

Mini review

I κ B kinase β (IKK β /IKK2/I κ BK β)—A key molecule in signaling to the transcription factor NF- κ B

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Abstract

IKK β /I κ BK β (I κ B kinase beta), also designated as IKK2, was named after its function of phosphorylating I κ B molecules, the inhibitors of NF- κ B transcription factors. The kinase activity of IKK β targets two adjacent serine residues of I κ B leading to ubiquitination and proteasomal degradation of the inhibitor, followed by release and activation of NF- κ B. Many signaling pathways that activate NF- κ B converge at the level of IKK β . Examples of stimuli leading to IKK β and subsequent NF- κ B activation include inflammatory cytokines (IL-1, TNF α), endotoxins (lipopolysaccharide), viral infection and double strand RNA as well as physical signals such as UV-irradiation.

Transcription factors of the NF- κ B protein family have a great variety of functions in regulating the immune system, cellular differentiation, survival and proliferation.

NF- κ B is an essential factor in acute as well as chronic inflammation, a pathological state which is either cause or co-factor in a great variety of diseases. Moreover, recent data suggest that many variants of cancer are characterized by elevated constitutive activity of NF- κ B, which can act as a survival factor for malignant cells by its predominantly anti-apoptotic function. Given the tight regulation of NF- κ B by I κ B molecules and the central role of IKK β in phosphorylation and degradation of the inhibitor, IKK β is a very promising target for pharmaceutical substances aiming at interfering with NF- κ B activation.

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Keywords: NF- κ B; Ubiquitination; Signaling cascades; Kinase inhibitors

1. Introduction

The currently best-documented function of IKK β is to activate members of the NF- κ B transcription factor family via the so-called classical (or canonical) pathway by phosphorylation of I κ B inhibitors [1–3]. NF- κ B transcription factors play an important role in the balance between cell survival and

apoptosis and are involved in the regulation of cell proliferation and development or differentiation of various cell types [4,5]. Changes in activity and/or regulation of IKK β and NF- κ B are found in many diseases associated with chronic or acute inflammation and more recently it became evident that NF- κ B exhibits higher constitutive activity or aberrant regulation in various forms of cancer [4,6–12].

The functional entities of NF- κ B transcription factors are homo- or heterodimers of members of this gene/protein family, consisting of the proteins NF- κ B1 (p50 and the precursor p105), NF- κ B2 (p52 and the precursor p100), RelA (p65), RelB and c-Rel. All these molecules contain a homologous DNA-binding domain (the Rel homology domain); however, just three of them (RelA/p65; RelB and c-Rel) contain a transactivation domain. Transcriptionally active NF- κ B dimers contain one of these three factors. In non-activated cells NF- κ B dimers are associated with molecules of

Abbreviations: I κ B, inhibitor of NF- κ B; IKK α , I κ B kinase α ; IKK β , I κ B kinase β ; IL-1, interleukin-1; NEMO, NF- κ B essential modulator; NF- κ B, nuclear factor-kappa B; TCR, T cell receptor; TNF α , tumor necrosis factor alpha.

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the I κ B protein family (mainly I κ B α , I κ B β and I κ B ϵ), which inhibit NF- κ B binding to DNA [13] and shift the steady state localization to the cytosol [4]. This model is supported by structural data of I κ B/NF- κ B complexes [14,15]. The precursor forms of p52 and p50 (p100 and p105, respectively) contain pro-domains, which are homologous to I κ B molecules and fulfill the same inhibitory role. Both NF- κ B and I κ B α molecules shuttle between cytosol and nucleus [16–18], but in the presence of I κ B α the predominant steady state localization of the complex is in the cytosol.

For full activation NF- κ B has to be released from I κ B, which is achieved by degradation of the inhibitor (or the inhibitory pro-domains of p100 and p105) by 26S proteasomes. Signal-induced proteasomal degradation of I κ B or inhibitory pro-domains requires prior polyubiquitination, which is carried out by SCF^{TrCP}-type E3 ligases [19–21]. This in turn is triggered by phosphorylation of I κ B on two adjacent serine residues (Ser32/Ser36 in I κ B α) in the N-terminal signal-response domain. Two kinases were reported to be capable of phosphorylating these residues: IKK α (I κ B kinase α , IKBKA, IKK1) and IKK β (IKBKB, IKK2, Fig. 1) [22–25]. IKK α and IKK β form heterodimers and are found in a 700–900 kDa complex with a non-enzymatic accessory molecule named IKK γ [26] or NEMO (NF- κ B essential modulator [27]). This complex, also known as IKK-signalosome, was postulated to contain two IKK-dimers and most likely a tetramer of IKK γ /NEMO [1]. IKK β turned out to be the crucial kinase of the IKK-signalosome for activation of NF- κ B by most inflammatory stimuli, which is considered the classical or canonical pathway of NF- κ B activation. Signals activating this pathway comprise the inflammatory cytokines TNF α and IL-1, bacterial components like lipopolysaccharide (LPS) which activate Toll-like receptors (TLR) and signals that activate T-cell receptors (TCR) [2,4,5]. Interestingly, recent data indicate that IKK β is dispensable for some pathways of canonical NF- κ B activation, as it was observed that IKK α can activate NF- κ B in response to IL-1, but not TNF α by forming functional IKK-complexes with NEMO even in the absence of IKK β [28].

Despite tedious studies, the exact molecular mechanisms leading from the different stimuli to activation of the IKK-complex are not clear and there are most probably different modes of activating IKK β . It was shown that various kinases (such as MEKK1, MEKK3, TAK1, NIK, NAK or PKC- θ , as reviewed in [4]) can activate IKK β by phosphorylating serine residues within its activation loop (Ser177 and Ser181). Gene deletion experiments verified the importance

of MEKK3 (mitogen-activated protein kinase/ERK kinase-3) and TAK1 (TGF β -activated kinase 1) in the canonical NF- κ B activation pathway [29,30]. Besides activation by upstream kinases there is evidence that IKK molecules can also activate themselves by a transphosphorylation mechanism of homo- or heterodimers in a proximity-induced self-activation process [31,32]. While all these studies led to the identification of a variety of possible upstream signaling pathways, the mechanistic details of these signaling events are still not fully understood. In the last few years, it became increasingly clear that ubiquitination cascades upstream of IKK signalosomes play a pivotal role in signaling to effector molecules.

In this article, we want to highlight recent insights in the activation of IKK β and NF- κ B including specific ubiquitination events. We describe recently identified substrates of IKK β which extend the role of IKK β beyond the NF- κ B signaling pathway. Furthermore, we report on pharmaceutical efforts to develop inhibitors or modulators of IKK β , as these substances have an enormous potential of application in a great variety of diseases.

2. Signaling and function of IKK β

2.1. Ubiquitination processes modulate signaling pathways converging on IKK β

The current view of the canonical pathway of NF- κ B activation is that specific and distinct ubiquitination processes are involved in the activation of the IKK-complex (Fig. 2) [3,33]. In fact, it was shown that the I κ B kinase activity requires non-degradative ubiquitination even before the molecular identification of IKKs [34]. In general, binding of ligands such as IL-1 or TNF α to respective receptors induces association of adaptor molecules with cytosolic receptor domains. These adaptor molecules include RING finger-proteins of the TRAF family (TNF-receptor associated factors), with TRAF6 being essential for IL-1-mediated IKK activation and TRAF2 or TRAF5 as crucial factors in TNF α -induced signaling. Biochemical analysis of factors linking TRAF6 to IKK activation led to the identification of Ubc13/Uev1A as a dimeric E2 ubiquitin-conjugating enzyme complex and demonstrated that the RING domain of TRAF6 acts as E3 ligase catalyzing the formation of lysine-63-linked polyubiquitin chains [35]. In contrast to lysine-48-linked polyubiquitin chains, which

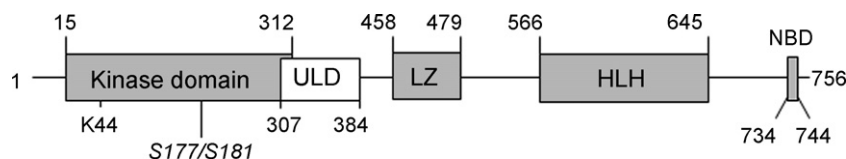


Fig. 1. Scheme of the IKK β domain structure. ULD, ubiquitin-like domain; LZ, leucine zipper; HLH, helix-loop-helix domain; NBD, NEMO-binding domain. Numbering of domain borders differ slightly between different references. The catalytic active site lysine residue (K44) is indicated and the two serine-residues (S177/S181) of the activation loop, which are phosphorylated upon activation, are shown in *italics*.

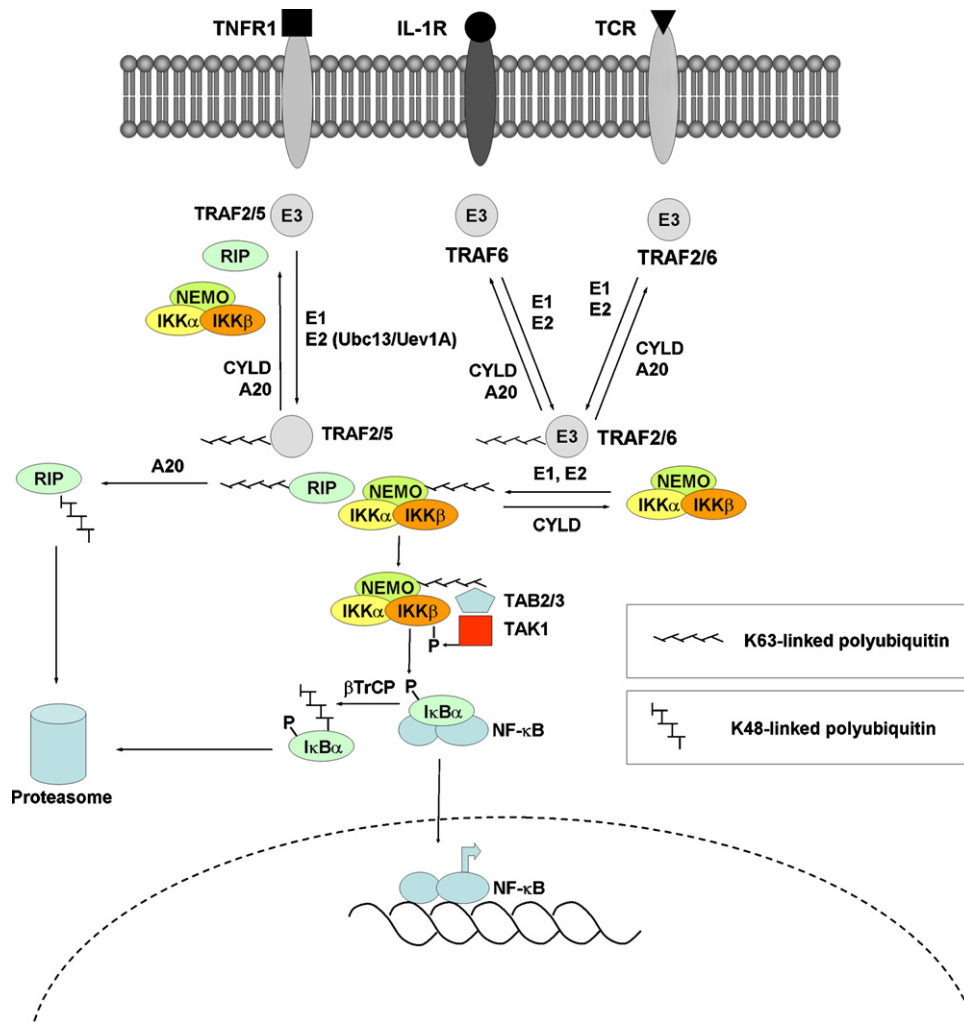


Fig. 2. Signaling pathways leading to activation of IKK β and ubiquitination processes involved therein. Binding of ligands to the respective receptors leads to association of TRAF molecules, which then act as E3 ligases to catalyze the formation of K63-linked polyubiquitin chains on themselves as well as on RIP and NEMO. These polyubiquitin chains create a binding platform for TAB2 or TAB3 together with TAK1, which activates IKK β by phosphorylation. Activated IKK β phosphorylates I κ B molecules, triggering their K48-linked polyubiquitination via β TrCP followed by proteasomal degradation of I κ B and release of active NF- κ B. Deubiquitinating enzymes such as CYLD or A20 counteract the signaling cascade by cleaving K63-polyubiquitin chains. A20 can also catalyze K48-linked, degradative polyubiquitination of RIP.

lead to proteasomal degradation, K63-linked polyubiquitins appear to serve as a platform for association of molecules with ubiquitin-binding domains and the subsequent activation of signaling molecules. For IL-1-mediated signaling, it was shown that TRAF6 catalyzes K63-linked autoubiquitination, as well as K63-linked polyubiquitination of NEMO, which leads to recruitment of the kinase TAK1 together with the ubiquitin-binding proteins TAB1 and TAB2 [36]. This results in activation of TAK1 which phosphorylates and activates IKK β . TAB2 or the homologous TAB3 have been identified as the essential ubiquitin-binding factors for association with K63-linked polyubiquitin chains of TRAF6. The molecular mechanism by which binding of TABs to autoubiquitinated TRAF6 leads to activation of TAK1 is still not clear, but it is supposed that it might facilitate oligomerization and self-activation of TAK1 by transphosphorylation [37].

For the TNF α -induced signaling pathway, it is assumed that TRAF2 and TRAF5 catalyze auto- and transubiquitination as well as K63-polyubiquitination of RIP1 (receptor-interacting protein-1) and IKK γ /NEMO. This induces binding and activation of TAK1 mediated by TAB2/3, followed by activation of IKK β by phosphorylation of serines 177 and 181 in the activation loop. The crucial role of TAK1 for both the TNF α - and the IL-1-mediated NF- κ B activation has recently been confirmed in a conditional knockout system [29].

Given the essential role of ubiquitination and ubiquitin-binding proteins, it is important to note that IKK β itself contains a ubiquitin-like domain (ULD, see Fig. 1), which was shown to be essential for activation of the kinase [38]. Interestingly, this domain cannot be replaced with the ubiquitin sequence and it does not contain lysines at positions equivalent to K48 or K63 of ubiquitin, indicating

that it is not a target of polyubiquitination. However, it might have a role in binding of co-factors such as TAB2/3.

In line with the model that ubiquitination processes are essential in signaling to IKKβ, deubiquitinating enzymes have been shown to be involved in termination and feedback inhibition of the IKK-mediated NF-κB activation. The known NF-κB inhibitory protein A20 [39,40] and the protein CYLD (cylindromatosis protein [41,42]) have been identified as deubiquitinating enzymes (DUBs) in the NF-κB pathway. CYLD cleaves K63-polyubiquitin chains of TRAF2 and NEMO, while the inhibitory action of A20 involves two concerted mechanisms: one domain of A20 cleaves the activating K63-polyubiquitin chains of RIP1 and a second domain catalyzes K48-linked polyubiquitination of RIP1 leading to its proteasomal degradation.

2.2. Substrates of IKKβ

IKKβ is activated by phosphorylation of S177 and S181 and catalyzes not only the phosphorylation of two crucial serine residues in IκB molecules, but also autophosphorylation on C-terminal serine residues. This is assumed to lead to self-inactivation representing a negative feedback loop [43], thereby being important for the termination of IKK activity in addition to phosphatases like PP2A or PP2Cβ [22,44]. Besides IκB and IKKβ itself, there are other molecules of the NF-κB pathway phosphorylated by IKKβ. One of them is RelA/p65, which is targeted by IKKβ at serine 536 [45,46]. Phosphorylation of this residue is important for full transcriptional activity of RelA/p65 and thus represents an enhancement of NF-κB activity. In the case of the NF-κB family member p105, phosphorylation by IKKβ leads to polyubiquitination and degradation similar to IκB [47]. As p105 is not only involved in the NF-κB pathway, but also binding effector molecules of other signaling pathways (e.g. TPL2/COT, a component of the MAPK pathway), its degradation can lead to liberation of these molecules and activation of the respective pathway [47,48]. Another substrate of IKKβ related to NF-κB activation is Bcl10 (B-cell lymphoma protein 10), a molecule involved in IKKβ activation by TCR signaling. In this case, IKKβ has a dual role: it is required for formation of the Carma1/Bcl10/

MALT1 complex essential for TCR-mediated NF-κB activation, and it also attenuates the signaling by phosphorylating Bcl10 [49].

In addition to the canonical pathway of NF-κB activation, there are also atypical pathways leading to IKKβ and NF-κB activation. For instance, genotoxic stress (e.g. UV-irradiation) induces DNA double strand breaks leading to activation of the kinase ATM (ataxia telangiectasia mutated), which phosphorylates a nuclear, sumoylated fraction of IKKγ/NEMO. This phosphorylation leads to replacement of the SUMO-1 modification by a mono-ubiquitination, which in turn triggers nuclear export of a NEMO–ATM complex. In the cytosol this complex then activates IKKβ in collaboration with the IKK-associated molecule ELKS [50].

Besides the well-documented role of IKKβ in the activation of NF-κB it could also be shown to phosphorylate other substrates than IκB or NF-κB molecules. One of these substrates is the Forkhead transcription factor FOXO3a [51], a tumor suppressor protein capable of inducing cell cycle arrest or apoptosis. IKKβ-mediated phosphorylation of FOXO3a results in its translocation to the cytoplasm and degradation. Another non-IκB substrate of IKKβ is 14-3-3β, which binds mRNAs containing AU-rich elements (ARE) in cooperation with the protein tristetraproline (TTP), leading to mRNA destabilization. Upon IKKβ-mediated phosphorylation of 14-3-3β, the complex with TTP is released and the corresponding mRNAs (including those coding for cytokines such as TNFα) are stabilized, providing a positive feedback loop for the NF-κB pathway [52]. Other newly identified substrates for IKKβ are insulin receptor substrate 1 (IRS1), where IKKβ-mediated phosphorylation is thought to inhibit tyrosine phosphorylation and impair insulin signaling [53], and the related protein DOK1 (docking protein 1), a tyrosine kinase substrate that promotes cell migration [54]. Given these recent new insights, it has to be expected that additional targets for IKKβ will be found in the future. Aligning the known IKK2 substrates in the region of their phosphorylated serine residue reveals a conserved core consensus site and additional conserved amino acids, about 15 amino acids N- and 11 amino acids C-terminal of the core region (Fig. 3).

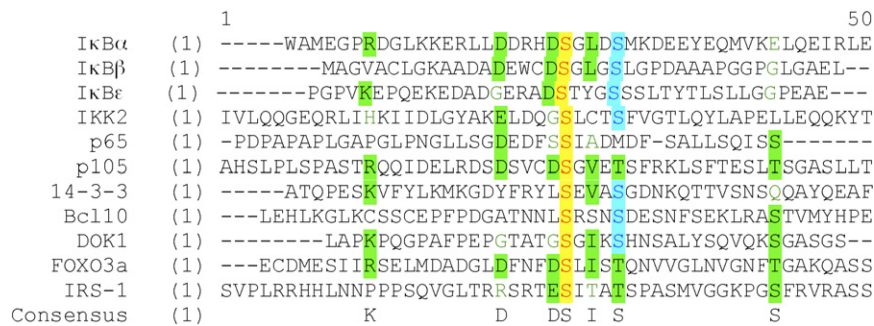


Fig. 3. IKKβ substrates and phosphorylation sites. Domains surrounding known phosphorylation sites of IKKβ substrates have been aligned with VectorNTI™ software (Invitrogen Inc.). The highly conserved phosphorylated serine residues are shaded in yellow.

2.3. Insights from knockout and transgene mouse models

While many different signaling molecules involved in activation or regulation of IKK β have been identified and studied by different cell cultures experiments *in vitro*, it soon became clear that physiological studies *in vivo* using knockout or transgene mouse models are required to fully elucidate the complex signaling network involved. Signaling molecules postulated to be essential for NF- κ B activation based on *in vitro* studies quite often turned out to be redundant and did not show the expected phenotype in knockout mice. In some cases, unexpected or tissue-specific effects could be observed (as reviewed in [55]).

Classical knockout mice with deletion of IKK β die at an embryonic stage (around E13) due to TNF-mediated apoptosis of hepatocytes [56]. This phenotype is very similar to that of RelA/p65 knockout mice [57], supporting the importance of IKK β for RelA/p65 activation downstream of TNF α signaling. Embryonic lethality can be rescued by additional deletion of TNF-receptor 1 supporting the notion that IKK β and RelA/p65 counteract the pro-apoptotic effect of TNF α in a sensitive phase of liver development [56].

Conditional knockout models of IKK β demonstrated the importance of this kinase in protecting macrophages [58], osteoclasts [59] or gut epithelium [60] from apoptosis triggered by Toll-like receptor signals. In contrast to the anti-apoptotic role of IKK β in these as well as many other cell types, it seems to have a pro-apoptotic role in particular cells such as neurons [61]. Cell-type specific differences are also observed for the role of IKK β in inflammation. While the kinase is essential for inflammatory signaling pathways in many cell types it was reported to have an anti-inflammatory role in keratinocytes [62]. Hepatocyte-specific deletion of IKK2 revealed that membrane-bound TNF elicits a different cellular response than soluble TNF. Mice lacking IKK β in hepatocytes were still protected from apoptosis triggered by soluble TNF α , while they were sensitive to treatment with Concanavalin A, an agent which triggers a membrane-bound TNF response [63]. This conditional knockout also helped in detailing the mechanism of liver regeneration after partial hepatectomy. It was shown that liver regeneration depends on NF- κ B and IKK β -mediated production of TNF α by non-parenchymal liver cells (mainly Kupffer cells representing liver macrophages) but not on IKK β and NF- κ B activation in hepatocytes themselves [63,64].

Conditional knockout of IKK β in other cells strengthened the notion that the function of IKK β varies significantly with the cell type. In macrophages it is important for synthesis of inflammatory cytokines [65], in osteoclasts it is involved in inflammation-induced bone loss [59], while it acts as an anti-inflammatory molecule in keratinocytes [62].

Conditional IKK β knockout models also revealed a role of IKK β in the development of obesity-induced insulin

resistance. These studies demonstrated that IKK β dependent production of inflammatory molecules by myeloid cells is required for the onset of type II diabetes [66]. B-cell specific deletion of IKK β results in a reduction of follicular and marginal zone B-cells supporting the role in B-cell development [67], and deletion of IKK β in the T-cell lineage prevents the development of NKT cells, as well as CD4+/CD25+ regulatory T-cells [68]. In addition to conditional knockouts of IKK β , transgenic mice expressing constitutively active IKK β have been generated. These contain a mutant of IKK β in which S177 and S181 are replaced by glutamic acids (IKK β ^{SS/EE}) mimicking the negative charge of phosphorylated serines in the activation loop. Tissue-specific expression of this mutant in skeletal muscle results in muscle wasting [69], indicating a role of IKK β in cachexia and muscle atrophy. Targeted expression of this constitutively active IKK β variant in the T-cell lineage confirmed that IKK β -dependent NF- κ B activation promotes thymocyte survival at a specific stage of T-cell development [70].

2.4. Efforts to develop inhibitors of IKK β to block NF- κ B activation

Following the elucidation of the key role of IKK β in inflammation and its importance in oncogenesis, pharmaceutical companies have undertaken a great effort in developing specific inhibitors. Generally, we may divide IKK β inhibitors into two groups: one, known drugs which have been shown to at least partly own their effectiveness to inhibiting IKK activity, and two, novel specific inhibitors, which often show strong inhibition at low concentrations but have yet to undergo clinical testing.

The first group includes the well-known anti-inflammatory agents aspirin, sodium salicylate and sulindac, which have been shown to influence several signal transduction pathways [71,72]. Their inhibition of IKK β activity likely contributes to their anti-inflammatory and anti-oncogenic activities, but the relative roles of different pathways are difficult to determine.

The immunomodulatory drug thalidomide, which also exhibits anti-inflammatory and anti-angiogenic effects, is another example of an I κ B kinase inhibitor [73]. Endogenous anti-inflammatory substances can also act by inhibiting IKK β , as has been shown for cyclopentenone prostaglandins [74]. Arsenic trioxide, which has been used for a long time for the treatment of chronic myelogenous leukaemia and more recently against promyelocytic leukaemia [75], similarly inhibits NF- κ B by mechanisms including the inhibition of IKK β [76]. The inhibition by arsenite is one example for a drug blocking cysteine residue 179, which lies between the activating phosphorylation sites serine 177 and serine 181, but is also critical for control of IKK activity by redox reactions through S-glutathionylation [77].

Specific IKK β inhibitors have been sought and found by a number of pharmaceutical companies. Celgene has

developed a series of quinazoline analogues including a molecule termed SPC 839, which inhibits IKK β with an IC₅₀ of 62 nM and has been shown to reduce paw oedema in a rat arthritis model [78]. This compound is one example for an ATP analog that shows specificity for IKK β compared to other kinases, as demonstrated by an about 200-fold higher IC₅₀ value for IKK α [79]. Other IKK β inhibitors acting as ATP analogs are: β -carboline, of which PS-1145 is being developed by Aventis and Millennium Pharmaceuticals [80], ML120B (Millennium Pharmaceuticals), a β -carboline demonstrated to be effective in a mouse apoptosis and a rat arthritis model, and SC-514, an aminothiophenecarboxamide [81–83]. Yet another mode of action is exemplified by BMS-345541 (Bristol-Myers-Squibb), which has been shown to inhibit IKK- β by binding at an allosteric site and was also successfully applied to *in vivo* inflammation models [84–86].

Several compounds pushed the limits with respect to effective inhibitory concentrations: some ureidocarboxamide thiophenes (AstraZeneca) show IC₅₀ values as low as 18 nM and were also effective in a rat arthritis model [79]. Bayer has developed pyridooxazin derivatives with reported IC₅₀ values of 2 nM [87]. CHS 828 (Leo Pharma), an antitumor agent undergoing clinical trials, was found to exert its actions through inhibition of IKK with an IC₅₀ value of 8 nM [88]. Interestingly, all of the compounds mentioned have been shown to have IC₅₀ values for IKK α which are several fold higher than for IKK β and can thus be considered specific for the latter isoform at the right concentration.

In vivo testing of IKK β inhibitors has not been restricted to inflammatory and cancer models. IMD-0354, a compound developed by the Institute of Medicinal Design (Japan), has been shown to ameliorate glucose intolerance in a mouse diabetes model [89].

Several other relevant small molecular inhibitors have been reviewed by Karin et al. [79].

Overall, there are more than 150 agents that have been shown to inhibit I κ B kinases based on *in vitro* assays [90]. Among those are natural inhibitors, synthetic compounds and gene-based inhibitors. Genetic approaches to inhibit I κ B kinases include the application of dominant-negative versions of IKK β , which carry mutations in the kinase activation loop (S177A, S181A) or in the kinase domain (K44A) [23,24]. Moreover, antisense approaches have been developed with therapeutic aims [79].

In addition to efforts targeting IKK β activity, strategies targeting the ubiquitination processes essential for activation of IKK β have been developed. An example is the enforced expression of deubiquitinating enzymes such as CYLD using viral transduction techniques [91]. Moreover, small molecule inhibitors targeting the ubiquitination of I κ B α have been described [92]. Future efforts may include screening for substances interfering with activating K63-linked polyubiquitination. However, the development of inhibitors targeting this reaction seems to be at an early

stage, most likely because the underlying molecular mechanisms have just very recently been elucidated.

One concern with IKK β inhibitors, as with NF- κ B inhibitors in general, is their applicability to conditions like chronic inflammatory diseases. This is due to the well-described role of the IKK β /NF- κ B pathway in regulation of apoptosis and in immunological functions and potential side-effects (e.g. pro-apoptotic) of IKK β inhibitors remain to be investigated in clinical trials. Moreover, IKK β has been described to have other targets than I κ B molecules (see above), and potential side-effects in clinical applications of inhibitors due to this heterogeneity remain to be described.

Altogether, this will determine the scope of IKK β inhibitors with respect to diseases. Some inhibitors are already in clinical trials with reference to anti-cancer therapy (e.g. CHS 828), but the function NF- κ B plays in different tumor types might differ, potentially limiting the inhibitors to certain cancers. Likewise, many companies aim to target different inflammatory diseases, with results from clinical trials still outstanding. However, IKK inhibitors seem also to have promise in conditions such as diabetes or muscle atrophy based on genetic mouse models and pharmacological *in vivo* animal studies [69,89,93]. Results from clinical trials will certainly be important for judging whether excitement on current IKK β inhibitors as potential drugs for such a wide range of diseases is justified.

3. Conclusion

After the identification of a great variety of signaling molecules involved in NF- κ B activation via IKK β , deciphering the exact pathways from cell surface receptors via adapter proteins and kinases to IKK β as converging point and key enzyme is an ongoing process. Recent data demonstrate that the signaling requires activating ubiquitinations which form K63-linked polyubiquitin chain platforms for the binding of signaling molecules. This may be crucial for scaffolding effector molecules in order to pass on the signal. Based on these findings, chemical substances interfering with activating ubiquitinations might be interesting future drugs.

Competing interests

The authors declare to have no competing interests.

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