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Novel functions of chromatin-bound $I\kappa B\alpha$ in oncogenic transformation

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The nuclear factor- κ B (NF- κ B) signalling pathway participates in a multitude of biological processes, which imply the requirement of a complex and precise regulation. I κ B (for Inhibitor of kappaB) proteins, which bind and retain NF- κ B dimers in the cytoplasm, are the main contributors to negative regulation of NF- κ B under non-stimulation conditions. Nevertheless, increasing evidences indicate that I κ B proteins exert specific nuclear roles that directly contribute to the control of gene transcription. In particular, hypophosphorylated I κ B β can bind the promoter region of TNF α leading to persistent gene transcription in macrophages and contributing to the regulation of the inflammatory response. Recently, we demonstrated that phosphorylated and SUMOylated I κ B α reside in the nucleus of the cells where it binds to chromatin leading to specific transcriptional repression. Mechanistically, I κ B α associates and regulates Polycomb Repressor Complex activity, a function that is evolutionary conserved from flies to mammals, as indicate the homeotic phenotype of *Drosophila* mutants. Here we discuss the implications of chromatin-bound I κ B α function in the context of tumorigenesis.

The nuclear factor- κ B (NF- κ B) family of transcription factors has an important role in the regulation of biological processes such as immunity and inflammation, apoptosis, stress response or ageing (Hayden and Ghosh, 2004). This family is composed of five members: RelA (p65), RelB and c-Rel, and the precursor proteins NF- κ B1 (p105) and NF- κ B2 (p100) that can be processed into p50 and p52, respectively. Nuclear factor- κ B transcription factors function as homo- and hetero-dimers that activate or repress gene expression in a context-dependent manner. Under resting conditions, most NF- κ B resides in the cytoplasm bound to particular inhibitory proteins of the inhibitor of kappaB (I κ B) family, I κ B α , IkB β or I κ B ϵ , which generate an additional degree of complexity. Phosphorylation of I κ B at specific serine residues by the I κ B kinase (IKK) complex induces its ubiquitynation and subsequent proteasomal degradation, thus releasing the NF- κ B factor leading to its nuclear translocation and gene transcription (Beg et al, 1992). However, recent studies have provided evidence that IkB proteins are more than NF-kB inhibitors. In 2010, Rao and colleagues demonstrated that following LPS stimulation, hypophosphorylated newly synthesised IkB β binds p65 and c-Rel at the promoter region of specific genes such as TNF α and protects the NF- κ B factor from IkBa association and chromatin release leading to persistent transcriptional activity (Rao et al, 2010). The

same mechanism operates at the IL1- β promoter (Scheibel *et al*, 2010).

Some years ago, we found that in fibroblasts nuclear $I\kappa B\alpha$ associates with NF- κ B-independent gene promoters, such as hes1 and herp2, which are general regulators of cell differentiation, correlating with their transcriptional repression. TNFa treatment induced IKK recruitment to these particular genes leading to $I\kappa B\alpha$ dissociation and transcriptional activation (Aguilera et al, 2004). Importantly, IKK was found constitutively bound to hes1 and herp2 promoters in colorectal cancer cells associated with increased gene expression (Fernandez-Majada et al, 2007a). Now, we have demonstrated that in keratinocytes there is a fraction of phosphorylated and SUMOylated I κ B α (PS-I κ B α) that binds to chromatin through direct association with histones leading to NF- κ B-independent gene regulation (Mulero *et al*, 2013). Interestingly, nuclear PS-I κ B α seems to be crucial for proper skin homeostasis, which might explain the severe skin phenotype of I κ B α -deficient mice that die 5 days after birth because of a massive skin inflammation likely associated with a defective barrier function (Beg et al, 1995; Klement et al, 1996; Rebholz et al, 2007; Table 1). In addition, our results strongly suggest that aberrant accumulation of cytoplasmic IκBα in keratinocytes promotes squamous cell carcinoma (SCC;

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Model	Phenotype	Reference
Conventional ΙκΒα-deficient mice	Increase on proliferative keratinocytes relative to differentiated cell types accompanied by a widespread dermatitis. Skin inflammation associated to high levels of IL-1 β and IFN- γ in the dermis and infiltration of CD8 + T cells and Gr-1 + neutrophils in the epidermis	Beg et al, 1995; Klement et al, 1996; Rebholz et al, 2007
Keratin5 promoter- ΙκΒα-deficient mice	Abnormal proliferation of keratinocytes without epidermal inflammation	Rebholz <i>et al,</i> 2007
Double $I\kappa B\alpha$ - and $TNF\alpha$ -deficient mice	Viable more than 3 months. Skin phenotype rescued	Shih <i>et al,</i> 2009
Keratin5 promoter- ΙκΒα-SR transgenic	Severe macroscopic phenotype characterised by flaky skin, hair loss, dysplasia of the epidermis and development of SCC and inflammatory response	van Hogerlinden <i>et al</i> , 1999; Seitz et al, 1998; van Hogerlinden <i>et al</i> , 2004
Human keratinocytes expressing I&Ba-SR and/or RAS Gly12Val transplanted into CB-17 scid mice	IκBα-SR alone showed mild hyperplasia. Co-expression of RAS and IκBα-SR produced large neoplasms resembling SCC	Dajee <i>et al,</i> 2003
NfkbiaNES/NES mice harbouring a triple point mutation in the NES	Defect on secondary lymphoid organ formation and impaired B-cell maturation. Expansion of the proliferative compartment and reduction of the differentiation layers in the skin	Wuerzberger-Davis <i>et al,</i> 2011; Mulero <i>et al,</i> 2013

Mulero et al, 2013), which is in agreement with the oncogenic phenotype of ectopic IkBa-SR expression in the skin (van Hogerlinden et al, 1999, 2004).

IκBα, AN OLD CYTOPLASMIC PROTEIN WITH A NOVEL NUCLEAR FUNCTION, OR VICE-VERSA

ΙκΒα regulates epidermal homeostasis. Mammalian epidermis consists of four different layers: basal, spinous, granular and cornified. The proliferating basal layer of the epidermis contains most of the stem and progenitor cells of this tissue, which then undergoes a differentiation process that culminates in their fully maturation and enucleation as they reach the surface layer, thus generating the cornified layer of keratinocytes. However, this is not an easy task for a tissue that is permanently exposed to a plethora of external insults such as UV radiation, extreme temperature variations and chemical exposure among others. The success of the skin differentiation process depends on the integration of intrinsic cellular programmes with external signals including the response of the immune system. Recently, we found that PS-I κ B α is predominantly distributed in the nucleus of keratinocytes bound to the promoter of genes such as HOX and IRX (Mulero et al, 2013), which control skin differentiation and proliferation but are also involved in the developmental regulation. Once in the chromatin, PS-IkBa facilitates the recruitment of polycomb repressive complex 2 to gene promoters and dictates their competence to be induced following $TNF\alpha$ stimulation, thus establishing a mechanistic link between inflammatory signals and skin homeostasis. Remarkably, this role for $I\kappa B\alpha$ as a regulator of polycomb function is operating during Drosophila development since mutations in Cactus (the IkBa orthologue in flies) enhanced the homeotic phenotype of Pc (Polycomb) mutations. These results together with the identification of $I\kappa B\alpha$ orthologues in the worm Caenorhabditis elegans that does not have a real NF-KB pathway suggest that this newly identified function of PS-I κ B α is an ancestral function previous to the specialisation of the immune system.

Nuclear IkBa as a tumour suppressor in the skin. Indicative of a tumour-suppressor function for PS-IkBa, immunohistochemical

analysis of a panel of human skin samples demonstrated that $I\kappa B\alpha$ remains nuclear in the keratinocytes of benign skin lesions such as elastosis, psoriasis, actinic keratosis and Bowen disease, but is specifically lost in the more malignant lesions such as SCC. Further analysis of a cohort of 112 patients with urogenital SCC at different stages of tumour progression showed that in samples corresponding to invasive and metastatic SCC, $I\kappa B\alpha$ was totally excluded from the nucleus but accumulated in the cytoplasm (Mulero et al, 2013), suggesting that beyond loss of nuclear IkBa, cytoplasmic IkBa (likely SUMOylated-I κ B α) might have additional pro-tumorigenic functions, which will be investigated. This possibility is in agreement with the skin phenotype of different mice strains ectopically expressing the I κ B α super-repressor mutant (I κ B α -SR), which develop SCC-resembling tumours in the skin (Dajee et al, 2003; van Hogerlinden et al, 1999, 2004; Table 1), what contrast with the dogma that constitutive NF- κ B activation results in protumorigenic phenotypes that are prevented following NF- κ B inhibition (Ben-Neriah and Karin, 2011). Similarly, Dajee et al (2003) demonstrated that mutant RASV12 failed to generate tumours when expressed in primary human keratinocytes (that were growth arrested), but it efficiently induced tumours resembling human SCC when co-expressed with IkBa-SR. Based on others and our results, we speculate that cytoplasmic accumulation of $I\kappa B\alpha$ in skin tumours might sequester nuclear co-represors and HDACs (Aguilera et al, 2004; Fernandez-Majada et al, 2007a, 2007b; Hoberg et al, 2004), thus promoting a global miss-regualtion of gene transcription. In this sense, specific HDAC proteins contain SUMO-binding elements that could favour their binding to PS-I κ B α either in the nucleus or the cytoplasm (model in Figure 1). Whether the cytoplasmic $I\kappa B\alpha$ that is found in SCC samples is SUMOylated and/or phosphorylated remains to be addressed.

More recently, a knock-in mouse containing an $I\kappa B\alpha$ protein with a mutated nuclear export sequence that is mostly localised in the nucleus of most cells has been characterised. These mutant mice show impaired canonical and alternative NF- κ B pathways in the mature B cells with the absence of secondary lymphoid organs, but they display functional skin with no evidence of critical barrier defects (Wuerzberger-Davis et al, 2011). However, a detailed analysis of mutant skins from 7- to 8-week-old animals revealed significant

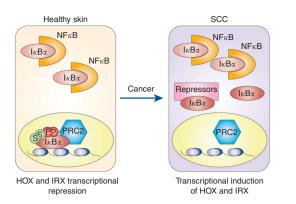


Figure 1. Schematic representation of PS-I κ B α structure depicting the six ankyrin repeats and the C-terminal PEST domain. SUMOylable lysines K21 and K22 are shown in green, whereas serines 32 and 36 (that are phosphorylated in PS-I κ B α) are indicated in red. Nuclear I κ B α is aberrantly localised in the cytoplasm of skin cancer cells. Thus, whereas in healthy skin, PS-I κ B α binds chromatin at the promoter of HOX and IRX family of genes repressing their transcription, in SCC, I κ B α is excluded from the nucleus and accumulates in the cytoplasm of the cells likely sequestering specific transcriptional repressors.

differences with wild-type mice including increased proliferation index, expansion of the K14-positive basal layer, and reduction on the thickness of the intermediate K10-positive skin layer (Mulero *et al*, 2013). Future experiments should address the question of whether constitutively nuclear $I\kappa B\alpha$ results in altered *Hox* and *Irx* expression in the basal or supra-basal layer of keratinocytes, and whether it protects these cells from undergoing tumorigenesis under specific transformation procedures or even with ageing.

IKB kinase alpha (IKK α) modulates IKB α localisation in keratinocytes. It is worth mentioning, that not only $I\kappa B\alpha$ but also the IKK α displays a predominantly nuclear distribution in the skin (Marinari et al, 2008; Zhu et al, 2007). Loss of IKKa associates with altered proliferation and differentiation of epidermal keratinocytes (Hu et al, 1999; Sil et al, 2004), whereas mutations that resulted in IKKa loss or in the generation of truncated proteins that failed to interact with chromatin led to the development of skin papillomas and SCC (Liu et al, 2006; Park et al, 2007). Conversely, chemically induced skin carcinogenesis is reverted by overexpression of wild-type IKKa (Liu et al, 2006). Our recent results indicated that active IKKa induced a partial accumulation of SUMOylated-IkBa in the cytoplasmic compartment of keratinocytes, and IKK activation correlates with cytoplasmic accumulation of $I\kappa B\alpha$ in human SCC samples (Mulero *et al*, 2013). These results open the possibility that $I\kappa B\alpha$ miss-regulation might contribute to the phenotypes observed downstream of IKKa alterations, although it remains to be studied how IKK α regulates I κ B α distribution. Because chromatin-bound $I\kappa B\alpha$ is already phosphorylated in the residues known to be targets of canonical IKK activity, and we found that this phosphorylation is IKK independent, we speculate that nuclear IKK α might induce PS-I κ B α chromatin release by regulating specific editing enzymes (i.e., phosphatase and desumoylase), scaffold proteins or proteins associated with the repressive PS-I κ B α complex such as histones or members of the polycomb repressive complex 2, resulting in a reduced affinity of $I\kappa B\alpha$ with chromatin.

Different I κ B α populations include different post-translational modifications. Several publications previously established the link between SUMOylation and transcriptional repression by specific transcription factors such as CtBP, KAP1 or Sp3 (reviewed in Garcia-Dominguez and Reyes (2009)). SUMOylated-I κ B α had previously been identified in different types of cells, however, no specific functions for this modified version of the molecule had been ascribed. In 1998, Desterro and colleagues detected the existence of endogenous SUMO-1-modified IkBa in a panel of cancer cell lines, being SUMO-1 linked to lysine 21 of IkBa. Because lysine 21 is involved in the signal-mediated degradation of I*κ*Bα (following poly-ubiquitination), SUMO1-I*κ*Bα was resistant to degradation and led to reduced NF- κ B activity in these cells. Interestingly, SUMOvlation was reduced in $I\kappa B\alpha$ mutant proteins mimicking serine 32 and 36 phosphorylation that is a mark for degradation (Desterro et al, 1998). Accumulation of SUMO-1bound $I\kappa B\alpha$ is also detected downstream of adenosine signalling during hypoxia and reoxigenation (Liu et al, 2009), although its functional contribution in this system is unknown. Recently, it was shown that $I\kappa B\alpha$ was modified by SUMO-2/3 but also by a combination of SUMO and ubiquitin chains (Culver et al, 2010) resulting in an I κ B α molecule that can still be regulated by degradation following NF- κ B activation (Aillet *et al*, 2012). The use of particular cell types, and the variations in the technical approaches (including the reagents used for stabilising SUMO chains and for detection) can explain the different results obtained by each group, however, it is still possible that several modifications coexist in particular $I\kappa B\alpha$ subpopulations leading to functional specificities. Interestingly, SUMOylable proteins are characterised by the presence of a specific WKxE/D motif, which is the case of IkBa but not of other IkB orthologues such as IkB β (Kracklauer and Schmidt, 2003). An extended consensus has also been reported, in which SUMOylation is imposed by negatively charged residues (including phosphorylated aminoacids) downstream of the Ψ KxE/D motif (Hietakangas *et al*, 2003). Thus, one could speculate that $I\kappa B\alpha$ SUMOvlation is subsequent to its phosphorylation at serines 32 and/or 36 by specific kinase/s other than IKK β (Mulero *et al*, 2013). Thus, it is of crucial importance to identify such kinases, investigate how they are regulated under specific conditions, different tissues or particular processes, and evaluate their contribution to $I\kappa B\alpha$ SUMOylation and function. Finally, studying the contribution of SUMO modifications to $I\kappa B\alpha$ function is not an easy job as mutants that fail to be SUMOylated (i.e., the K21-22 mutant) are also unable to be ubiquitinated and degraded, thus leading to strong NF-kB phenotypes. To circumvent this problem, we are currently generating SUMO-I κ B α fusion proteins, which will be tested for their chromatin- or NF-kBrelated activities.

The discovery that PS-I κ B α exerts a nuclear function that affects NF- κ B-independent transcription in response to NF- κ B-related stimuli such as TNF α is also a temptation to re-examine previous results that might have misinterpreted because of the most prominent role of cytoplasmic I κ B α . A putative involvement of PS-I κ B α in other types of cancer should also be studied; mainly in those that are associated with aberrant or chronic IKK activity such is the case of inflammation-related ones.

On the other hand, it is possible that specific elements of the chromatin-bound $I\kappa B\alpha$ complex are directly involved in $I\kappa B\alpha$ SUMOylation. For example, Pc2, one of the mammalian orthologues of the *Drosophila* Polycomb (PRC1) that we found as functionally associated with $I\kappa B\alpha/Cactus$ during *Drosophila* development, is a SUMO E3 ligase (Kagey *et al*, 2003). Moreover, it is not just $I\kappa B\alpha$ but other chromatin components such as the histones and elements of the PRC complex including EZH2 and SUZ12 are capable to be SUMOylated, which might impact on their capacity to recruit transcriptional repressors at specific genomic regions, which will be addressed in a near future.

Future therapeutic perspectives based on I\kappaB\alpha. The importance of investigating the mechanisms involved in I κ B α and PS-I κ B α regulation and their functional relevance in tumour progression is evidenced by the fact that over 250 000 patients are diagnosed with

SCC in the world each year. Squamous cell carcinoma is the second most common skin cancer that arises in any region of the body but more frequently in areas exposed to the UV light. Although infrequent (about 10% of the cases), the appearance of metastasis in SCC patients has a very bad prognosis because the absence of treatments, especially in aged patients. Moreover, to date there are no good biomarkers that predict metastatic SCC potential beyond the previous appearance of local relapse, tumour staging or the presence of MYC amplifications (Toll *et al*, 2009). We are currently investigating whether detection of cytoplasmic I κ B α or PS-I κ B α , or/and nuclear-active IKK α identifies the small fraction of SCC patients that will develop tumour relapse or metastasis. Those patients could be then selected for more aggressive therapies, but also as candidates for future personalised treatments based on I κ B α /IKK α -based therapies.

CONCLUSIONS

Initially, IkB proteins were described as cytoplasmic regulators of the NF- κ B pathway; however, several studies focused on I κ B α and I κ B β demonstrated the existence of specific nuclear roles for both proteins. First, it was found that IkBa contains a functional nuclear localisation signal that is essential for the efficient post-activation termination of NF- κ B signalling by facilitating chromatin release of p50-p65 dimers (Arenzana-Seisdedos et al, 1997). However, IkB α can be retained bound to the chromatin at specific promoter regions through its interactions with histones H2A and H4, thus playing an essential contribution to skin differentiation. We propose that PS-IkBa can exert both pro-oncogenic and tumoursuppressor functions, which need to be investigated in detail. In contrast, nuclear I κ B β is mainly associated with the regulation of the inflammatory response, through the maintenance of persistent cytokine expression in macrophages. The finding that this polycomb-associated IkBa function is conserved in the Drosophila development, together with and the identification of IkB homologues in worms lacking a truly NF- κ B pathway suggests that this is an ancestral function that might exert a more general contribution to the cellular physiology. Finally, the identification of specific post-translational modifications that are restricted to chromatin-bound IkBa converts its modifying enzymes and PS- $I\kappa B\alpha$ in attractive targets for novel therapeutic strategies specific for particular IkBa-associated pathologies and patients.

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