h later the splenocytes were isolated from the mice and stained with FITC–anti-TCR-β (BD Pharmingen) and PE–anti-B220 (BD Pharmingen) Abs. The ratio of T cells (TCR-β) to B cells (B220) was determined by flow cytometry. The number of apoptotic cells was determined by TUNEL assay using In Situ Cell Death Detection Kit, TMR Red (Roche Diagnostics) by FACS.

Staphylococcal enterotoxin B-induced T cell deletion in vivo
WT or STAP-2 KO mice (10 wk old) were treated i.p. with 2 μg staphylococcal enterotoxin B (SEB) (Toxin Technology) in 200 μl PBS on days 1, 3, and 5. On days 0 and 7, peripheral blood taken from the tail vein was used to stain PE–anti-V b8 (clone F23.1) or FITC–anti-V b6 (clone RR4-7; BD Pharmingen). The percentage of SEB-responsive (V b8+) or SEB-unresponsive (V b6+) CD4⁺ T cells were analyzed by flow cytometry.

Apoposnosis of OVA-reactive CD4⁺ T cells
Detection of apoptotic OVA-reactive CD4⁺ T cells was described previously (22). Mice were immunized s.c. in the hind footpads with 100 μg chicken OVA (Sigma-Aldrich) emulsified in CFA (Wako; OVA/CFA). For the indicated periods after OVA/CFA immunization, popliteal lymph node systems, Gaithersburg, MD).

Statistical methods
The significance of differences between group means was determined by Student t test.

Results
STAP-2 enhances PHA- and DR-mediated apoptosis in Jurkat T cells
To initially examine the role of STAP-2 in T cell apoptosis, we used Jurkat T cells overexpressing STAP-2 (Jurkat/STAP-2 cells).
We observed significantly enhanced cell death in Jurkat/STAP-2 cells after PHA treatment compared with empty vector-expressing Jurkat T cells (Jurkat/pcDNA3 cells; Fig. 1A). Next, we examined the involvement of STAP-2 in DR-mediated cell death. Fas-mediated cell death was induced in Jurkat T cells by exposure to a Fas agonist mAb. Jurkat/STAP-2 cells displayed higher susceptibility to cell death than Jurkat/pcDNA3 cells. Similarly, Jurkat/STAP-2 cells showed enhanced cell death in response to TNF-α and TRAIL, although their susceptibilities to cell death were lower than that for Fas stimulation. We then examined the involvement of STAP-2 in the Bim-dependent mitochondrial apoptotic pathway in T cells. We used etoposide and staurosporine as Bim-dependent apoptotic stimuli. No significant differences in cell death in response to these drugs were observed between STAP-2-overexpressing and control Jurkat T cells (Supplemental Fig. 1A). Thus, the enhanced cell death displayed in the STAP-2 transfectants is selective for the DR-mediated apoptotic pathway.

**FIGURE 1.** STAP-2 enhances Fas-mediated apoptosis and caspase activation in Jurkat T cells. (A) Jurkat/pcDNA3 (filled circle), Jurkat/STAP-2#1 (filled triangle) or Jurkat/STAP-2#2 (filled square) cells (2 × 10⁴/well) were cultured in 96-well plates in the absence or presence of the increasing amount of PHA (24 h), anti-Fas Ab (24 h), TNF-α (48 h) or TRAIL (48 h). The cell viability was measured using a Cell Counting Kit-8. The data are the means of triplicate experiments, which generally varied by ±10%. Similar results were obtained in three independent experiments. (B) Jurkat/pcDNA3 or Jurkat/STAP-2 cells (1 × 10⁵) were stimulated without (−) or with (+) anti-Fas Ab (10 ng/ml). At 12 h after stimulation, apoptotic cells were determined by flow cytometry using TUNEL-staining. Similar results were obtained in three independent experiments. (C) Jurkat/pcDNA3 or Jurkat/STAP-2 cells (1 × 10⁵) were stimulated with anti-Fas Ab (10 ng/ml) for the indicated periods. The cells were then lysed, and total cell lysate (TCL) was immunoblotted (IB) with anti–caspase-8, anti-cleaved caspase-8, anti–caspase-3, anti-cleaved caspase-3, anti–caspase-7, anti-cleaved caspase-7, anti-PARP, anti-cleaved PARP, anti-Myc, or anti-actin Ab. (D) Jurkat/pcDNA3 or Jurkat/STAP-2 cells (1 × 10⁵) were stimulated with increased amounts of anti-Fas Ab (0, 1, 5, 10 ng/ml). The cells were then assessed for caspase-8 (3 h after stimulation) or caspase-3/7 (5 h after stimulation), and activity was analyzed as described in Materials and Methods. Data are expressed relative to the value of control samples without Fas stimulation. Results are representative of three independent experiments, and the error bars represent the SD of means. (E) Jurkat/STAP-2 cells (2 × 10⁵/well) were cultured in 96-well plates without or with anti-Fas Ab (0.5 ng/ml) and increased concentrations of Z-VAD-fmk (0.5, 1 μM) or Z-IETD-fmk (20, 40 μM) for 24 h. The cell viability was measured using a Cell Counting Kit-8. Similar results were obtained in three independent experiments. Data are the means of triplicate experiments, and the error bars represent the SD of means. *p < 0.05 (Student t test).
Increased caspase activation through Fas in STAP-2-expressing Jurkat T cells

We focused on effects of STAP-2 on Fas-mediated apoptosis, because Fas and FasL have a major role in AICD of T cells. To determine whether STAP-2 affected the susceptibility of Jurkat cells to Fas-mediated cell death, apoptosis of the stable transfectants was evaluated with TUNEL staining (Fig. 1B) as well as annexin V staining (Supplemental Fig. 1B) after the treatment with an anti-Fas mAb. Enhanced induction of apoptosis upon Fas stimulation was detected in Jurkat/STAP-2 cells. We then analyzed the activation of caspases after Fas stimulation. As shown in Fig. 1C, the cleavage of caspase-3, -7 and -8 as well as that of PARP was significantly increased in Jurkat/STAP-2 cells compared with control cells. These findings were confirmed by observations that Fas stimulation markedly increased the caspase enzymatic activities in Jurkat/STAP-2 cells (Fig. 1D), although slightly enhanced basal caspase activation was observed. To confirm the requirement for caspase-8 in the STAP-2-mediated apoptotic process, cells were cultured in the presence of a general caspase inhibitor, Z-VAD, or a caspase-8-specific inhibitor, IETD. Pretreatment with these compounds completely blocked Fas-mediated cell death in Jurkat/STAP-2 cells (Fig. 1E). Therefore, enhanced activation of caspase-8 is a critical step in the increased susceptibility to Fas-mediated cell death exhibited in STAP-2 transfectants.

Caspase-8 is recruited to the multiprotein Fas-DISC that is rapidly formed on the cytoplasmic portion of the Fas receptor after ligand engagement by FADD. Therefore, we examined the effect

FIGURE 2. STAP-2 influences Fas-DISC formation. (A–C) Jurkat/pcDNA3 or STAP-2 cells were stimulated with anti-Fas Ab (20 ng/ml) at the indicated periods. The immunoprecipitate with anti-IgM Ab was separated on SDS-PAGE and immunoblotted with anti-caspase-8 (A), anti-FADD (B), or anti-Myc (C, upper panel). An aliquot of TCL was blotted with the indicated Abs (lower panels). Similar results were obtained in three independent experiments. (D) Jurkat/pcDNA3 or STAP-2 cells (1 \times 10^7) were lysed after stimulation at the indicated times with anti-Fas Ab (20 ng/ml). The cells were lysed, immunoprecipitated (IP) with anti–caspase-8 Ab and immunoblotted with the indicated Abs (upper panels). TCL was also blotted with indicated Abs (lower panels). (E) 293T cells (1 \times 10^5) were transfected with HA-tagged caspase-8 (8 \mu g) without or with Myc-tagged STAP-2 (10 \mu g). At 36 h after transfection, the cells were lysed, immunoprecipitated with anti-Myc Ab, and immunoblotted with the indicated Abs (upper panels). TCL was blotted with indicated Abs (lower panels). (F) Human T cell lymphoma, HUT78 cells (1 \times 10^5) were lysed, immunoprecipitated with control IgG or anti–caspase-8 Ab, and immunoblotted with anti–STAP-2 (upper panel) or anti–caspase-8 (lower panel) Ab. (G) 293T cells (1 \times 10^5) were transfected with HA-tagged caspase-8 (15 \mu g), FLAG-tagged FADD (20 \mu g) and increasing amount of Myc-tagged STAP-2 (0, 1.5, 5 \mu g). At 36 h after transfection, the cells were lysed, immunoprecipitated with anti-HA Ab, and immunoblotted with the indicated Abs (upper panels). TCL was blotted with the indicated Abs (lower panels).
of STAP-2 on the Fas-DISC formation. Anti-Fas mAb treatment led to caspase-8 association with Fas in the Fas-DISC, and cleaved caspase-8 was produced (Fig. 2A). Importantly, the amount of caspase-8 in the Fas-DISC was remarkably increased in Jurkat/STAP-2 cells compared with control cells. The amount of FADD in the Fas-DISC was also increased in Jurkat/STAP-2 cells (Fig. 2B). Notably, STAP-2 itself existed in the Fas-DISC in Jurkat/STAP-2 cells (Fig. 2C). Moreover, the association of caspase-8 with FADD was markedly enhanced by overexpression of STAP-2 (Fig. 2D). Thus, STAP-2 is likely to enhance the Fas-DISC formation after Fas stimulation. We then examined effects of STAP-2 on caspase-8 aggregation. Aggregation of caspase-8 in the absence of 2-ME was markedly increased in 293T and Jurkat cells overexpressing STAP-2 (Supplemental Fig. 2A, 2B). These findings indicate that STAP-2 enhances caspase-8 aggregation in the Fas-DISC.

Association of STAP-2 with caspase-8

As shown in Fig. 2E, the immunoprecipitates for STAP-2 contained caspase-8 protein in samples from 293T cells expressing HA-caspase-8 and Myc-STAP2. A similar interaction between STAP-2 and caspase-8 was also observed in Jurkat/STAP-2 cells expressing Myc-tagged STAP-2 (Supplemental Fig. 2C). The immunoprecipitates for STAP-2 contained caspase-8 protein even in the absence of Fas stimulation, suggesting that the interaction between STAP-2 and caspase-8 occurred spontaneously. To confirm the endogenous association of the two proteins, we used a T cell lymphoma cell line, HUT78, which abundantly expressed both endogenous STAP-2 and caspase-8. The immunoprecipitates with the anti-caspase-8 Ab contained endogenous STAP-2 protein, whereas those with the control Ab did not (Fig. 2F). In addition, both endogenous STAP-2 and caspase-8 existed in the Fas-DISC (Supplemental Fig. 2D). Thus, STAP-2 constitutively associates with caspase-8 in cells. Next, we examined whether STAP-2 interacts with FADD, another component of the Fas-DISC. STAP-2 failed to interact with FADD in samples of 293T cells expressing FLAG-FADD and Myc-STAP2 (Supplemental Fig. 2E). Similarly, an association between STAP-2 and FADD was not observed in Jurkat/STAP-2 cells (Supplemental Fig. 2F). However, coexpression of STAP-2 with caspase-8 and FADD caused an enhanced interaction between caspase-8 and FADD, which is consistent with the data shown in Fig. 2G. These findings strongly suggest that STAP-2 has an important role in the complex formation between caspase-8 and FADD.

Next, we determined the caspase-8-interacting domain in STAP-2 using a series of Myc-tagged STAP-2 deletion mutants (Fig. 3A). Deletion mutants of the C-terminal domain or the PH domain of STAP-2 as well as full length of STAP-2 showed interactions with caspase-8, but a deletion mutant lacking the SH2 domain failed to bind to caspase-8 (Fig. 3B). To further confirm these findings, a series of deletion mutants of STAP-2 fused with GST (GST-STAP-2

**FIGURE 3.** Interacting domains of STAP-2 with caspase-8. (A) Schematic diagrams of the domain structures of the STAP-2 deletion mutant fragments, the GST-fused STAP-2 mutant fragments, and the domain structure of the caspase-8 deletion mutant fragments. (B) 293T cells (1 x 10⁶) were transfected with HA-tagged caspase-8 (8 μg) or a series of Myc-tagged STAP-2 WT or deletion mutants (10 μg). At 36 h after transfection, the cells were lysed, immunoprecipitated with anti-Myc Ab, and immunoblotted with the indicated Abs (upper panels). TCL was blotted with indicated Abs (lower panels). (C) 293T cells (1 x 10⁶) were transfected with HA-tagged caspase-8 (15 μg) and/or a series of GST-fused STAP-2 WT or mutants (10 μg). At 36 h after transfection, the cells were lysed, pulled down with glutathione-Sepharose, and immunoblotted with anti-HA or anti-GST Ab (upper panels). TCL was blotted with anti-HA or anti-GST Ab (lower panels). (D) 293T cells (1 x 10⁶) were transfected with Myc-tagged STAP-2 (8 μg) and/or a series of FLAG-tagged caspase-8 deletion mutants (15 μg). At 36 h after transfection, the cells were lysed, immunoprecipitated with anti-FLAG Ab, and immunoblotted with the indicated Abs (upper panels). TCL was blotted with indicated Abs (lower panels). (E) Jurkat transfectants (2 x 10⁶/well) were cultured in 96-well plates with the indicated amounts of anti-Fas Ab for 24 h. The cell viability was measured using a Cell Counting Kit-8. The data are the means of triplicate samples, which generally varied by <10%. Similar results were obtained in three independent experiments. (F) Jurkat transfectants (1 x 10⁶) were stimulated without or with anti-Fas Ab (10 ng/ml) for 3 h. The cells were then assessed for caspase-8 activities. Data are expressed relative to the value of control samples without Fas stimulation. Results are representative of three independent experiments, and the error bars represent the SD of means. *p < 0.05 (Student t test).
PH, GST-STAP-2 SH2, and GST-STAP-2 C) were used (Fig. 3A). The precipitates for the GST–STAP-2 SH2 protein clearly contained caspase-8 protein (Fig. 3C). However, no caspase-8 protein was detected in the precipitates for GST–STAP-2 PH protein or GST–STAP-2 C protein. These findings further indicate that the SH2-like domain of STAP-2 interacts with caspase-8. We also determined the STAP-2–interacting domain on caspase-8 using a series of caspase-8 deletion mutants (Fig. 3A). The two N-terminal death effector domain (DED) domains of caspase-8 showed obvious interactions with STAP-2 as strong as full-length caspase-8 did, whereas the catalytic domain failed to bind to STAP-2 (Fig. 3D). Therefore, caspase-8 interacts with STAP-2 through its N-terminal DED domains.

To assess the physiologic roles of the association between STAP-2 and caspase-8, we used stable Jurkat cell transfectants expressing an empty vector (pcDNA3), WT STAP-2 or STAP-2 ΔSH2, which lacks the SH2-like domain. Significant cell death in response to Fas stimulation was observed in Jurkat/STAP-2 WT cells compared with Jurkat/pcDNA3 cells (Fig. 3E). However, the Fas-induced cell death in Jurkat/STAP-2 ΔSH2 cells was moderate. We also found that the enhanced Fas-induced caspase-8 enzymatic activity was significantly reduced in Jurkat/STAP-2 ΔSH2 cells compared with Jurkat/STAP-2 WT cells (Fig. 3F). Therefore, the association of STAP-2 with caspase-8 through its SH2-like domain enhances Fas-induced cell death and caspase-8 enzymatic activation in Jurkat T cells.

Proteolytic cleavage of STAP-2 by caspase-8 is required for Fas-mediated signaling

As seen in Fig. 2A, Fas-mediated proteolytic cleavage of STAP-2 was observed in Jurkat/STAP-2 WT cells after Fas stimulation. Therefore, we focused on the potential role of STAP-2 proteolysis during Fas-mediated signaling. First, we examined the proteolytic cleavage of endogenous STAP-2 after Fas stimulation using HUT78 cells. Cleaved STAP-2 as well as cleaved caspase-8 was observed in HUT78 cells treated with the anti-Fas Ab (Fig. 4A). We then investigated which domains of STAP-2 were cleaved in response to Fas stimulation. Jurkat cells expressing a series of Myc-tagged STAP-2 deletion mutants were treated with an anti-Fas Ab. Mutants lacking the PH or SH2 domain, but not a deletion mutant for the C-terminal domain of STAP-2, successfully generated cleaved STAP-2 within 1 h after Fas stimulation (Fig. 4B), indicating that the proteolytic cleavage site of STAP-2 may exist in the C-terminal domain. To examine the involvement of caspases in the Fas-mediated processing of STAP-2, we transfected specific siRNAs for caspase-3 (nos. 1 and 2) or caspase-8 (nos. 1 and 2) into Jurkat/STAP-2 cells. Reduction in caspase-8 expression resulted in a marked decrease in STAP-2 cleavage after Fas stimulation, whereas the reduction in caspase-3 expression did not (Fig. 4C). We next tested whether recombinant active caspase-8 can cleave the STAP-2 protein in vitro. As shown in Fig. 4D, recombinant active caspase-8 cleaved the partially purified STAP-2 protein from the Myc-STAP-2–transfected 293T cells. Furthermore, Z-VAD treatment inhibited generation of the cleaved STAP-2.
Thus, caspase-8 is required for the STAP-2 processing during Fas-mediated signaling. In general, caspases cleave their substrates specifically at the C-terminal side of aspartic acid (the P1 site), which is dictated by arginine and glutamine residues (24). Indeed, the consensus caspase-8 cleavage site was reported to be (I/L/V) EXD (25). Thus, we searched for this consensus sequence in the C-terminal domain of STAP-2, because a deletion mutant of the C-terminal domain failed to produce the cleaved fragment after Fas stimulation. We found a VEAD sequence (residues 257–260) as a potential caspase-8 cleavage site (Fig. 5A). To further evaluate the potential cleavage of STAP-2 at this site, we generated an STAP-2 mutant with substitution of alanine for aspartic acid at

**FIGURE 5.** Caspase-8–dependent STAP-2 cleavage occurs at the position of Asp260. (A) The consensus caspase-8 cleavage site in STAP-2 and the substitution of Asp (D)–260 to Ala (A) or Glu (E) in STAP-2 are schematically shown. (B) Jurkat cells (1 × 10^7) were transiently transfected with Myc-tagged STAP-2 WT, DA, or DE (10 μg), stimulated with anti-Fas Ab (20 ng/ml) for the indicated periods. The cells were lysed, and an aliquot of TCL was immunoblotted (IB) with anti-Myc or anti-actin Ab. (C) Jurkat/pcDNA3, Jurkat/STAP-2 WT, and Jurkat/STAP-2 DA cells (1 × 10^7) were stimulated with anti-Fas Ab (20 ng/ml) for the indicated periods. The cells were lysed, and an aliquot of total cell lysate (TCL) was immunoblotted (IB) with anti–caspase-8, anti–caspase-3, anti-Myc, or anti-actin Ab. (D and E) Time course analysis of Fas-DISC formation was performed as described in Materials and Methods. Jurkat/pcDNA3, Jurkat/STAP-2 WT, or Jurkat/STAP-2 DA cells (2 × 10^6) were stimulated with anti-Fas Ab (20 ng/ml) at the indicated periods. The immunoprecipitate with anti-IgM Ab was separated on SDS-PAGE and immunoblotted with anti–caspase-8 (D) or anti-FADD Ab (E, upper panel). An aliquot of TCL was blotted with anti-caspase-8 (D), anti-FADD (E), anti-Myc Ab (D, E, lower panels). The data are representative of three independent experiments. (F) Jurkat/pcDNA3, Jurkat/STAP-2 WT, or Jurkat/STAP-2 DA cells (1 × 10^7) were stimulated without or with anti-Fas Ab (10 ng/ml). The cells were then assessed for caspase-8 (3 h after stimulation) or caspase-3/7 (5 h after stimulation) activities as described in Materials and Methods. The data are indicated as a relative caspase activity from triplicate experiments, and the error bars represent the SD. *p < 0.05 (Student t test). (G) Jurkat/pcDNA3, Jurkat/STAP-2 WT, or Jurkat/STAP-2 DA cells (1 × 10^6) were stimulated without or with TNF-α (100, 500 ng/ml). The cells were then assessed for caspase-8 (3 h after stimulation) activity as described in Materials and Methods. The data are indicated as a relative caspase activity from triplicate experiments, and the error bars represent the SD. *p < 0.05 (Student t test). (H) Jurkat/pcDNA3, Jurkat/STAP-2 WT, or Jurkat/STAP-2 DA cells (1 × 10^6) were stimulated without or with anti-Fas Ab (10 ng/ml). At 20 h after stimulation, apoptotic cells were determined by flow cytometry using annexin V staining. Data are expressed relative to the value of control samples without Fas stimulation. Results are representative of three independent experiments. (I) Jurkat/pcDNA3 (filled circle), Jurkat/STAP-2 WT#1 (filled square), Jurkat/STAP-2 DA#1 (filled triangle), or Jurkat/STAP-2 DA#2 (open triangle) cells (2 × 10^5) were cultured in 96-well plates with the indicated amounts of anti-Fas Ab (24 h). The cell viability was measured using a Cell Counting Kit-8. The data are the means of triplicate experiments, which generally varied by <10%. Similar results were obtained in three independent experiments.
STAP-2 associates with Fas. (A) 293T cells (1 × 10^7) were transfected with Myc-tagged STAP-2 WT or DA (6 μg) and with or without HA-tagged caspase-8 (10 μg). At 36 h after transfection, the cells were lysed and immunoprecipitated with anti-HA Ab and immunoblotted with anti-Myc or anti-HA Ab (upper panels). TCL was blotted with anti-Myc or anti-HA Ab (lower panels). (B) 293T cells (1 × 10^7) were transfected with Myc-tagged STAP-2 WT (6 μg) and with or without Halo-tagged Fas (10 μg). At 36 h after transfection, the cells were lysed and immunoprecipitated with anti-Myc Ab and immunoblotted with anti-Fas or anti-Myc Ab (upper panels). TCL was blotted with anti-Fas or anti-Myc Ab (lower panels). (C) 293T cells (1 × 10^7) were transfected with Myc-tagged STAP-2 WT or DA (6 μg) and with or without Halo-tagged Fas (10 μg). At 36 h after transfection, the cells were lysed and pulled down with HaloLink resin and immunoblotted with anti-Myc or anti-Fas Ab (upper panels). TCL was blotted with anti-Myc or anti-Fas Ab (lower panels).

STAP-2 DE were transiently expressed into Jurkat cells and cells were stimulated anti-Fas mAb for the indicated periods. Although substitution of Asp260 with a neutral amino acid, Ala, differing in size and polarity, resulted in a slightly faster mobility in the SDS-PAGE gels, Fas-mediated cleavage of STAP-2 was not observed in Jurkat cells expressing either STAP-2 DE or STAP-2 DA (Fig. 5B). Therefore, Fas/caspase-8-mediated processing of STAP-2 occurs at Asp260 in its C-terminal domain.

Activation of caspase-3 and -8 was greatly decreased in Jurkat/STAP-2 DA cells compared with Jurkat/STAP-2 WT cells (Fig. 5C). Furthermore, the amount of caspase-8 or FADD, or both, in the Fas-DISC was also reduced in Jurkat/STAP-2 DA cells compared with Jurkat/STAP-2 WT cells (Fig. 5D, 5E). We further examined whether enhanced enzymatic activation of caspsases by STAP-2 was affected by this mutation. As shown in Fig. 5F, Fas-induced caspase-3 and -8 enzymatic activities in Jurkat/STAP-2 DA cells were markedly reduced compared with Jurkat/STAP-2 WT cells. Moreover, TNF-α-induced caspase-8 enzymatic activity in Jurkat/STAP-2 DA cells was also significantly reduced compared with Jurkat/STAP-2 WT cells (Fig. 5G), suggesting that the cleavage of STAP-2 at Asp260 by caspase-8 is required for other DR-mediated apoptotic pathways. Fas-induced apoptosis in Jurkat/STAP-2 DA cells was weaker than that in Jurkat/STAP-2 WT cells, and at a level similar to that in Jurkat/pcDNA cells (Fig. 5H, 5I). Therefore, proteolytic cleavage of STAP-2 at Asp260 by caspase-8 is required for the enhancement of Fas-induced apoptosis and caspase-8 enzymatic activation by STAP-2 in Jurkat T cells.

We examined the molecular mechanisms related to how the STAP-2 DA mutant affects the Fas-DISC formation. We tested the association of caspase-8 with STAP-2 WT and DA in 293T cells. As shown in Fig. 6A, both STAP-2 WT and DA interacted with caspase-8. Because STAP-2 interacted with Fas (Fig. 6B), we tested the association of Fas with STAP-2 WT and DA in 293T cells.
STAP-2 KO (filled circle) mice (6–8 wk old) were immunized s.c. in the hind footpads with OVA/CFA (100 μg) in CD4+ T cells calculated according to the formula: % apoptosis = (% annexin V+ apoptotic cells at indicated day in CD4+ T cells/% annexin V+ apoptotic cells at day positive and FITC-CD4–positive cells were detected by FACS. (20 h after injection, isolated splenocytes were stained with anti–TCR-α/β, anti-CD3, and anti-CD8 Abs and determined the T cell-to-B cell ratio by FACS. Each circle represents data from one mouse; horizontal bars represent the mean; n = 6–9; t value for CD3/WT versus CD3/KO, p < 0.01 (Student t test). (B) Splenocytes from WT or STAP-2 KO mice injected with anti-CD3 Ab or control Ig (5 μg) for 20 h were stained with FITC-CD4 and TUNEL. TUNEL-positive and FITC-CD4+ positive cells were detected by FACS. (C and D) WT or STAP-2 KO mice were injected i.p. with SEB. Percentages of Vβ8+CD4+ T cells (Fig. 8A). However, no significant reduction was observed in those of STAP-2–deficient mice. Similar results were obtained when apoptotic cells were evaluated by TUNEL staining (Fig. 8B). Finally, we treated mice with a superantigen, SEB, that leads to the elimination of Vβ8+ (superantigen responsive) T cells in a Fas-dependent manner (26). SEB injection caused STAP-2–deficient mice to display a decreased ability to eliminate Vβ8+ CD4+–responsive cells compared with WT mice (Fig. 8C), but did not lead to elimination of the Vβ6+CD4+ T cell population (unresponsive to SEB) in either WT or STAP-2–deficient mice (Fig. 8D). We further investigated the more physiologic role of STAP-2 in AICD by studying apoptosis in Ag-specific CD4+ T cells in STAP-2–deficient mice induced by immunization with OVA/CFA. The above findings suggest that absence of STAP-2 results in longer life span of Ag-stimulated CD4+ T cells because of lowered sensitivity to AICD. Notably, the frequencies of apoptotic CD4+ T cells in the draining lymph nodes decreased after immunization in STAP-2–deficient mice (Fig. 8E). However, DEX-induced cell death in splenic T cells was not altered by STAP-2 deficiency (Supplemental Fig. 3C). In addition, DO11.10 T cells overexpressing STAP-2 responded to DEX as strong as control cells (Supplemental Fig. 3D). Therefore, these data support the notion that STAP-2 has a physiologic role in the ability of the immune system to eliminate activated T cells.

Discussion

The domain structure of STAP-2 contains several potential tyrosine phosphorylation sites as well as PH- and SH2-like domains, and STAP-2 shows the characteristics of an adaptor protein that can interact with several other signaling molecules. In this study, we identified new functions of STAP-2, specifically that it is a member of the Fas-DISC components and enhances Fas-mediated apoptosis in T cells. The STAP-2–mediated effect is selective for the DR-
mediated pathway because STAP-2 expression does not alter the sensitivity of Jurkat cells to Bim-dependent apoptotic stimuli. The critical target of the STAP-2-mediated effects is the activation of caspase-8, a key initiator caspase in the Fas signaling pathway. Indeed, stable expression of STAP-2 leads to a marked increase in caspase-8 activation upon Fas engagement, and the addition of a caspase-8 inhibitor blocks Fas-mediated cell death in STAP-2-transfected cells. Splenic T cells from STAP-2-deficient mice exhibit a reduced ability to undergo AICD, as well as defects in the SEB-mediated elimination of Vβ8*CD4+ T cells. These findings indicate that STAP-2 can control T cell apoptosis by modulating one of the critical initiating events in the Fas signaling cascade.

In general, caspase-8 activation within the Fas-DISC is believed to occur in two steps. For the first step, recruitment of FADD to Fas promotes dimerization and conformational changes of caspase-8, and allows caspase-8 to gain full enzymatic activity. Next, active caspase-8 undergoes autoproteolytic processing and leaves the Fas-DISC to access its substrates. Among the Fas-DISC components, FLASH associates with procaspase-8 in nonapoptotic cells (27). After Fas signaling is stimulated, FADD and then a FLASH–procaspase-8 complex are recruited into the intracellular domain of the aggregated Fas, resulting in the promotion of caspase-8 activation. Similar to FLASH, STAP-2 recognized the DED domain of caspase-8, even under steady-state conditions, and enhanced the interaction between FADD and caspase-8 as well as the aggregation and activation of caspase-8 during Fas signaling. Although STAP-2 did not bind to FADD, the molecular mechanisms for how FLASH and STAP-2 enhance Fas-induced apoptosis may be similar. For example, STAP-2 may control the local concentration and intracellular distribution of procaspase-8 before Fas stimulation. Alternatively, STAP-2 may promote a conformational change of procaspase-8 to allow dimerization or rapidly expose its autoproteolytic active sites in the Fas-DISC.

STAP-2 has a consensus caspase-8 cleavage sequence, VEAD, in its C-terminal domain, and was clearly cleaved by caspase-8 after Fas stimulation. It is noteworthy that processing of STAP-2 was crucial for Fas-induced apoptosis. Consequently, STAP-2 may participate in the Fas-DISC as a suicide substrate to enhance Fas-induced apoptosis. For example, activated caspase-8 may easily leave the Fas-DISC after processing of STAP-2. Although FLASH is also proteolytically cleaved during Fas signaling, the requirement for the cleavage is likely to differ between STAP-2 and FLASH. In the case of FLASH, its C-terminal region contains a potential cleavage site for caspase-8 and a nuclear localization signal (27). Thus, the cleaved FLASH C-terminal is thought to translocate into the nucleus. Although not a Fas-DISC component, hematopoietic progenitor kinase 1 (HPK1), a mammalian Ste20-related protein kinase, is a substrate of caspases (28, 29). HPK1 is crucial for TCR-mediated NF-κB activation; therefore, AICD-resistant naive T cells contain full-length HPK1. Following the proliferation of activated T cells, HPK1 is cleaved into N- and C-terminal fragments (HPK1-N and HPK1-C, respectively). The kinase-inactive HPK1-C inhibits NF-κB by binding to IκK-α and IκK-β, and sequestering the IκK complex in its inactive state. Therefore, HPK1-C blocks the induction of prosurvival genes and sensitizes T cells to AICD (8, 28, 29). At the present time, the roles of the cleaved STAP-2 fragments remain unknown. Further detailed studies are required to clarify this issue.

Our data also indicate that both the SH2 domain and a cleaved site of STAP-2 are essential for full activation of caspase-8 after Fas-stimulation. We have proposed possibility that STAP-2 SH2 is involved in recruitment of caspase-8 into the Fas-DISC and that STAP-2 cleavage is required for the activation of caspase-8 itself. Although our data are reproducible, there are some questions against these molecular events in the Fas-DISC. One question is how STAP-2 ΔSH2, lacking the binding capacity to caspase-8, was cleaved by caspase-8 (Fig. 4B). This might suggest that STAP-2 cleavage is independent on tight binding between STAP-2 and caspase-8, because both proteins may exist closely enough in the Fas-DISC. The other question is why STAP-2 DA inhibited recruitment of caspase-8 into the Fas-DISC (Fig. 5D). For the possible mechanism, the caspase-8–cleaved site might bind to another Fas-DISC component. Indeed, we showed that STAP-2 DA could recognize caspase-8, but not Fas (Fig. 6A, 6C). Because molecular events in the DISC during Fas-stimulation are complicated, further analysis will clarify these strange phenomena regarding to STAP-2.

Notably, expression of FLIP-like inhibitory protein (FLIP), an inhibitory protein of Fas-mediated apoptosis (30), was slightly decreased in Jurkat/STAP-2 cells (Supplemental Fig. 4A). Furthermore, STAP-2-deficient T cells also showed a slightly increased FLIP expression (Supplemental Fig. 4B). Thus, the involvement of STAP-2 in FLIP expression is likely to be another possible mechanism for the DISC formation, although we need more careful examinations in this regard.

Given that STAP-2 interacts with a variety of signaling molecules, an attractive hypothesis is that the presence or absence of specific partners may modulate the ability of STAP-2 to function in several signaling pathways. In this study, we identified caspase-8 as a novel partner of STAP-2 in T cells. Future investigations will clarify when and how STAP-2 acts as a regulator of caspase-8 activation in vivo.

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References


