Apoptotic pathways are selectively activated by granzyme A and/or granzyme B in CTL-mediated target cell lysis

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Purified cytolytic T lymphocyte (CTL) proteases granzyme (gzm)A and gzmB with sublytic dose of perforin (perf) initiate distinct proapoptotic pathways. Their physiological relevance in CTL-mediated target cell apoptosis is elusive. Using ex vivo virus-immune CD8⁺ T cells from mice deficient in perf, gzmA and/or gzmB, and the Fas-resistant EL4.F1.5 tumor target cell, we show that (a) CTL from gzmA−/− or gzmB−/− mice similarly induced early proapoptotic features, such as phosphatidyl serine (PS) exposure on plasma membrane, ΔΨm loss, and reactive oxygen radical generation, though with distinct kinetics; (b) CTL from gzmA−/− but not from gzmB−/− mice activate caspase 3 and 9; (c) PS exposure induced by CTL from gzmA−/− or gzmB−/− mice is prevented, respectively, by caspase inhibitors or by reactive oxygen scavengers without interfering with target cell death; and (d) all gzm-induced apoptotic features analyzed depend critically on perf. Thus, perf is the principal regulator in CTL-mediated and gzm-facilitated intracellular processes. The ability of gzmA and gzmB to induce multiple independent cell death pathways may be the hosts response to circumvent evasion strategies of pathogens and tumors.

Introduction

Cytolytic leukocytes, Natural Killer (NK) and CD8⁺ T (cytotoxic T lymphocyte [CTL]) cells, are key components of the hosts immune system against intracellular parasites and tumors. NK and CTL exert their biological activity via two distinct mechanisms. One is the synthesis and release of soluble mediators such as IFN-γ (Boehm et al., 1997), TNF-α (Vassalli, 1992), and interleukins (Biron, 1994), which may act proximal and distal to the effector cell. The other is direct cytolyis and induction of programmed cell death, apoptosis, in target cells by either or both of two cytopathic pathways (Kagi et al., 1994; Lowin et al., 1994). One is the Fas pathway involving the Fas ligand (FasL) on the effector cell engaging the Fas receptor (Fas or CD95) on the target cell (Rouvier et al., 1993; Nagata and Golstein, 1995; Krammer, 1999). The other, executed via the granula exocytosis pathway, is mediated by perforin (perf; Podack, 1986; Henkart, 1994) and the two principal granzymes (gzm), gzmA and gzmB (Simon and Kramer, 1994; Tschopp, 1994). These components are stored in cytoplasmic granules and are released into the immunological synapse formed between effector cells and their targets (Podack, 1986; Henkart, 1994; Stinchcombe et al., 2001). Although gzmA and gzmB can get access to target cells independent of perf via the mannose 6-phosphate receptor pathway or by other means (Motyka et al., 2000; Trapani et al., 2003; Dressel et al., 2004), their delivery to the cytosol and/or nucleus, where they initiate alternative proteolytic processes to trigger apoptosis, is critically dependent on perf (Froelich et al., 1996; Trapani et al., 1998).

Significant advances in our understanding of the molecular basis for gzmA- and gzmB-induced cell death are based on experiments using the mast-cell exocytosis model (Nakajima et al., 1995) and from in vitro studies using purified effector molecules. It was concluded that gzmB initiates cell death through various pathways, either involving activation of caspases, directly or indirectly, and resulting in disruption of mitochondrial
integrity (Barry et al., 2000; Heibein et al., 2000; Sutton et al., 2000, 2003; Alimonti et al., 2001; Goping et al., 2003; Metkar et al., 2003), by derepressing the endonuclease CAD (Thomas et al., 2000; Sharif-Askari et al., 2001) or by cleaving key structural proteins in the nuclear membrane or cytoskeleton (Browne et al., 2000; Zhang et al., 2001a,b). In contrast, gzmA seems to induce apoptosis by caspase-independent pathways (Beresford et al., 1999; Shresta et al., 1999). Besides other substrates of gzmA, like lamins (Zhang et al., 2001a) and histones (Zhang et al., 2001b), a special target seems to be the endoplasmic reticulum–associated SET complex (Fan et al., 2002). This complex contains three gzmA substrates, the nucleosome assembly protein SET, the DNA binding protein HMG-2, and the base excision repair endonuclease Ape1. The SET complex also contains the tumor suppressor protein pp32 and the DNase assembly protein SET, the DNA bending protein HMG-2, and the DNase complex contains three gzmA substrates, the nucleosome assembly protein SET, the DNA binding protein HMG-2, and the base excision repair endonuclease Ape1. The SET complex also contains the tumor suppressor protein pp32 and the DNase complex contains three gzmA substrates, the nucleosome assembly protein SET, the DNA binding protein HMG-2, and the base excision repair endonuclease Ape1. The SET complex also contains the tumor suppressor protein pp32 and the DNase complex contains three gzmA substrates, the nucleosome assembly protein SET, the DNA binding protein HMG-2, and the base excision repair endonuclease Ape1. 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These findings, principally obtained with purified effector molecules, emphasize the complexity of intracellular events triggered by gzmA and gzmB. However, it is unclear to what extent these in vitro observations reflect the biologically relevant interaction of NK and CTL with target cells in vivo. In particular, factors such as the quality of the proteins involved, the way and context of their delivery, and/or their accessibility to cellular compartments may play a crucial role in the outcome of cytolytic function. The present work uses ex vivo–derived virus-immune CD8+ T cells from mice with targeted gene defects in perf or gzmA and/or gzmB to examine for the first time the apoptotic pathways activated by CTL via the two gzms in an in vitro cytotoxic assay using Fas-resistant tumor target cells.

Results

Perf-mediated cytotoxicity of EL4.F15 by CTL: loss of plasma membrane integrity and mitochondrial membrane potential is similarly and independently induced by gzmA and gzmB

To study a physiologically relevant model for granule exocytosis–executed apoptotic cell death, in particular mediated by gzms and independent of Fas, we used an in vitro CTL-target cytotoxic assay. Ex vivo–derived virus-immune CD8+ T cells (day eight after infection) from B6 mice or those deficient in gzm(s) (gzmA<sup>-/-</sup>, gzmB<sup>-/-</sup>, and gzmA×B<sup>-/-</sup>) or perf (perf<sup>-/-</sup>) infected with LCMV 8 d before, were used as effector cells. As target cell, the tumor cell line EL4.F15 was chosen because it is Fas resistant and at the same time sensitive to both gzmA- and gzmB-induced apoptosis (Pardo et al., 2002). Confirming previous studies, splenocytes from 8-d LCMV-immune B6, gzmA<sup>-/-</sup>, and gzmB<sup>-/-</sup> mice contained similar numbers (11, 6, and 9%, respectively) of gp33/D<sup>8</sup>tetramer<sup>+</sup>/CD8<sup>+</sup> T cells (Fig. 1 Aa). As shown previously (Simon et al., 1997; Pardo et al., 2002), enriched CD8<sup>+</sup> T cells from all three mouse strains readily induced specific nucleolysis in gp33-pulsed EL4.F15 target cells (4-h assay), which was similar in magnitude for B6 and gzmA<sup>-/-</sup> and somewhat lower for gzmB<sup>-/-</sup> T cells (Fig. 1 Ab).

Changes of cellular parameters occurring in EL4.F15 cells were analyzed after incubation with LCMV-immune CD8+ T cells (2 h), by gating effector/target mixtures for CD8 negative cells. CD8+ T cell populations from B6, gzmA<sup>-/-</sup>, and gzmB<sup>-/-</sup> mice similarly induced loss of plasma membrane integrity of gp33-pulsed EL4.F15 cells, as monitored by exposure of phosphatidyl serine (PS) at the plasma membrane and incorporation of propidium iodide (PI). This finding is revealed by the fact that numbers of annexinV/PI-positive cells was increased in gp33-pulsed as compared with mock-treated targets (51, 40, and 40% vs. 9, 14, and 13% for B6, gzmA<sup>-/-</sup>, and gzmB<sup>-/-</sup> T cells, respectively; Fig. 1 Ac). Gliotoxin, a hydrophobic fungal metabolite with apoptotic potential for mammalian cells, served as positive control for induction of the aforementioned parameters (Waring et al., 1999; Fig. 1 Ac). Furthermore, upon specific CTL–target cell interaction (2 h), all three CD8<sup>+</sup> T cell populations induced severe mitochondrial perturbation in EL4.F15 targets. This result can be deduced by the comparable reduction of the mitochondrial transmembrane potential (∆Ψ<sub>m</sub>, 88 to 33%, 83 to 42%, and 81 to 45% for B6, gzmA<sup>-/-</sup>, and gzmB<sup>-/-</sup> T cells, respectively) and an increase in the generation of reactive oxygen species (ROS), when mock-treated were compared with gp33-pulsed EL4.F15 cells (3 to 38%, 4 to 35%, and 3 to 38% for B6, gzmA<sup>-/-</sup>, and gzmB<sup>-/-</sup> T cells, respectively; Fig. 1 Ad). The data suggest that CTL-induced loss of plasma membrane and mitochondrial integrity can be elicited to the same extent by gzmA or gzmB and independently of each other. However, when tested at earlier time points of CD8<sup>+</sup> T cell–target cell interaction (i.e., at 30 or 60 min) loss of plasma membrane and mitochondrial integrity was more pronounced with B6 and gzmA<sup>-/-</sup> as compared with gzmB<sup>-/-</sup> CD8<sup>+</sup> T cells (Fig. 1 Ae). Moreover, at these two time points but not later (2 h), annexinV reactivity preceded membrane permeability by B6 and gzmA<sup>-/-</sup> effectors.

Induction of loss of plasma membrane integrity and mitochondrial membrane potential elicited by CTL via gzmA or gzmB is dependent on perf

To determine if loss of plasma membrane and mitochondrial integrity in EL4.F15 target cells induced by gzmA- or gzmB-deficient CTL is dependent on perf, ex vivo–derived (day eight after infection) and CD8-enriched LCMV-immune splenic T cells from B6, perf<sup>-/-</sup>, and gzmA×B<sup>-/-</sup> mice were tested under the same conditions (2 h) for their potential to induce the same apoptotic parameters described in the previous paragraph. Effector cell populations from all three mouse strains contained similar numbers of gp33/D<sup>8</sup>tetramer<sup>+</sup>/CD8<sup>+</sup> T cells (10, 11, and 9% for B6, perf<sup>-/-</sup>, and gzmA×B<sup>-/-</sup> T cells, respectively; Fig. 1 Ba). As previously found (Simon et al., 1997; Pardo et al., 2002), only CD8<sup>+</sup> T cells from B6, but
not from perf−/− or gzmA×B−/−, mice were able to induce specific nucleolysis in EL4.F15 target cells (Fig. 1 Bb, 4-h assay). Therefore, target cell survival upon interaction with either B6-, perf−/−, or gzmA×B−/−-derived CTL was inversely proportional to nucleolysis (Fig. 1 Bc). From the three effector cell populations, only CD8+ T cells from B6 mice readily induced loss of plasma membrane integrity in EL4.F15 target cells, whereas CD8+ T cells from perf−/− or gzmA×B−/− mice were, if at all, only marginally effective (Fig. 1 Bd). Similarly, only CD8+ T cells from B6 mice were able to opti-
mally induce ΔΨm loss (from 82 to 59%) and ROS generation (from 8 to 25%, in the absence vs. presence of gp33 peptide). In contrast, ΔΨm loss and ROS generation was much lower when CD8+ T cells from gzmA−/− or gzmB−/− mice were used (ΔΨm: 83 to 77%, ROS: 7 to 13%; in the absence vs. presence of gp33 peptide) and not detectable with CTL from perf−/− mice (Fig. 1 Be). These data demonstrate that for gzm-facilitated loss of plasma membrane and mitochondrial integrity in EL4.F15 target cells during specific CTL attack, the presence of perf is critical. In addition, in the absence of gzmA and gzmB, perf is able on its own or together with as yet unknown factors to induce, though only slightly, ΔΨm loss and ROS generation, however without affecting the survival of target cells (Fig. 1 B, e vs. c).
LCMV-immune CD8⁺ T cells from B6, gzmA⁻/⁻, and gzmB⁻/⁻ mice were incubated with gp33-pulsed or mock-treated EL4.F15 target cells (2 h), and activation of intracellular caspase 3 was assessed using the mAb C92-605. Fig. 2 A shows that effectors from B6 and gzmA⁻/⁻ mice specifically and comparably induced activation of caspase 3 in ~30% of target cells, whereas those from gzmB⁻/⁻ mice did not (Fig. 2 Aa, top). The presence of blocking anti-FasL mAb did not alter activation of caspase 3 by the two CD8⁺ T cell populations (Fig. 2 Aa, bottom). This excludes a contribution of the Fas pathway and suggests that the CTL-mediated effect is solely elicited via the exocytosis pathway (Pardo et al., 2002). When caspase activation in EL4.F15 cells was tested under similar conditions by applying intracellular staining with the caspase 3--specific agent SRH-DEVD-fmk, comparable results were obtained (Fig. 2 Ab, top). Gp33-pulsed but not mock-treated target cells incubated with either B6- or gzmA⁻/⁻--derived LCMV-immune CD8⁺ T cells stained positive for active caspase 3 (44 vs. 6% and 60 vs. 15%, respectively). Again, the presence of blocking anti-FasL mAb did not alter activation of caspase 3 by B6 and gzmA⁻/⁻ CTL (Fig. 2 Ab, middle, + gp33 peptide). In both cases, pretreatment of targets with the specific inhibitor Z-DEVD-fmk (Fig. 2 Ab, orange) leads to a drastic reduction in positively staining cells (Fig. 2 Ab, bottom). Surprisingly and in contrast to results obtained using the specific mAb for active caspase 3, a small fraction of gp33-pulsed EL4.F15 cells (30 vs. 17% for mock-treated cells) also stained positively with SRH-DEVD-fmk after incubation with gzmB⁻/⁻--LCMV-immune CD8⁺ T cells (Fig. 2 Ab, top). However, the number of EL4.F15 cells staining for active caspase 3 were only marginally reduced by the specific inhibitor Z-DEVD-fmk (Fig. 2 Ab, bottom). This finding indicates that the apparent caspase 3 activation observed by using the fluorescent substrate (but not the mAb) is due to unspecific binding of the substrate to a molecule distinct from caspase 3 (Amastad et al., 2001).

The CTL-induced intracellular activation of caspase 9 was monitored by using the specific agent FAM-LEHD-fmk. As shown in Fig. 2 Ac (top) LCMV-immune CD8⁺ T cells from B6 and gzmA⁻/⁻ mice specifically activated caspase 9 in a fraction of EL4.F15 cells (gp33 vs. mock peptide: 52% vs. 28% and 56% vs. 21%, respectively). In both cases, activation was totally inhibited upon pretreatment of EL4.F15 cells with the specific inhibitor of caspase 9, Z-LEHD-fmk (Fig. 2 Ac, bottom, orange). Again, incubation of EL4.F15 cells with gzmB⁻/⁻--derived LCMV-immune CD8⁺ T cells resulted in an increase of target cells staining with FAM-LEHD-fmk (Fig. 2 Ac, top). However, this effect was not or only marginally altered upon pretreatment with the specific inhibitor Z-LEHD-fmk (Fig. 2 Ac, bottom, orange), indicating that FAM-LEHD-fmk binds to a protein(s) distinct from caspase 9 (Amastad et al., 2001). Specific activation of caspase 9 by B6 and gzmA⁻/⁻ CTL was not inhibited in the presence of anti-FasL mAb (Fig. 2 Ac, middle).

To determine whether or not CTL-induced and gzmB-facilitated activation of caspase 3 is also dependent on perf, EL4.F15 cells were cocultured with LCMV-immune CD8⁺ T cells from B6, perf⁻/⁻, and gzmA×B⁻/⁻ mice. Fig. 2 Ab shows that only CTL from B6 mice were able to specifically induce activation of caspase 3, as monitored with the mAb C92-605 in a fraction of EL4.F15 cells (23 vs. 2% for mock-treated cells). Similar results were obtained when SRH-DEVD-fmk was used to detect active caspase 3 (Fig. 2 Bb, top). As expected, the number of cells staining positive with SRH-DEVD-fmk, upon incubation with B6 CTL, was drastically reduced after preincubation of EL4.F15 cells with Z-DEVD-fmk (Fig. 2 Bb, bottom, orange). A considerable increase in positive staining cells for SRH-DEVD-fmk was also seen after incubation with LCMV-immune gzmA×B⁻/⁻--derived CD8⁺ T cells (Fig. 2 Bb, top). However, fluorescence was not altered after preincubation of cells with Z-DEVD-fmk (Fig. 2 Bb, bottom), indicating that SRH-DEVD-fmk binds to a protein(s) distinct from caspase 3.

Similarly, only effector cells from B6 mice were able to specifically induce activation of caspase 9, as observed with FAM-LEHD-fmk (52 vs. 15% for mock-treated cells; Fig. 2 Bc, top), which was inhibited in the presence of Z-LEHD-fmk (52 to 36%; Fig. 2 Bc, bottom, orange). In contrast, LCMV-immune CD8⁺ T cells from perf⁻/⁻ mice did not induce activation of caspase 9. Furthermore, the increase in intracellular staining of EL4.F15 cells for FAM-LEHD-fmk after incubation with gzmA×B⁻/⁻--LCMV-immune CD8⁺ T cells (47 vs. 15% for mock-treated cells) was not inhibited by Z-LEHD-fmk (47 vs. 53%; Fig. 2 Bc, bottom).

GzmB-activated caspases contribute to loss of plasma membrane integrity and mitochondrial membrane potential

We tested if in the course of CTL-mediated cytolysis, activation of caspases is essential for gzm-induced PS exposure on plasma membrane, cell death (PI incorporation), ∆Ψm loss, and ROS generation. For this purpose, LCMV-immune CD8⁺ T cells from B6, gzmA⁻/⁻, or gzmB⁻/⁻ mice were incubated with EL4.F15 cells in the presence of the universal caspase inhibitor Z-VAD-fmk or with the caspase 3 inhibitor Z-DEVD-fmk. As shown in Fig. 3 A (A and B; mean of three independent experiments), the number of annexin V⁺ and PI⁺ cells was drastically reduced by either Z-DEVD-fmk or Z-VAD-fmk when gzmA⁻/⁻--derived CTL were used, only partially in the presence of B6 CTL, and not at all with gzmB⁻/⁻ CTL. Furthermore, ∆Ψm loss and ROS generation induced by B6- and gzmA⁻/⁻-- but not gzmB⁻/⁻--derived CTL were also reduced, though only partially, in the presence of Z-DEVD-fmk or Z-VAD-fmk (Fig. 3 C and D). These data suggest that CTL-mediated induction of plasma membrane perturbation is critically dependent on functional active caspases when elicited by gzmB but not by gzmA and reveals caspase-dependent and -independent mechanisms of gzmB-induced mitochondrial de-
polarization. In both cases, a DEVD-sensitive caspase, in particular caspase 3, may be the main executor of these caspase-dependent processes.

Synergy between caspase 3 and 9 in CTL-mediated target cell lysis

To clarify if the level of active caspase 3 generated during CTL-mediated cytolysis is regulated by caspase 9, which is only produced in its active form after mitochondrial perturbation and cytochrome c release (Li et al., 1997; Boatright et al., 2003), LCMV-immune CD8\(^+\) T cells from B6 and gzmA\(^{-/-}\) mice were incubated with EL4.F15 cells in the presence of the caspase 9 inhibitor Z-LEHD-fmk. As shown in Fig. 3 E, Z-LEHD-fmk (orange) considerably reduced specific activation of caspase 3, as monitored with mAb C92-605. This result was independent of the effector cell population used (from 58 to 25% for B6 CTL and from 55 to 24% for gzmA\(^{-/-}\) CTL; Fig. 3 E, bottom).

To see whether or not the generation of functional active caspase 9 as monitored with the specific substrate FAM-LEHD-fmk was dependent on previous activation of caspase 3, aliquots of the cytotoxicity assay (CML) cultures derived from B6 and gzmA\(^{-/-}\) mice were incubated in the presence of inhibitors for either caspase 3 (Z-DEVD-fmk, gray) or caspase 9 (Z-LEHD-fmk, orange). Fig. 3 F shows that specific induction of caspase 9 activity by both CTL populations (top) is completely inhibited by Z-LEHD-fmk (from 36 to 13% for B6 CTL and from 36 to 14% for gzmA\(^{-/-}\) CTL; Fig. 3 F, middle) and also by Z-DEVD-fmk (from 36 to 16% for B6 CTL and from 36 to 17% for gzmA\(^{-/-}\) CTL; Fig. 3 F, bottom). Together, these results suggest that in CTL-mediated cytolysis activation of caspase 3 is a prerequisite for caspase 9 activation and that the generation of the former caspase is amplified by the latter.

Effect of oxidative stress on gzmA- and gzmB-induced loss of plasma membrane integrity and mitochondrial membrane potential

As shown in the first paragraph of Results, incubation of EL4.F15 cells with either B6, gzmA\(^{-/-}\), or gzmB\(^{-/-}\) LCMV-immune CD8\(^+\) T cells leads to ROS generation. To evaluate the requirement for ROS generation in gzmA- and gzmB-mediated apoptotic processes, the respective CML cultures were incubated with targets (2 h) previously treated with the antioxidant N-acetylcysteine (NAC) and tested for the annexinV\(^+/\)PI\(^-\) phenotype, \(\Delta \Psi_m\) loss, and presence of active caspases 3 and 9. As expected, ROS formation is similarly suppressed after pretreatment of EL4.F15 cells with NAC, irrespective of the source of CTL (Fig. 4 D). The number of cells with the annexinV\(^+/\)PI\(^-\) phenotype was significantly reduced in NAC-treated as compared with mock-treated EL4.F15 cells after culture with B6- and gzmA\(^{-/-}\)-derived CTL and reduced to near background level when cultured with gzmB\(^{-/-}\)-derived...
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with either B6- or gzmA
considerably reduced activation of caspase 9 after incubation
mAb C92-605 fluorescence (Fig. 4 E, left), but resulted in
had no effect on the activation of caspase 3, as monitored by
annexin V-FITC; A) and PI uptake (B) and, in parallel,
caspase 9 activity was determined by using the specific fluorescent sub-
(FITC-labeled mAb against the active form of the enzyme (left), whereas
ting with FAM-LEHD-fmk (Fig. 4 E, right). Upon addi-
case 9 activity was determined by using the specific fluorescent sub-
strate FAM-LEHD-fmk (right) by two-color flow cytometry in the cell popu-
lation negative for CD8 expression (target cells). Numbers correspond to
the percentage of cells positive for the labeling in each case, indicated by
the horizontal bars.

Figure 4. PS exposure induced by gzmB−/− CTL is blocked in the absence of ROS, but mitochondrial depolarization is still observed. Gp33-pulsed
EL4.F15 cells were incubated with ex vivo virus-specific CD8+ cells (MACS selected, ≥95% CD8+ cells) from wild-type B6, gzmA−/−, and/or
gzmB−/− mice for 2 h at a 10:1 effector/target ratio, in the presence
or absence of the ROS scavenger NAC at 15 mM. PS exposure on
plasma membrane (annexin-V-FITC; A) and PI uptake (B) and, in parallel,
ΔΨm loss (DIOC6(3) staining; C) and ROS generation (2′-HE; D) were an-
alyzed by three-color flow cytometry in the cell population negative for
CD8 expression. Results are the mean of two independent experiments
and are given as the difference of percentages in the presence or absence
of gp33 (SD was always lower that 5% of the mean). (E) Alternatively,
CML cultures were incubated in the absence (red or green) or presence
(blue) of NAC (15 mM). Caspase 3 activation was determined using an
FITC-labeled mAb against the active form of the enzyme (left), whereas
or gzmB−/− mice were incubated with gp33 peptide or mock-treated EL4.F15 cells (Fig. 6 A, top) or in the presence of either Z-VAD-fmk or Z-DEVD-
fmk (Fig. 6 A, middle) or after pretreatment of target cells with
NAC (Fig. 6 A, bottom). Target cell survival was estimated by
extended culture under growth conditions unsuitable for CTL
and by adding fresh inhibitors every 24 h. Neither treatment of
target cells with Z-VAD-fmk nor Z-DEVD-fmk was able to res-
cue target cells from death, irrespective of the CTL population
used. Furthermore, pretreatment of EL4.F15 cells with NAC
did not prevent their death by either B6, gzmA−/−, or gzmB−/−
CTL. The lack of inhibition of target cell death was
most likely not due to loss of inhibitor activity of any of the
three agents. This is indicated by the finding that supernatant of
cell cultures still retained most of the inhibitor activity after 24 h
of culture, as tested by its effect on either anti-Fas mAb medi-
atid killing of L1210.Fas cells (Fig. 6 Ba, for Z-VAD-fmk and
Z-DEVD-fmk activities) or on generation of gliotoxin-induced
ROS in EL4.F15 cells (Fig. 6 Bb, for NAC activity). However,
even with this control, the possibility that during CTL-mediated
apoptosis caspases were not completely inhibited and contrib-
ted to cell death cannot be formally excluded.

Discussion

The evolution of multiple strategies by intracellular pathogens
and transformed cells to evade the immune system has brought
about a multitude of effector mechanisms for CTL, the biologically most relevant being the ability to induce apoptosis. By using ex vivo-derived CTL from mice deficient in either gzmA and/or gzmB or perf, we show here that induction of cell death, as monitored by a cell survival assay, only occurs when at least one of the two gzms, gzmA and gzmB, is present, and that perf is the ultimate regulator of the underlying processes. The data reveal that gzmA and gzmB independently induce several similar or distinct morphological and biochemical events now recognized as characteristic features of the apoptotic program, including PS exposure at the plasma membrane, mitochondrial depolarization, caspase activation, and Ape-1 cleavage. Moreover, results obtained with inhibitors of caspasess or ROS generation suggest that individual gzm-facilitated proapoptotic pathways are effective on their own in inducing cell death but that the latter process is amplified by their concerted action. The finding that gzmA×B−/− but not perf−/−-derived CTL express residual potential to induce certain apoptotic features indicates the involvement of additional effector molecules, besides gzmA and gzmB, in perf-mediated cell death. However, these factors do not contribute to cell death of the target used in the present study.

The findings that during CTL-target cell killing, perf-induced plasma membrane disturbance in EL4.F15 target cells, as revealed by PS exposure, occurs faster with gzmB as compared with gzmA and that in the case of gzmB annexin-V reactivity precedes membrane permeabilization are new. Together with the fact that this proapoptotic program was greatly repressed by universal and specific caspase inhibitors only in case of gzmA−/−, but not gzmB−/−, CTL supports recent findings with purified perf and gzms (Sarin et al., 1998; Heibein et al., 1999) and suggests that activation of caspase(s) contributes, together with other pathways (i.e., mitochondria; see below in Discussion), to the accelerated process by gzmB. This finding also emphasizes the notion that CTL-mediated apoptosis elicited in the presence of both gzms is greatly influenced by the quality of the individual target cell (Pardo et al., 2002).

The result that PS exposure on EL4.F15 cells was only marginally increased upon incubation with gzmA×B−/− CTL makes it unlikely that additional molecules, besides gzmA and gzmB, contribute to plasma membrane perturbation. However, because the targeted null mutation of gzmB also affects other downstream genes in the domain, including gzmC, -D, -E, -F, and -G (Pham et al., 1996), their involvement in this CTL-mediated pathway cannot be excluded. Especially as it was recently shown that purified gzmC together with perf induces PS exposure on plasma membrane in a process distinct from gzmB (Johnson et al., 2003). In addition, other gzms, termed orphan gzms (Grossman et al., 2003), such as gzmK and gzmM, with cellular expression patterns distinct from gzmA and gzmB may also facilitate this proapoptotic process (Shresta et al., 1997; MacDonald et al., 1999; Kelly et al., 2004).

The finding that the ROS scavenger NAC completely blocks the induction of PS exposure on plasma membrane of EL4.F15 cells by gzmB−/− but not gzmA−/− CTL is novel and indicates that ROS synergize with gzmA but not gzmB in CTL-induced plasma membrane perturbation. This finding is remarkable in the context of a recent paper demonstrating the coupling of actin cytoskeleton dynamics and the production of ROS in cell death of yeast and most probably also mammalian cells (Gourlay et al., 2004). Thus, we speculate that gzmA is destabilizing the actin cytoskeleton in target cells by cleaving a yet unknown substrate, leading to depolarization of mitochondrial membrane and ROS generation, and that the latter amplifies PS exposure at the plasma membrane, thereby accelerating cell death and/or uptake of targets by phagocytes via the PS receptor (Savill and Fadok, 2000; Danial and Korsmeyer, 2004). Alternatively, as the SET complex, a major substrate of gzmA (Fan et al., 2002, 2003a,b), is associated with the ER, gzmA may initiate apoptotic processes by perturbing ER membrane and inducing Ca2+ release from ER stores. This cell death pathway is elicited by interorganelle flow of Ca2+ and facilitated by direct physical connections between ER and mitochondria (Newmeyer and Ferguson-Miller, 2003), leading to caspase-independent ΔΨm loss and ROS generation (Demaurex and Distelhorst, 2003; Orrenius et al., 2003).
Mitochondria are implicated in CTL-mediated pathways of apoptosis, but the contribution of ΔΨm loss and ROS generation to this process is still controversial (MacDonald et al., 1999; Barry et al., 2000; Heibein et al., 2000; Danial and Korsmeyer, 2004). The data that gzmA−/− and gzmB−/−, but not perf−/−, CTL induce ΔΨm reduction and ROS generation in EL4.F15 target cells to a similar extent indicates that both processes are dependent on perf, but are similarly and independently elicited by gzmA or gzmB. In addition, the finding that activation of the mitochondrial pathway is inhibited, at least partially, by Z-VAD-fmk and DEVD-fmk in the case of gzmA−/− but not gzmB−/− CTL argues that gzmA and gzmB induce ΔΨm loss via distinct molecular pathways. Furthermore, it indicates that gzmA induces mitochondrial depolarization in a caspase-independent manner, whereas gzmB may use both caspase-dependent and -independent pathways and supports previous findings (Heibein et al., 1999; Barry et al., 2000; Alimonti et al., 2001; Pinkoski et al., 2001; Goping et al., 2003; Sutton et al., 2003). Understanding how these complex processes induced by gzmA and gzmB interrelate and facilitate target cell lysis by CTLs requires further analysis.

The present demonstration that CTL from B6 and gzmA−/−, but not from gzmB−/−, perf−/−, or gzmA×B−/−, mice induced activation of caspase 3 and 9 in EL4.F15 cells corroborates and extends previous work with purified proteins and CTL on the differential effect of gzmA and gzmB in the perf-facilitated caspase pathway (Heibein et al., 1999; Pardo et al., 2002; Goping et al., 2003; Metkar et al., 2003; Sutton et al., 2003). However, because the targeted null mutation of gzmB also affects other downstream gzm genes in the domain (gzmC-G; Pham et al., 1996), their putative effect on these processes cannot be assessed. Activation of caspase 3 and 9 by wild-type B6 and gzmA−/− CTL was completely blocked by pretreatment of EL4.F15 cells with the caspase 3–specific inhibitor Z-DEVD-fmk. In contrast, using similar conditions, the caspase 9–specific inhibitor Z-LEHD-fmk completely inhibited activation of caspase 9, but only partially that of caspase 3. Thus we conclude that in gzmB-mediated cytolysis, activation of caspase 3 is an early event in target cell apoptosis and is a prerequisite for the generation of the caspase 9 apoptosome—most likely via mitochondrial permeabilization—which in turn cleaves additional procaspase 3. Such an amplification loop between caspase 3 and 9 has been proposed before with purified gzmB and perf (Metkar et al., 2003).

Ape-1, a multifunctional component of the SET complex (Fan et al., 2003b) expressing both endonuclease activity and the potential to repair oxidative damage to DNA and oxidative changes to transcription factors (Bennett et al., 1997; Hirota et al., 1997; Evans et al., 2000), is similarly cleaved in EL4.F15 cells, irrespective of whether CTL from either B6, gzmA−/−, or gzmB−/− mice are used as effectors. Cleavage of Ape-1 was also observed, though at reduced levels, with gzmA×B−/− CTL, but was absent in perf−/− CTL. Fan et al. (2003b) have shown that gzmA specifically binds Ape-1 and destroys its known oxidative repair function by proteolytic cleavage. Our data indicate that CTL contain additional enzymatic activity(ies) distinct from gzmA and gzmB-G, such as gzmK (Shresta et al., 1997), which is able to block cellular repair in a perf-dependent manner. However, this gzmA/gzmB-independent process does not seem to be relevant for the induction of cell death, as demonstrated by survival of EL4.F15 cells after their incubation with gzmA×B−/− CTL (Fig. 2 C).

The lack of inhibition of CTL-mediated cell death of EL4.F15 cells, as monitored by target cell survival, by either the universal caspase inhibitor Z-VAD-fmk, the caspase 3 inhibitor DEVD-fmk, or the antioxidant agent NAC when effector cells from B6, gzmA−/−, or gzmB−/− mice were used emphasizes the multitude of gzmA- and gzmB-facilitated effector pathways elicited by CTL. Moreover, the data reiterate the notion that gzmB-induced cell death similarly occurs via caspase-
dependent and -independent intracellular processes, whereas all gzmA-induced cell death events are caspase independent and also occur in the absence of ROS generation. This enormous versatility of CTL probably evolved in response to the multiple strategies of pathogens and tumors to evade immune-mediated apoptosis (Benedict et al., 2002; Igney and Krammer, 2002; Trapani and Smyth, 2002).

In conclusion, the present study is the first account on gzmA- and/or gzmB-initiated intracellular processes during CTL-target cell interaction, a model of which is schematically represented in Fig. 7. Although the biological significance of the multiple overlapping and nonoverlapping proapoptotic pathways observed with ex vivo–derived CTLs reported herein for their in vivo performance is still elusive, this type of in vitro cytotoxic assay should help to provide a physiologically relevant perspective for gzm-mediated control of infections and cancer.

Materials and methods

Mouse strains

Inbred C57BL/6 (B6) and mouse strains deficient for perf (perf−/−), gzmA (gzmA−/−), gzmB (gzmB−/−), and gzmA−/B (gzmA−/B−/−) bred on the B6 background were maintained at the Max-Planck-Institut für Immunobiologie and analyzed for their genotypes as described previously (Simon et al., 1997; Balkow et al., 2001). Male mice of 8 to 10 wk of age were used in all experiments and were conducted in accordance with the ethical guidelines of the Federation of European Laboratory Animal Science Association.

Generation of ex vivo CD8+ cells

Mice were infected with 10⁵ pfu LCMV-WE i.p. according to established protocols (Balkow et al., 2001). On day eight after infection, CD8+ cells were positively selected from spleen using α-CD8-MicroBeads (Miltenyi Biotec) with an autoMACS (Miltenyi Biotec) and resuspended in MEM/2 mg/ml BSA before use in cytotoxic assays. Purity of selected CD8+ cells was assessed by FACS staining and found to be between 95–98%.

Target cells

The mouse tumor lines EL4.F15 and L1210.Fas were used as target cells (Pardo et al., 2002). Cell lines were cultured in MEM supplemented with 10% heat-inactivated FCS and 2-mercaptoethanol (10⁻⁵ M) at 7% CO₂, as described previously (Pardo et al., 2002).

CMLs

The DNA release assay and the target cell survival assay was performed as described previously (Müllbacher et al., 1999). For LCMV-immune CTL-mediated lysis, target cells were pretreated with the synthetic peptide KAVYNTATC [gp33] as described previously (Balkow et al., 2001).

Online supplemental material

For analysis of intracellular apoptotic processes in target cells, effector and target cells were incubated at a ratio of 10:1 (effector/target) and aliquots of CML cultures (10⁵ targets/experimental point) were stained with anti-CD8 mAb. CD8-negative targets were subsequently analyzed for proapoptotic processes and cell death, including plasma membrane disintegration, mitochondrial perturbation, caspase activation, Apel cleavage, and thymidine release/cell survival. Online supplemental material consists of the following methods: [3H] DNA release and cell survival assay; analysis of inhibitor stability; flow cytometry, including cell surface phenotype analysis, exposure/incorporation of annexin V/PI, and reduction of mitochondrial membrane potential/generation of ROS (i.e., ∆Ψm/ROS); activation of caspases; and proteolytic degradation of Apel-1. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200406115/DC1.

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Materials and methods

**[H] DNA release and cell survival assays**

[1H] DNA release assay was described previously (Pardo et al., 2002). Percentage of specific lysis was calculated by the following formula: % specific lysis = ([experimental release - medium release] / [maximum release - medium release]) × 100. Data given are the means of triplicate determinations. SEM values were always <2%.

Target cell survival assay was performed as described previously (Mullichaker et al., 1999). Caspase inhibitors (Z-DEVD-fmk and Z-VAD-fmk [Bachem] and Z-LEHD-fmk [BD Biosciences]) or ROS scavengers (N-acetylcysteine [NAC]; Sigma-Aldrich) were used. Target cells were preincubated with the respective agent for 1 h at indicated concentrations before the addition of effector cells. For cell survival assays, fresh inhibitor was added every 24 h in order to ensure the permanent presence of active inhibitor. In some experiments, effector cells were preincubated for 30 min in 20 ng/ml of v-FAS antibody MFL-3 (BD Biosciences) or Ig isotype control (hamster IgG; Dianova) before their addition to target cells.

**Analysis of inhibitor stability**

For monitoring inhibitor stability, aliquots of cell culture supernatants [SN] were taken 24 h after incubation and inhibitor activity was released. Z-VAD-fmk and ZDEVD-fmk was tested for its potential to inhibit caspase-mediated apoptosis in L1210.Fas cells. NAC was tested for its potential to inhibit gliotoxin-induced ROS generation in BuL15 cells. Accordingly, L1210.Fas cells were incubated with anti-Fas mAb [1 μg/ml Jo-2 (BD Biosciences)] for 20 h in the presence or absence of 100 μM of either Z-VAD-fmk or ZDEVD-fmk or with SN (24 h) of cell cultures. BuL15 cells were incubated for 3 h with glutathione [100 or 200 μM] in the presence of either NAC (15 mM) or SN (24 h) of cell cultures.

**Flow cytometry**

All mAbs were obtained from BD Biosciences. In all cases, cells were incubated with control antibody clone 2.4G2) before the first staining step. In all cases, labeled cells were examined in the FACSCalibur (Becton Dickinson) and analyzed with CellQuest software (Becton Dickinson).

**Phenotypic analysis**

The phenotypes of ex vivo-derived LCMV-immune spleen cells was determined by FACS, analyzed before and after enrichment of CD8+ T cells using the following mAbs: FITC-labeled αCD4 (clone H129.19), αCD25/αCD122 (clone RA3-6B2), αCD44/αCD69 (clone 1D3), αCD8-APC (clone 53–6.7), or αCD45RITC (clone 53–6.7). All fluorescence-conjugated mAbs were diluted in PBS/1% FCS/0.1% sodium azide to final concentrations of 2–5 μg/ml. Stained cells were fixed in PBS containing 1% PFA, examined in the FACSCalibur and analyzed with CellQuest software.

**Detection of LCMV-immune CTL**

Detection of LCMV-immune CTL was conducted by double staining with αCD8-APC (clone 53–6.7) and gp33-labeled tetramers (H-2Db, tel-PE; Altman et al., 1999).

**Annexin V (FLICA) and / or ROS**

Phosphatidyl serine (PS) exposure on plasma membrane and incorporation of propidium iodide (PI), changes in their Δψm, and the levels of reactive oxygen species (ROS) were measured by three-color flow cytometry. After preincubation of aliquots from CML cultures with αCD4-APC mAb, cell mixtures were incubated with either Annexin V-FLICA and PI according to the manufacturer’s protocol (BD Biosciences) or with 2 μM of hydroxyethidine [detection of ROS; Molecular Probes] and 10 nM DIOC6 (3,3'-dihexyloxacarbocyanine Molecular Probes) for 30 or 15 min, respectively. Fluorescence was measured using a FACSCalibur and analyzed with CellQuest software.

**Activation of caspases**

Intracellular activation of caspase-3 and caspase-9 was monitored using the fluorescence substrates S Hirudin-fmk and FAMDEVD-fmk (BioCarta), respectively, according to the instructions of the manufacturers. To control for specificity of the individual enzymes, target cells were preincubated with the respective inhibitors (Z-DEVD-fmk for caspase-3 and ZLEHD-fmk for caspase-9) before the addition of fluorescent substrate. Before FACS analysis, cells were labeled with αCD8-APC mAb, washed with PBS, and fixed with 1% PFA in PBS.

Intracellular activation of caspase-3 was monitored using a FITC-labeled rabbit antibody preparation (clone C92-605; BD Biosciences); Ig isotype antibody (BD Biosciences) served as control. Aliquots of CML cultures were labeled with αCD4-APC mAb and washed (PBS) and fixed for 15 min with PFA 2.5% in PBS. After repeated washings, cells were permeabilized for 10 min with 1% of 0.1% saponin in PBS and analyzed with FACS by using a FACSCalibur with Cell Quest software.

**Proteolytic degradation of Ape-1**

For the analysis of Ape-1 cleavage, a polyclonal rabbit antibody (H-300; Santa Cruz Biotechnology, Inc.) was used. Aliquots of CML cultures were treated with αCD8-APC mAb, washed with PBS, and fixed for 15 min with 1% PFA in PBS. Cells were washed and permeabilized with 100 μl of 0.1% saponin in PBS + 5% goat serum for 10 min on ice. 2 μl of anti-Ape-1 or 0.4 μl of rabbit IgG isotype control antibody (1 mg/ml) were added for 25 min at RT. Cells were washed twice with 0.02% saponin in PBS and resuspended in 100 μl of 1% goat serum + 5% FCS, resuspended in 100 μl of 1% FCS in PBS, and analyzed by FACS using a FACSCalibur with Cell Quest software.

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