REVIEW

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Apoptosis pathways in cancer and cancer therapy

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Abstract Activation of apoptosis pathways is a key mechanism by which cytotoxic drugs kill tumor cells. Also immunotherapy of tumors requires an apoptosis sensitive phenotype of target cells. Defects in apoptosis signalling contribute to resistance of tumors. Activation of apoptosis signalling following treatment with cytotoxic drugs has been shown to lead to activation of the mitochondrial (intrinsic) pathway of apoptosis. In addition, signalling through the death receptor (extrinsic) pathways, contributes to sensitivity of tumor cells towards cytotoxic treatment. Both pathways converge finally at the level of activation of caspases, the effector molecules in most forms of cell death. In addition to classical apoptosis, non-apoptotic modes of cell death have recently been identified. Mechanisms to overcome apoptosis resistance include direct targeting of antiapoptotic molecules expressed in tumors as well as re-sensitization of previously resistant tumor cells by re-expression of caspases and counteracting apoptotis inhibitory molecules such as Bcl-2 and molecules of the IAP family of endogenous caspase inhibitors. Molecular insights into regulation of apoptosis and defects in apoptosis signalling in tumor cells will provide novel approaches to define sensitivity or resistance of tumor cells towards antitumor therapy and provide new targets for rational therapeutic interventions for future therapeutic strategies.

Keywords Apoptosis · Cancer therapy · Resistance mechanisms · Cytotoxic drugs · Immunotherapy · Apoptosis defects

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Introduction

Killing of tumor cells by diverse cytotoxic approaches such as anticancer drugs, γ -irradiation, suicide genes, or immunotherapy has been shown to be mediated through induction of apoptosis in target cells [1, 2, 3, 4, 5, 6, 7]. Apoptosis or programmed cell death is a distinct, intrinsic cell death program that occurs in various physiological and pathological situations [8]. The underlying mechanism for initiation of an apoptosis response upon cytotoxic therapy may vary for different stimuli and is only partially understood. However, damage to DNA or to other critical molecules and/or subcellular structures appears to be a common early hit by some inducers which is then propagated by the cellular stress response [9]. Multiple stress-inducible molecules-e.g., INK, MAPK/ERK, NFkB, or ceramide-may have a profound impact on apoptosis pathways [2, 10, 11, 12]. On the other hand, cytotoxic T cells or NK cells may release compounds such as granzyme B which directly activates downstream apoptosis effector mechanisms inside the cell [8]. Apoptosis is characterized by typical morphological and biochemical hallmarks including cell shrinkage, nuclear DNA fragmentation, and membrane blebbing [8]. Protelolytic enzymes such as caspases play an important role as effector molecules in apoptosis including cytotoxic therapy-induced cell death [13, 14, 15, 16, 17, 18, 19]. Because of the potentially detrimental effects on cell survival in case of inappropriate caspase activity, activation of caspases has to be tightly controlled. The antiapoptotic mechanisms regulating activation of caspases have also been postulated to be involved in drug resistance to tumor cells [20, 21, 22]. However, the concept that anticancer therapies primarily act by triggering apoptosis has also been challenged, since a consistent link between the ability of tumor cells to undergo apoptosis in vitro and their susceptibility to anticancer therapy in vivo has not always been observed [23]. Therefore, nonapoptotic modes of cell death-e.g., necrosis or some forms of cell

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death that cannot be easily classified at present—may mediate the cell death response to cytotoxic therapy [24, 25]. Also, non-caspase-dependent apoptosis has been found to be induced by anticancer drugs in some cells [26, 27, 28]. Thus, a better understanding of these diverse modes of tumor cell death following cytotoxic therapies will provide a molecular basis for new strategies targeting caspase-dependent and independent death pathways in apoptosis-resistant forms of cancer.

Mechanisms of apoptosis

Most signaling pathways activated by anticancer drugs ultimately result in activation of caspases, a family of cysteine proteases that act as common death effector molecules in various forms of cell death [8, 13, 14, 15, 16, 17, 18]. Caspases are synthesized as inactive zymogens and activated by proteolytic cleavage-i.e., cleavage between the large and the small subunit followed by cleavage between the large subunit and the prodomain [13, 14, 15, 16, 17, 18]. Caspases involved in apoptosis signaling are currently categorized into initiator and effector caspases, respectively [13, 14, 15, 16, 17, 18]. Initiator caspases transduce various signals into protease activity and are directly linked to deathinducing signaling complexes (DISCs): caspase-8 or caspase-10 via their death effector domain (DED) interact with adaptor proteins (FADD), recruited and bound to activated death receptors, while caspase-9 is recruited to the apoptosome via its CARD domain [13]. Effector caspases cleave various cytoplasmatic or nuclear substrates, which mark many of the morphologic features of apoptotic cell death [13, 14, 15, 16, 17, 18]. For example, polynucleosomal DNA fragmentation is initiated by cleavage of ICAD (inhibitor of caspase-activated DNase), the inhibitor of the endonuclease CAD (caspase-activated DNase) that cleaves DNA into the characteristic oligomeric fragments [8]. DNA condensation is caused by AIF, a mitochondrial protein that translocates to the nucleus upon death triggering, and by Acinus, which stands for "apoptotic chromation condensation inducer in the nucleus" [29, 30]. AIF may also mediate caspaseindependent cleavage of DNA into larger fragments [29, 30]. Likewise, loss of overall cell shape is due to proteolysis of cytoskeletal proteins including fodrin, gelsolin, actin, plectrin, and cytokeratin, while nuclear shrinking and budding occurs after degradation of lamin [8].

Activation of caspases can principally be triggered by two different mechanisms. According to the induced proximity model, initiator caspases such as caspase-8 or caspase-9 are activated in a multimeric complex—e.g., caspase-8 in the death-inducing signaling complex (DISC) and caspase-9 in the apoptosome [8, 13, 31, 32, 33]. Alternatively, caspases are activated by catalytic processing of the zymogens at specific cleavage sites [13]. Caspase activation can be initiated through different

entry sites-e.g., at the plasma membrane by death receptor mediated signaling (receptor pathway) or at the mitochondria (mitochondrial pathway) [8, 13]. Stimulation of death receptors of the tumor necrosis factor (TNF) receptor superfamily such as CD95 (APO-1/Fas) or TRAIL receptors results in receptor aggregation and recruitment of the adaptor molecule Fas-associated death domain (FADD) and capase-8 [31, 32, 33]. Upon recruitment, caspase-8 becomes activated and initiates apoptosis by direct cleavage of downstream effector caspases [31, 32, 33]. The mitochondrial pathway is initiated by the release of apoptogenic factors such as cytochrome c, apoptosis-inducing factor (AIF), Smac/ Diablo, Omi/HtrA2, endonuclease G, caspase-2 or caspase-9 from the mitochondrial intermembrane space [34, 35, 36, 37, 38, 39]. The release of cytochrome c into the cytosol triggers caspase-3 activation through formation of the cytochrome-c/Apaf-1/caspase-9-containing apoptosome complex [40, 41]. Smac/Diablo and Omi/ HtrA2 promote caspase activation by neutralizing the inhibitory effects on IAPs, while AIF and endonuclease G cause DNA condensation [30, 38, 39, 42, 43].

The receptor and the mitochondrial pathway can be interconnected at different levels [44]. Following death receptor stimulation, activation of caspase-8 may result in cleavage of Bid, a BH3 domain containing protein of the Bcl-2 family, which assumes cytochrome-*c*-releasing activity upon cleavage, thereby initiating a mitochondrial amplification loop [43, 44]. In addition, mitochondria-triggered caspase-6 cleavage may feed back to the receptor pathway by cleaving caspase-8 [16].

Signaling pathways in cancer therapy

Apoptosis in response to cancer therapy proceeds through activation of the core apoptotic machinery including the receptor and the mitochondrial signaling pathway [2, 3, 4,]. The relative contribution of the receptor and the mitochondrial pathway to drug-induced apoptosis has been a subject of controversial discussion [2, 3, 4,]. While a number of initial studies suggested that cancer therapy-triggered apoptosis involves activation of the CD95 receptor/ligand system, compelling evidence subsequently indicated that the majority of cytotoxic drugs initiate cell death by triggering the cytochrome-c/Apaf-1/caspase-9-dependent pathway through the mitochondria [45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68]. To this end, targeted disruption of genes involved in the mitochondrial pathway points to a crucial and indispensable role of this pathway for apoptosis in response to anticancer drug treatment [66, 67]. Caspase- $9^{-/-}$ embryonic stem cells and Apaf- $1^{-/-}$ thymocytes are resistant to cytotoxic drugs but remain sensitive to death receptor triggering [66, 67]. In contrast, FADD^{-/-} and caspase-8^{-/-} embryonic fibroblasts are refractory to death receptor stimulation, but equally sensitive to cytotoxic drugs suggesting that the death receptor pathway has a dispensable role in druginduced apoptosis, at least in these particular nontransformed cells [64, 65]. However, the relative contribution of the death receptor versus the mitochondrial pathway may depend on the cytotoxic drug, dose, and kinetics, or on differences between certain cell types similar to the cell type-dependent signaling in the CD95 pathway [52, 68]. Importantly, this amplification of the chemoresponse through activation of the CD95 system may be clinically meaningful, since it may critically affect the time required for execution of the death program. Multiple proapoptotic and antiapoptotic signaling paths as discussed below regulate the net outcome of signaling through the core apoptotic machinery [2, 4].

Proapoptotic signaling in cancer therapy

Caspases

Given the important role of caspases as effector molecules in various forms of cell death including drug-induced apoptosis, the ability of anticancer agents to trigger caspase activation appears to be a critical determinant of sensitivity or resistance to cytotoxic therapies [2, 4]. As a consequence, inhibition of caspase activation may be an important factor in chemoresistance [2, 4].

Expression levels of individual caspases may have an impact on their overall activity, since deficient expression levels of caspases may simply impair activation of caspases [69, 70, 71]. For example, MCF-7 breast carcinoma cells completely lack caspase-3 expression due to a frameshift mutation within exon 3 of the caspase-3 gene [70]. These cells can be sensitized by transfection of pro-caspase-3 toward treatment with cytotoxic drugs [71]. Moreover, caspase expression may be impaired by epigenetic alterations such as promoter hypermethylation. Accordingly, caspase-8 expression was found to be frequently inactivated by hypermethylation of regulatory sequences of the caspase-8 gene in a number of different tumor cells derived from neuroblastoma, malignant brain tumors, Ewing tumors, and small lung cell carcinoma both in vitro and also in vivo in primary tumor samples [72, 73]. Importantly, restoration of caspase-8 expression by gene transfer or by demethylation treatment, sensitized resistant tumor cells to death receptor-induced or drug-induced apoptosis [73]. Conversely, enhanced transcription of caspase genes in response to cytotoxic treatment may increase expression levels [74]. Thus, treatment with IFN- γ resulted in enhanced expression of caspase proteins mediated by direct activation of Stat-1, a downstream transcription factor involved in IFN- γ signaling [75]. Moreover, transcriptional upregulation of caspase-3 or caspase-8 was found upon drug treatment independent of Stat-1 [76].

Antiapoptotic signaling in cancer therapy

Bcl-2 proteins

Bcl-2 family proteins play a pivotal role in the regulation of the mitochondrial pathway, since these proteins localize to intracellular membranes, in particular the mitochondrial membrane [77]. They comprise both antiapoptotic members-e.g., Bcl-2, Bcl-X_L, and Mcl-1-as well as proapoptotic molecules such as Bax, Bek, and Bad, and BH3 domain-only molecules which link the death receptor pathway to the mitochondrial pathway (Bid, Bim, Puma, and Noxa) [77]. Upon apoptosis induction, proapoptotic Bcl-2 proteins with multidomains such as Bax translocate from the cytoplasm to the outer mitochondrial membrane, where they oligomerize to form a pore-like structure, thereby promoting cytochrome-c release [78]. This translocation to mitochondria can be triggered by Bcl-2 proteins, which have a BH3 domain only [77]. BH3 domain-only proteins include Bid, which is activated by caspase-8-mediated cleavage; Bim, a microtubule-associated protein, or Noxa and PUMA, two p53-induced proteins [77]. Bcl-2 or Bcl-X_L exert their antiapoptotic function, at least in part, by sequestering BH 3 domain-only proteins in stable mitochondrial complexes, thereby preventing activation and translocation of Bax or Bak to mitochondria [78]. In addition, Bcl-2 and Bcl-X_L block apoptosis by preventing cytochromec release through a direct effect on mitochondrial channels such as the voltage-dependent anion channel (VDAC) or the permeability transition pore complex (PTPC) [35, 36]. Mutations or altered expression of proapoptotic or antiapoptotic Bcl-2 family proteins can drastically alter drug response in experimental systems [79]. In addition, several clinical correlative studies have provided support that high level expression of antiapoptotic Bcl-2 proteins confers a clinically important chemoresistant phenotype on cancer cells, including AML, ALL, CLL, multiple myeloma, prostate carcinoma, malignant brain tumors, and neuroblastoma [22, 80, 81, 82]. Likewise, reduced Bax levels have been associated with poor responses to chemotherapy and shorter overall survival in breast or colorectal carcinoma [83]. Conversely, enhanced Bax levels correlated in several cell types with response to chemotherapy in vivo [84].

Inhibitor of apoptosis proteins (IAPs)

Inhibitor of apoptosis proteins (IAPs) have been reported to directly inhibit active caspase-3 and caspase-7 and to block caspase-9 activation [85, 86, 87]. In addition to regulation of apoptosis, IAP members such as survivin have been found to be involved in the regulation of mitosis [87]. The activity of IAPs are controlled at various levels—e.g., by the transcription factor NFkB that has been reported to stimulate expression of cIAP1, cIAP0, and XIAP [85]. IAPs are negatively regulated by

caspase-mediated cleavage [85]. In addition, Smac/Diablo and Omi, two proteins released from mitochondria upon apoptosis induction, neutralize IAPs through binding to IAPs thereby displacing them from their caspase partners [86]. Likewise, XAF1 has been found to displace IAPs from bound caspases in the nucleus [86]. Inhibition of apoptosis by IAPs in response to cytotoxic therapy has been suggested by several experimental studies [88, 89, 90, 91]. XIAP, cIAP1, or cIAP2 suppressed apoptosis in vitro following treatment with cisplatin, cytarabine, TRAIL, or staurosporine, or after γ -irradiation [92, 93]. Also, increased IAP expression correlated with poor treatment response in myeloid leukemia cells, and elevated survivin expression predicted adverse prognosis in several tumors-e.g., neuroblastoma, AML, colon, lung and esophagus carcinoma [88, 89, 90, 91].

The discovery that the IAP-inhibitor Smac/Diablo, one of the photogenic factors released from mitochondria, is required to fully activate caspases in many instances, has prompted interest in expressing Smac/ Diablo in the erythroplasma of tumor cells to overcome IAP-mediated inhibition of apoptosis induction in tumors. Thus, cytoplasmic localization of Smac by transfection-enforced overexpression or by using cell permeable peptides as Smac agonists has shown efficacy in sensitizing previously resistant tumors to apoptosis induction [92, 93].

NFkB

The ability of the transcription factor NFkB to suppress apoptosis is thought to confer resistance to cytotoxic therapies [96]. As outlined above, NFkB may be constitutively active in certain tumor types such as pancreatic carcinoma [96]. In addition, NFkB activity is induced in response to a variety of stimuli-e.g., in response to cellular stress and anticancer agents [96]. NFkB is composed of heterodimers or homodimers of the NFkB/Rel family of proteins, which mediate protein dimerization, nuclear import, and specific DNA binding [96]. In most cell types, NFkB is sequestered in the cytoplasm by its interaction with IkB proteins and therefore remains inactive [96]. Upon stimulation, IkB becomes phosphorylated following activation of the IKK complex and is degraded via the proteasome, thereby releasing NFkB to translocate into the nucleus for transcription of target genes [96]. NFkB target genes include several antiapoptotic proteins-e.g., cIAP1, cIAP2, TRAF1, TRAF2, Bfl-1/A1, Bcl-X_L, and FLIP [96]. Interestingly, NFkB also controls promoter activation of certain proapoptotic factors such as CD95L, CD95, TRAIL-R1, and TRAIL-R2, an observation consistent with reports that NFkB can promote apoptosis under certain circumstances [96]. The NFkB-signaling pathway has been linked to death receptor signaling because RIP, which serves as an adaptor molecule for the TNFRI receptor to the NFkB pathway, can be cleaved by caspases, thereby modulating the balance between proapoptotic and antiapoptotic signals upon TNF receptor signaling and may even stimulate an autocrine "death loop" [96]. Since certain types of anticancer treatments result in induction of NFkB transcriptional activity, inhibition of NFkB in parallel with chemotherapy strongly enhanced the cytotoxic effect of chemotherapy [96]. Thus, NFkB may play an important role in inducible chemoresistance, and inhibition of NFkB may serve as a potential new adjuvant approach to chemotherapy [2, 4, 96].

Caspase-independent and nonapoptotic modes of cell death

Although a large body of data points to an essential role of caspase-dependent apoptosis in mediating tumor cell death upon cytotoxic therapy, this concept has also been challenged [1, 2, 3, 4, 5, 6, 7, 23]. Thus, a clear, consistent link between the cells' ability to undergo apoptosis and their susceptibility to anticancer therapy could not be observed [23]. In addition, p53 status did not always correlate with the ability of a tumor cell to respond to treatment [97]. Cells harboring wild-type p53 may fail to respond, and those lacking functional p53 may even respond better [97]. Thus, "nonclassical apoptosis," or nonapoptotic modes of cell death-e.g., necrosis or some forms of cell death that cannot be easily classified at present-have also been taken into consideration as a response to cytotoxic therapy [23, 24, 25, 26, 27, 28]. Also, delayed suppression of tumors upon irradiation, for example, has been taken as evidence against a predominant apoptotic mode of cell death, since apoptosis appears to be induced fairly rapidly in vitro and in vivo upon appropriate stimulation [23]. Although the signaling pathways and molecules involved in these alternative forms of cell death have not yet been exactly defined, noncaspase proteases such as calpains and cathepsins, Bax or Bax-like molecules, and AIF or endonuclease G may be involved [8, 23, 24, 25, 26, 27, 28]. The relative contribution of these different modes of cell death for chemoresponses in vitro and in vivo remains to be defined.

Conclusion

Numerous studies over the last years have indicated that anticancer therapies primarily act by activating the apoptosis response pathway in tumor cells [1, 2, 3, 4, 5, 6, 7]. However, several points remain to be addressed in future studies: Firstly, most of the apoptosis signaling components have not been studied in clinical samples [2, 4, 6, 7, 22]. Secondly, while many experimental studies indicate that alterations in components of the apoptotic machinery have an impact on sensitivity of tumor cells toward cytotoxic therapy, this premise remains to be tested in clinical settings [1, 2, 3, 4, 5, 22]. Moreover, the biology that determines the individual responses of different tumors to cytotoxic therapies warrants further investigation to provide the basis for more specific therapeutic interventions. In this context, the multiple connections between death receptor signaling and the cellular stress response and even cytokine mediated modulation of pathways may be particularly important in vivo [98, 99, 100].

Finally, the concept that "classical" apoptosis represents the major mechanism by which tumor cells are eliminated by cytotoxic therapies may not universally apply and thus caspase-independent modes of cell death should also be considered [23, 24, 25, 26, 27, 28]. Nonetheless, studies on the regulation of apoptosis signaling pathways triggered by anticancer therapies have provided substantial insights into the molecular mechanisms regulating the response of tumor cells toward current therapies. Future studies on the role of apoptosis signaling molecules in individual tumors both in vitro and in vivo in tumor cells of patients undergoing chemotherapy—e.g., using DNA microarrays or proteomic studies-may provide the basis for "tailored" tumor therapy and may identify new targets for therapeutic intervention.

In addition to the identification of novel therapeutic strategies, it is expected that a more in-depth understanding of apoptosis signaling will help us to molecularly guide established therapies using chemotherapeutical drugs and irradiation. Altering the thresholds of tumor cells to apoptosis induction by interference with apoptosis resistance to sensitize tumor cells to established therapy protocols is expected to contribute to progress in cancer therapy in the future.

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