

The Nuclear Protein I κ B ζ Forms a Transcriptionally Active Complex with Nuclear Factor- κ B (NF- κ B) p50 and the *Lcn2* Promoter via the N- and C-terminal Ankyrin Repeat Motifs*

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The nuclear protein I κ B ζ , comprising the N-terminal *trans*-activation domain and the C-terminal ankyrin repeat (ANK) domain composed of seven ANK motifs, activates transcription of a subset of nuclear factor- κ B (NF- κ B)-dependent innate immune genes such as *Lcn2* encoding the antibacterial protein lipocalin-2. *Lcn2* activation requires formation of a complex containing I κ B ζ and NF- κ B p50, a transcription factor that harbors the DNA-binding Rel homology region but lacks a *trans*-activation domain, on the promoter with the canonical NF- κ B-binding site (κ B site) and its downstream cytosine-rich element. Here we show that I κ B ζ productively interacts with p50 via Asp-451 in the N terminus of ANK1, a residue that is evolutionarily conserved among I κ B ζ and the related nuclear I κ B proteins Bcl-3 and I κ B_{NS}. Threonine substitution for Asp-451 abrogates direct association with the κ B-site-binding protein p50, complex formation with the *Lcn2* promoter DNA, and activation of *Lcn2* transcription. The basic residues Lys-717 and Lys-719 in the C-terminal region of ANK7 contribute to I κ B ζ binding to the *Lcn2* promoter, probably via interaction with the cytosine-rich element required for *Lcn2* activation; glutamate substitution for both lysines results in a loss of transcriptionally active complex formation without affecting direct contact of I κ B ζ with p50. Both termini of the ANK domain in Bcl-3 and I κ B_{NS} function in a manner similar to that of I κ B ζ to interact with promoter DNA, indicating a common mechanism in which the nuclear I κ Bs form a regulatory complex with NF- κ B and promoter DNA via the invariant aspartate in ANK1 and the conserved basic residues in ANK7.

Nuclear factor- κ B (NF- κ B)² plays central roles in host defense and inflammation as a homo- or heterodimer of NF- κ B/Rel family proteins by controlling the expression of genes for pro-inflammatory cytokines, chemokines, and antibacterial proteins (1–4). The mammalian NF- κ B family is com-

posed of five structurally related polypeptides: p50, p52, p105 (the precursor of p50), p100 (the precursor of p52), p65 (also known as RelA), RelB, and c-Rel. They share the Rel homology region, which mediates dimerization, nuclear translocation, binding to specific DNA sequences known as NF- κ B-binding elements (κ B sites), and association with one of the I κ B family proteins (1–4). Among the members of the family, p65, RelB, and c-Rel have an ability to activate transcription by themselves via the C-terminal *trans*-activation domain, which is absent in the smaller p50 and p52 proteins. In resting cells, NF- κ B dimers are retained in the cytoplasm by associating with a member of the prototypical/cytoplasmic I κ B proteins including I κ B α , I κ B β , and I κ B ϵ (1–4). Cell activation with appropriate stimuli such as bacterial LPS leads to phosphorylation-induced degradation of cytoplasmic I κ Bs and resultant liberation of NF- κ B dimers (1, 5, 6). The released NF- κ B dimers subsequently translocate to the nucleus and thus induce the expression of primary response genes via binding to κ B sites on their promoter/enhancer regions (1–4).

The primarily induced gene products include the atypical/nuclear I κ B proteins Bcl-3 (7, 8), I κ B ζ (also known as MAIL or INAP) (9–11), and I κ B_{NS} (12), which are not expressed in resting cells. In contrast to the cytoplasmic I κ Bs, which preferentially associate with NF- κ B dimers that possess at least one p65 or c-Rel subunit such as the p50-p65 heterodimer (13), the nuclear I κ Bs prefer the p50 (or p52) homodimer as a partner to directly regulate the activation of secondary response genes for appropriate host defense responses (14–19). Thus, a part of the secondary response genes is controlled by NF- κ B-dependent induction of nuclear I κ Bs and their subsequent association with NF- κ B. For instance, the secondarily induced genes *Lcn2* (encoding the antibacterial protein lipocalin-2) and *Ptx3* (encoding the antibacterial protein pentraxin 3) are activated by the nuclear I κ B protein I κ B ζ (20–24), which serves as a key regulator in the immune system (16, 18, 25, 26). On the other hand, Bcl-3 participates in transcriptional control of the chemokine-encoding genes *Ccl2* for monocyte chemoattractant protein-1 (MCP-1) and *Cxcl10* for interferon- γ -induced protein 10 (IP-10) (27), and I κ B_{NS} regulates transcription of *Il6* (encoding the pro-inflammatory cytokine interleukin-6) and *Il12b* (encoding interleukin-12 subunit p40) (28, 29).

The I κ B proteins are characterized by the presence of the ankyrin repeat domain (ARD). The ARD of the cytoplasmic or nuclear I κ Bs contains six or seven ankyrin repeat (ANK) motifs, respectively. The ANK is an evolutionarily conserved protein

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² The abbreviations used are: NF- κ B, nuclear factor- κ B; ARD, ankyrin repeat domain; ANK, ankyrin repeat; MEF, mouse embryonic fibroblast; BMM, bone marrow-derived macrophage; HDAC, histone deacetylase; TSA, trichostatin A; MBP, maltose-binding protein; CBB, Coomassie brilliant blue.

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motif of about 33 amino acid residues that forms an L-shaped structure comprising a β hairpin and two antiparallel α helices. Consecutive ANK motifs generally stack together to serve as an underlying architecture of a modular specific protein-interacting interface (30–32). The ARD of I κ Bs mediates the association with NF- κ B dimers via direct binding to the NF- κ B Rel homology region (23, 33, 34). Although the ARD of nuclear I κ Bs displays a high sequence similarity to that of cytoplasmic I κ Bs except for the additional seventh motif ANK7 (10, 12, 35, 36), the preference for NF- κ B dimer species differs between the nuclear and cytoplasmic I κ Bs, as described above (7–9, 12, 16, 37). Furthermore, there exists a difference in interaction with κ B DNA. Although I κ B α promotes the dissociation of a p65-containing dimer from the promoter DNA (38), the nuclear I κ Bs are generally assumed to interact indirectly with the κ B site via binding to NF- κ B p50 or p52 (7, 8, 23, 33, 34). In addition, we have recently shown that I κ B ζ interaction with the *Lcn2* promoter also requires a region downstream of the κ B site (23). However, the molecular mechanism underlying assembly of the nuclear I κ B-containing regulatory complex has not been well elucidated.

In the present study, we show that I κ B ζ , containing the N-terminal *trans*-activation domain and the C-terminal ARD, forms a transcriptionally active complex with the *Lcn2* promoter via both Asp-451-mediated association with the κ B-site-binding protein p50/p52 and Lys-717/Lys-719-dependent interaction with the downstream extra κ B site on the *Lcn2* promoter. Asp-451, an invariant residue among the nuclear I κ Bs, is present in the N terminus of ANK1; Lys-717 and Lys-719 exist in the region C-terminal to the second α helix of ANK7, and the corresponding sites are also occupied by basic residues in Bcl-3 and I κ B_{NS}. Both termini of the ARD in these proteins serve in a manner similar to that of I κ B ζ , indicative of a common mechanism by which nuclear I κ Bs form a p50/p52-containing regulatory complex on target gene promoters.

Results

The Invariant Aspartate in ANK1 of I κ B ζ and Other Nuclear I κ Bs Is Crucial for Interaction with NF- κ B—It is known that the ARD of the nuclear I κ B proteins I κ B ζ , I κ B_{NS}, and Bcl-3 (Fig. 1A) is responsible for binding to NF- κ B p50 (33, 34). To determine the N-terminal boundary of the I κ B ζ region required for interaction with p50, we expressed and purified a series of N-terminally truncated I κ B ζ as GST-fused proteins and tested their ability to bind to p50. As shown in Fig. 1B, I κ B ζ -(449–728) fully interacted with p50, as did I κ B ζ -(414–728). On the other hand, I κ B ζ -(453–728) failed to bind to p50 (Fig. 1B), suggesting a role for amino acid residues 449–452. Among the four residues, Asp-451 in ANK1 is the only one that is completely conserved during evolution (Fig. 1A). Intriguingly, the aspartate also exists in the other nuclear I κ B proteins I κ B_{NS} and Bcl-3 (Asp-60 and Asp-127, respectively) but is replaced by threonine or serine in cytoplasmic I κ B members (Fig. 1A). Consistent with the conservation, the replacement of Asp-451 by threonine impaired I κ B ζ binding to p50 in a GST pulldown assay (Fig. 1C). The D451T substitution in I κ B ζ also resulted in a loss of its co-immunoprecipitation with p50 when FLAG-tagged full-length I κ B ζ and HA-p50 were expressed in HEK293T cells

(Fig. 1D). Thus, the invariant residue Asp-451 in ANK1 plays a crucial role in I κ B ζ interaction with p50.

We next investigated the role of the corresponding aspartate residue in other nuclear I κ B proteins (Asp-60 in I κ B_{NS} and Asp-127 in Bcl-3). Threonine substitution for Asp-60 in I κ B_{NS} led to an impaired interaction with p50 both in a GST pulldown assay using purified proteins (Fig. 1E) and in a co-immunoprecipitation assay using proteins expressed in HEK293T cells (Fig. 1F). Similarly, compared with wild-type Bcl-3, a mutant protein with threonine substitution for Asp-127 interacted with p50 much less efficiently both *in vitro* (Fig. 1E) and *in vivo* (Fig. 1G). These findings highlight a conservative role for the invariant aspartate of ANK1 in direct interaction of nuclear I κ Bs with p50.

Nuclear I κ B proteins are also known to form a complex with NF- κ B p52, a protein homologous to p50 (7, 12, 37). As expected from the homology, *in vitro* complex formation with p52 was impaired by threonine substitution for the invariant aspartate in ANK1 of nuclear I κ Bs: Asp-451 in I κ B ζ , Asp-60 in I κ B_{NS}, and Asp-127 in Bcl-3 (Fig. 2A). The critical role for the aspartates was confirmed by co-precipitation of p52 with I κ B ζ (Fig. 2B), I κ B_{NS} (Fig. 2C), and Bcl-3 (Fig. 2D) when ectopically expressed in HEK293T cells. Thus, p52 likely interacts with nuclear I κ B proteins in a manner similar to the way p50 does.

Asp-451 of I κ B ζ Is Involved in Transcriptional Activation—As we have shown previously (23), expression of I κ B ζ along with p50 results in transcriptional activation of the promoter of the lipocalin-2-encoding gene *Lcn2* in p50/I κ B ζ -deficient mouse embryonic fibroblasts (MEFs) (*Nfkb1*^{-/-}; *Nfkbiz*^{-/-} MEFs) (Fig. 3A). To examine the role for Asp-451 of I κ B ζ in p50-dependent *Lcn2* activation, we used p50/I κ B ζ -deficient MEFs in which a luciferase reporter is regulated by the *Lcn2* promoter (23). As shown in Fig. 3A, I κ B ζ (D451T), defective in associating with p50, activated the *Lcn2* promoter much less effectively than the wild-type protein even in the presence of p50. We next tested the role for Asp-451 of ANK1 in I κ B ζ -mediated activation of the endogenous *Lcn2* gene. As shown in Fig. 3B, exogenous expression of wild-type I κ B ζ in I κ B ζ -deficient bone marrow-derived macrophages (BMMs) resulted in time-dependent activation of the endogenous *Lcn2* gene in response to LPS. On the other hand, I κ B ζ (D451T), a mutant protein defective in direct interaction with NF- κ B p50 (Fig. 1), failed to activate the endogenous *Lcn2* gene, although I κ B ζ (D451T) was expressed at a level similar to that of the wild-type protein (Fig. 3B). Thus, the interaction between I κ B ζ and p50 appears to be involved in transcriptional activation of *Lcn2*.

We also investigated the function of Bcl-3 Asp-127, a residue that corresponds to Asp-451 in I κ B ζ and is crucial for binding to p50 and p52 (Figs. 1 and 2), in gene activation. As shown in Fig. 3C, Bcl-3 (D127T) activated a reporter of the *Ccl2* promoter in LPS-stimulated RAW264.7 cells that ectopically expressed p52 but to a significantly lesser extent than the wild-type protein. Thus, Bcl-3 binding to p52 plays a role in *Ccl2* activation. On the other hand, I κ B ζ did not activate *Lcn2* in combination with p52 under conditions where p50 fully supported I κ B ζ (Fig. 3D). This raises the possibility that p52 is incapable of directly interacting with the *Lcn2* promoter DNA, although p52 binds to I κ B ζ as p50 does (Fig. 2B). To address this

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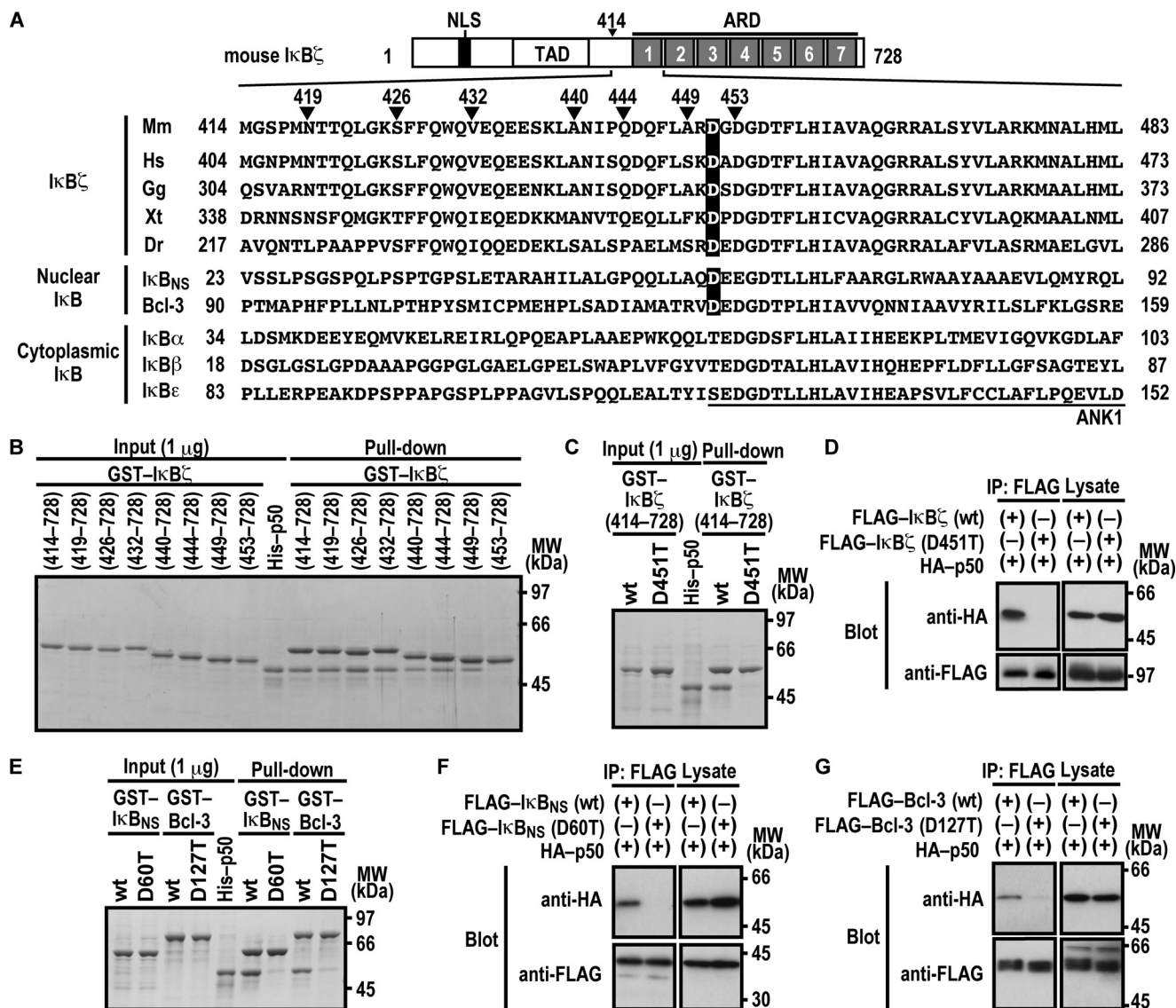


FIGURE 1. Asp-451 in ANK1 of I κ B ζ and the corresponding residues of I κ B ζ and Bcl-3 are involved in interaction with NF- κ B p50. A, domain organization of mouse I κ B ζ and comparison of the amino acid sequences of ANK1 and its N-terminally flanking region. Mouse I κ B ζ of 728 amino acids contains the nuclear localization signal (NLS), the trans-activation domain (TAD), and the ARD comprised of seven ANK motifs. The amino acid sequences of ANK1 and its N-terminally flanking region of I κ B ζ from various species and those of other mouse I κ B proteins are aligned. *Mm*, *Mus musculus*; *Hs*, *Homo sapiens*; *Gg*, *Gallus gallus*; *Xt*, *Xenopus tropicalis*; *Dr*, *Danio rerio*. B, the I κ B ζ N-terminal boundary required for interaction with NF- κ B p50. GST-fused I κ B ζ with the indicated truncation was incubated with His-p50 and pulled down with glutathione-Sepharose-4B beads, followed by SDS-PAGE analysis with CBB staining. MW, molecular weight. C and E, the role for I κ B ζ Asp-451, I κ B ζ Asp-60, and Bcl-3 Asp-127 in interaction with NF- κ B p50 *in vitro*. GST-fused I κ B ζ (C), I κ B ζ (E), or Bcl-3 (E) with or without the indicated amino acid substitution was co-expressed with HA-p50 in HEK293T cells, and proteins in the cell lysate were immunoprecipitated (IP) with anti-FLAG antibody, followed by immunoblot analysis with the indicated antibody (Blot). Positions for marker proteins are indicated in kilodaltons.

question, we analyzed the formation of the protein-promoter complex using a DNA-binding assay in which DNA bound to a tagged protein is pulled down with tag affinity beads and amplified by PCR (for details, see "Experimental Procedures"). As shown in Fig. 3E, the *Lcn2* promoter efficiently interacted with wild-type p50 but not with p50 (Y57A/E60D), a mutant protein defective in binding to the κ B site (23), or p65. In contrast to p50, wild-type p52 failed to directly bind to the *Lcn2* promoter (Fig. 3E). Thus, I κ B ζ appears to activate *Lcn2* by specifically interacting with p50.

*Lys-717 and Lys-719 in ANK7 of I κ B ζ Participate in *Lcn2* Activation*—We next studied the role for the C-terminal region of the I κ B ζ ARD, which comprises seven ANK repeats (Fig. 4A).

For this purpose, we expressed a series of C-terminally truncated I κ B ζ proteins in *Nfkb1*^{-/-}; *Nfkbiz*^{-/-} MEFs to test their ability to activate the *Lcn2* promoter. As shown in Fig. 4B, I κ B ζ -(1-721) was as active as full-length I κ B ζ of 728 amino acids. By contrast, *Lcn2* was activated much more weakly by I κ B ζ -(1-718) and only marginally by I κ B ζ -(1-716) (Fig. 4B), indicating a crucial role for the C-terminal region of I κ B ζ ANK7 (amino acids 717-721) in *Lcn2* activation. On the other hand, this region was dispensable for direct contact of I κ B ζ with p50, as estimated by the GST pull-down assay (Fig. 4C). The dispensability is in contrast with the involvement of I κ B ζ ANK1 in direct interaction with p50 (Fig. 1) as well as in *Lcn2* activation (Fig. 3). The I κ B ζ C-terminal region crucial for *Lcn2* activation

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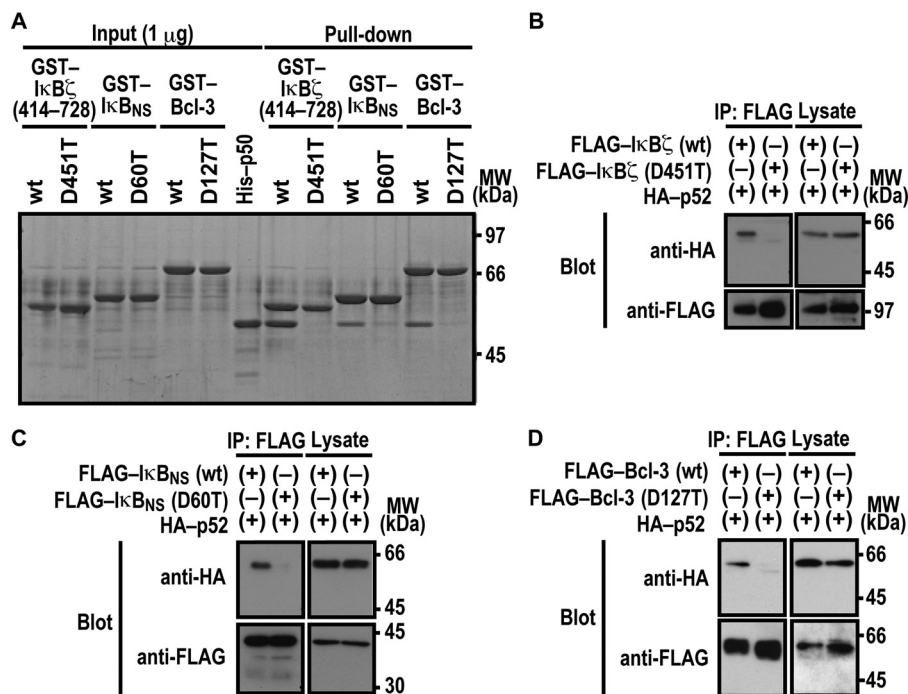


FIGURE 2. Asp-451 in ANK1 of I κ B ζ and the corresponding residue of I κ B_{NS} and Bcl-3 are involved in interaction with NF- κ B p52. *A*, the role for I κ B ζ Asp-451, I κ B_{NS} Asp-60, and Bcl-3 Asp-127 in interaction with NF- κ B p50 *in vitro*. GST-fused I κ B ζ , I κ B_{NS}, and Bcl-3 with or without the indicated amino acid substitution were incubated with His-p52(1–341), and pulled down with glutathione-Sepharose-4B beads, followed by SDS-PAGE analysis with CBB staining. MW, molecular weight. *B–D*, the role of I κ B ζ Asp-451, I κ B_{NS} Asp-60, and Bcl-3 Asp-127 in interaction with NF- κ B p50 *in vivo*. FLAG-tagged I κ B ζ (*B*), I κ B_{NS} (*C*), or Bcl-3 (*D*) with or without the indicated amino acid substitution was co-expressed with HA-p52 in HEK293T cells, and proteins in the cell lysate were immunoprecipitated (IP) with the anti-FLAG antibody, followed by immunoblot analysis with the indicated antibody (Blot). Positions for marker proteins are indicated in kilodaltons.

contains the basic residues Lys-717 and Lys-719, both of which are evolutionarily well conserved (Fig. 4A). The *Lcn2* promoter was activated by a mutant I κ B ζ carrying substitution of the acidic residue glutamate for Lys-717, but to a lesser extent than the wild-type protein (Fig. 4D), and double glutamate substitution for Lys-717 and Lys-719 led to an almost complete loss of *Lcn2* activation (Fig. 4D) without affecting the ability to directly interact with p50 (Fig. 4E). Furthermore, LPS-induced activation of the endogenous *Lcn2* gene was not observed in BMMs expressing a mutant I κ B ζ with the K717E/K719E substitution (Fig. 3B). In contrast, simultaneous replacement of Lys-717 and Lys-719 by the other basic residue arginine hardly affected *Lcn2* activation (Fig. 4F). These observations imply a possible role for the positive charge at amino acid positions 717 and 719 in I κ B ζ ANK7.

*Lys-717 and Lys-719 in ANK7 of I κ B ζ Participate in Complex Formation with the *Lcn2* Promoter and Not via p50*—It should be noted that the basic residues lysine and arginine are both capable of not only forming a salt bridge with a phosphate group of DNA but also of directly interacting with a base of DNA, especially guanine (39, 40). Furthermore, we have shown recently that a cytosine-rich region downstream of the κ B site is involved in formation of the active three-species complex I κ B ζ -p50-DNA (23), suggesting that the extra- κ B site makes a direct contact with p50, I κ B ζ , or both. It seems thus possible that the arginine-replaceable residues Lys-717 and Lys-719 in ANK7 participate in I κ B ζ interaction with the *Lcn2* promoter DNA. To test this possibility, we analyzed the *in vitro* formation of the I κ B ζ -p50-DNA complex using the method used in Fig. 3E.

Under conditions where the *Lcn2* promoter fragment was fully co-precipitated with wild-type I κ B ζ , the co-precipitation was not caused by I κ B ζ (D451T), defective in direct binding to p50 (Fig. 5A). The D451T substitution also disrupted I κ B ζ interaction with the endogenous promoter of *Lcn2*, as shown by ChIP analysis using cells that stably expressed the wild-type or mutant protein (Fig. 5B). Further analysis with the anti-RNA polymerase II antibody revealed that the impairment of I κ B ζ -p50 association resulted in loss of the *in vivo* formation of a transcriptionally active complex on the *Lcn2* promoter (Fig. 5B). The requirement of I κ B ζ -p50 association for interaction with the promoter is in good agreement with the following observation. Both p50 protein and the p50-binding site on the promoter (the κ B site) were required for I κ B ζ interaction with DNA (Fig. 5A). Thus, Asp-451 indirectly participates in complex formation with the *Lcn2* promoter via direct binding to p50. On the other hand, Lys-717 and Lys-719 in I κ B ζ may directly interact with target DNA because the K717E/K719E substitution abolished not only the recruitment to the *Lcn2* endogenous promoter for subsequent active complex formation (Fig. 5B) but also the *in vitro* interaction with the target DNA without affecting binding to p50 (Fig. 5A). As indicated from the finding that arginine can replace Lys-717 and Lys-719 in *Lcn2* activation (Fig. 4F), the replacement did not affect active complex formation with the *Lcn2* promoter (Fig. 5D). These findings indicate that I κ B ζ interacts with the *Lcn2* promoter via the arginine-replaceable residues Lys-717 and Lys-719 in a manner independent of direct binding to p50.

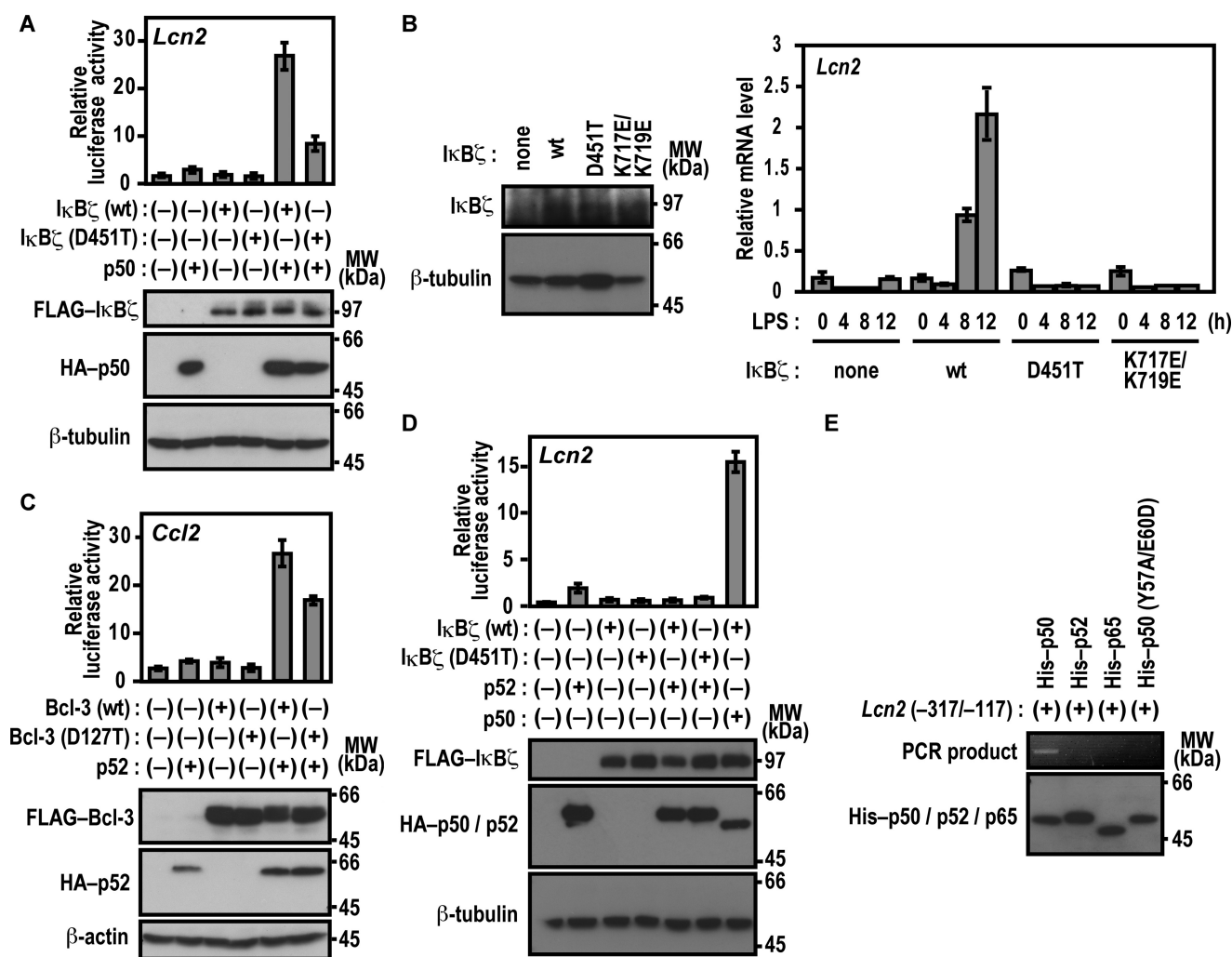


FIGURE 3. Asp-451 of IκBζ and Asp-127 of Bcl-3 participate in transcriptional activation. A and D, the role of IκBζ Asp-451 in *Lcn2* activation. p50/IκBζ-deficient MEFs were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of *Lcn2* (−1031/+54), the internal control plasmid pRL-TK, pcDNA3 for expression of FLAG-IκBζ (WT) or FLAG-IκBζ (D451T), and HA-p50 (A) or HA-p52 (D). Luciferase activities were determined as described under “Experimental Procedures.” Each graph represents the mean ± S.D. obtained from three independent transfections. Cell lysates were analyzed by immunoblot with anti-FLAG, anti-HA, or anti-β-tubulin antibody. MW, molecular weight. B, IκBζ-mediated activation of the endogenous *Lcn2* gene. IκBζ-deficient BMMs were retrovirally transduced for expression of WT IκBζ or a mutant protein with the D451T or K717E/K719E substitution. Proteins in the cell lysates were analyzed by immunoblot with the anti-IκBζ or anti-β-tubulin antibody (left panel). The transduced BMMs were stimulated for the indicated time with LPS, and the relative amounts of mRNA transcribed from the endogenous *Lcn2* gene were estimated by quantitative real-time RT-PCR as described under “Experimental Procedures” (right panel). Each graph represents the mean ± S.D. in triplicate determinations. C, the role of Bcl-3 Asp-127 in *Ccl2* activation. RAW264.7 cells were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of *Ccl2* (−2777/+76), the internal control plasmid pRL-TK, and pcDNA3 for expression of FLAG-Bcl-3 (WT) or FLAG-Bcl-3 (D127T) and HA-p52. Luciferase activities were determined as described under “Experimental Procedures.” Each graph represents the mean ± S.D. obtained from three independent transfections. Cell lysates were analyzed by immunoblot with anti-FLAG, anti-HA, or anti-β-actin antibody. E, association of p50 with the *Lcn2* gene promoter. His-tagged p50 (WT), p52 (WT), p65 (WT), or p50 (Y57A/E60D) was incubated with the *Lcn2* gene promoter (−317/−117). After the protein-DNA complex was pulled down with COSMOGEL® His-Accept, the co-precipitated DNA was amplified by PCR, and the product was analyzed by agarose gel electrophoresis. The precipitated proteins were subjected to immunoblot analysis with anti-His antibody. Positions for marker proteins are indicated in kilodaltons.

Furthermore, proline substitution for the evolutionarily well conserved residue Gly-718, which locates between Lys-717 and Lys-719 in IκBζ ANK7 (Fig. 4A), resulted in a loss of both interaction with the *Lcn2* promoter (Fig. 5A) and *Lcn2* activation (Fig. 5C). The observation suggests that correct orientation of Lys-717 and Lys-719 toward the target DNA may be required for association of IκBζ to the *Lcn2* promoter. On the other hand, neither S720A nor I721S substitution affected *Lcn2* activation (Fig. 5C).

Acetylation of IκBζ Does Not Seem to Be Involved in Lcn2 Activation—The significance of Lys-717 and Lys-719 of IκBζ in *Lcn2* activation may suggest the involvement of posttransla-

tional modification of these lysine residues, such as acetylation. To test this possibility, we treated cells with the potent histone acetyltransferase inhibitor anacardic acid (41, 42) and nicotinamide, an agent that inhibits the NAD⁺-dependent class III (sirtuin) family of histone deacetylases (HDACs) (43, 44). *Lcn2* activation by IκBζ remained unaffected by these inhibitors (Fig. 6, A and B). Under conditions where histone acetylation was significantly enhanced by the presence of trichostatin A (TSA), an inhibitor of class I/II HDAC (43, 44), lysine residues in IκBζ were not acetylated (Fig. 6C). Furthermore, a mobility shift of IκBζ on an SDS-PAGE gel, which was expected to occur by posttranslational modification, was not induced by TSA (Fig.

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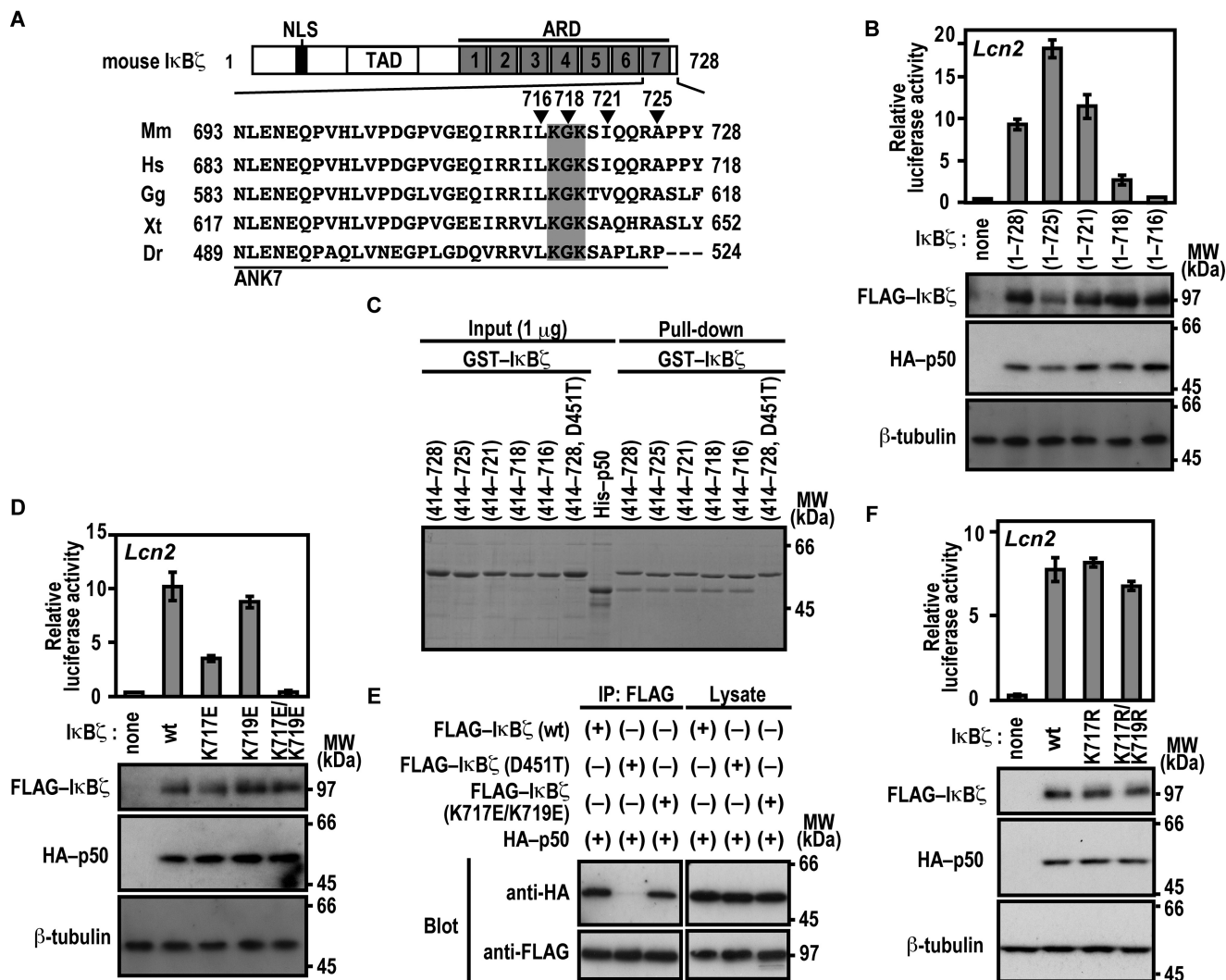


FIGURE 4. Lys-717 and Lys-719 in ANK7 of $\text{I}\kappa\text{B}\zeta$ are crucial for activation of the *Lcn2* gene. *A*, amino acid sequence alignment of ANK7 in $\text{I}\kappa\text{B}\zeta$ from various species. TAD, trans-activation domain; Mm, *Mus musculus*; Hs, *Homo sapiens*; Gg, *Gallus gallus*; Xt, *Xenopus tropicalis*; Dr, *Danio rerio*. *B*, the $\text{I}\kappa\text{B}\zeta$ C-terminal boundary required for *Lcn2* activation. p50- $\text{I}\kappa\text{B}\zeta$ -deficient MEFs were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of *Lcn2* (-1031/+54); the internal control plasmid pRL-TK, and pcDNA3 for expression of FLAG- $\text{I}\kappa\text{B}\zeta$ with the indicated truncation and HA-p50. Luciferase activities were determined as described under "Experimental Procedures." Each graph represents the mean \pm S.D. obtained from three independent transfections. Cell lysates were analyzed by immunoblot with anti-FLAG, anti-HA, or anti- β -tubulin antibody. MW, molecular weight. *C*, the $\text{I}\kappa\text{B}\zeta$ C-terminal boundary required for interaction with NF- κB p50. GST-fused $\text{I}\kappa\text{B}\zeta$ with the indicated truncation was incubated with His-p50 and pulled down with glutathione-Sepharose-4B beads, followed by SDS-PAGE analysis with CBB staining. *D*, the role of Lys-717 and Lys-719 of $\text{I}\kappa\text{B}\zeta$ ANK7 in *Lcn2* activation. The ability of FLAG- $\text{I}\kappa\text{B}\zeta$ with the indicated amino acid substitution was analyzed as in *B*. *E*, the role of Lys-717 and Lys-719 of $\text{I}\kappa\text{B}\zeta$ ANK7 in interaction with NF- κB p50 *in vivo*. FLAG-tagged $\text{I}\kappa\text{B}\zeta$ with the K717E/K719E or D451T substitution was co-expressed with HA-p50 in HEK293T cells, and proteins in the cell lysate were immunoprecipitated (IP) with anti-FLAG antibody, followed by immunoblot analysis with the indicated antibody (Blot). *F*, the effect of arginine substitution for Lys-717 and Lys-719 on $\text{I}\kappa\text{B}\zeta$ -mediated *Lcn2* activation. The ability of FLAG- $\text{I}\kappa\text{B}\zeta$ with the indicated amino acid substitution was analyzed as in *B*. Positions for marker proteins are indicated in kilodaltons.

6C). These observations suggest that acetylation of Lys-717 or Lys-719 of $\text{I}\kappa\text{B}\zeta$ does not participate in *Lcn2* activation, which also appears to be supported by the finding that neither gene activation nor promoter association are prevented by replacement of the lysines with arginine, a residue that does not undergo acetylation (Figs. 4F and 5D).

Basic Residues in ANK7 of $\text{I}\kappa\text{B}_{\text{NS}}$ and Bcl-3 Are Involved in Association with Target DNA—Lys-717 and Lys-719 of $\text{I}\kappa\text{B}\zeta$ are predicted to follow the second α helix in ANK7, and basic residues also exist at the corresponding sites in ANK7 of $\text{I}\kappa\text{B}_{\text{NS}}$ and Bcl-3 (Fig. 7A). As shown in Fig. 7B, association of $\text{I}\kappa\text{B}_{\text{NS}}$ with the promoter of the $\text{I}\kappa\text{B}_{\text{NS}}$ -regulated gene *Il6* was prevented by simultaneous glutamate substitution for Lys-316, Arg-317, and

Arg-319 in ANK7, although the substitution did not affect $\text{I}\kappa\text{B}_{\text{NS}}$ binding to p50. Similarly, glutamate substitution for Arg-354 and Lys-356 in ANK7 of Bcl-3 resulted in a loss of complex formation with the promoter of the Bcl-3-dependent gene *Cxcl10* without affecting Bcl-3 interaction with p50 (Fig. 7C), and Bcl-3 (R354E/K356E) also failed to associate with the endogenous promoter of *Cxcl10*, as indicated by ChIP analysis (Fig. 7D). Thus, in $\text{I}\kappa\text{B}_{\text{NS}}$ and Bcl-3, basic residues that follow the second α helix in ANK7 appear to be involved in recognition of their target gene promoters. Furthermore, the R354E/K356E substitution in Bcl-3 resulted in loss of the p52-dependent *Ccl2* activation in LPS-stimulated RAW264.7 cells (Fig. 7E), confirming the significance of the basic residues in ANK7.

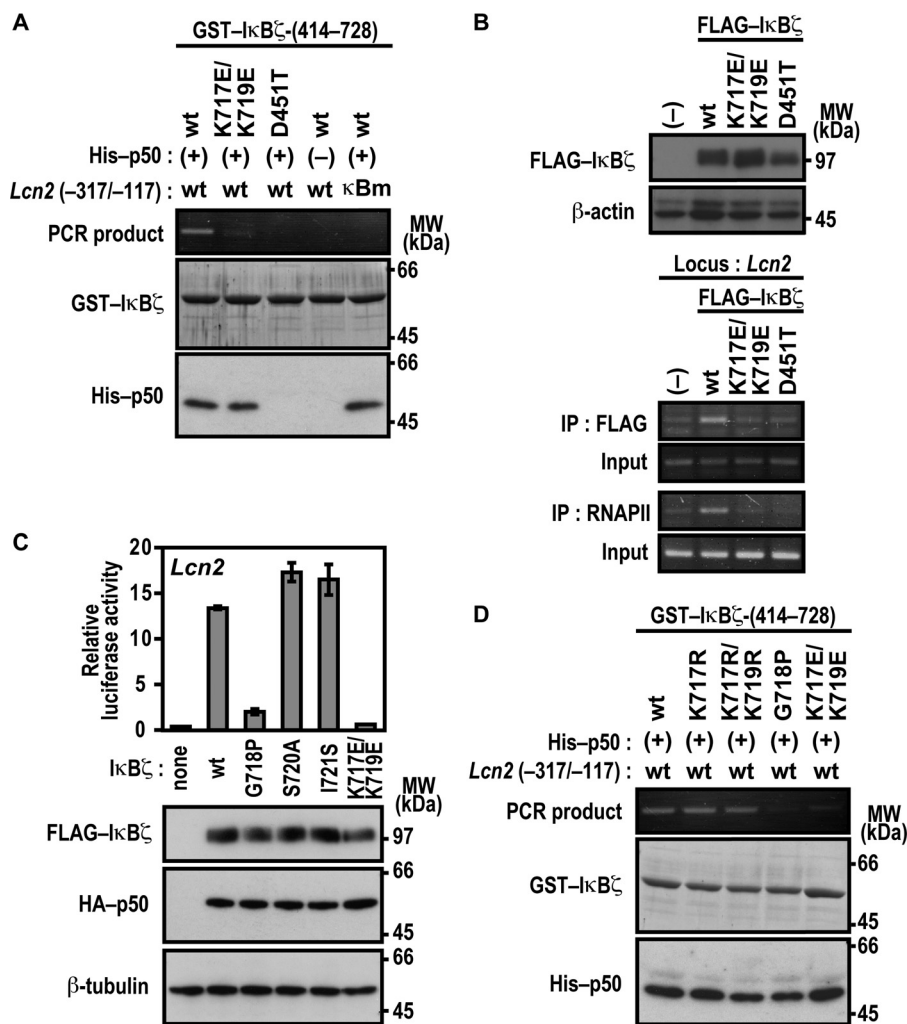


FIGURE 5. Lys-717 and Lys-719 in ANK7 of IκBζ are crucial for association with the *Lcn2* promoter DNA. *A* and *D*, GST-fused IκBζ-(414–728) or a mutant IκBζ carrying the indicated substitution were incubated with His-p50 in the presence of WT *Lcn2* (–317/–117) or a mutated κB site (κBm)-carrying *Lcn2* (–317/–117). After the protein-DNA complex was pulled down with glutathione-Sepharose-4B beads, the co-precipitated DNA was amplified by PCR, and the product was analyzed by agarose gel electrophoresis. The precipitated proteins were subjected to SDS-PAGE, followed by staining with CBB or immunoblot with anti-His antibody. *MW*, molecular weight. *B*, formaldehyde-fixed chromatin was prepared from RAW264.7 cells stably expressing FLAG-IκBζ (WT), FLAG-IκBζ (K717E/K719E), or FLAG-IκBζ (D451T) (*top panel*) and subjected to ChIP assay using anti-FLAG (M2) mouse monoclonal antibody or anti-RNA polymerase II antibody (*bottom panel*). Precipitated DNA was analyzed by PCR using primers corresponding to the *Lcn2* locus. The results are representative of experiments from at least three independent experiments. *IP*, immunoprecipitation. *C*, the role of Gly-718, Ser-720, and Ile-721 in *Lcn2* activation. p50-IκBζ-deficient MEFs were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of *Lcn2* (–1031/+54), the internal control plasmid pRL-TK, and pcDNA3 for expression of FLAG-IκBζ with the indicated amino acid substitution and HA-p50. Luciferase activities were determined as described under “Experimental Procedures.” Each graph represents the mean ± S.D. obtained from three independent transfections. Cell lysates were analyzed by immunoblot with anti-FLAG, anti-HA, or anti-β-tubulin antibody. Positions for marker proteins are indicated in kilodaltons.

The DNA-binding assays also revealed that the invariant aspartate residues in ANK1 of IκB_{NS} (Asp-60) (Fig. 7*B*) and Bcl-3 (Asp-127) (Fig. 7, *C* and *D*) participate in association with their target gene promoters via direct binding to p50, similar to the corresponding residue of IκBζ (Asp-451) (Fig. 5*A*).

Activation of *Lcn2* Involves Promoter Association with IκBζ via an Extra-κB Site in a Sequence-specific Manner—Activation of the mouse *Lcn2* gene requires promoter association with the IκBζ-p50 complex via both the κB site (5′-GGGAAT-GTCCC-3′ at positions –230 to –220 relative to the transcription start site) and its downstream region of 5′-CCCCTC-3′ at positions –212 to –207 (23) (see Fig. 8*A*). To elucidate base specificity in the downstream sequence, we constructed a series of mutant *Lcn2* promoters and tested their ability. Substitution of either guanine or adenine for cytosine at position –212 led to

a loss of both interaction with IκBζ and IκBζ-mediated *Lcn2* activation (Fig. 8*B*). On the other hand, they were only marginally impaired by thymine replacement at the corresponding position (Fig. 8*B*). Adenine but not thymine or guanine partially replaced cytosine at position –211 (Fig. 8*C*). At positions –210 (Fig. 8*D*) and –209 (Fig. 8*E*), cytosine was strictly required for both IκBζ binding to the *Lcn2* promoter and IκBζ-mediated *Lcn2* activation. By contrast, any of four bases fully functioned at positions –208 (Fig. 8*F*) and –207 (Fig. 8*G*). In the sequence CCCCTC at positions –212 to –207 of the mouse *Lcn2* promoter, the preference for cytosine at positions –212 to –209 but not at position –208 or –207 (Fig. 8, *B–G*) appears to be consistent with the conservation of the first four cytosines but not the last two bases in the corresponding region from other mammals (Fig. 8*A*). These mutational analyses indicate that the

I κ B ζ Ankyrin Repeats Bind to NF- κ B p50 and Promoter DNA

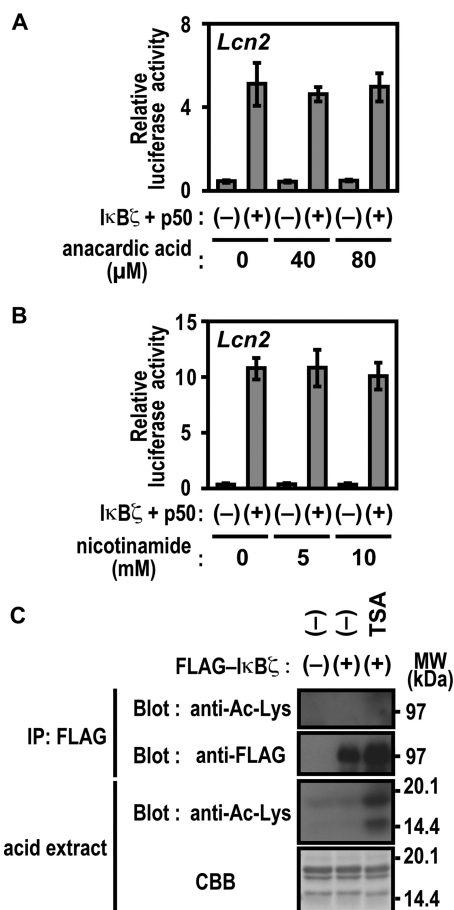


FIGURE 6. Protein acetylation is not involved in I κ B ζ -mediated *Lcn2* activation. *A* and *B*, effect of anacardic acid (*A*) and nicotinamide (*B*) on I κ B ζ -mediated *Lcn2* activation. p50-/I κ B ζ -deficient MEFs were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of *Lcn2* (-1031/+54), the internal control plasmid pRL-TK, and the pcDNA3 vector or pcDNA3 for expression of FLAG-I κ B ζ and HA-p50. Cells were incubated for 12 h with the indicated concentrations of the histone acetyl transferase inhibitor anacardic acid (*A*) or the HDAC inhibitor nicotinamide (*B*), and luciferase activities were determined as described under "Experimental Procedures." Results are means \pm S.D. for three independent transfections. *C*, effect of the HDAC inhibitor TSA on I κ B ζ . HEK293T cells expressing FLAG-I κ B ζ were incubated for 6 h with 2 μ M TSA. The cell lysates were applied to immunoprecipitation (IP) with anti-FLAG antibody. Precipitated FLAG-I κ B ζ as well as acid extracted histones in the nuclear extracts were analyzed by immunoblot with the indicated antibodies or by staining with CBB. Positions for marker proteins are indicated in kilodaltons.

I κ B ζ -responsive element (positions -212 to -209) requires the sequence 5'-YCCC-3' (Y is pyrimidine). Taken together with the present findings, I κ B ζ activates the endogenous *Lcn2* gene both via Asp-451-dependent direct interaction with p50 and Lys-717/Lys-719-involved association with the sequence 5'-YCCC-3' downstream of the κ B site.

Discussion

The nuclear I κ B proteins I κ B ζ , Bcl-3, and I κ B_{NS} are thought to regulate NF- κ B-dependent transcription by directly interacting with a p50 or p52 homodimer that binds to the κ B site on target genes. However, the mechanism for formation of the regulatory complex has not been fully elucidated. In the present study, we show that I κ B ζ , comprising the N-terminal trans-activation domain and the C-terminal ARD composed of seven ANK motifs, forms a transcriptionally active complex on its

target gene *Lcn2* both via Asp-451-mediated binding to p50 and via Lys-717/Lys-719-dependent interaction with the extra- κ B site of the *Lcn2* promoter. Asp-451 is present in the N-terminal region of ANK1, whereas the basic residues Lys-717 and Lys-719 exist in the C-terminal region of ANK7. We also demonstrate similar roles for both termini of the ARD in Bcl-3 and I κ B_{NS}, proposing a model for a common mechanism by which nuclear I κ Bs form a p50/p52-containing complex on target gene promoters.

Asp-451 in I κ B ζ ANK1 is strictly conserved during evolution (Fig. 1). Replacement of Asp-451 by threonine abrogates both association with a homodimer of the NF- κ B subunit p50 (Fig. 1) and activation of *Lcn2* via formation of the I κ B ζ -p50-DNA complex on the promoter (Figs. 3 and 5). The aspartate residue is also conserved among the nuclear I κ Bs, including Bcl-3 and I κ B_{NS}; however, it is replaced by threonine or serine in cytoplasmic I κ Bs such as I κ B α and I κ B β (Fig. 1), which associate with a p50/p52 homodimer much less efficiently (13). The conservation among the nuclear I κ Bs is consistent with the present finding that the corresponding aspartate residues (Asp-127 in Bcl-3 and Asp-60 in I κ B_{NS}) are also crucial for interaction with a p50 or p52 homodimer (Figs. 1 and 2). It should be noted that Asp-451 in I κ B ζ is one of the very few residues that are completely conserved among nuclear I κ Bs but replaced in cytoplasmic I κ Bs. On the other hand, the presence of aspartate at this position by itself does not seem to be sufficient because a mutant I κ B α carrying aspartate substitution for Thr-71 at the corresponding position of ANK1 as well as the wild-type protein fails to bind to a p50 homodimer (data not shown).

Although little is known about the tertiary structure of nuclear I κ B-NF- κ B complexes, crystal structures of the cytoplasmic I κ B proteins I κ B α and I κ B β complexed with a p65-p50 heterodimer and a p65 homodimer, respectively, have been solved (45–47). If I κ B ζ interacts with NF- κ B subunits in a manner similar to the cytoplasmic I κ Bs, then it seems likely that Asp-451 in I κ B ζ is positioned toward the C-terminally localized nuclear localization signal (NLS) in p50, a region that is required not only for nuclear localization of p50 but also for direct interaction of p50 with I κ B ζ (23, 48). Because of the dual role of the p50 NLS-containing region, the requirement of direct p50-I κ B ζ interaction for gene activation has not been established, although an NLS-truncated p50 protein did not activate I κ B ζ -dependent transcription, and thus I κ B ζ was assumed to interact with the promoter DNA via association with p50, which directly binds to the κ B site (23, 48). The conclusion appears to be strongly supported by the present findings that the D451T substitution in I κ B ζ abrogates interaction with p50 (Fig. 1), complex formation on both endogenous and exogenous *Lcn2* promoter (Fig. 5), and activation of *Lcn2* transcription (Fig. 3).

In addition to direct association with the κ B-site-binding protein p50, I κ B ζ activates *Lcn2* transcription by interacting with the extra- κ B site of the *Lcn2* promoter in which the basic residues Lys-717 and Lys-719 in the C-terminal region of I κ B ζ ANK7 likely play a major role (Figs. 4 and 5). The association does not appear to be mediated via direct binding to p50 because the K717E/K719E substitution in I κ B ζ leads to a loss of both promoter association and *Lcn2* activation without affect-

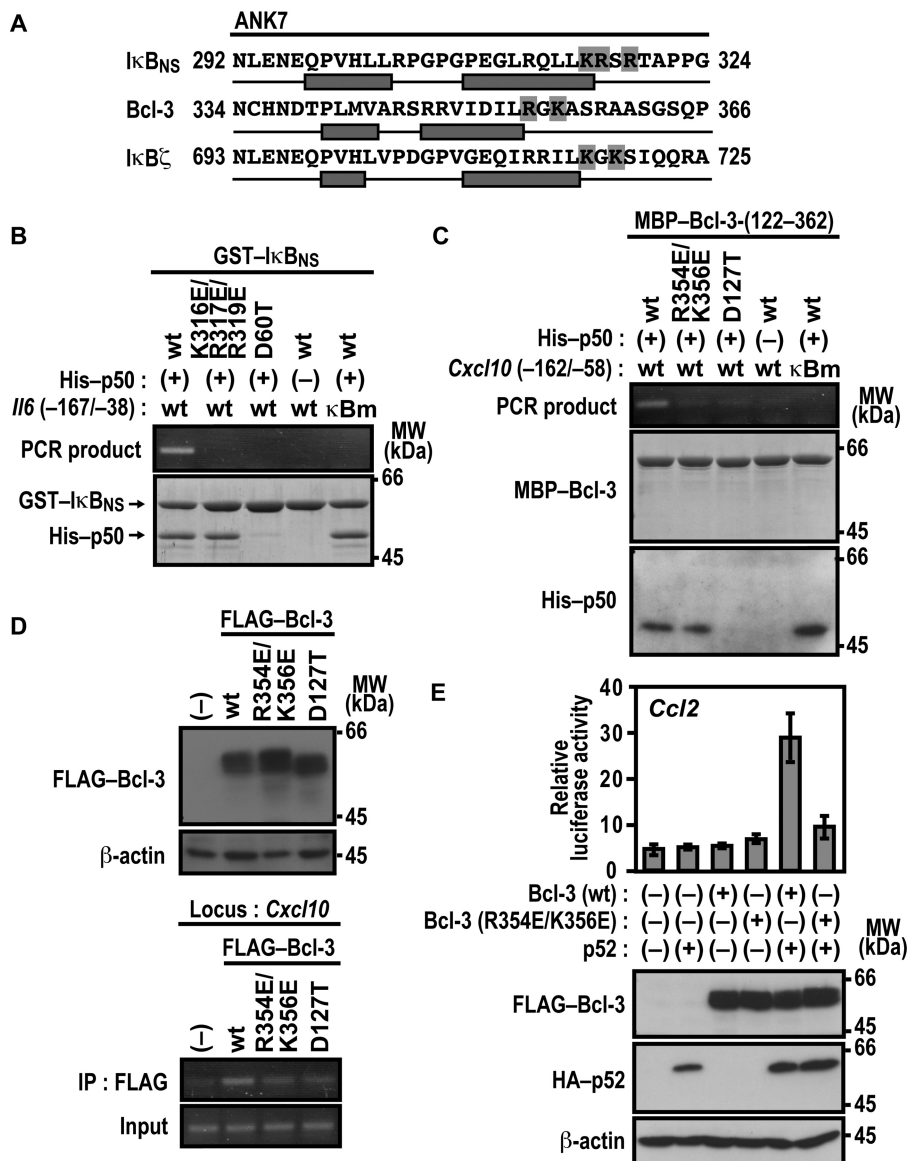


FIGURE 7. Basic residues in ANK7 of IκB_{NS} and Bcl-3 participate in association with their target gene promoter. *A*, amino acid sequence alignment of ANK7 in the mouse nuclear IκB proteins IκB_ζ, Bcl-3, and IκB_{NS}. The two antiparallel α helices in ANK7 of Bcl-3 were determined in crystal structures of Bcl-3 (36), whereas those of IκB_ζ and IκB_{NS} were predicted from their primary sequences by using the program PSIPRED (45, 46). Residues boxed in gray are the basic residues that follow the second α helix of ANK7. *B*, complex formation of IκB_{NS} with p50 and the *Il6* promoter. GST-fused WT IκB_{NS} or a mutant IκB_{NS} with the K316E/R317E/R319E or D60T substitution was incubated with or without His-p50 in the presence of WT *Il6* (-167/-38) or a mutated κB site (κBm)-carrying *Il6* (-167/-38). After the protein-DNA complex was pulled down with glutathione-Sepharose-4B beads, the co-precipitated DNA was amplified by PCR, and the product was analyzed by agarose gel electrophoresis. The precipitated proteins were subjected to SDS-PAGE, followed by staining with CBB. MW, molecular weight. *C*, complex formation of Bcl-3 with p50 and the *Cxcl10* promoter. MBP-fused WT Bcl-3-(122-362) or a mutant protein with the R354E/K356E or D127T substitution was incubated with or without His-p50 in the presence of *Cxcl10* (-162/-58) or a mutated κB site (κBm)-carrying *Cxcl10* (-162/-58). After the protein-DNA complex was pulled down with amylose resins, the co-precipitated DNA was analyzed as in *B*. The precipitated proteins were subjected to SDS-PAGE, followed by staining with CBB or immunoblot with the anti-His antibody. *D*, formaldehyde-fixed chromatin was prepared from RAW264.7 cells stably expressing FLAG-Bcl-3 (WT), FLAG-Bcl-3 (R354E/K356E), or FLAG-Bcl-3 (D127T) (top panel) and subjected to ChIP assay using anti-FLAG (M2) mouse monoclonal antibody (bottom panel). Precipitated DNA was analyzed by PCR using primers corresponding to the *Cxcl10* locus. The results are representative of experiments from at least three independent experiments. *IP*, immunoprecipitation. *E*, the role of Arg-354 and Lys-356 of Bcl-3 ANK7 in *Ccl2* activation. RAW264.7 cells were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of *Ccl2* (-2777/+76), the internal control plasmid pRL-TK, and pcDNA3 for expression of FLAG-Bcl-3 (WT) or FLAG-Bcl-3 (R354E/K356E) and HA-p52. Luciferase activities were determined as described under "Experimental Procedures." Each graph represents the mean ± S.D. obtained from three independent transfections. Cell lysates were analyzed by immunoblot with anti-FLAG, anti-HA, or anti-β-actin antibody. Positions for marker proteins are indicated in kilodaltons.

ing direct contact of IκB_ζ with p50 (Figs. 4 and 5). In addition, the function of the lysine residues does not seem to require their modification, such as acetylation (Fig. 6), which is supported by the finding that arginine, a residue insusceptible to acetylation, fully serves in place of them (Figs. 4 and 5).

The extra-κB site required for IκB_ζ-dependent *Lcn2* activation localizes seven bases downstream of the κB site in the *Lcn2*

promoter (23) and strictly requires the sequence 5'-YCCC-3' as an IκB_ζ-responsive element, as shown in this study (Fig. 8). In both promoter association and *Lcn2* activation, Lys-717 and Lys-719 in IκB_ζ are fully replaced by arginine residues (Figs. 4 and 5). It is known that lysine and arginine, but not glutamate, are often involved in direct interaction with DNA, which can be mediated not only via nonspecific interaction with the phos-

IκBζ Ankyrin Repeats Bind to NF-κB p50 and Promoter DNA

A 5'-upstream region of mouse *Lcn2*

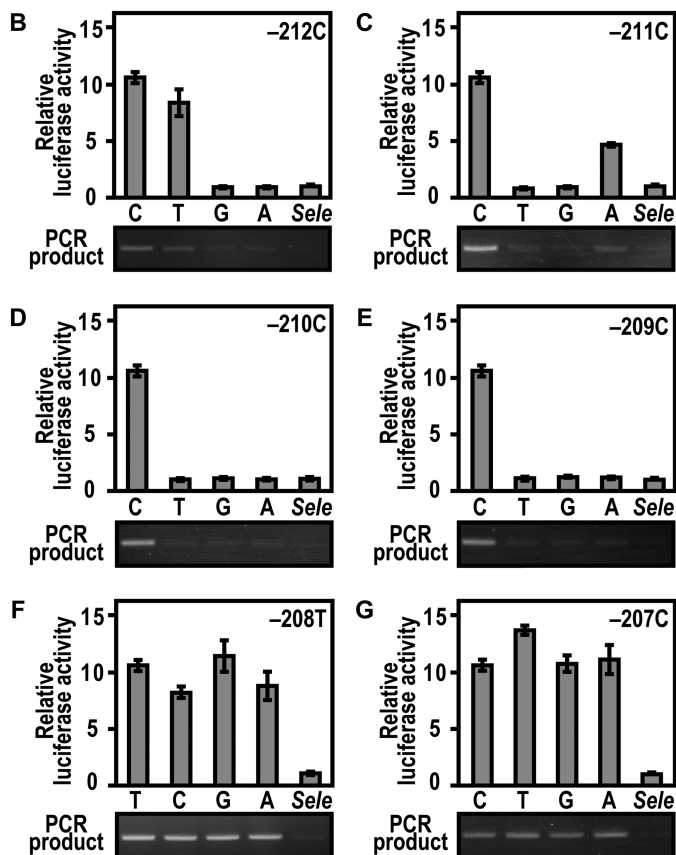
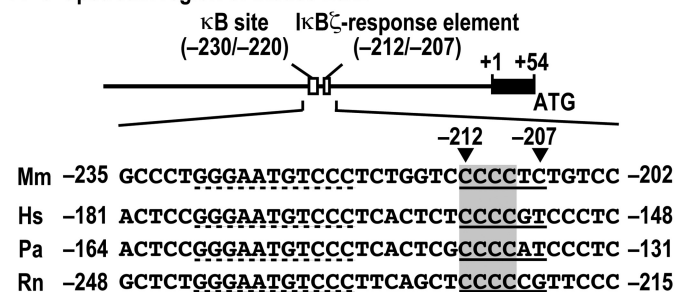


FIGURE 8. Interaction of IκB_ζ with the *Lcn2* promoter, and its activation requires the 5'-YCCC-3' sequence downstream of the κB site. A, the 5' upstream promoter region of the mouse *Lcn2* gene. The κB site and its downstream IκB_ζ-response element in the region are underlined. The nucleotide sequences of the corresponding region from various species are aligned. Mm, *Mus musculus*; Hs, *Homo sapiens*; Pa, *Papio anubis*; Rn, *Rattus norvegicus*. B–G, base preference of the extra-κB site in *Lcn2* activation (top panels) and in formation of the three-species complex containing IκB_ζ, p50, and promoter DNA (bottom panels). For estimation of *Lcn2* activation, p50/IκB_ζ-deficient MEFs were transfected with the following plasmids: the luciferase reporter plasmid pGL3-Basic containing the upstream region of wild-type *Lcn2* (–500/+50); a mutant *Lcn2* with the indicated base replacement, or the IκB_ζ-independent gene *Sele* (–445/+105); the internal control plasmid pRL-TK; and pcDNA3 for expression of FLAG-IκB_ζ and HA-p50. Luciferase activities were determined as described under "Experimental Procedures." Each graph represents the mean ± S.D. obtained from three independent transfections. For estimation of protein-DNA complex formation, GST-IκB_ζ was incubated with His-p50 in the presence of the DNA fragment of wild-type *Lcn2* (–500/+50), a mutant *Lcn2* with the indicated base replacement, or *Sele* (–445/+105). After the complex was pulled down with glutathione-Sepharose-4B beads, the co-precipitated DNA was amplified by PCR, and the product was analyzed by agarose gel electrophoresis.

phate moiety of DNA but also via recognition of a DNA base, especially a guanine (39, 40). In this context, it should be noted that the IκB_ζ-responsive element (5'-YCCC-3') of the *Lcn2*

promoter is abundant in the Lys/Arg-recognizing base guanine in the antisense strand. The presence of multiple guanines in the element may be in agreement with the present conclusion that Lys-717 and Lys-719 each contribute to element recognition because single glutamate substitution for either lysine residue results in only a partial loss of the activity of IκB_ζ (Fig. 4). Correct orientation of the side chains of Lys-717 and Lys-719 toward target DNA also seems to be important for element recognition, as indicated by the finding that replacement of the flexible residue Gly-718, which is the intervening amino acid between the lysines and is strictly conserved during evolution, by the inflexible residue proline abrogates both binding to the *Lcn2* promoter and transcription of *Lcn2* (Fig. 5).

The NF-κB family proteins serve as a homo- or heterodimer to bind to a κB DNA response element in the promoters of distinct inducible genes, thereby playing their respective roles in gene regulation (1–4). The transcriptional specificity of NF-κB dimers is generally thought to be coded within the κB site sequences (27, 49). Indeed, in the case of the *Lcn2* promoter, its κB site effectively interacts with the NF-κB p50 homodimer but not with the p52 homodimer (Fig. 3), although both homodimers are capable of binding to IκB_ζ (Fig. 2). As a result, in contrast to p50, p52 fails to induce IκB_ζ-dependent activation of the *Lcn2* gene (Fig. 3). In addition to the κB site sequence itself, the ability of NF-κB dimers to function on a particular promoter is also considered to be determined by extra-κB sites recognized via co-activator proteins (16, 50). However, such a co-activator was not previously identified. This study demonstrates that IκB_ζ, a co-activator of p50, activates the *Lcn2* gene not only via binding to p50 but also by associating with the IκB_ζ-responsive element (5'-YCCC-3') downstream of the κB site, providing evidence that an extra-κB site and its interacting co-activator do determine the transcriptional specificity of NF-κB dimers.

Bcl-3 and IκB_{NS} are the putative second and third examples that determine the transcriptional specificity of NF-κB dimers via association with extra-κB sites. These nuclear IκB proteins, capable of binding to a p50 and p52 homodimer (Figs. 1 and 2), have conserved basic residues that follow the second α helix in the C-terminal region of ANK7; the residues appear to be involved in association of Bcl-3 and IκB_{NS} with promoters of their target genes (Fig. 7). The crucial role for Arg-354 and Lys-356 of Bcl-3 ANK7 in promoter binding and gene activation agrees well with a model in which the C-terminal region of Bcl-3 ARD in complex with the p50 homodimer is placed near the promoter DNA (36). Future studies should aim to elucidate a Bcl-3- or IκB_{NS}-interacting *cis* element out of κB sites in Bcl-3- or IκB_{NS}-dependent gene promoters, respectively.

Combined with the present observation that the aspartate residue in the N terminus of the ARD of Bcl-3 and IκB_{NS} as well as that of IκB_ζ plays a crucial role in direct interaction with a p50 or p52 homodimer (Figs. 1 and 2), we propose a common mechanism for nuclear-IκB-mediated regulation of NF-κB-dependent genes. The nuclear IκB proteins with seven ANK motifs (IκB_ζ, Bcl-3, and IκB_{NS}) form a p50/p52-containing regulatory complex on promoter DNA via the following two interactions: direct association with the κB-site-binding protein p50/p52 via the invariant aspartate residue in the N-terminal

region of ANK1 and interaction with an extra- κ B site via recognition by the conserved lysine/arginine residues that locate C-terminally to the second α helix of ANK7.

Experimental Procedures

Cells, Antibodies, and Reagents—MEFs doubly deficient in NF- κ B p50 and I κ B ζ (*Nfkb1*^{-/-};*Nfkbiz*^{-/-} MEFs) were prepared as described previously (23). Mouse BMMs were obtained as described previously (22, 24). All animals were housed and maintained in a specific pathogen-free animal facility at Kyushu University. All experiments were performed in strict accordance with the guidelines for proper conduct of animal experiments (Science Council of Japan). The experimental protocol was approved by the Animal Care and Use Committee of Kyushu University (permit numbers: A24-042 and A26-102). All efforts were made to minimize the numbers of animals and their suffering. MEFs, BMMs, HEK293T cells, and mouse macrophage-like RAW 264.7 cells were maintained in Dulbecco's modified Eagle's medium supplemented with 10% heat-inactivated fetal bovine serum, penicillin (100 units/ml), and streptomycin (100 μ g/ml) at 37 °C under 5% CO₂.

Anti-FLAG (M2) (catalog no. F3165) and anti- β -tubulin (TUB 2.1, catalog no. T4026) mouse monoclonal antibodies and anti-FLAG rabbit polyclonal antibodies (catalog no. F7425) were purchased from Sigma-Aldrich, an anti-HA rat monoclonal antibody (3F10) (catalog no. 11 867 431 001) from Roche Applied Science, an anti-His₅ monoclonal antibody (catalog no. 34660) from Qiagen, an anti- β -actin mouse monoclonal antibody (catalog no. sc-47778) and anti-RNA polymerase II rabbit polyclonal antibody (catalog no. sc-899) from Santa Cruz Biotechnology, and an anti-acetylated lysine rabbit polyclonal antibody (catalog no. 9441) from Cell Signaling Technology. Anti-I κ B ζ rabbit polyclonal antibodies were raised against I κ B ζ -(1–100) and prepared as described previously (51). TSA and anacardic acid were purchased from Calbiochem and nicotinamide from Sigma-Aldrich.

Plasmid Construction—The mouse cDNAs encoding full-length I κ B ζ (amino acid residues 1–728), I κ B ζ -(414–728), p50 of 366 amino acid residues, and p65 of 325 amino acids were prepared as described previously (9, 33). The cDNA for mouse full-length I κ B_{NS} (amino acid residues 1–327) were prepared by RT-PCR using mRNA from mouse BMMs stimulated with LPS (List Biological Laboratories). The cDNAs for mouse full-length Bcl-3 (amino acid residues 1–448) and p52 of 415 amino acid residues were prepared by RT-PCR using mRNA from LPS-stimulated RAW 264.7 cells. The cDNA fragments encoding Bcl-3-(122–362) and p52-(1–341) for bacterial expression were prepared by PCR using their respective full-length cDNAs. Mutations leading to the indicated amino acid substitutions or truncations were introduced by PCR-mediated site-directed mutagenesis. The cDNA fragments were ligated to the following expression vectors: pGEX-6P-2 (GE Healthcare) and pMALc2 (New England Biolabs) for bacterial expression of proteins fused to GST and maltose-binding protein (MBP), respectively; pRSFDuet-1 (Novagen) modified for expression of hexahistidine (His)-tagged proteins in *Escherichia coli* (52); pcDNA3 (Invitrogen) for expression of FLAG- or HA-tagged proteins in mammalian cells; and pBABE-puro (Cell Biolabs)

for retroviral transduction in BMMs. The 5' upstream region (–1031/+54 or –500/+50) of the lipocalin-2-encoding gene *Lcn2* or the 5' upstream region (–445/+105) of the E-selectin-encoding gene *Sele* was ligated to the luciferase reporter plasmid pGL3-Basic (Promega) as described previously (23). The 5' upstream regions of the following genes were amplified by PCR using mouse genomic DNA as a template and subcloned into pGL3-Basic: the IL-6-encoding gene *Il6* (–1217/+50), the IP-10-encoding gene *Cxcl10* (–500/+50), and the MCP-1-encoding gene *Ccl2* (–2777/+76). Mutations in the κ B site of the following gene promoters were introduced by PCR-mediated site-directed mutagenesis: *Lcn2* (–230/–220), 5'-TGGGAATGTCCCT-3' to 5'-TAATAATGTTAAT-3' (23, 24); *Il6* (–73/–64), 5'-TGGGATTTTCCCA-3' to 5'-TAATATTTTAAA-3'; and *Cxcl10* (–113/–103), 5'-AGGGGACTTCCCT-3' to 5'-ATAACTACTTTAAT-3' (note that mutated nucleotides are underlined). All of the constructs were sequenced for confirmation of their identity.

GST Pulldown Assay—GST- and His-tagged proteins were purified as described previously (52, 53) and incubated for 20 min at 4 °C in 500 μ l of buffer A (137 mM NaCl, 2.7 mM KCl, 0.5% Triton X-100, 1 mM DTT, 8.1 mM Na₂HPO₄, and 1.5 mM KH₂PO₄ (pH 7.4)). A slurry of glutathione-Sepharose 4B beads (GE Healthcare) was subsequently added, followed by further incubation for 40 min at 4 °C. After washing three times with the buffer above, the proteins were eluted from the beads with 20 mM glutathione in 150 mM NaCl, 2 mM DTT, and 100 mM Tris-HCl (pH 8.8). The eluate was subjected to SDS-PAGE, followed by staining with Coomassie Brilliant Blue (CBB).

Immunoprecipitation Analysis—HEK293T cells were transfected with the indicated expression plasmids using X-tremeGENE HP DNA Transfection Reagent (Roche Applied Science) and cultured for 24 or 48 h. Cells were lysed by sonication at 4 °C in 500 μ l of lysis buffer (137 mM NaCl, 2.7 mM KCl, 1% Nonidet P-40, 8.1 mM Na₂HPO₄, and 1.5 mM KH₂PO₄ (pH 7.4)) supplemented with Complete™ Protease Inhibitor Cocktail (Roche Applied Science). Proteins in the cell lysate were immunoprecipitated using anti-FLAG antibody (M2) and protein G-Sepharose (GE Healthcare). The precipitants were analyzed by immunoblot with the anti-FLAG rabbit polyclonal antibody or the anti-HA (3F10) rat monoclonal antibody. The blots were developed using ECL-Prime (GE Healthcare) for visualization of the antibodies.

Detection of Acetylated Proteins—FLAG-I κ B ζ expressed in HEK293T cells was incubated for 6 h with 2 μ M TSA and immunoprecipitated from the cell lysates as described above, with the exception that 2 μ M TSA and 20 mM nicotinamide were used during immunoprecipitation to prevent deacetylation. The precipitated proteins were applied to immunoblot analysis with anti-acetylated lysine rabbit polyclonal antibody. Histones were prepared from HEK293T cells by acid extraction as described by Nightingale *et al.* (54). For detection of acetylated histones, the acid extracts were subsequently analyzed by immunoblot with the anti-acetylated lysine rabbit polyclonal antibody.

Luciferase Reporter Assay—*Nfkb1*^{-/-};*Nfkbiz*^{-/-} MEFs or RAW264.7 cells were transfected with the luciferase reporter plasmid pGL3-Basic containing the indicated promoter, the

I κ B ζ Ankyrin Repeats Bind to NF- κ B p50 and Promoter DNA

internal control plasmid pRL-TK (Promega), and the indicated plasmids for protein expression using X-tremeGENE HP DNA Transfection Reagent. The luciferase activities were determined by the Dual-Luciferase[®] reporter assay system (Promega). For estimation of protein levels, cell lysates were analyzed by immunoblot with anti-FLAG (M2), anti-HA, anti- β -tubulin, or anti- β -actin antibody.

Analysis of Protein-DNA Interaction—Analysis of protein-DNA interaction was performed as described previously (23). GST-I κ B ζ , GST-I κ B_{NS}, or MBP-Bcl-3 was incubated with His-p50 for 20 min at 4 °C in 500 μ l of buffer A containing salmon sperm DNA (0.1 mg/ml), or His-p50, His-p52, or His-p65 alone was incubated for 20 min at 4 °C in 500 μ l of buffer B (150 mM NaCl, 5% glycerol, 1 mM DTT, 0.5% Triton X-100, and 25 mM Tris-HCl (pH 8.0)) containing salmon sperm DNA (0.1 mg/ml). A slurry of glutathione-Sepharose 4B, Amylose Resin (New England Biolabs), or COSMOGEL[®] His-Accept (Nacalai Tesque) was added in a GST, MBP, or His pulldown assay, respectively. The indicated DNA fragment (0.1 pmol) was subsequently added to the mixture, followed by further incubation for 40 min at 4 °C. After washing with buffer A for a GST or MBP pulldown assay or with buffer B containing 25 mM imidazole for a His pulldown assay, the protein-DNA complex was eluted from glutathione-Sepharose 4B with an elution buffer (20 mM glutathione, 150 mM NaCl, 2 mM DTT, and 100 mM Tris-HCl (pH 8.8)), from amylose resin with buffer A containing 20 mM maltose, or from COSMOGEL[®] His-Accept with buffer B containing 1 M imidazole. The eluted protein was applied to SDS-PAGE, followed by CBB staining or immunoblot analysis with the anti-His₅ monoclonal antibody. The DNA in the eluted complex was analyzed by PCR using the following primer pairs: 5'-TACAGGGTTATGGGAGTGGAC-3' and 5'-TCTGTTGAAATACTTGGCAAGAT-3' for detection of the *Lcn2* promoter region; 5'-CCATGGAAGACGCCAAAAACA-3' and 5'-CATATCGTTTCATAGCTTCTGC-3' for the 263-bp region of the pGL3-Basic vector (23); 5'-CTTAATAAGGTTTCCAATCAGCC-3' and 5'-GTCTCATCTTTATTA-GGAGTCAAC-3' for the *Il6* promoter region; and 5'-TCCAAGTTCATGGGTCACAA-3' and 5'-TGATTGGCTGACTT-TGGAGA-3' for the *Cxcl10* promoter region.

Activation of the Endogenous *Lcn2* Gene by I κ B ζ —Retroviral expression of wild-type I κ B ζ or a mutant protein with the D451T or K717E/K719E substitution was performed according to the method of He *et al.* (55). Briefly, HEK293T cells were transfected with the Moloney Murine Leukemia virus- Ψ E helper plasmid and pBABE-puro-3 \times FLAG-I κ B ζ , and the culture supernatant containing the retrovirus was collected. I κ B ζ -deficient BMMs were infected with the retrovirus and cultured for 2 days. The cells were treated for 4, 8, or 12 h with or without LPS (100 ng/ml). Expression of I κ B ζ was detected by immunoblot with the anti-I κ B ζ antibody. The mRNA product of the endogenous *Lcn2* gene was estimated by quantitative real-time RT-PCR as described previously (56). Briefly, total RNAs were extracted using TRIreagent (BIOLINE) according to the instructions of the manufacturer, and 1 μ g of the RNA was reverse-transcribed by ReverTra Ace[®] reverse transcriptase (TOYOBO) using an oligo(dT) primer, followed by real-time PCR using SYBR[®] premix Ex Taq[™]

(Takara Bio) on the Roter-Gene 6200 system (Corbett). The primer pairs used were 5'-AAGGAGCTGTCCCCTGA-ACT-3' and 5'-GGTGGGGACAGAGAAGATGA-3' for *Lcn2* and 5'-AAGCGAAACTGGCGGAAAC-3' and 5'-TAACCG-ATGTTGGGCATCAG-3' for the control gene *Rpl32*.

ChIP Analysis—RAW264.7 cells expressing I κ B ζ or Bcl-3 under the control of the sheep metallothionein Ia promoter (−600/+72) were prepared as described previously (22). The stable transformants were incubated in the presence of 50 μ M ZnSO₄ and LPS (100 ng/ml), and ChIP analysis was performed according to a method described previously (24, 56). Cells were fixed for 10 min at 25 °C with 1% formaldehyde and washed with ice-cold phosphate-buffered saline. After sonication, a chromatin-containing solution was precleared with Protein G-Sepharose 4 Fast Flow (GE Healthcare), followed by incubation overnight at 4 °C with the indicated antibody. Antigen-antibody complexes on the resin were washed sequentially with a low-salt wash buffer (150 mM NaCl, 2 mM EDTA, 0.1% SDS, 1% Triton X-100, and 20 mM Tris-HCl (pH 8.0)), a high-salt wash buffer (500 mM NaCl, 2 mM EDTA, 0.1% SDS, 1% Triton X-100, and 20 mM Tris-HCl (pH 8.0)); a LiCl wash buffer (250 mM LiCl, 1 mM EDTA, 1% sodium deoxycholate, 1% Nonidet-P40, and 10 mM Tris-HCl (pH 8.0)), and TE (1 mM EDTA and 10 mM Tris-HCl (pH 8.0)). DNA-protein complexes were eluted with elution buffer containing 1% SDS and 100 mM sodium bicarbonate. After cross-links were reversed by overnight incubation at 65 °C, Proteinase K (0.1 mg/ml) was added and incubated for 3 h at 45 °C. Purified DNA was subjected to PCR to detect the following regions using specific primers as follows: the *Lcn2* promoter region containing the CCCCTC element (−212/−207), 5'-CCCCTCTGTCCCCTGCAGC-3', and 5'-TCTGTTGAAATACTTGGCAAGAT-3' and the *Cxcl10* promoter region, 5'-TCCAAGTTCATGGGTCAA-3' and 5'-GGGAAGTCCCCTGTAAACCGA-3'.

Secondary Structure Prediction—The secondary structure of the ANK7 in I κ B ζ and I κ B_{NS} was predicted using the server-side program PSIPRED (57, 58).

Author Contributions—A. K., S. Y., and H. S. designed the study. A. K. performed the experiments. A. K., S. Y., and H. S. analyzed the data and wrote the paper. All authors analyzed the results and approved the final version of the manuscript.

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