

Targeting c-FLIP in cancer

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Abbreviations: CDDP, cisplatin; VP16, etoposide; 5FU, 5-Fluorouracil; DISC, Death-Inducing Signaling Complex; DcR2, TRAIL-R4 or Decoy Receptor 2; DR5, TRAIL-R2; DR4, TRAIL-R1.

Abstract

Cellular-FLICE inhibitory protein (c-FLIP) is a key anti-apoptotic regulator that inhibits cell death mediated by the death receptors Fas, DR4, DR5, and TNFR1. Three splice variants of c-FLIP function at the DISC level by blocking the processing and activation of procaspase-8 and -10. Overexpression of c-FLIP has been identified in many different tumor types, and its downregulation in vitro has been shown to restore apoptosis mediated by CD95L and TRAIL. c-FLIP therefore represents a promising target for cancer therapy. This review focuses on the molecular mechanisms that control c-FLIP expression and current research into inhibitors of the protein. Increasing evidence supports the investigation of c-FLIP as a therapeutic target to restore an apoptotic response in cancer cells.

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1 Introduction

Apoptosis is crucial for tissue homeostasis and normal development. Two major signaling pathways engage the apoptotic program: the mitochondrial-dependent intrinsic pathway that is activated upon intracellular signals, and the extrinsic pathway that is triggered upon binding of ligands such as TRAIL, Fas, and TNF α with their cognate death receptors at the cell surface. Ligand binding induces oligomerization of the receptors, allowing the formation of macromolecular complexes formed by homotypic interactions by means of the Death Domain (DD) and Death Effector Domains (DEDs) of adaptor proteins such as FADD or TRADD, initiator caspases, the procaspase-8 and -10. Binding of Fas ligand and TRAIL to death receptors recruits initiator caspases to the membrane, within the death-inducing signaling complex (DISC) (Figure 1A). Upon assembly of the DISC, the dimerization and transproteolytic cleavage of procaspase-8 results in the release of the catalytically active p10-p18 subunit heterotetramer [1]. Recruitment and activation of initiator caspases upon TNF-R1 engagement takes place in complex II, a cytosolic complex generated sequentially from TNF-R1 DISC, which at the membrane contains TRADD and RIP but lacks FADD and caspase-8 [2]. This event triggers a proteolytic cascade, leading to the activation of executioner caspases-3 and -7, which drive apoptotic cell death (Figure 1A).

2 c-FLIP

2.1 *c-FLIP isoforms*

c-FLIP, also known as Casper, iFLICE, FLAME-1, CASH, CLARP, MRIT or usurpin, is a crucial negative regulator of the apoptotic pathway [3]. Thirteen splice variants of the gene have been identified, but only three of these have been shown to be translated to protein. These are c-

FLIP_L, c-FLIP_S, and c-FLIP_R (Figure 1B). c-FLIP_L is a 55 kDa protein that is structurally similar to procaspase-8, with two N-terminal DED domains and a C-terminal caspase-like domain [4]. The C-terminal domain of c-FLIP_L lacks the catalytic cysteine residue, which confers the proteolytic activity of caspases. c-FLIP_L is thus devoid of enzymatic activity. c-FLIP_S (26 kDa) and c-FLIP_R (24 kDa) also contain two N-terminal DEDs, but with a shorter carboxy terminus than c-FLIP_L. The C-terminal tails of the short forms of c-FLIP play an important role in the ubiquitylation and degradation of the proteins, as well as contributing to apoptotic function [5; 6]. All three isoforms of c-FLIP can be recruited to the DISC through an interaction of their tandem DED domains with the adaptor protein FADD.

2.2 c-FLIP functions

Recruitment of c-FLIP_S to the DISC or to complex II inhibits procaspase-8 dimerization and activation, thus blocking the activation of the apoptotic cascade. c-FLIP_L, on the other hand, forms a heterodimeric complex with caspase-8, but unlike c-FLIP_S, heterodimerization of c-FLIP_L with procaspase-8 induces caspase-8 activation in the absence of cleavage [7]. Limited activation of caspase-8 in these complexes results in the generation of p43-c-FLIP and the p41/43 caspase-8 subunits. However, as no further processing occurs due to the lack of proteolytic activity of c-FLIP_L, cleaved products remain bound at the DISC, preventing further transduction of the apoptotic signal (Figure 1A). Nevertheless, active caspase-8 has access to a limited subset of substrates, including RIP [7]. Differential cleavage RIP at the membrane, could therefore account for the differential regulation of downstream signaling pathways such as c-Fos or NF-κB by c-FLIP_L and c-FLIP_S upon Fas ligand stimulation [8]. A puzzling detail with respect to the inhibitory potential of this protein, is the finding that c-FLIP_L expression levels in some tumor cells are sometimes much lower than the levels of caspase-8 itself [9], yet c-FLIP clearly protects

against ligand mediated cell death. This inhibitor appears in fact to be preferentially recruited within the DISC [10] or complex II [2], with caspase-8. The molecular mechanisms behind this preferential recruitment are unknown, but since the heterodimer c-FLIP_L-Caspase-8 is more stable than the homodimer [7; 10], it cannot be excluded that the heteromers may stabilize DISC formation more efficiently than the caspase-8 homodimers, but this hypothesis awaits further investigation.

2.3 Overexpression of cFLIP in tumors

c-FLIP has been found at elevated levels in a number of different cancers. Studies of cell lines have demonstrated increased levels of c-FLIP in colorectal carcinoma [11], gastric adenocarcinoma [12], pancreatic carcinoma [13], melanoma [14], ovarian carcinoma [15], and prostate carcinoma [16]. Studies in primary tissues from patients have also demonstrated that there are increased levels of c-FLIP in malignant cells in B-cell chronic lymphocytic leukemia [17; 18], bladder urothelial carcinoma [19], lung adenocarcinoma [20], gallbladder carcinoma [21] and hepatocellular carcinoma [22]. Analysis of primary cells from patients also confirmed the upregulation of c-FLIP in gastric carcinoma [23; 24], Hodgkins lymphoma [25], non small cell lung carcinoma [26], and melanoma [27]. It is of interest to note that in primary Ewing sarcoma, including metastases, c-FLIP was shown to be abundantly expressed in 18 of 18 patients [28].

In the majority of cases it is the c-FLIP_L isoform that is overexpressed in malignancy, however there are some studies showing upregulation of c-FLIP_S. Gastric carcinoma SNU-216 cells demonstrated high levels of c-FLIP_S [12], as did pancreatic cancer cell lines [29]. Tissue samples from lung adenocarcinoma patients also showed an overexpression of c-FLIP_S, but not c-

FLIP_L [20].

Overexpression of c-FLIP is associated with an increased resistance to apoptosis mediated by Fas and TRAIL, and studies have demonstrated that in some tissue types, high levels of c-FLIP expression correlates with a more aggressive tumor [30]. Studies of patients with colorectal carcinoma [31], cervical carcinoma [32], Burkitt's lymphoma [33], non-Hodgkin's lymphoma [34], and bladder urothelial carcinomas [19] have demonstrated that elevated levels of c-FLIP in tumor tissue is correlated with a poor prognosis. To our knowledge only one study suggested that c-FLIP levels did not have any correlation with survival in ovarian cancers [35]. Altogether these findings demonstrate that c-FLIP isoforms are often found to be overexpressed in tumors. Their expression levels should thus not only be considered with regard to death receptor targeted therapies, but also to conventional chemotherapy since c-FLIP was shown to inhibit anticancer drug-induced cell death in preclinical models [36; 37].

3 Transcriptional regulation of c-FLIP expression

c-FLIP is a transcriptional target of several transcription factors including NF- κ B [38; 39], p53 [40], p63 [41], the forkhead transcription factor FOXO3a [42], EGR1 [43], AR [44; 45], sp1 [44], E2F1 [20], c-myc [46], IRF5 [47], c-Fos [48], NFATc2 [49] and hnRNPk [50]. NF- κ B, p53, p63, NFAT, EGR1, hnRNP K, AR and sp1 induce c-FLIP expression, while c-myc, Foxo3a, c-Fos, IRF5 or sp3 inhibit c-FLIP transcription (Figure 2). Activation of these transcription factors can be mediated by a large panel of signaling pathways, including TNF ligands, growth factors, interleukins, chemokines, DNA damaging agents or non-conventional chemotherapeutic agents (Table 1) [51]. Activation of NF- κ B by TNF α or CD40 ligand leads to c-FLIP upregulation and to inhibition of Fas-, TNFR1- and TRAIL receptor-induced apoptosis [38; 52; 53]. Likewise,

activation of the PI3K (phosphatidylinositol-3 kinase)/Akt, MAPK (mitogen-activated protein kinase) pathways, or growth factor stimulation, induces the transcriptional upregulation of c-FLIP expression and affords protection to apoptosis induced by death receptors [3]. More recently, the chemokine IL-8 was shown to increase c-FLIP_S and c-FLIP_L mRNA levels through both NF-κB- and androgen-receptor dependent transcriptional activation in prostate cancer cell lines [54]. Alternatively, inhibition of c-FLIP expression has been shown to occur through interferon β-mediated IRF5 activation [47], as well as PMA or TRAIL-induced activation of c-Fos [55; 56].

Regulation of c-FLIP isoforms is still, however, not completely understood, but appears to depend both on the transcription factor itself or the signaling pathway that is activated, and on the specific cell line. For example, in lung cancer cells, E2F1 was shown to inhibit c-FLIP_S expression, but not c-FLIP_L [20]. In another study, up-regulation of c-FLIP_S in activated T-cells was shown to specifically rely on NFATc2 [49]. Regulation of the c-FLIP_R isoform is less characterized. CD40-mediated upregulation of c-FLIP_R was demonstrated to inhibit Fas ligand-induced cell death in primary precursor B-ALL [57]. Interestingly, although c-FLIP_S and c-FLIP_L expression are both regulated by NF-κB, c-FLIP_R expression was shown to be induced upon TNF stimulation in a NF-κB-independent manner in the erythroleukemic cell line, TF-1 [58]. Moreover, a RNAi screen aimed at defining p63 targets, in HaCat cells, further highlighted the findings that c-FLIP isoforms may be differentially regulated by a single transcription factor. It was found in this study that p63 could induce specifically c-FLIP_R expression, while repressing that of c-FLIP_S without affecting the transcription levels of c-FLIP_L [41].

The increasing number of transcriptional regulators found to bind CFLAR promoter, thus certainly account for the differential regulation of c-FLIP isoforms, in cell-type dependent manner, and ultimately determine cell fate from a given stimulus [51]. However, the molecular mechanisms that regulate the alternative splicing of the c-FLIP gene, CFLAR, are still

incompletely understood and require further efforts.

4 Post-translational regulation of c-FLIP expression

Besides, transcriptional regulation, c-FLIP isoforms are also heavily regulated at the post-transcriptional level by a plethora of compounds that induce c-FLIP degradation and afford sensitization to death receptor induced apoptosis (Table 1). c-FLIP isoforms are short lived proteins whose expression can easily be attenuated by the use of protein or RNA synthesis inhibitors [11; 59]. Their expression was shown to be regulated by heat stress [60], JNK activation via the E3 ubiquitin ligase ITCH [61] and by the ubiquitin proteasomal pathway [62], through phosphorylation dependent or independent mechanisms (Figure 3).

The pathways for the degradation of c-FLIP by the proteasome are surprisingly complex, partly due to the different mechanisms that exist for the long and the short forms, and to our incomplete understanding of the post-translational modifications that can target c-FLIP isoforms. The short form of c-FLIP is more prone to ubiquitylation and degradation, due to its unique C-terminal tail [5]. The E3 ubiquitin ligase ITCH, which is under control of JNK, builds polyubiquitin chains on c-FLIP to target it for degradation at the proteasome [61]. Initially it was established that only the long form of c-FLIP could be ubiquitylated by ITCH, however more recent work has demonstrated that ITCH is also a key regulator of c-FLIP_S ubiquitylation and stability [63; 64]. Interestingly, ubiquitylation of c-FLIP_L was shown to be independent of CUL3, the E3 ligase that mediates caspase-8 ubiquitylation upon TRAIL stimulation [65]. c-FLIP_L and c-FLIP_S can also be degraded in a JNK-independent manner [66; 67; 68].

Phosphorylation events also play important roles in the regulation of c-FLIP protein levels. Phosphorylation at the serine 193 residue of the c-FLIP_S form inhibits its polyubiquitylation, thus

stabilizing c-FLIP_S levels in the cell [69] and enhancing cell survival. Akt can phosphorylate c-FLIP_L at serine residue 273, which is important in the reduction of c-FLIP levels, though in a JNK and ITCH dependent manner [70]. Conversely, Akt can also enhance the polyubiquitylation and degradation of the E3 ligase ITCH, which acts to stabilize c-FLIP_S levels [63]. Another mechanism has been identified in mouse macrophages undergoing *Mycobacterium*-induced apoptosis, where the protein kinases p38 and c-Abl phosphorylate specific residues on c-FLIP_S, facilitating an interaction between c-FLIP_S and the E3 ligase c-Cbl. Ubiquitylation of c-FLIP_S results in its degradation by the proteasome [71]. It may be important to note that the authors in this paper discuss c-FLIP_S, rather than c-FLIP_R, which is the only short isoform of c-FLIP present in murine cells [49].

Finally, a role for reactive oxygen species (ROS) has also been described for the regulation of c-FLIP, however it is still not clearly understood how this particular mechanism works. ROS were described to induce FLIP downregulation through the proteasome in FasL mediated apoptosis [72]. It has also been demonstrated that NF- κ B can inhibit JNK activation by suppressing the levels of ROS in cells [73], which could lead to a decrease in the activity of Itch, thus stabilizing the levels of c-FLIP. This indicates that modulation of NF- κ B can affect c-FLIP levels at both the transcriptional and posttranscriptional level.

5 Targeting c-FLIP for cancer therapy

There is a strong correlation between the overexpression of c-FLIP and resistance to FasL- or TRAIL-induced apoptosis, and many *in vitro* studies have demonstrated that inhibiting c-FLIP directly or indirectly can overcome this resistance. Thus targeting c-FLIP may be a promising strategy for cancer therapy, especially if combined with other treatments, such as TRAIL or

conventional chemotherapy [36; 74; 75; 76; 77].

5.1 *Transcriptional regulators*

Treatment with DNA damaging agents has shown some promise with regard to decreasing c-FLIP levels, however the effect on expression levels varies between cell types. This finding was at first rather unexpected since c-FLIP was shown to be a p53 target [40]. However, the upregulation of c-FLIP by chemotherapeutic drugs has not yet been documented at the protein level. On the contrary, some chemotherapeutic drugs have been shown to downregulate levels of c-FLIP (Table 1.). Cisplatin, in particular, has been well studied in ovarian cancer cell lines, and shown to induce ubiquitylation and degradation of c-FLIP in a p53 dependent manner, through the formation [78] of a ternary complex with both p53 and Itch [79]. Ubiquitylation of c-FLIP_{S/L} by this ternary complex was recently shown to be under the control of the Akt pathway in these ovarian cancer cells [80]. An earlier study also indicated that cisplatin could downregulate c-FLIP_S expression in melanoma cells, but not the long. Instead c-FLIP_L was found to be dephosphorylated upon cisplatin stimulation as evidence by 2D-gel analysis in resistant melanoma cells [78]. Based on earlier studies showing that phosphorylation of c-FLIP_L by CaMKII can promote c-FLIP recruitment and inhibition of caspase-8 within the DISC [81], it was proposed that dephosphorylation of c-FLIP_L would impair its inhibitory activity in glioma cells [78]. In line with the involvement of p53 in regulating c-FLIP expression, oxaliplatin and CPT11 were shown to induce c-FLIP_{S/L} downregulation in the p53 wt colon carcinoma cell line HCT116, but not in the p53^{-/-} isogenic clone [75]. However c-FLIP_{S/L} were also deregulated in the p53 mutated HT29 cell line and sensitization to TRAIL-induced cell death by these drugs was achieved irrespective of the p53 status [75]. Histone deacetylase inhibitors and topoisomerase I inhibitors are two additional emerging cancer therapies which have been shown to regulate c-

FLIP levels. Trichostatin A treatment downregulated c-FLIP_L mRNA and protein levels in ovarian cancer cells, with no effect on c-FLIP_S. Interestingly, treatment with inhibitors of the EGRF signaling pathway blocked the regulation of c-FLIP_L by trichostatin A[82]. Two other HDACis, ITF2357 and valproic acid, were studied in hepatocellular carcinoma cells. These two agents were also shown to decrease c-FLIP mRNA and protein levels, though the study did not differentiate between the different isoforms [83]. More recently, 4-(4-Chloro-2-methylphenoxy)-N-hydroxybutanamide (CMH), a small molecule inhibitor of c-FLIP, identified using a high-throughput chemical library screen [84; 85], was demonstrated to induce killing in the breast cancer cell line MCF7. CMH induced apoptosis through c-FLIP_L and c-FLIP_S mRNA downregulation [86]. The use of DNA-damaging agents to target c-FLIP or presents some difficulties, as the effect on c-FLIP varies from cell type to cell type, and can affect either both or just one of the isoforms.

5.2 Genetic approaches : siRNAs

Directly inhibiting translation through RNA interference represents the most specific method of downregulating c-FLIP, and this approach has been used in many in vitro studies to sensitize cells to TRAIL or FasL mediated killing [36; 74; 75]. However, there are many limitations for siRNA *in vivo*, and clinical trials using siRNA to target c-FLIP are probably still some time away.

5.3 Targeting c-FLIP for degradation

General metabolic inhibitors were among the first compounds used to study the mechanics of inhibiting c-FLIP expression. c-FLIP has been shown to be downregulated by several compounds that have a broad activity on the cell. For example, cycloheximide [29; 87; 88; 89], or anisomycin

[85], two protein synthesis inhibitors, like the RNA synthesis inhibitor actinomycin D [11; 14; 17; 78], have been shown to downregulate the long and the short forms of c-FLIP (Table 1). Chemotherapy with fluorouracil (5-FU) has also been demonstrated to downregulate both the long and short isoforms of c-FLIP in colon cancer cell lines [75; 90].

The protease inhibitor bortezomib has been widely studied in many different cell lines, with differing outcomes depending on the type of cell line studied. c-FLIP levels in Hodgkins and Reed-Sternberg cells [91], astrocytoma and oligoastrocytoma [92], esthesioneuroblastoma [93], myeloid leukaemia cells [94], and myeloma cell lines [95; 96] were decreased after treatment with bortezomib. While most studies have mainly focused on c-FLIP_L, it should be noted however that in at least two studies where the short isoform was analyzed in parallel, c-FLIP_L deregulation was associated with the up-regulation of c-FLIP_S, [93; 97]. Likewise, studies on the small molecule proteasome inhibitor MG-132 have also demonstrated both increases and decreases in cellular c-FLIP levels in different cell lines [51]. Strikingly, both bortezomib and MG132 sensitized each of these cell types to TRAIL-induced cell death, indicating that deregulation of both the long and the short isoforms is not an absolute requirement for the restoration of apoptosis. Much effort needs to be made to understand why the remaining c-FLIP isoform fails to protect cells from death ligands.

6 Conclusions

Many in vitro studies have demonstrated the importance of the role of c-FLIP in resistance to apoptosis induced by death receptors and, to a lesser extent, to conventional chemotherapy. Elevated expression of c-FLIP is often identified in malignant cancers, and is strongly correlated with a poor prognosis. Many studies in cell lines demonstrate that sensitivity

to Fas ligand or TRAIL induced apoptosis can be restored by decreasing the levels of c-FLIP in malignant cells. However, as covered in this review, c-FLIP is highly regulated through many different pathways, and the existence of the three separate isoforms, which appear to be differentially modulated, adds another level of complexity with regard to targeting c-FLIP for cancer therapy.

Particularly, it remains unclear whether c-FLIP isoforms may play different regulatory functions in different types of cancer. While most c-FLIP inhibitors described so far target c-FLIP_L and c-FLIP_S isoforms simultaneously, some compounds affect only one isoform. In line with this is the finding that bortezomib can inhibit the expression of c-FLIP_L and induce that of c-FLIP_S, but nevertheless can sensitize cells to death receptor induced apoptosis. Post-translational modifications of c-FLIP, including phosphorylation of serine 193, may selectively inactivate one isoform by preventing its recruitment at the DISC level. A better understanding of these post-translational modifications and the systematic analysis of the different isoforms of c-FLIP could in the future help address this question.

Thus far, apart from siRNAs, the inhibitors that have been studied act indirectly on c-FLIP. The development of compounds targeting c-FLIP directly, either at the mRNA or protein level, would be of great interest for further study, but this presents a major challenge. As a key negative regulator of the death receptor apoptotic machinery, c-FLIP represents a promising target for cancer therapy. However c-FLIP is enzymatically inactive, and structurally very similar to caspase-8. Specific targeting of c-FLIP may be difficult and has so far not been achieved. One strategy would be to develop compounds that interfere with the recruitment of c-FLIP to the DISC through the DED domains, however, such compounds would have to be designed so that they would not inhibit recruitment of caspase-8, with its highly homologous DED. Alternatively, some of the inhibitors found so far to target c-FLIP to proteosomal degradation, may in fact act

indirectly at the transcriptional level, and could simultaneously induce the stabilization or degradation of transcription factors found to regulate CFLAR expression. These include p63 which, like c-FLIP, can be targeted to proteosomal degradation by the E3 ligase ITCH [98], or c-myc [99], c-Fos [100] and Foxo3a [101], to name a few. Kinase inhibitors targeting Akt and NF- κ B, or multikinase inhibitors such as sorafenib, could also lead to transcriptional and post-transcriptional regulation of c-FLIP expression and function.

The preclinical data clearly indicate that selective inhibitors of c-FLIP, in combination with a ligand such as TRAIL or FasL, or a conventional chemotherapy such as 5-FU, could represent an effective anti-tumor therapy, however, selective inhibition of c-FLIP may be more difficult than anticipated. A deeper understanding of the regulation of the protein, and the role of the different isoforms would be probably required for the rational design or for chemical library screens of selective c-FLIP inhibitors. An ideal situation would be the development of a panel of compounds that can to restore sensitivity to death receptor induced cell death through the specific regulation of the cFLIP isoforms. Using these compounds it could be possible to regulate the levels, or even modulate the ratios of the different isoforms in malignant cells, offering a way in which to control ligand-mediated apoptosis as a therapy for cancer. The future will tell whether such compounds can be obtained.

Conflicts of interest

None declared.

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	Primary mode of action	Agent	References
Transcriptional	Alkylating agent	Cisplatin Oxaliplatin	[75; 78; 79; 102; 103]
	Intercalating of DNA	Doxorubicin	[104]
	Histone deacetylase inhibitor	Vorinostat, Trichostatin, Droxinostat, Valproic acid	[82; 83; 105; 106]
	Topoisomerase I inhibitor	Camptothecin, 9-NC, Irinotecan	[32; 75; 107; 108; 109]
	Modulation of Ras/PI3K/NF-κB pathway	Lupeol (triterpene)	[110]
	Suppression NF-κB pathway	Celastrol, Zerumbone (sesquiterpene), Withaferin A (steroidal lactone) Quinacrine	[111; 112] [113; 114]
	Decreases TNFα mediated NF-κB activation	Chrysin (flavanoid)	[115]
	Inhibition of STAT3 activation	CDDO-Imidazolidine – synthetic triterpenoid	[116]
Postranscriptional	RNA interference	siRNAs	[36; 117]
	? – phosphorylation of long form	Cisplatin	[78]
	RNA synthesis inhibitor	Actinomycin D	[11; 14; 17]
	Protein synthesis inhibitor	Cycloheximide Anisomycin	[29; 85; 87; 88; 89; 118]
	Thymidylate synthase inhibitor	Fluorouracil (5-FU)	[75; 90]
	Proteasome inhibitor	PS-34 (bortezomib)	[91; 94; 95; 96; 97]
	Small molecule proteasome inhibitor	MG-132	[48; 119]
	PPARγ modulating agent	Troglitazone	[120; 121; 122]
	Multikinase inhibitor	Sorafenib	[123; 124]
	Antimicrotubule agent	Taxol (paclitaxel), Nocodazole	[66; 125]
	Downregulation Akt and NF-κB	Genistein (isoflavone)	[126]
	?	Silibinin (Flavonoid)	[67]
	COX-2 inhibitor	Celecoxib	[127]
	?	CDDO-Me	[68]

Table 1. Inhibitors of c-FLIP and their main modes of action.

Figure 1. c-FLIP forms and interaction at the DISC. *A* c-FLIP is expressed as three different isoforms in the human cell. c-FLIP_L contains a caspase-like domain. The two aspartate proposed cleavage sites are indicated. c-FLIP_R contains a unique sequence at the C-terminus. *B* Interaction of the long and the short c-FLIP isoforms at the DISC. **1-** In the absence of c-FLIP, procaspase-8 dimerization induce full processing and activation of caspase-8, leading to the release of active caspase-8 to the cytosol and activation of apoptosis. **2-** In the presence of c-FLIP_S, procaspase-8 remains mostly uncleaved and thus non functional. **3-** When c-FLIP_L is present, procaspase-8 forms heterodimers with c-FLIP_L limiting procaspase-8 autoprocessing. Autoprocessing occurs either between the prodomain and the caspase domain or between the p20 and p10 subunits of the caspase domain. The active heterodimer remains associated with the DISC complex where it can cleave a limited number of substrates including RIP leading to enforced NF-κB activation of the activation of non apoptotic signaling pathways such as ERK. Like c-FLIP_S, c-FLIP_L prevents death-receptor induced apoptosis.

Figure 2. Signaling pathways leading to the upregulation or downregulation of c-FLIP. See text for details.

Figure 3. Posttranslation modifications and regulation of degradation of c-FLIP. JNK activates the E3 ubiquitin ligase ITCH to mediate accelerated turnover of c-FLIP_L and c-FLIP_S through polyubiquitylation and degradation by the proteasome. Different compounds have been identified which accelerate the degradation of either c-FLIP_L, c-FLIP_S. Phosphorylation events by p38 and c-Abl allow polyubiquitylation of c-FLIP_S by c-Cbl, resulting in degradation. Akt phosphorylates the c-FLIP_L form, enhancing an ITCH independent degradation of the protein. Conversely, loss of PTEN and activation of Akt are events in a pathway that bring about the ubiquitylation of ITCH, which results in stabilization of c-FLIP_S. Protein kinase C (PKC) has been shown to phosphorylate c-FLIP_S at a specific serine, decreasing its ubiquitylation and stabilizing levels of c-FLIP_S. Finally, generation of ROS, can also enhance degradation of cFLIP.

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