

NF- κ B Activation Coordinated by IKK β and IKK ϵ Enables Latent Infection of Kaposi's Sarcoma-Associated Herpesvirus

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All herpesviruses share a remarkable propensity to establish latent infection. Human Kaposi's sarcoma-associated herpesvirus (KSHV) effectively enters latency after *de novo* infection, suggesting that KSHV has evolved with strategies to facilitate latent infection. NF- κ B activation is imperative for latent infection of gammaherpesviruses. However, how NF- κ B is activated during *de novo* herpesvirus infection is not fully understood. Here, we report that KSHV infection activates the inhibitor of κ B kinase β (IKK β) and the IKK-related kinase epsilon (IKK ϵ) to enable host NF- κ B activation and KSHV latent infection. Specifically, KSHV infection activated IKK β and IKK ϵ that were crucial for latent infection. Knockdown of IKK β and IKK ϵ caused aberrant lytic gene expression and impaired KSHV latent infection. Biochemical and genetic experiments identified RelA as a key player downstream of IKK β and IKK ϵ . Remarkably, IKK β and IKK ϵ were essential for phosphorylation of S⁵³⁶ and S⁴⁶⁸ of RelA, respectively. Phosphorylation of RelA S⁵³⁶ was required for phosphorylation of S⁴⁶⁸, which activated NF- κ B and promoted KSHV latent infection. Expression of the phosphorylation-resistant RelA S⁵³⁶A increased KSHV lytic gene expression and impaired latent infection. Our findings uncover a scheme wherein NF- κ B activation is coordinated by IKK β and IKK ϵ , which sequentially phosphorylate RelA in a site-specific manner to enable latent infection after KSHV *de novo* infection.

Human Kaposi's sarcoma-associated herpesvirus (KSHV, also known as human herpesvirus 8, or HHV-8) belongs to lymphotropic gammaherpesvirus 2 family (1). KSHV infection is causatively linked to Kaposi's sarcoma (KS), primary effusion lymphoma (PEL), and multicentric Castleman's disease (MCD) (2–5). KS is the leading cause of mortality and morbidity in immunocompromised patients, whereas PEL and MCD are rare lymphomas. Similar to other herpesviruses, KSHV infection has two phases, i.e., lytic replication and latency. Interestingly, cells supporting lytic replication and those carrying latent KSHV genomes are consistently found in KSHV-associated tumors, e.g., KS lesions (6, 7). In human KS lesions, the majority of the tumor comprises KSHV latently infected spindle cells that have been infiltrated with immune cells, displaying characteristics of an excessive inflammatory response (8).

A feature of KSHV is its remarkable propensity to establish latent infection after *de novo* infection. KSHV infection *ex vivo* in a variety of cell lines leads to latent infection by default (9, 10). Although latently infected cells can be induced to enter the lytic cycle, biological and chemical reagents are relatively poor in reactivating KSHV and viral yield is low, suggesting tight control of lytic replication (11). By using KSHV latent lymphoma cell lines, KSHV lytic gene expression and productive replication can be induced with exogenous expression of the viral replication transactivator (RTA). Accumulating studies point to RTA as the regulatory node that integrates diverse physiological signaling events to determine the fate of KSHV-infected cells. Thus, RTA-mediated transcription is the paramount regulatory hub during KSHV infection. An array of events that influence RTA expression and RTA-mediated transcription have been reported thus far (12–17). Moreover, RTA-interacting proteins, either of host or viral origin, can alter its activity during viral infection (13, 15). Finally, microRNA and posttranslational events, e.g., phosphorylation and acetylation, can further tune RTA-dependent gene expression (16–19). These findings demonstrate the crucial roles of RTA in determining the fate of KSHV infection and suggest that RTA-

mediated transcription is highly suppressed after *de novo* KSHV infection.

In response to viral infection, innate immune signaling events are immediately initiated to defeat viral replication. Despite the diversity of pattern recognition receptors (PRRs) that sense viral infection, upstream signaling events converge at two kinase complexes, i.e., the inhibitor of κ B kinase (IKK), consisting of IKK α , IKK β , and IKK γ , and the IKK-related TBK1-IKK ϵ complex (20). Activated kinases phosphorylate key transcription factors or inhibitors thereof to upregulate the expression of antiviral genes, thereby establishing an antiviral state (21, 22). As obligate pathogens, viruses have evolved with strategies to evade and exploit host innate immune signaling events. Positive-strand RNA viruses cleave adaptor molecules upstream of IKK $\alpha\beta\gamma$ or TBK1-IKK ϵ kinases to disarm the host innate immune defense (23–26). Large DNA herpesviruses dedicate significant portions of their genomes to modulators of host innate and adaptive immune responses. Notable examples are the diverse mechanisms that deregulate the interferon (IFN)-dependent antiviral pathways by various pathogens. Strikingly, our recent studies showed that murine gamma-herpesvirus 68 (γ HV68), a model herpesvirus for human KSHV and Epstein-Barr virus (EBV), usurped the IKK β kinase to phosphorylate RTA and promote viral transcriptional activation (27). Loss of IKK β or components of the same pathway severely impaired γ HV68 lytic replication. Moreover, IKK β was exploited by γ HV68 to terminate NF- κ B activation and to avoid antiviral cytokine production (28, 29). These findings highlight the dynamic and intricate interactions between viruses and their human host.

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Downstream of IKK α β or TBK1-IKK ϵ kinases, NF- κ B transcription factors are key players in regulating antiviral gene expression, specifically that of inflammatory cytokines and IFNs. Among five members of the NF- κ B family, RelA is the most abundantly and ubiquitously expressed (30). Moreover, RelA is the transcriptionally active subunit of the predominant RelA-p50 dimer. Posttranslational modifications of the RelA subunit, e.g., phosphorylation and acetylation, are important means to regulate NF- κ B-dependent gene expression (31–34). However, how multiple events are coordinated to achieve regulated gene expression is not clear. Here, we report that KSHV *de novo* infection activates IKK β , and IKK ϵ , which enable the phosphorylation of serine 536 (S⁵³⁶) and S⁴⁶⁸ of RelA, respectively, to promote NF- κ B activation and KSHV latent infection. Phosphorylation of S⁵³⁶ of RelA is required for phosphorylation of S⁴⁶⁸, the latter of which potentially inhibited KSHV lytic replication. Conversely, knockdown of IKK β and IKK ϵ impaired NF- κ B activation and elevated KSHV lytic gene expression, resulting in reduced KSHV latent infection. Our findings have uncovered a scheme wherein two closely related kinases are activated to coordinate NF- κ B activation in enabling KSHV latent infection and reveal an intimate link between innate immune signaling and viral persistent infection.

MATERIALS AND METHODS

Plasmids. Unless otherwise specified, IKK α , IKK β , IKK ϵ , TBK1, RelA, and RelA mutants carrying an S⁴⁶⁸A, S⁴⁶⁸E, S⁵³⁶A, S⁵³⁶E, S⁵²⁹A, or S^{468,536}A mutation and Flag-tagged RTA were cloned into pCDNA5/FRT/TO (Invitrogen) and pCDH-puro for transient and stable expression, respectively. All cloned cDNAs were validated by DNA sequencing.

Cells and viruses. Human ECV endothelial cells and 293T, iSLK-Bac16, and iSLK.219 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum and 100 U penicillin-streptomycin. iSLK-Bac16 cells were maintained with G418 (250 μ g/ml), hygromycin (1.2 mg/ml), and puromycin (1 μ g/ml). iSLK.219 cells were maintained with G418 (250 μ g/ml), hygromycin (400 μ g/ml), and puromycin (10 μ g/ml). Recombinant KSHV was induced from iSLK-Bac16 or iSLK.219 cells with doxycycline (1 μ g/ml) for up to 96 h, as described previously (35, 36). Recombinant KSHV was concentrated via ultracentrifugation at 32,000 rpm for 2 h at 4°C.

Luciferase reporter assay. As previously described (37), 293T cells were seeded into 24-well plates (1 \times 10⁵ cells/cm²). Sixteen hours later, cells were transfected with a total of 500 ng of plasmid cocktail per well by calcium phosphate precipitation. To determine the effects of human I κ B α kinases or RelA on the transcriptional activation of RTA, we transfected 293T cells with a plasmid cocktail that comprised 100 ng of open reading frame 57 (ORF57) or polyadenylated nuclear (PAN) luciferase reporter plasmid, 2 ng of RTA, 200 ng of pCMV- β -galactosidase (β -Gal) plasmid, and 50 ng or 150 ng of IKK or RelA plasmid. At 20 h posttransfection, the activity of firefly luciferase and β -Gal in whole-cell lysates was determined by using a FLUOstar Omega microplate reader (BMG Labtech.). Data from reporter assays represent at least three independent experiments.

Protein expression and purification. Glutathione S-transferase (GST) and GST-fusion proteins containing the N-terminal region of I κ B α or the carboxyl terminus of IFN regulatory factor 3 (IRF3) were expressed after isopropyl- β -D-thiogalactopyranoside induction and purified with glutathione-conjugated Sepharose as previously described (38, 39). Eluted proteins were resuspended in 25% glycerol and stored at –80°C for kinase assays.

Reverse transcript-PCR and qRT-PCR. To determine the relative level of cellular and viral transcripts, reverse transcription-PCR and quantitative real-time PCR (qRT-PCR) were performed as previously described (27, 28). Briefly, total RNA was extracted from ECV, iSLK.219, or BJAB cells by using TRIzol reagent (Invitrogen). To remove genomic

DNA, total RNA was digested with RNase-free DNase I (New England BioLabs) at 37°C for 1 h. DNase I digestion was quenched by heat inactivation at 70°C for 20 min, and total RNA was purified with TRIzol reagent. cDNA was prepared with 1.5 μ g total RNA, reverse transcriptase (Invitrogen), and oligo(dT)_{12–19} primer. RNA was then removed by incubation with RNase H (Epicentre). The abundance levels of cellular and viral mRNAs were assessed by qRT-PCR by using a StepOnePlus real-time PCR system (Applied Biosystems). Human β -actin was used as an internal control. To determine the relative viral genomes in KSHV-infected ECV cells, total genomic DNA was purified by phenol-chloroform extraction and ethanol-sodium acetate precipitation after digestion with proteinase K (Qiagen). The abundance of the KSHV genome in 20 ng total genomic DNA was determined by real-time PCR using primers specific for RTA (also known as ORF50) and ORF9. All primers were synthesized by Integrated DNA Technologies and validated individually.

In vitro kinase assay. Endogenous IKK β and IKK ϵ were analyzed in *in vitro* kinase assays. Briefly, ECV cells were harvested at the indicated time points after KSHV infection. Whole-cell lysates were precipitated with an antibody against IKK γ (also known as NEMO) to obtain the IKK β kinase complex, or with rabbit anti-IKK ϵ to obtain the IKK ϵ -containing kinase complex. The kinase reaction mixture consisted of 0.5 μ g GST or GST-fusion proteins 100 μ Ci [γ -³²P]ATP, and precipitated kinase in 20 μ l of kinase buffer. The reaction mixture was incubated at room temperature for 40 min, and denatured proteins were analyzed by SDS-PAGE and autoradiography.

Immunoprecipitation and immunoblotting. Commercial antibodies used in this study included mouse M2 anti-Flag (Sigma), mouse anti- β -actin (Abcam), rabbit anti-IKK ϵ (Sigma), rabbit anti-RelA (C-20; Santa Cruz Biotech), rabbit anti-RelA S⁴⁶⁸p (Bethyl), rabbit anti-RelA S⁵³⁶p (Cell Signaling), and rabbit anti-GST (Santa Cruz Biotech) antibodies. Antibodies against IKK β and IKK γ were kindly provided by E. Zandi, and anti-RTA antibody was a gift from Y. Izumiya (40).

Immunoprecipitation and immunoblotting were carried out as described previously (38, 41, 42). Briefly, cells were harvested and lysed with NP-40 buffer (50 mM Tris-HCl [pH 7.4], 150 mM NaCl, 1% NP-40, 5 mM EDTA) supplemented with a protease inhibitor cocktail. Then, centrifuged cell lysates were precleared with Sepharose 4B beads and incubated with the indicated antibodies and protein A/G-agarose (Thermo Scientific) or antibody-conjugated agarose (Sigma) at 4°C for 4 to 6 h. The agarose beads were washed three times with the corresponding lysis buffer and eluted with 1 \times SDS sample buffer by boiling at 95°C for 5 min. Immunoblotting analysis was performed with the indicated primary antibodies, and proteins were visualized with IRDye800- or IRDye680-conjugated secondary antibodies (Licor) and an Odyssey infrared imaging system (Licor).

Statistical analysis. The statistical significance (*P* value) was calculated by using an unpaired two-tailed Student's *t* test. A *P* value of <0.05 was considered statistically significant.

RESULTS

IKK β and IKK ϵ potentially inhibit RTA-mediated transcriptional activation. We previously showed that IKK β was usurped by murine gammaherpesvirus 68 (γ HV68) to promote viral lytic replication via phosphorylation of RTA (27). We reasoned that IKK and IKK-related kinases likely impact KSHV gene expression driven by RTA as well. To assess the effects of these innate immune kinases on KSHV RTA transcriptional activation, we performed luciferase assays with KSHV lytic promoters, i.e., those of PAN RNA and ORF57, a key player of viral RNA metabolism (43). As shown in Fig. 1A, RTA expression upregulated the gene expression levels driven by PAN and ORF57 promoters by ~65- and 30-fold, respectively. Exogenous expression of IKK β and IKK ϵ , but of neither IKK α nor TBK1, potentially inhibited the gene expression driven by PAN and ORF57 promoters in a dose-dependent

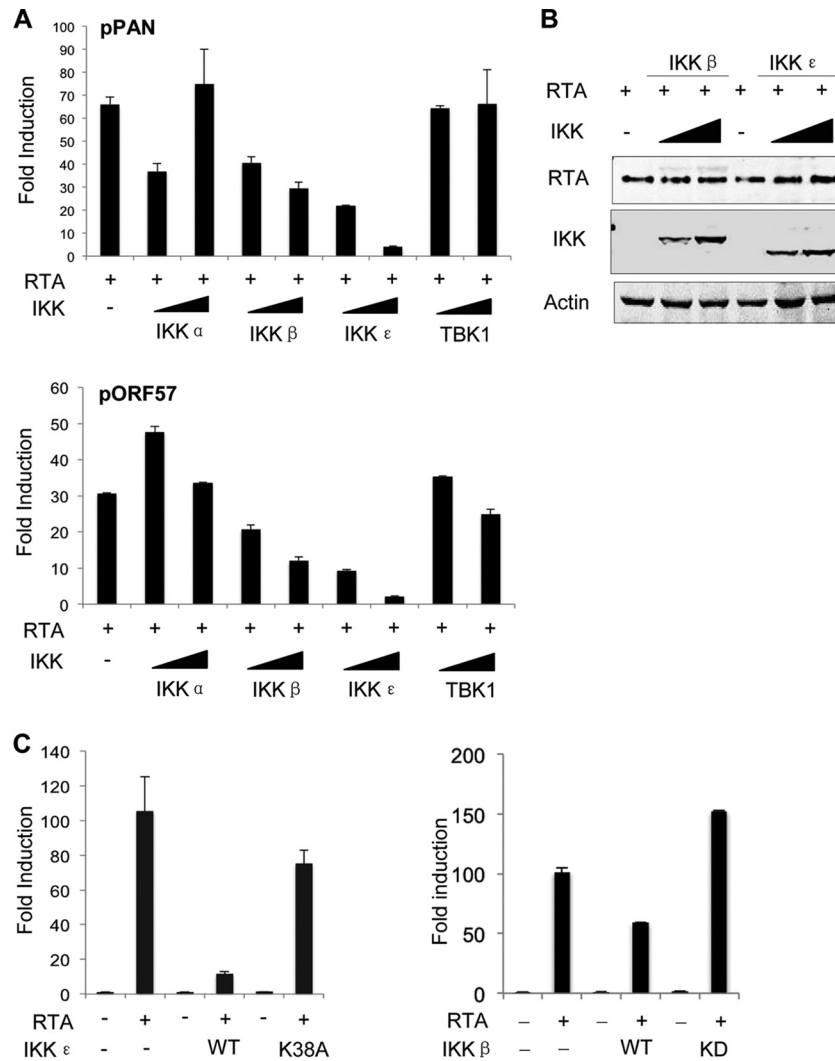


FIG 1 IKK β and IKK ϵ inhibit RTA-mediated gene expression. (A and B) 293T cells were transfected with a reporter plasmid cocktail and plasmids containing the indicated genes. At 24 h posttransfection, luciferase activity and β -galactosidase activity in whole-cell lysates were determined (A). Whole-cell lysates were analyzed by immunoblotting with the indicated antibodies (B). (C) Transfection with BJAB cells and luciferase reporter assays were carried out as described for panel A, except a plasmid containing the kinase-dead mutant of IKK ϵ (IKK ϵ K38A) or that of IKK β (IKK β KD) was included. WT, wild type.

manner. The effect of IKK ϵ was more robust than that of IKK β , and these two kinases were equally expressed (Fig. 1B). To determine whether the kinase activity of IKK ϵ was required for the inhibition of RTA-dependent transcriptional activation, we utilized the kinase-dead mutant of IKK ϵ , IKK ϵ K38A, for a reporter assay. Compared to wild-type IKK ϵ , the IKK ϵ K38A mutant had a marginal effect on RTA-mediated gene expression (Fig. 1C). Similarly, the kinase-dead mutant of IKK β , IKK β KD, failed to inhibit RTA-mediated transcription. Thus, IKK β and IKK ϵ potentially inhibit RTA-mediated transcriptional activation in a kinase-dependent manner.

Knockdown of IKK β and IKK ϵ upregulates KSHV lytic gene expression and impairs KSHV latent infection. Compared to human umbilical vein endothelial cells (HUVEC), ECV endothelial cells express high levels of IKK β and IKK ϵ and can be easily amplified for biochemical studies. Thus, we employed ECV cells to investigate innate immune signaling in KSHV latent infection. To probe the roles of IKK β and IKK ϵ in KSHV infection, we knocked

down their expression with short hairpin RNA (shRNA) and assessed KSHV infection. Two separate shRNAs, expressed via lentivirus infection, reduced the IKK ϵ protein level in human ECV endothelial cells without affecting the IKK β protein level (Fig. 2A). After infection with shRNA-expressing lentivirus, ECV cells were then infected with recombinant KSHV.219 (rKSHV.219), which carries green fluorescent protein (GFP) as an infection marker and red fluorescent protein (RFP; under the control of the PAN promoter) as a lytic replication marker (44). rKSHV.219 infection in ECV cells expressing shRNA27 yielded cells with higher GFP intensity, likely due to viral genome replication. In support of this, knockdown of IKK ϵ greatly elevated RFP⁺ cells as well, suggesting more robust lytic gene expression when IKK ϵ expression was suppressed (Fig. 2B). shRNA36 had a mild effect on KSHV lytic gene expression, as judged by the number of RFP⁺ cells (data not shown). Indeed, qRT-PCR analysis using primers specific for KSHV lytic genes, including RTA, PAN, ORF57, ORF21, and K8.1, showed that knockdown of IKK ϵ increased viral

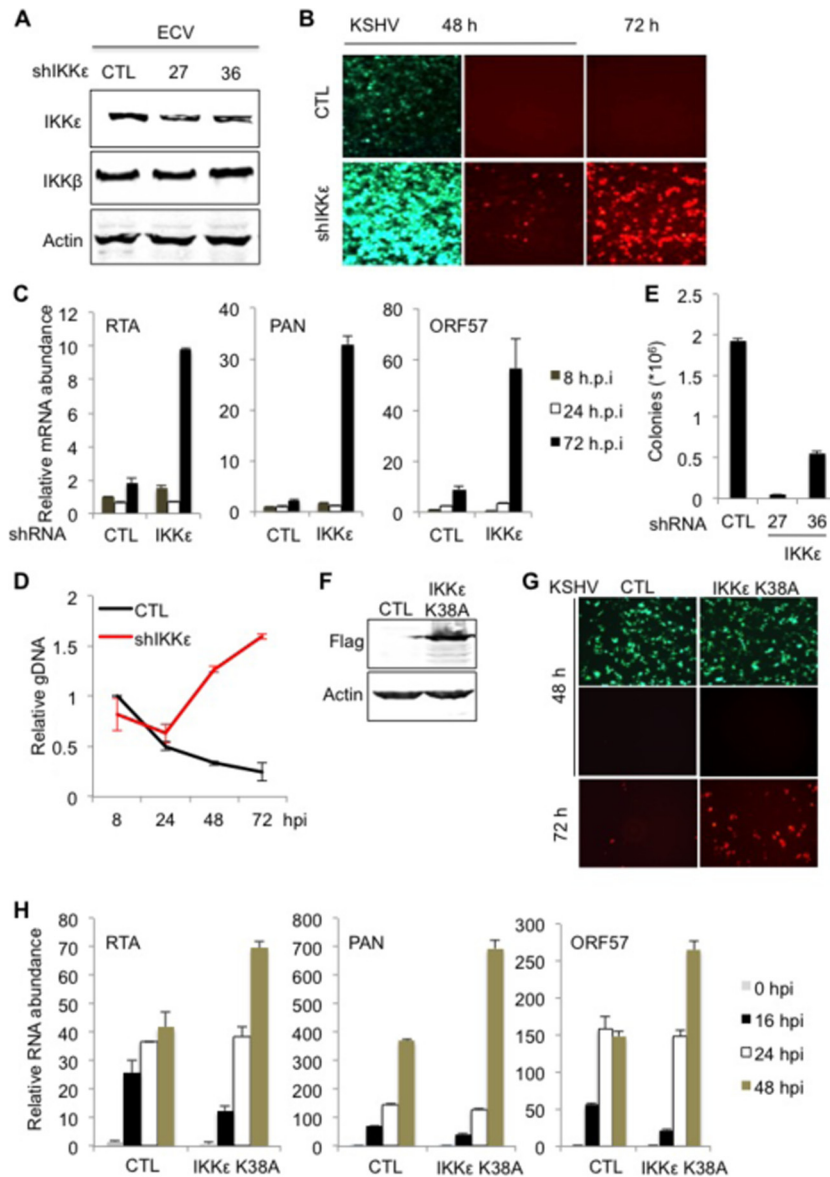


FIG 2 Knockdown of IKK ϵ increases KSHV lytic gene expression and impairs latent infection. ECV cells were infected with lentivirus expressing control (CTL) shRNA or shRNA27 and shRNA36 of IKK ϵ and then selected with puromycin. (A) Whole-cell lysates were analyzed by immunoblotting with the indicated antibodies. (B) ECV cells were infected with KSHV at a multiplicity of infection (MOI) of 2 and monitored by fluorescence microscopy at 48 and 72 h postinfection. (C and D) Total RNA (C) or genomic DNA (D) was extracted from ECV cells at the indicated time points after KSHV infection. The mRNA abundance of selected viral genes (C) or the copy number of viral episomes (D) was analyzed by qRT-PCR. (E) ECV cells were infected with rKSHV derived from BAC16 at an MOI of 0.5. At 72 hpi, cells were selected with hygromycin and colonies were counted. (F, G, and H) ECV cells were infected with control lentivirus or lentivirus containing Flag-IKK ϵ K38A. Whole-cell lysates were prepared and analyzed by immunoblotting with the indicated antibodies (F). ECV cells were infected with rKSHV.219 at an MOI of 0.5. Lytic replication was analyzed by fluorescence microscopy (G) and quantitative real-time PCR with total RNA (H).

lytic transcripts by \sim 5-fold for RTA, ORF57, ORF21, and K8.1, whereas PAN RNA was elevated by more than 10-fold at 72 h postinfection (hpi) (Fig. 2C). Consistent with increased viral gene expression, the viral genome copy number gradually increased in ECV cells in which IKK ϵ was knocked down, whereas it gradually decreased in control ECV cells (Fig. 2D). By 72 hpi, the copy number of the KSHV genome in IKK ϵ knockdown cells was approximately 6-fold higher than that in control ECV cells. To quantitatively measure KSHV latent infection, we used recombinant KSHV derived from BAC16, which permits selection with hygromycin, accommodating the puromycin resistance conferred by

shRNA expression vectors. ECV cells were infected with lentivirus expressing IKK ϵ shRNA and selected with puromycin. Cells were then infected with recombinant KSHV generated from BAC16 (hygromycin resistant) and selected with puromycin and hygromycin for latently infected KSHV episomes. When ECV cells were selected with puromycin and hygromycin for latently infected cells, knockdown of IKK ϵ in ECV cells reduced KSHV latently infected cells by more than 95% for shRNA27 and by \sim 75% for shRNA36 (Fig. 2E).

We further examined the effects of the kinase-dead IKK ϵ K38A mutant on KSHV latent infection. When IKK ϵ K38A was ex-

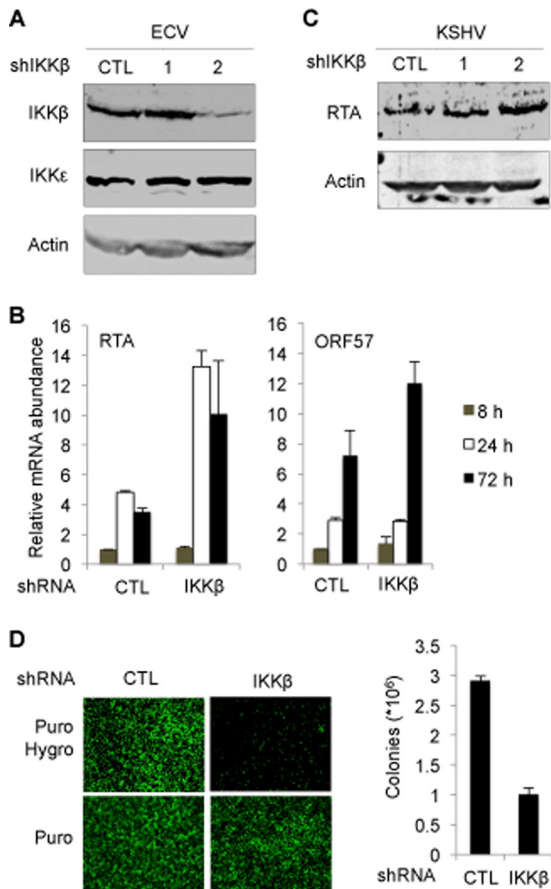


FIG 3 Depletion of IKK β promotes KSHV lytic gene expression and impairs latent infection. ECV cells were infected with lentivirus expressing control (CTL) shRNA or shRNA1 and shRNA2 of IKK β and selected with puromycin. (A) Whole-cell lysates were analyzed by immunoblotting with the indicated antibodies. (B and C) ECV cells were infected with KSHV at a multiplicity of infection (MOI) of 2. Total RNA was extracted and analyzed by qRT-PCR (B). Whole-cell lysates were prepared at 48 h postinfection and analyzed by immunoblotting with anti-RTA and anti- β -actin antibodies (C). (D) ECV cells were infected with KSHV at an MOI of 0.5. At 72 hpi, cells were selected with hygromycin, fluorescence of surviving cells was recorded by using a fluorescence microscope (left), and colonies were counted (right).

pressed in ECV cells (Fig. 2F), we observed an increase in RFP⁺ cells at 72 hpi (Fig. 2G). qRT-PCR analysis, using primers specific for KSHV lytic genes, showed that the expression of IKK ϵ K38A increased the abundance of various lytic transcripts, although its effects at 24 or 48 hpi were marginal (Fig. 2H). The effects of IKK ϵ knockdown and exogenously expressed IKK ϵ K38A on KSHV lytic gene expression were prominent at late time points during KSHV infection, i.e., 72 hpi, implying its temporal effect during KSHV infection. Taken together, these results indicate that IKK ϵ is crucial for KSHV latent infection.

Similarly, we examined the roles of IKK β in KSHV latent infection with shRNA-mediated knockdown. ECV cells were infected with lentivirus expressing shRNAs specific for IKK β . Of two shRNAs, one caused diminished IKK β protein expression, as determined by immunoblotting analysis (Fig. 3A). qRT-PCR analysis showed that IKK β knockdown resulted in an increase of the mRNAs for ORF57 and RTA by \sim 2- to 3-fold (Fig. 3B). The effect of IKK β knockdown on KSHV gene expression was not as

robust as that of IKK ϵ knockdown, in agreement with the lower inhibition of IKK β than that of IKK ϵ for RTA-mediated transcriptional activation in reporter assays. Furthermore, the increased RTA mRNA abundance correlated with a higher protein level in ECV cells infected with KSHV (Fig. 3C). Finally, we examined the outcome of IKK β knockdown on KSHV latent infection. Knockdown of IKK β diminished cells latently infected with KSHV, as assessed by fluorescence microscopy. Semiquantitative measurement showed that shRNA knockdown of IKK β reduced KSHV latent infection by \sim 65%, indicating that IKK β is necessary for KSHV latent infection (Fig. 3D).

KSHV *de novo* infection activates IKK β and IKK ϵ . IKK and IKK-related kinases are key signaling molecules in innate immune responses against viral infections (22, 45). We reasoned that KSHV *de novo* infection activates IKK β and IKK ϵ , which in turn impinge on KSHV lytic gene expression and latent infection. To test this hypothesis, we monitored the kinase activities of IKK β and IKK ϵ after KSHV infection in an *in vitro* kinase assay. Human ECV endothelial cells were infected with rKSHV.219, and the IKK β kinase complex was precipitated with anti-IKK γ . An *in vitro* kinase assay showed that KSHV infection gradually increased IKK β kinase activity by up to \sim 3-fold at 4 hpi (Fig. 4A). Interestingly, we found that the kinase activity of IKK ϵ was much more robustly induced by KSHV infection, with an \sim 5- to 10-fold increase in its ability to phosphorylate IRF3C (Fig. 4B). To corroborate the activation of IKK β and IKK ϵ in *in vitro* kinase assays, we carried out qRT-PCR analysis and assessed the expression of host inflammatory genes, represented by IFN- α 1, IFN- α 2, IFIT3, CCL5, interleukin-8 (IL-8), and IFN- γ -inducible protein 10 (IP10). Interestingly, IFN α 1, IFN α 2, IFIT3, and CCL5 shared similar expression patterns (Fig. 4C). The levels of these cytokine mRNAs were reduced at 4 hpi and then induced at 8 hpi by \sim 2- to 5-fold. At 24 hpi, these mRNAs returned to levels below those for mock-infected cells. By contrast, IL-8 and IP10 were gradually induced up to 6- and 4-fold at 24 hpi, respectively. Evidently, the first four cytokines are the faster responders upon KSHV infection, and the other two chemokines, i.e., IL-8 and IP10, perhaps represent the slower responders. When viral lytic transcripts, i.e., RTA and ORF57, were examined by qRT-PCR, we observed a gradual and robust increase in viral gene expression, indicating the progression of viral infection (Fig. 4D). Notably, both lytic and latent genes are expressed during the first 24 h postinfection to facilitate the establishment of KSHV latent infection (46). These results collectively indicate that KSHV *de novo* infection activates both IKK β and, more potently, IKK ϵ .

RelA is an effector downstream of IKK β and IKK ϵ that inhibits RTA-mediated transcriptional activation. We previously reported that IKK β can phosphorylate γ HV68 RTA to promote viral transcriptional activation (27). To this end, we extensively analyzed RTA phosphorylation by IKK β and IKK ϵ in an *in vitro* kinase assay and via mass spectrometry. Although the *in vitro* kinase assay identified three phosphorylation sites within the carboxy terminus of RTA, the ability of IKK ϵ to phosphorylate these sites was not confirmed by mass spectrometry analysis when we used RTA purified from transfected 293T cells (data not shown). Moreover, RTA mutants carrying phosphorylation-resistant mutations demonstrated a similar ability to activate gene expression in reporter assays and in iSLK.219 cells that ectopically expressed RTA (data not shown). These results suggest that RTA phosphor-

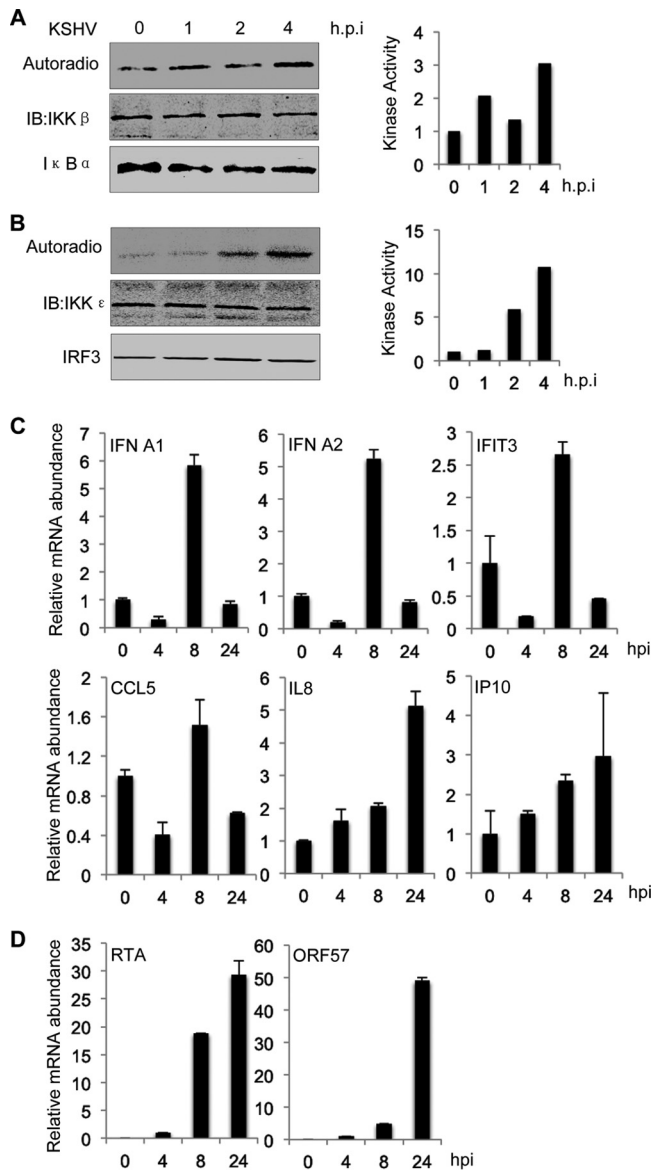


FIG 4 KSHV *de novo* infection activates IKK β and IKK ϵ . (A and B) IKK β and IKK ϵ were precipitated from ECV cells at the indicated time points after KSHV infection. GST fusion proteins carrying the N terminus of I κ B α or the C terminus of IRF3 (IRF3C) were added to precipitated IKK β (A) and IKK ϵ (B), respectively. Phosphorylation of GST fusion proteins and other proteins were analyzed by autoradiography and immunoblotting (IB), respectively. Phosphorylation was also quantified with densitometry; results are shown in the graphs on the right. Data represent three independent experiments. (C and D) Total RNA was extracted from ECV cells at the indicated time points after KSHV infection and analyzed by qRT-PCR for mRNA abundance of selected host (C) and viral (D) genes.

ylation by IKK β and IKK ϵ does not contribute to suppression of KSHV lytic replication by these two kinases.

Because IKK β and IKK ϵ are important for NF- κ B activation which, in turn, enables the latent infection of gammaherpesvirus, we surmised that NF- κ B activation is a major player downstream of IKK β and IKK ϵ . To test this hypothesis, we examined the inhibitory effects of IKK β and IKK ϵ on RTA-mediated transcriptional activation in reporter assays in which the three transcrip-

tionally active subunits of NF- κ B, i.e., RelA, RelB, and c-Rel, were knocked down with shRNAs. We found that knockdown of RelA, but not that of RelB or c-Rel, diminished the inhibition of RTA-dependent gene expression by IKK β (Fig. 5A). Similar results were obtained for the inhibition of RTA-mediated transcriptional activation by IKK ϵ . These results identified RelA as a key player downstream of IKK β and IKK ϵ for inhibition of RTA-mediated transcription. The efficiencies of knockdown of all three Rel family members were validated by qRT-PCR analysis, the results of which demonstrated a reduction of gene expression of >60% (Fig. 5B). To further corroborate the role of RelA downstream of IKK β and IKK ϵ , we performed an electrophoresis mobility shift assay. KSHV infection elevated the nuclear binding activity of an NF- κ B probe, indicative of NF- κ B activation (Fig. 5C). Moreover, an antibody against RelA further retarded the migration of the NF- κ B-DNA complex, indicating that KSHV-induced NF- κ B contains RelA (Fig. 5C). These results collectively support that RelA is an important effector downstream of IKK β and IKK ϵ .

To examine the role of RelA in KSHV latent infection, we knocked down RelA expression in ECV cells and examined KSHV infection. While shRNA1 reduced the RelA protein level by ~38.8%, shRNA2 nearly abolished the RelA protein (Fig. 5D). Moreover, knockdown of RelA resulted in an increase in viral lytic transcripts, including PAN, ORF57, and ORF21, by ~2- to 3-fold (Fig. 5E). By using rKSHV.219, which expresses RFP as a lytic marker, we found that knockdown of RelA elevated lytic replicating cells by ~5- to 10-fold at 72 hpi. Whereas the RFP⁺ cells were not detected at 48 hpi in ECV cells expressing control shRNA, RFP⁺ ECV cells were prominent in those cells expressing RelA shRNA (Fig. 5F). Finally, quantitative measurement of KSHV latently infected cells indicated that RelA knockdown reduced KSHV latent infection by ~80% (Fig. 5F). These results indicate that RelA, an effector downstream of IKK β and IKK ϵ , is critical for suppressing KSHV lytic gene expression, thereby enabling KSHV latent infection.

IKK ϵ and IKK β are required for phosphorylation of S⁴⁶⁸ and S⁵³⁶ of RelA, respectively, to inhibit RTA-mediated transcriptional activation. Although IKK β and IKK ϵ were shown to phosphorylate the inhibitor of κ B (I κ B, e.g., I κ B α), these kinases can directly phosphorylate NF- κ B subunits such as RelA, representing a regulatory step likely functioning at post-nuclear translocation. In fact, RelA phosphorylation of S⁵³⁶ and S⁴⁶⁸ are implicated in distinct outcomes of NF- κ B, depending on cellular conditions (31, 47). Considering that IKK β and IKK ϵ remained highly active at 4 hpi, we reasoned that events after NF- κ B subunits released from I κ B, e.g., RelA phosphorylation by IKK β and IKK ϵ , are likely important to influence NF- κ B activation and KSHV latent infection. We thus examined RelA phosphorylation of S⁴⁶⁸ (S⁴⁶⁸p) and S⁵³⁶ (S⁵³⁶p), both of which are important for NF- κ B activation. Upon KSHV infection, the level of RelA S⁴⁶⁸p gradually increased within the first 4 hpi, whereas that of RelA S⁵³⁶p increased at 1 and 2 hpi and then declined to levels below that of mock-infected cells at 4 hpi (Fig. 6A). To test whether RelA phosphorylation of S⁴⁶⁸ and S⁵³⁶ is important for the inhibitory effect of RelA, we overexpressed RelA or its mutants and examined RTA-mediated transcriptional activation in reporter assays. In agreement with a previous report (48), RelA expression potentially inhibited RTA-mediated transcriptional activation on the ORF57 promoter (Fig. 6B). Interestingly, RelA S⁴⁶⁸A failed to inhibit gene expression driven by the RTA-dependent ORF57 promoter, whereas RelA

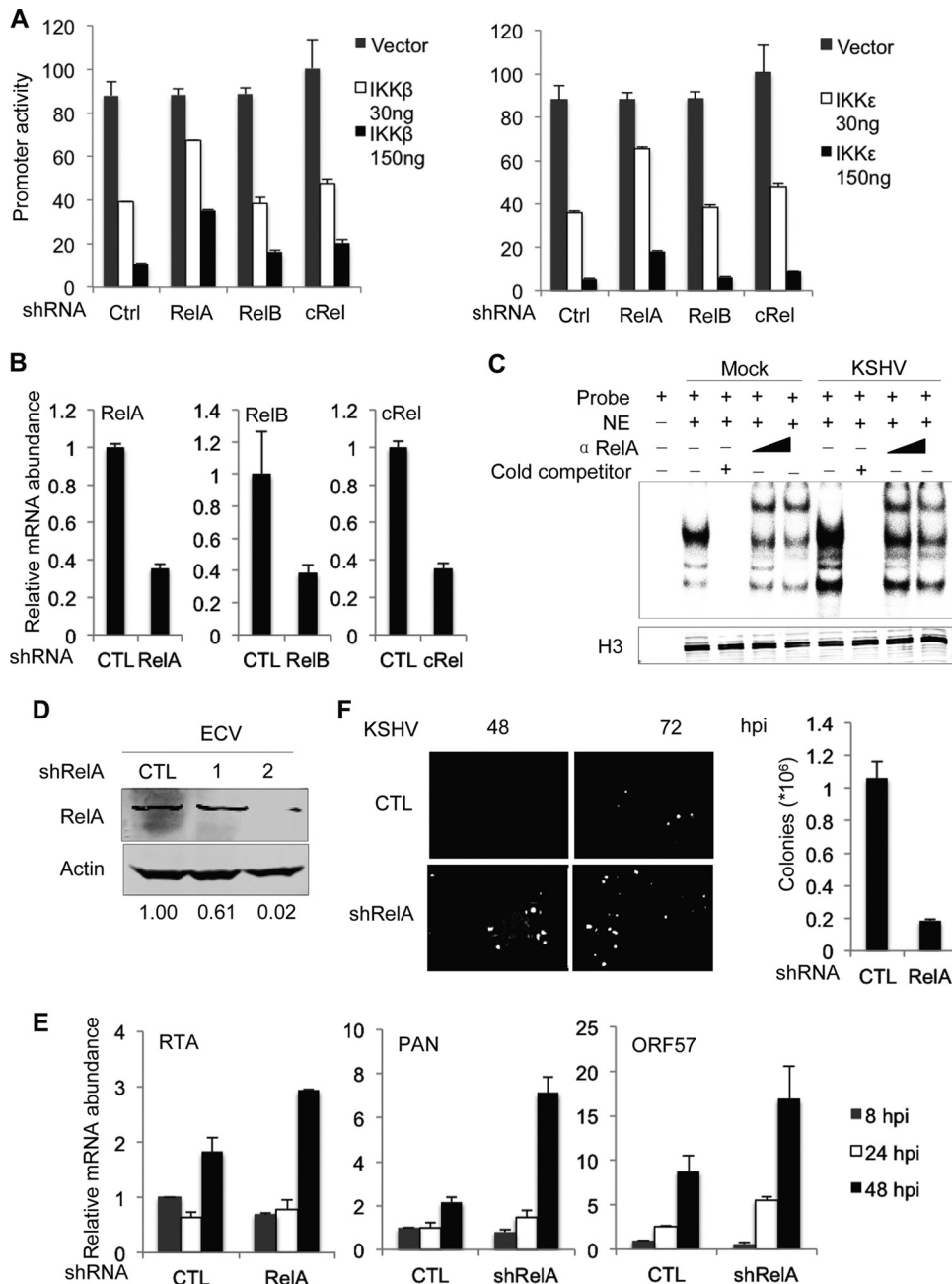


FIG 5 RelA is an effector downstream of IKK β and IKK ϵ . 293T cells were infected with lentivirus expressing control (Ctrl) shRNA or shRNA specific for RelA, RelB, or c-Rel. (A) 293T cells were used to determine the inhibition of IKK β (left) and IKK ϵ (right) on RTA-dependent transcriptional activation in a luciferase reporter assay. (B) Total RNA was extracted for qRT-PCR analysis using primers specific for RelA, RelB, and c-Rel. (C) Nuclear extract was incubated with a [γ -³²P]ATP and analyzed by polyacrylamide gel electrophoresis. (D) Whole-cell lysates were analyzed by immunoblotting with the indicated antibodies. Numbers below the blots indicate the remaining RelA, which was determined by densitometry analysis. (E and F) ECV cells were infected with lentivirus expressing control (CTL) or RelA-specific shRNA, selected with puromycin, and infected with KSHV at a multiplicity of infection of 2. Viral lytic gene expression was analyzed by qRT-PCR (E) and fluorescence microscopy (F).

S⁴⁶⁸E, a phosphorylation mimetic mutant, was as potent as wild-type RelA. Moreover, a dose-dependent expression of RelA wild type and RelA S⁴⁶⁸E showed that RelA S⁴⁶⁸E was not more potent than RelA wild type, suggesting that RelA phosphorylated by endogenous kinases is sufficient to inhibit RTA-mediated transcription (Fig. 6C). Interestingly, RelA S⁵³⁶A greatly increased RTA-dependent transcription, potentially exerting a dominant negative

effect on endogenous RelA. The S⁵³⁶E mutation reduced the inhibitory effect of RelA, although RelA S⁵³⁶E increased the basal promoter activity of ORF57 (Fig. 6B). These results suggest that RelA S⁵³⁶ phosphorylation is required, but not sufficient, for RelA-mediated inhibition. On the other hand, RelA S⁴⁶⁸ phosphorylation is sufficient to inhibit RTA-dependent transcription. To probe the roles of IKK β and IKK ϵ in phosphorylating S⁴⁶⁸

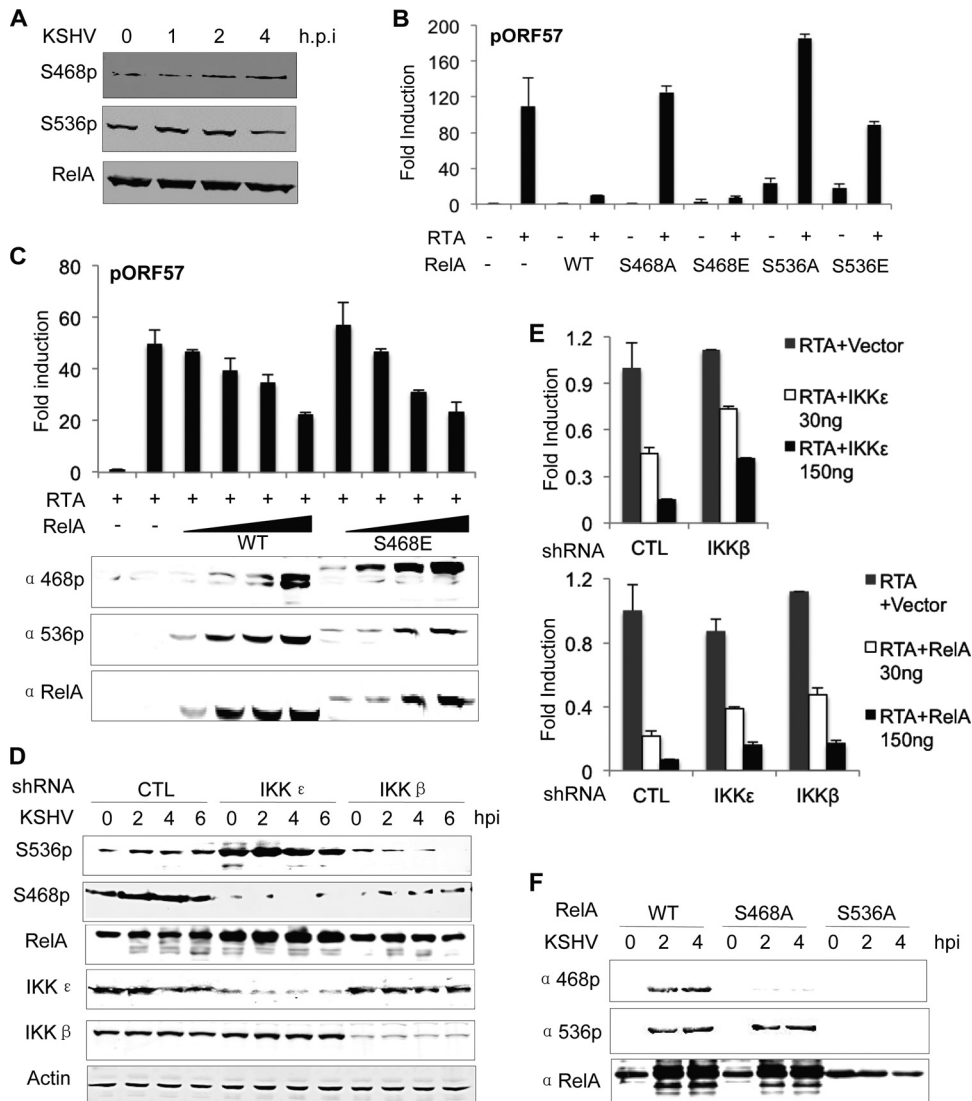


FIG 6 Phosphorylation of RelA is coordinated by IKK β and IKK ϵ during KSHV infection. (A) ECV cells were infected with KSHV and harvested at the indicated time points postinfection. Whole-cell lysates were analyzed for RelA phosphorylation of S⁴⁶⁸ and S⁵³⁶ by immunoblotting with the indicated antibodies. (B) RTA activation was determined in a luciferase reporter assay in 293T cells with plasmids carrying RelA wild type (WT) or mutants, as indicated. (C) Reporter assays were carried out as described for panel B, except with an increasing amount of plasmid containing RelA WT or RelA S^{468E}. (D) ECV cells were infected with lentivirus expressing control shRNA or shRNA specific for IKK ϵ and IKK β and selected with puromycin. At various time points after KSHV infection, RelA phosphorylation was analyzed by immunoblotting with the indicated antibodies. (E) IKK ϵ -mediated (top) or RelA-mediated (bottom) repression of RTA-dependent transcriptional activation in control or IKK knockdown ECV cells was analyzed in luciferase reporter assays. (F) ECV cells expressing RelA WT, RelA S^{468A}, or RelA S^{536A} were infected with KSHV, and whole-cell lysates were analyzed by immunoblotting with the indicated antibodies.

and S⁵³⁶ of RelA, we knocked down IKK β and IKK ϵ and examined RelA phosphorylation after KSHV infection. In control ECV cells, KSHV infection resulted in an increase of RelA S^{536p} by 50% and a more robust increase of RelA S^{468p} (Fig. 6D). IKK ϵ knockdown in ECV cells diminished RelA S^{468p} and increased RelA S^{536p}, indicating that IKK ϵ is necessary for RelA S⁴⁶⁸ phosphorylation (Fig. 6D). The increase in RelA S536p upon IKK ϵ depletion suggested that RelA S536p is subsequently phosphorylated and targeted for degradation by IKK ϵ . Surprisingly, IKK β knockdown resulted in low levels of both RelA S^{536p} and RelA S^{468p} (Fig. 6D). This result indicates that IKK β is necessary for phosphorylation of both S⁴⁶⁸ and S⁵³⁶ of RelA. Taken together, these results suggest a possibility that RelA S⁵³⁶ phosphorylation is necessary for RelA

S⁴⁶⁸ phosphorylation. Under this scenario, IKK β is responsible for phosphorylation of S⁵³⁶, whereas IKK ϵ is responsible for phosphorylating RelA at S⁴⁶⁸. We thus surmised that the inhibition of IKK ϵ on RTA-mediated transcriptional activation depends, at least partly, on IKK β . To test this hypothesis, we knocked down IKK β and examined RTA-dependent transcription when IKK ϵ was expressed. As expected, knockdown of IKK β partly restored the transcriptional activity of RTA that was inhibited by IKK ϵ (Fig. 6E). When IKK β or IKK ϵ was knocked down with shRNA, RelA inhibition of RTA-mediated transcriptional activation was partially restored (Fig. 6E). Finally, we constructed a RelA mutant carrying the S^{536A} or S^{468A} mutation and examined the phosphorylation of S⁴⁶⁸ and S⁵³⁶ in ECV cells infected with KSHV. We

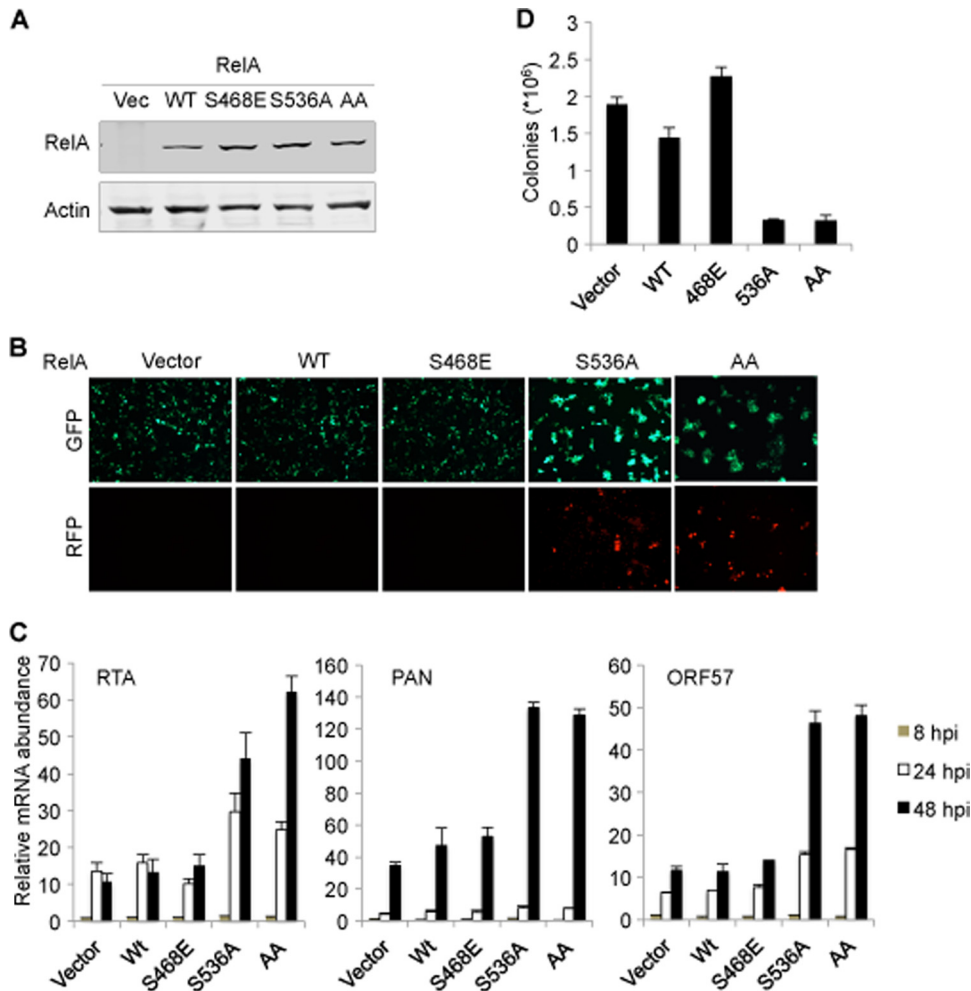


FIG 7 RelA S536A promotes KSHV lytic gene expression and impairs latent infection. ECV cells were infected with lentiviruses expressing RelA wild type (WT), RelA S^{468E}, RelA S^{536A}, or RelA S^{468,536A} (AA). (A) Whole-cell lysates were analyzed by immunoblotting with the indicated antibodies. (B) Cells were infected with rKSHV.219, and fluorescence was determined by using a fluorescence microscope at 72 hpi. (C) Total RNA was extracted and analyzed by qRT-PCR with primers specific to the indicated genes. (D) Cells were selected with hygromycin at 72 hpi, and colonies were counted.

found that KSHV infection robustly elevated the S⁵³⁶ phosphorylation of RelA wild type and RelA S^{468A}, but not the phosphorylation of S⁴⁶⁸ of the RelA S^{536A} mutant (Fig. 6F). These results further confirmed that S⁵³⁶ and its phosphorylation are required for the phosphorylation of S⁴⁶⁸.

NF- κ B activation enables KSHV latent infection. To determine the roles of NF- κ B activation on KSHV latent infection, we utilized the loss-of-function and dominant negative mutant of RelA, RelA S^{536A}, to examine the effect of NF- κ B activation on KSHV latent infection. Although RelA S^{468A} lost its ability to inhibit RTA-mediated transcriptional activation, it did not have a dominant negative effect. Thus, we used RelA S^{468E} to probe the phosphorylation of S⁴⁶⁸ in KSHV lytic gene expression and latent infection. ECV cells stably expressing RelA S^{536A}, RelA S^{468E}, or RelA S^{468,536A} were established with lentivirus infection (Fig. 7A) and infected with rKSHV.219. Fluorescence microscopy analysis indicated that expression of RelA S^{536A} and RelA S^{468,536A}, but not that of RelA wild type or RelA S^{468E}, increased RFP⁺ cells, which also correlated with elevated GFP fluorescence (Fig. 7B). We then examined viral lytic gene expression by qRT-PCR and found that

RelA S^{536A} expression increased viral mRNA transcripts of RTA, ORF57, and K8.1 by ~5-fold. A similar effect on KSHV lytic gene expression was observed for the RelA S^{468,536A} mutant. By contrast, expression of RelA S^{468E} or RelA wild type had minimal effects on KSHV lytic gene expression, suggesting that endogenous RelA is sufficient to inhibit KSHV lytic gene expression (Fig. 7C). This result indicated that NF- κ B activation driven by RelA is a potent inhibitor of KSHV lytic replication. We further examined the effects of these two RelA mutants on KSHV latent infection. Using hygromycin to select for stable episomes of KSHV in ECV cells, we found that the expression of RelA S^{536A} and RelA S^{468,536A} reduced KSHV latently infected cells by ~75% after *de novo* infection (Fig. 7D). In contrast, the expression of the RelA S^{468E} mutant or RelA wild type had a marginal effect on KSHV colony formation. The fact that RelA S^{468,536A} and RelA S^{536A} demonstrated the same level of inhibition on KSHV latent infection and promotion on KSHV lytic gene expression supports the conclusion that phosphorylation of RelA S⁵³⁶ is a critical step for RelA-mediated inhibition. Collectively, these results indicate that RelA S^{536A} impairs KSHV latent infection by promoting lytic gene expression.

DISCUSSION

NF- κ B activation is crucial for a plethora of biological processes, ranging from fundamental development to highly diseased clinical conditions (49). Not surprisingly, NF- κ B is a key determinant of and crucially required for the latent infection of gammaherpesviruses. Specifically, NF- κ B activation is likely exploited by gammaherpesviruses to suppress viral lytic gene expression during latent phase (50–53). For human KSHV and murine γ HV68, NF- κ B activation is sufficient to inhibit RTA-dependent transcriptional activation (48). Conversely, RTAs of KSHV and γ HV68 were also shown to induce RelA degradation and terminate NF- κ B activation (29, 54). This likely contributed to the efficient lytic replication of γ HV68 via evasion of antiviral cytokine production, although the significance of RelA degradation by KSHV RTA remains less clear. In fact, γ HV68 hijacks MAVS and IKK β to induce RelA degradation, in conjunction with RTA serving as an E3 ligase to ubiquitinate RelA (29). These findings highlight the dynamic regulation of NF- κ B as being important for the outcome of KSHV and γ HV68 infection. Given the propensity of KSHV to establish latent infection, we have addressed the importance of NF- κ B activation during KSHV infection. In determining the roles of IKK β and IKK ϵ in KSHV infection, we found that these two kinases are coordinated to promote NF- κ B activation which, in turn, enables KSHV latent infection by suppressing viral lytic gene expression.

The IKK complex is composed of two kinase subunits, IKK α and IKK β , and a scaffold subunit, IKK γ . IKK ϵ is an IKK-related kinase, and its function remains less understood, despite its presumed redundant function with TBK1 in phosphorylating interferon regulatory factors (55, 56). However, IKK ϵ is largely dispensable for proinflammatory cytokine production in response to viral infection (57). Instead, IKK ϵ was shown to regulate IFN-mediated signal transduction downstream of interferon receptors (58, 59). Upon viral infection, these innate immune kinases are activated to provoke antiviral cytokine production, which acts to defeat viral infection. Our recent studies of murine γ HV68 suggested the possibility that these immune kinases directly phosphorylate KSHV RTA to influence viral transcription (27). Indeed, IKK β and IKK ϵ potently phosphorylated KSHV RTA in an *in vitro* kinase assay (data not shown). However, we were unable to confirm RTA phosphorylation in cells and to establish the biological significance of RTA phosphorylation when we used recombinant KSHV (data not shown). Thus, we determined that NF- κ B activation is an effector downstream of IKK β and IKK ϵ . By employing shRNA-mediated knockdown, we showed that RelA, but neither RelB nor c-RelA, contributed to the inhibition of IKK β and IKK ϵ on RTA-mediated transcriptional activation and KSHV lytic gene expression. The viral lytic gene expression also conversely correlated with latent infection of KSHV. However, knockdown of RelA only partly restored the inhibition of IKK β and IKK ϵ on RTA-dependent transcriptional activation, implying that additional cellular or viral factors are inhibited by IKK β and IKK ϵ during KSHV infection. This was further supported by the observation that a fraction of the NF- κ B–DNA complex was shifted by an anti-RelA antibody.

A key component downstream of IKK β and IKK ϵ is NF- κ B, which is activated by phosphorylation and degradation of the inhibitor of κ B (I κ B). Unleashed from I κ Bs, NF- κ B dimers translocate into the nucleus to upregulate expression of diverse cellular

inflammatory genes. Notably, posttranslational modifications, e.g., phosphorylation, further influence NF- κ B activation and impinge on the outcome of infection by gammaherpesviruses. Among the multiple phosphorylated forms of RelA identified thus far, phosphorylations of S⁵³⁶ and S⁴⁶⁸ have been relatively well defined. RelA S⁵³⁶p was reported to enable NF- κ B activation via recruitment of coactivators, such as p300, to promote targeted gene expression (31). However, phosphorylation of RelA S⁴⁶⁸ was originally identified for its role in priming RelA for degradation by the ubiquitin/proteasome system (60). In agreement with this, we previously showed that murine γ HV68 induced RelA S⁴⁶⁸ phosphorylation to promote its degradation (28). In this study, we showed that RelA phosphorylation of S⁴⁶⁸ is necessary for NF- κ B activation and KSHV latent infection. These findings support the conclusion that the outcome of RelA phosphorylation is context dependent. Nevertheless, we found that RelA S⁴⁶⁸A failed to inhibit RTA-mediated transcriptional activation, implying that S⁴⁶⁸ phosphorylation is necessary for RelA-mediated inhibition. Recently, we also found that the G protein-coupled receptor of KSHV enables NF- κ B activation via phosphorylation of S⁴⁶⁸, which is relayed by IKK ϵ (61). These results collectively support the corollary that S⁴⁶⁸ phosphorylation marks RelA for activation and perhaps undergoes immediate degradation, thereby coupling RelA degradation to its activation. This notion is consistent with the observation that many transcriptional factors are kept at low expression levels via the coupling of degradation to transcriptional activation. In support of this, depletion of IKK ϵ elevated the levels of RelA S536p, which presumably accumulated due to lack of phosphorylation at S468 and impaired degradation thereof.

In this study, we report that both IKK β and IKK ϵ are critical for NF- κ B activation and that these two kinases are coordinated to phosphorylate S⁵³⁶ and S⁴⁶⁸ of RelA, respectively. Moreover, RelA S⁵³⁶ phosphorylation is necessary for subsequent phosphorylation of S⁴⁶⁸, highlighting the sequential actions of IKK β and IKK ϵ in activating NF- κ B. This is the first example wherein two closely related kinases are activated by a pathogen to enable NF- κ B activation via site-specific phosphorylation. It is not clear how these closely related kinases achieve site-specific phosphorylation in cells. When purified, IKK β and IKK ϵ did not display selectivity to phosphorylate S⁵³⁶ and S⁴⁶⁸ of RelA *in vitro* (data not shown), suggesting that other cellular factors are required for the specific phosphorylation of RelA by IKK β and IKK ϵ in cells. Alternatively, it is also possible that specific phosphorylation is mediated by other kinases, which are selectively activated by IKK β and IKK ϵ . Surprisingly, IKKs, IKK-related kinases, and IRAK1 were previously reported to phosphorylate S⁵³⁶ or S⁴⁶⁸ of RelA under various physiological conditions (28, 60–63). Our recent studies further validate these phosphorylation events for RelA that occur in KSHV-infected cells. Notably, the KSHV G protein-coupled receptor (kGPCR) also activates IKK ϵ , which promotes the phosphorylation of S⁴⁶⁸ of RelA to activate NF- κ B, and NF- κ B activation by IKK ϵ is critical for kGPCR tumorigenesis (61). Here, we found that IKK ϵ also phosphorylates RelA S⁴⁶⁸ to enable NF- κ B activation and inhibition of KSHV lytic gene expression, thereby promoting KSHV latent infection. These studies support the possibility that RelA S⁴⁶⁸p is an activated form of NF- κ B, and our results also suggest that IKK ϵ is an important signaling molecule in activating NF- κ B under diverse physiological conditions.

The assembly of the IKK kinase complex and subsequent activation by phosphorylation of a serine residue within the so-called

activation loop defines a prototypical activation mechanism of IKK β . Surprisingly, the S \rightarrow E mutation within the equivalent activation loop of IKK ϵ resulted in reduced kinase activity (64–66), suggesting a new mechanism of kinase activation distinct from those of IKK α and IKK β . Our recent studies involving KSHV infection have provided compelling evidence that IKK ϵ is critical for NF- κ B activation, and the findings suggest that KSHV deploys viral factors, e.g., kGPCR, to activate IKK ϵ . The identification of viral activators (e.g., kGPCR and others) will offer useful tools to dissect IKK ϵ activation and determine its role in fundamental biological processes.

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We declare no conflict of interest.

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