Mitogen-activated kinase kinase kinase 1 inhibits hedgehog signaling and medulloblastoma growth through GLI1 phosphorylation

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Abstract. The aberrant activation of hedgehog (HH) signaling is a leading cause of the development of medulloblastoma, a pediatric tumor of the cerebellum. The FDA-approved HH inhibitor, Vismodegib, which targets the transmembrane transducer SMO, has shown limited efficacy in patients with medulloblastoma, due to compensatory mechanisms that maintain an active HH-GLI signaling status. Thus, the identification of novel actionable mechanisms, directly affecting the activity of the HH-regulated GLI transcription factors is an important goal for these malignancies. In this study, using gene expression and reporter assays, combined with biochemical and cellular analyses, we demonstrate that mitogen-activated kinase kinase 1 (MEKK1), the most upstream kinase of the mitogen-activated protein kinase (MAPK) phosphorylation modules, suppresses HH signaling by associating and phosphorylating GLI1, the most potent HH-regulated transcription

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factor. Phosphorylation occurred at multiple residues in the C-terminal region of GLI1 and was followed by an increased association with the cytoplasmic proteins 14-3-3. Of note, the enforced expression of MEKK1 or the exposure of medulloblastoma cells to the MEKK1 activator, Nocodazole, resulted in a marked inhibitory effect on GLI1 activity and tumor cell proliferation and viability. Taken together, the results of this study shed light on a novel regulatory mechanism of HH signaling, with potentially relevant implications in cancer therapy.

Introduction

The Sonic hedgehog (SHH) pathway regulates postnatal cerebellar development and its aberrant activation causes SHH-dependent medulloblastoma (SHH-MB), an aggressive pediatric cerebellar tumor (1). Hedgehog signaling is activated by the interaction of the HH ligand with the inhibitory receptor patched (PTCH). This allows the activation of the transmembrane transducer smoothened (SMO), which primes a signaling cascade that involves changes in the interactions between the cytoplasmic transducer SUFU and the GLI transcription factors: GLI1, GLI2 and GLI3. GLI1 and GLI2 act as activators, while GLI3 is a suppressor of hedgehog (HH)-dependent transcription (2).

GLI1 is the most potent activator, and plays a key role in tumorigenesis (3). Mutations typically found in SHH-MB include loss of function mutations of *PTCH* or *SUFU* or activating mutations of *SMO* or *GLI2* amplifications (4). Tumors carrying *PTCH* or *SMO* mutations are eligible to be treated with the drug, Vismodegib, an FDA-approved SMO inhibitor. However, despite the initial positive response, these tumors promptly develop compensatory mechanisms (i.e., *SMO* mutations or the activation of collateral pathways) that restore HH signaling to the post-receptor level (5). Furthermore, Vismodegib is not effective in tumors carrying genetic alterations of SUFU or GLI, thus implying that the identification of molecules with the ability to block the signaling at the post-receptor level, i.e., at the GLI level, would be a preferable choice. In this regard, different inhibitors have been characterized to date, some directly targeting GLI, others targeting GLI modifiers (6).

GLI transcription factors are finely regulated at the post-translational level by various modifications, such as phosphorylation (7), ubiquitination (8), acetylation (9,10) and SUMOylation (11). It has previously been demonstrated that targeting some of these GLI modifications may prove to be an additional avenue with which to inhibit HH-regulated transcriptional output (12). For instance, we have previously found that the pharmacological induction of GLI1 acetylation, using selective HDAC inhibitors, efficiently turns off HH signaling, counteracts tumor growth and improves survival in preclinical models of HH-dependent tumors (13).

Phosphorylation is another key modification that plays a relevant role in the regulation of GLI function. Indeed, phosphorylation regulates proteolytic cleavage, stability, compartmentalization and the activity of GLI, which in most cases are followed by transcriptional repression (3). Hence, drugs targeting specific kinases may be used as alternative tools to prevent GLI function in medulloblastoma and other HH-driven malignancies. In this context, our group and others have found that human GLI1 is a substrate for the energy sensor AMP kinase at serine 408 (Ser408) and that this modification destabilizes GLI1 and reduces tumor formation (14,15), thus implying that AMPK agonists may be used to restrain SHH-MB growth. However, since Ser408 is conserved only in primates, preclinical studies using these compounds to test their efficacy in relevant animal models of medulloblastoma are unfortunately not feasible.

In a recent study, it was shown that also the mitogen-activated kinase kinase kinase 2 and 3, two members of the most upstream mitogen-activated protein kinase (MAPK) phosphorylation modules, phosphorylate and inhibit GLI1 and medulloblastoma growth (16). In this study, we investigated the role of another key member of the same phosphorylation module, the mitogen-activated kinase kinase kinase 1 (MEKK1) (17), in HH-dependent function and tumorigenesis. We demonstrate that MEKK1 binds and phosphorylates GLI1 at multiple residues, thus causing the inhibition of HH/Gli1 signaling and reducing HH-dependent medulloblastoma cell growth.

Materials and methods

Plasmids and reagents. The pcDNA3 MEKK1 WT, pcDNA3 MEKK1 KD plasmids were a gift from Dr G. Johnson (Addgene plasmid #12180); 8xGLI-Luc was provided by the H. Sasaki Laboratory, RIKEN Center for Developmental Biology, Kobe, Japan; 12xGLI-Luc, TK-*Renilla*, P1A WT-Luc and P1A Mut-Luc were from Dr R. Tofgard, Karolinska Institute, Stockholm, Sweden; FlagGLI2 was a gift from Dr A. Dlugosz, University of Michigan, Ann Arbor, MI, USA (18); pcDNA3 FlagGLI1, pcDNA3 FlagGLI1(2-413), pcDNA3 GLI1(2-413)Vp16,

Gal4GLI1(424-1106) and the 5xGal-Luc reporters were as previously described in the study by Canettieri *et al* (9).

The pcDNA3 His-MLK3, CMV sport6-TAK1, CMV sport6-ASK1, pcDNA3TPL2 plasmids were provided by Dr U. Jhala, University of San Diego, San Diego, CA, USA. Sag was purchased from Adipogen Life Sciences (Liestal, Basel, Switzerland). Nocodazole was purchased from Sigma-Aldrich, St. Louis, MO, USA (cat. no. M1404) and calf intestinal alkaline phosphatase was purchased from New England Biolabs (cat. no. M0290S), Ipswich, MA, USA.

Cell culture and treatments. The NIH3T3 and 293T cell lines (cat. no. RL-1658 and cat. no. CRL-3216, respectively) were purchased from ATCC (Manassas, VA, USA) and were cultured and maintained according to the manufacturer's recommendations; the Med1-MB cells (19), a mouse medulloblastoma cell line of the SHH subgroup (SHH-MB) were generated in the Laboratory of Dr Matthew Scott (Standford University, Standford, CA, USA) from patched PTCH+/-;LacZ mouse and were cultured and maintained as previously described (13,19,20). For Sag treatment, the NIH3T3 cells were incubated in 0.5% of fetal bovine serum, overnight, to allow a full HH response and were then exposed to 200 nM Sag for the indicated periods of time (24 h Fig. 3B, 36 h and 48 h Fig. 4B). For Nocodazole treatments, the cells were incubated with 1 μ g/ml Nocodazole or the vehicle control (DMSO for the indicated periods of time (24 h Fig. 4A; 36 h and 48 h Fig. 4B, 48 h Fig. 9C).

Luciferase/Renilla assays. The 293T or NIH3T3 cells were transfected with the plasmids indicated in the figures, using Lipofectamine 2000 reagent or Lipofectamine and Plus reagent (Invitrogen/Thermo Fisher Scientific, Waltham, MA, USA) respectively, according to the manufacturer's recommendations. After 24 h (Figs. 1, 2B, 3A and 6A) or 48 h (Fig. 4A) from transfection Luciferase/*Renilla* assays were performed as previously described (9,21).

RNA analysis and reverse transcription-quantitative PCR (RT-qPCR). The NIH3T3 or 293T cells were treated with Sag or transfected with pcDNA3, pcDNA3 Flag GLI1, pcDNA3 MEKK1, pcDNA3 MEKK1 KD, as indicated in the figures, and RNA was then extracted using TRIzol reagent. Reverse transcription was performed using the SensiFAST cDNA Syntesis kit (cat. no. BIO-65054) and qPCR was performed as previously described (9,22), using SYBR-Green reagent SensiFAST (cat. no. BIO-94020) (both from Bioline, Memphis, TN, USA). Each amplification reaction was performed in triplicate and the average of the three threshold cycles was used to calculate the amount of transcript in the sample (using ViiA[™] 7 software; Life Technologies/Thermo Fisher Scientific). The results were expressed as the fold induction relative to the control samples using the $\Delta\Delta$ Ct method (23) as previously described (6). HPRT or GAPDH were used where indicated as endogenous controls. The thermocycling conditions used for the PCR were as follows: 95°C, 2 min; (95°C, 5 sec; 60°C, 15 sec) 40 cycles SYBR-Green oligos used are listed below: hGLI1 forward, GGTGGTTCACATGCGCAG and reverse, GGTGCGTCTTC AGGTTTTGC; hPTCH forward, TAGGAGTGGAGTTC ACCGTT and reverse,

ATCCAGGACGGGTGCAAACAT; *hHPRT* forward, GAAGAGCTATTGTAATGACCAGTC and reverse, CAAGCTTGCGACCTTGACCATC; *mGli1* forward, AAGCCAACTTTATGTCAGGG and reverse, AGAGCCCGC TTCTTTCTTAA; *mHprt* forward, GCTTCCTCCTCAGAC CGCTT and reverse, GGTCATAACCTGGTTCATCATC; and *mGapdh* forward, GACGGCCGCATCTTCTTGT and reverse, CCTGGTGACCAGGCGC.

Immunoprecipitation, western blot analysis and antibodies. The 293T cells were lysed with RIPA buffer (0.5% sodiumdehoxycolate, 50 mM Tris HCl pH 7.6, 1% NP-40, 0.1% SDS, 140 mM NaCl and 5 mM EDTA pH 8), supplemented with protease and phosphatase inhibitors (5 mM sodium pyrophosphate, 1 mm b-glycero phosphate and 1 mM sodium orthovanadate). Immunoprecipitation was performed by incubation for 2 h in 1 mg of lysate with anti-Flag M2 Affinity Gel (cat. no. A2220, IP 30 µl; Sigma-Aldrich). Proteins were eluted and analyzed by SDS-PAGE (polyacrylamide percentages: 6% Fig. 5; 12% Fig. 6B; 10% Fig. 8B), blotted onto a nitrocellulose membrane (Perkin-Elmer, Waltham, MA, USA). The membranes were blocked in 5% milk in Tris-buffered saline with 0.1% Tween-20, and incubated overnight at 4°C with the primary antibodies. The following antibodies were used: anti-Flag M2 (1:1,000; cat. no. A8592; Sigma-Aldrich), anti-phosphoserine (1:500; cat. no. 16-455; Millipore, Billerica, MA, USA), anti-14-3-3e (1:1,000; cat. no. sc-1020), anti-MEKK1 (1:1,000; cat. no. sc-449) (both from Santa Cruz Biotechnology, Inc., Santa Cruz, CA, USA), anti-GLI1 (1:1,000; cat. no. 2553S; Cell Signaling Technology, Danvers, MA, USA). Filters were incubated with the following secondary antibodies for 30' at room temperature: Anti-mouse HRP-conjugated (1:10,000; cat. no. A-90-116P); anti-rabbit HRP-conjugated (1:10,000; cat. no. A120-108P) (both from Bethyl Laboratories, Inc., Montgomery, TX, USA). Signals were detected with Western Lightning Plus-ECL (Perkin-Elmer).

Mass spectrometry. Plasmids expressing Flag-GLI1 (424-1106), MEKK1 or empty vector were transfected in to the 293T cells using Lipofectamine 2000. After 24 h, the cells were washed with PBS and lysed in 1% NP-40, 50 mM HEPES pH 7.5, 150 mM NaCl, 1 mM EDTA, 10% glycerol, 10 mM NaF, 1 mM Na₃VO₄, 1 mM DTT and protease inhibitors. Lysates were centrifuged and the supernatants incubated with anti-Flag M2 agarose conjugated beads (A2220; Sigma-Aldrich) overnight at 4°C. At the end of incubation, the agarose beads were washed extensively with lysis buffer and then with PBS. The immunocomplexes were eluted with 0.1 mg/ml Flag peptide, precipitated with 5% TCA and the pellet washed twice with acetone and analyzed as previously described (9,24).

MTT assay. The Med1-MB cells were treated with Nocodazole $(0.1 \,\mu g/ml)$ or transfected with MEKK1 or the empty vector, using Lipofectamine 2000. For the transfected cells, after 2 weeks of selection with G418 0.8 mg/ml, stable cell lines were used for MTT assay. For this purpose, the cells were seeded in triplicate in 96-well plates at a density of 2x10⁴ cells/ml. At the indicated time-points (24 or 48 or 72 h Fig. 9B; 48 h Fig. 9C), 10 μ l of a 5 mg/ml MTT stock solution (purchased from Sigma-Aldrich; cat. no. M2128) was added to each well and the plates were

incubated for 3 h at 37°C. Following incubation, 100 μ l of DMSO were added to each well to solubilize the crystals. The plates were shaken for 15 min and the absorbance was read with a Wallac Victor 2 1420 Spectrophotometer (Perkin-Elmer) at 570 nm.

RNA interference. RNA knockdown was performed with pools of siRNA duplexes (50 to 100 nM) transfected into the NIH3T3 cells using Lipofectamine 2000. The following siRNA purchased from Dharmacon were used: siControl cat. no. D-001206-13-20; siMekk1 cat. no. L-040605-00-0020.

Colony formation assay. The Med1-MB cells were transfected using Lipofectamine 2000 as previously described (13) with a control vector or MEKK1. After 24 h, the cells were counted and equally diluted on new plates in presence of Neomycin (0.8 mg/ml). After 10 days, the foci were stained with Coomassie blue (cat. no. B0149; Sigma-Aldrich) for 10 min at room temperature rinsed with PBS, and counted using ImageJ Software 1.50i. The experiments were performed 3 times in triplicate.

Statistical analysis. Statistical significance was determined using a paired Student's t-test or one-way ANOVA followed by Tukey's post hoc test using GraphPad Prism 6.0 software. A value of P<0.05 was considered to indicate a statistically significant difference.

Results

The kinase MEKK1 inhibits HH-GLI1 activity. We examined the effect of 5 different MAP3K (MEKK1, TPL2, MLK3, ASK1 and TAK1) on the activity of ectopically expressed GLI1, using a luciferase reporter vector containing 12 repeats of a GLI-Bs, upstream of the TK promoter (12xGLI-Luc) (Dr R. Tofgard, Karolinska Institute). Among the kinases tested, ASK1, MLK3 and MEKK1 exerted a significant inhibitory effect, while the others did not markedly affect GLI1 activity (Fig. 1A). Since the most potent effect was achieved by MEKK1, we focused our study on this kinase. We confirmed the inhibition on a different GLI-Luc reporter, containing 8 repeats of the GLI binding site (8xGLI-Luc), indicating that the effect was specific for GLI-Bs (Fig. 1B). The inhibition was dose-dependent and was very robust at the doses of the transfected plasmids as low as 5 ng (Fig. 1B). We then examined the effect of the ectopic expression of MEKK1 on the activity of GLI2, the early effector of HH signaling. As shown in Fig. 1C, this transcription factor was also potently inhibited by the kinase, suggesting the involvement of a conserved region of the two proteins.

To determine whether MEKK1 also has an effect on a native HH responsive promoter, we examined the transcriptional response of the *PTCH1* gene, which is induced by HH signaling through a conserved GLI binding site in its promoter region (9). The overexpression of GLI1 in mouse NIH3T3 cells caused an increase in the endogenous *PTCH1* mRNA levels, as measured by RT-qPCR (Fig. 2A). Consistently, the ectopic expression of GLI1 led to an increase in PTCH-Luc reporter (P1A) activity. In both cases, the induction achieved with the overexpression of GLI1 was prevented by the co-expression of WT MEKK1, but not of a kinase death (KD) mutant (Fig. 2), indicating that MEKK1 inhibition requires the catalytic activity of the protein. GLI1 and

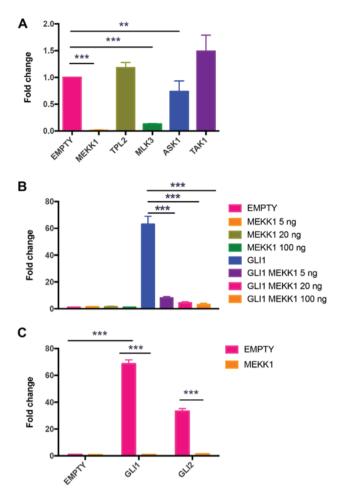


Figure 1. Regulation of the GLI1 promoter by MEKK1. (A) 293T cells were co-transfected with the expression plasmid encoding Flag-GLI1 and expression vectors for MEKK1, TPL2, MLK3, ASK1, TAK1 or control vector (Flag-pcDNA3), and a 12x-GLI luciferase promoter reporter. Plasmid TK-Renilla was transfected to normalize the transfection efficiency. Data are expressed as the fold change of the ratio between luciferase to Renilla activity. (B) 293T cells were transfected with 8x-GLI luciferase promoter reporter and TK Renilla plasmids and with vectors expressing Flag-pcDNA3 or Flag-GLI1 and increasing amounts of MEKK1 plasmid (5, 20 and 100 ng), where indicated. Data are shown as the fold change of the ratio of luciferase reporter to Renilla activity. (C) 293T cells were co-transfected with 8x-GLI luciferase reporter and TK Renilla plasmids and Flag-GLI1 or Flag-GLI2 expression vectors or control vector (Flag-pcDNA3). Data are expressed as the fold change of the ratio between luciferase to Renilla activity. Results are the means \pm SD of 3 independent experiments, each performed in triplicate. **P<0.01 and ***P<0.001 (determined by ANOVA with Tukey's post hoc test).

MEKK1 failed to exert any significant effect on a PTCH-Luc vector mutated on the *GLI* binding site (P1Amut) (Fig. 2B), demonstrating that the inhibition is specific for GLI target genes and cannot be attributed to effects on other promoter regions. To confirm the effects of endogenous MEKK1 on HH signaling, we performed siRNA-mediated knockdown. The ablation of the kinase resulted in increased basal and GL11-induced activity of a GLI-Luc reporter and of basal and Sag-induced levels of *GL11* mRNA (Fig. 3), indicating that endogenous MEKK1 exerts an inhibitory effect on GL11 activity. To further support this observation, we examined the effect of Nocodazole, a MEKK1 activator (25), on HH-GLI signaling. The exposure of the cells to Nocodazole caused a robust decrease in GL11-induced luciferase activity of a GLI-Luc reporter (Fig. 4A) and of the Sag-induced

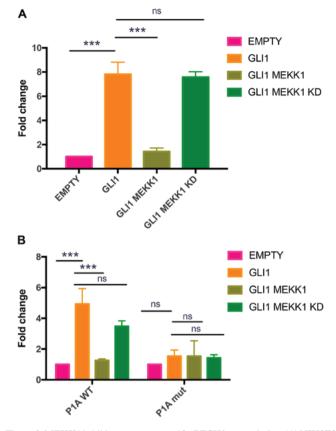


Figure 2. MEKK1 inhibits promoter-specific *PTCH1* transcription. (A) NIH3T3 cells were transfected with Flag-GLI1 or control vector and MEKK1 expression plasmids. Relative expression of *PTCH1* mRNA was evaluated by RT-qPCR. Data were normalized to *HPRT* mRNA levels and are expressed as the fold change relative to control sample. (B) 293T cells were transiently transfected with P1A WT and P1A mutant promoter luciferase constructs, and the TK *Renilla* encoding gene as reporters, and plasmids encoding GLI1, MEKK1 WT or KD or empty vector. Data are expressed as the fold change of the ratio between luciferase to *Renilla* activity. The results are the means \pm SD of 3 independent experiments, each performed in triplicate. ***P<0.001; ns, not significant (calculated by ANOVA with Tukey's post hoc test).

expression of *GL11* mRNA (Fig. 4B), further demonstrating the ability of endogenous MEKK1 to modulate the HH signaling.

MEKK1 binds and pxhosphorylates GLI1. Having observed that MEKK1 inhibits GLI1 activity, we first wished to determine whether this effect was related to the ability of the kinase to associate with this transcription factor. Immunoprecipitation of Flag-GLI1 revealed an association of the transcription factor with ectopically expressed His-MEKK1. This binding was readily competed by the addition of the Flag peptide (Fig. 5A) in molar excess, demonstrating the specificity of the interaction.

We then examined whether MEKK1 phosphorylates GLI1, by co-transfecting Flag tagged GLI1 together with MEKK1 or its empty vector into 293T cells. As shown in Fig. 5B, following Flag immunoprecipitation, the band corresponding to GLI1 exhibited a retarded migration in the presence of MEKK1 compared to the control. To prove that this retarded band was due to GLI1 phosphorylation, we incubated the immunocomplex from Flag immunoprecipitation with calf intestinal phosphatase (CIP) and observed that the GLI1 band was no longer retarded by the kinase (Fig. 5C), leading us to conclude that MEKK1 phosphorylates GLI1.

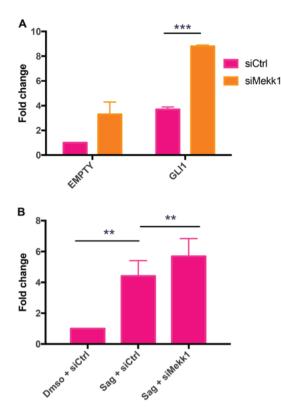


Figure 3. MEKK1 ablation increases HH/GLI1 activity. (A) NIH3T3 cells were transiently transfected with control siRNA (siCtrl, 100 nM) or *Mekk1* siRNA (siMekk1, 100 nM) and 12x-GLI and TK *Renilla* luciferase reporters. Cells were harvested and analyzed for luciferase activity. Data are expressed as the fold change of the ratio between luciferase to *Renilla* activity. (B) *GLI1* mRNA expression levels in Sag-treated NIH3T3 cells expressing control siRNA (siCtrl, 100 nM) or *Mekk1* siRNA (siMekk1, 100 nM) were evaluated by RT-qPCR. *GLI1* mRNA levels were normalized to *HPRT* mRNA levels and expressed as fold change relative to control sample. Data are the means ± SD of at least 3 independent experiments, each performed in triplicate. **P<0.01 and ***P<0.001 (determined by ANOVA with Tukey's post hoc test).

To elucidate which region of GLI1 is regulated by MEKK1, we then performed biochemical and functional analyses of the N-terminal (2-413) and C-terminal (424-1106) fragments of GLI1. Since the N-terminal region contains the GLI DNA binding domain, but not a transactivation domain, we used a chimeric construct consisting of this region fused to the VP16 transactivation domain (TAD) co-transfected with an 8xGLI-Luc reporter. Conversely, since the C-terminal region contains the TAD domain of GLI1, but not the DNA binding domain (DBD), we used a vector containing the C-terminus fused to a Gal4 DBD together with a 5x Gal4-Luc reporter (Fig. 6A) (9). The ectopic expression of MEKK1 inhibited Gal4-GLI1(424-1106), but not GLI1(2-413)-Vp16 activity (Fig. 6A), indicating that the MEKK1 regulation occurs in the C-terminal portion. Consistently, we observed that MEKK1 caused a retardation of the electrophoretic migration of the C-Terminal GLI1 fragment, but did not affect the mobility of the N-Terminal region (Fig. 6B). Thus, MEKK1 binds and phosphorylates GLI1 at its C-terminal region.

To identify the modified residue/s of GLI1 and understand the molecular consequences of the phosphorylation, we performed mass spectrometric analysis on immunoprecipitated Flag-GLI1 C-Term in 293T cells. We observed that GLI1 was phosphorylated in 27 residues in the presence of MEKK1,

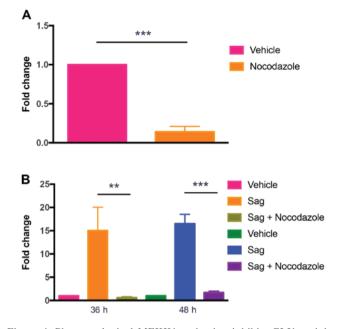


Figure 4. Pharmacological MEKK1 activation inhibits GLI1 activity. (A) Luciferase reporter activity in 293T cells transiently transfected with 12x-GLI luciferase and TK *Renilla* reporters. Cells were treated with Nocodazole (1 μ g/ml) for 24 h and analyzed for luciferase activity. Data are expressed as the fold change of the ratio between luciferase to *Renilla* activity. (B) *GLI1* mRNA expression levels in Sag-treated NIH3T3 cells exposed to Nocodazole (0.1 μ g/ml) for 36 and 48 h. *GLI1* were analyzed by RT-qPCR and normalized to *GAPDH* mRNA levels. Results are expressed as the fold change relative to the control (vehicle) sample. Data are the means ± SD of at least 3 independent experiments, each performed in triplicate. **P<0.01 and ***P<0.001 [calculated using the Student's t-test (A) or ANOVA with Tukey's post hoc test (B)].

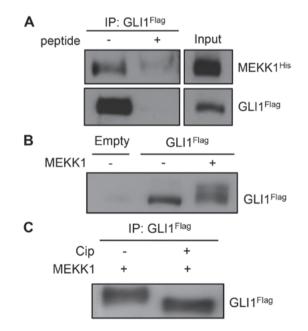


Figure 5. MEKK1 binds and phosphorylates GL11. (A) 293T cells were transfected with constructs encoding Flag-GL11 and His-MEKK1 and cell lysates were immunoprecipitated with anti-Flag antibody without or with 0.1 mg/ml blocking peptide. MEKK1 and GL11 were revealed with anti MEKK1 and anti-Flag antibodies, respectively. Input: 5%. (B) Western blot analysis of cellular lysates from 293T cells expressing Flag-Gl11 alone or in combination with His-MEKK1. Flag-GL11 was revealed with anti-Flag antibody. (C) 293T cells transfected with plasmids encoding Flag-GL11 and His-MEKK1. Cell lysates were immunoprecipitated and immunocomplexes were incubated in the absence or presence of calf intestinal phosphatase (CIP).

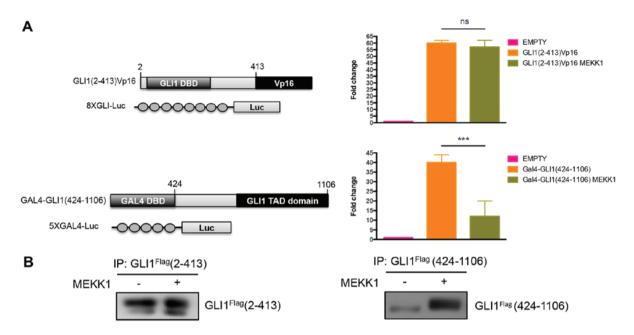


Figure 6. MEKK1 inhibits GL11 transcriptional activity and phosphorylates the C-terminal region of GL11. (A) Left panel, schematic representation of fusion vectors expressing GL11(2-413)Vp16 and 8xGL1 luciferase reporter or Gal4-GL11(424-1106) and 5xGal4 luciferase reporter plasmids. Right panel, luciferase assay on 293T cells transfected with GL11(2-413)Vp16 and 8xGli-Luc or Gal4-GL11(424-1106) and 5xGal4-Luc vectors, with or without MEKK1 expression plasmid. Plasmid encoding TK *Renilla* was transfected to normalize transfection efficiency. Data are expressed as the fold change of the ratio between luciferase to *Renilla* activity. (B) Western blot analysis of immunoprecipitates from 293T cells transfected with expression vectors for Flag-GL11(2-413) or Flag-GL11(424-1106), with or without MEKK1. Flag-GL11 was revealed with anti-Flag antibody. Results are expressed as the means ± SD of at least 3 independent experiments, each performed in triplicate. ***P<0.001; ns, not significant (calculated by ANOVA with Tukey's post hoc test).

Without	MEKK1

without h									
10	20	30	40	50	60	70	80	90	100
SCTEGPLFSS	PRSAVKLTKK	RALSISPLSD	ASLDLOTVIR	TSPSSLVAFI	NSRCTSPGGS	YGHLSIGTMS	PSLGFPAQMN	HQKGPSPSFG	VQPCGPHDSA
110	120	130	140	150	160	170	180	190	200
RGGMIPHPQS	RGPFPTCQLK	SELDMLVGKC	REEPLEGDMS	SPNSTGIQDP	LLGMLDGRED	LEREEKREPE	SVYETDCRWD	GCSQEFDSQE	QLVHHINSEH
210	220	230	240	250	260	270	280	290	300
IHGERKEFVC	HWGGCSRELR	PFKAQYMLVV	HMRRHTGEKP	HKCTFEGCRK	SYSRLENLKT	HLRSHTGEKP	YMCEHEGCSK	AFSNASDRAK	HONRTHSNEK
310	320	330	340	350	360	370	380	390	400
			AHVTKRHRGD					SPGAQSSCSS	
410	420	430	440	450	460	470	480	490	500
			GLSTLRRLEN						
510	520	530	540	550	560	570	580	590	600
			ARYASARGGG						
610	620	630	640	650	660	670	680	690	700
		- -	SITENAAMDA						
710	720	730	740	750	760	770	780	790	800
			PGPKALGGTY					A	
810	820	830	840	850	860	870	880	890	900
QSGPYTQPPP 910	DYLPSEPRPC 920	LDFDSPTHST 930	GQLKAQLVCN 940	YVQSQQELLW 950	EGGGREDAPA 960	QEPSYQSPKF 970	LGGSQVSPSR 980	AKAPVNTYGP 990	GFGPNLPNHK 1000
			LLPPLPTCYG						
1010	1020	1030	1040	1046	CGHPEVGREG	GGPALIPPPE	GOACHETDET	DEDNIQUDEV	AILDEPQGL5
			LLRSLPGETE						
1110002000	0000000000	1 Millit Oldiby	DDRODI ODI D	1 BROOM					
With ME	K 1								
With ME	<k1 20</k1 	30	40	50	60	70	80	90	100
10	20		40 ASLDLQTVIR						
10	20								
10 SCTEGPLFSS 110	20 PRSAVKLTKK 120	RALSISPLSD 130	ASLDLQTVIR	TSPSSLVAFI 150	NSRCTSPGGS 160	YGHLSIGTMS 170	PSLGFPAQMN 180	HQKGPSPSFG 190	VQPCGPHDSA 200
10 SCTEGPLFSS 110 RGGMIPHPQS 210	20 PRSAVKLTKK 120 RGPFPTCQLK 220	RALSISPLSD 130 SELDMLVGKC 230	ASLDLQTVIR 140 REEPLEGDMS 240	TSPSSLVAFI 150 SPNSTGIQDP 250	NSRCTSPGGS 160 LLGMLDGRED 260	YGHLSIGTMS 170 LEREEKREPE 270	PSLGFPAQMN 180 SVYETDCRWD 280	HQKGPSPSFG 190 GCSQEFDSQE 290	VQPCGPHDSA 200 QLVHHINSEH 300
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR	RALSISPISD 130 SELDMLVGKC 230 PFKAQYMLVV	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP	PSLGFPAQMN 180 SVYETDCRWD 280 YMCEHEGCSK	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR 320	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370	PSLGFPAQMN 180 SVYETDCRWD 280 YMCEHEGCSK 380	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 PYVCKLPGCT	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRHRGD	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT	PSLGFPAQMN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 PYVCKLPGCT 410	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR 420	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD 430	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS 450	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470	PSLGFPAQMN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 PYVCKLPGCT 410 TDSGVEMTGN	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR 420 AGGSTEDLSS	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD 430 LDEGPCIAGT	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440 GLSTLRRLEN	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 SLSHTGETVS	PSLGFPAQNN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 RRVGPPVSLE	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYTVSRRS5
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 PYVCKLPGCT 410 TDSGVEMTGN 510	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR 420 AGGSTEDLSS 520	RALSISPLSD 130 SELDMLVGKC 230 FFKAQYMLVV 330 KHVKTVHGPD 430 LDEGPCIAGT 530	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440 GLSTLRRLEN 540	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR 550	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP 560	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 SLSHTGTVS 570	PSLGFPAQMN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 RRVGPPVSLE 580	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RR <mark>SSSSS6FFS</mark> 590	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYTVSRRS5 600
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 PYVCKLPGCT 410 TDSGVEMTGN 510 LASPFPPGSP	20 PRSAVKLTKK 120 RGFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR 420 AGGSTEDLSS 520 PENGASSLPG PENGASSLPG	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD 430 LDEGPCIAGT 530 LMPAQHYLLR	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440 GLSTLRRLEN 540 ARYASARGGG	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR 550 TSPTAASSLD	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP 560 RIGGLPMPPW	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 515HTGFTVS 570 RSRAEPFGWN	PSLGFPAQNN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 RRVGPPVSLE 580 PNAGVTRRAS	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RF SSFSFS 590 DPAQAADRPA	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYIVSRRS5 600 PARVQRFKSL
10 SCTEGPLFSS 110 RGGMIFHPQS 210 IHGERKEFVC 310 PYVCKLPGCT 410 TDSGVENTGN 510 LASPFPPGSP 610	20 PRSAVKLTKK 120 RGFFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR 420 AGGSTEDLSS 520 PENGASSLPG 620	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD 430 LDEGPCIAGT 530 LMPAQHYLLR 630	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440 GLSTLRRLEN 540 ARYASARGGG 640	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR 550 650	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP 560 RIGGLPMPPW 660	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 SCHTCHTVS 570 RSRAEMPGIN 670	PSLGFPAQNN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 RRVGPPVSLE 580 PNAGVTRRAS 680	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RRESERVEN 590 DPAQAADRPA 690	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYIVSRRS5 600 PARVQRFKSL 700
10 SCTEGPLFSS 110 RGGMIPHOS 210 IHGERKEFVC 310 PYVCKLPGCT 410 TDSGVEMTGN 510 LASPFPCSP 610 GCVETPFVA	20 PRSAVKLTKK 120 RGFPTCQLK 220 HWGCCSRELR 320 KRYTDPSSLR 420 AGGSTEDLSS 520 PENCASSLPG 620 GGGQNFDPYL	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD 430 LDEGPCIAGT 530 LDPAQHYLLR 630 PTSVYSPQPP	ASLDLQTVIR 140 REEPLBCDMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440 GLSTLRRLEN 540 ARYASARGGG 640 SITENAAMDA	TSPSSLVAFI 150 SPNSTGIODP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR 550 TFFTAASSLD 550 RGLQEEPEVG	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP 560 RIGGLPMPPW 660 TSMVGSGLNP	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 510 STENTGETVS 520 RSRAEPGYN 670 YMDFPPTDTL	PSLGFPAOMN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPOP 480 RRVGPPVSLE 580 PNAGVTRRAS 680 GYGGPEGAAA	HQKGPSPSFG 190 GCSQEPDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RFSSESSFS 590 DPAQAADRPA 690 EPYGARGPGS	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYIVSRR55 600 PARVQRFKSL 600 PARVQRFKSL LPLGPGPPTN
10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 PYVCKLPGCT 410 TDSGVEMTCM 10 LASPPPPGSP 610 GCVHTPPTVA 710	20 PRSAVKLTKK 120 RGFPTCQLR 220 HWGGCSRELR 320 KRYTDPSSLR 420 AGGSTEDLSS 520 PENGASSLPG 620 GGGQNFDPYLL 720	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD LDEGPCIAGT 530 LMPAQHYLLR 630 PTSVYSPQPP 730	ASLDLQTVIR 140 REEPLEGDMS 240 HMRRHTGEKP 340 AHVTKRIRGD 440 GLSTLRALEN 540 ARYASARGGG 640 SITENAAMDA 740	TSPSSLVAFI 150 SPNSTGIQDP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR 550 RGLQEEPEVG 650 RGLQEEPEVG 750	NSRCTSPGGS 160 260 SYSRLENLKT 360 TVEPKRRREG 460 PIGTRGLKLP 560 RIGGLPMPPW 660 TSMVGSGLNP 760	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 520 RSRAEDPGTN 670 YMDFPPTDTL 770	PSLGFPAQMN 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 RRVGPPVSLE 580 PNAGVTRRAS 680 GYGGPEGAAA 780	HQKGPSPSFG 190 GCSQEFDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RISSESFS 590 DPAQAADRPA 690 EPYGARGPGS 790	VQPCGPHDSA 200 QLVHIINSEH 300 HQNRTHSNEK 400 DHSPAGSAN 500 SAYLVSRE 600 PARVQRFKSL 700 LPLGPGPPTN 800
10 SCTEGPLESS 210 IHGERKEFVC 310 PYVCKLPGCT TDSGVEHTGN LASPFPGSP GCVHTPPTVA 710 GCVHTPPTVA 710 YGPNCCFQQA	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSRELR 320 KRYTDPSSLR 420 PENGASCEDLSS 520 PENGASCEDLSS 520 GGGQNFDPYL GGGQNFDPYL 720 SYPDPTQETW	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHGPD 430 LDEGPCIAGT 530 LDEGPCIAGT 630 PTSVYSPOPP 730 GEFPSHSGLY	ASLDLQTVIR 140 REEPLEGMS 240 HMRRHTGEKP 340 AHVTKRHRGD 440 GLSTLRKLEN 540 ARYASARGGG SITENAAMDA 740 PGPKALGGTY	TSPSSLVAFI 150 SPNSTGIODP 250 HKCTFEGCRK 350 GPLPRAPSIS 450 LRLDQLHQLR 550 RGLQEEPEVG 750 SQCPRLEHYG	NSRCTSPGGS 160 LLGMLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP 560 RIGGLPMPPW 660 TSMVGSGLNP 760 QVQVKFPGGC	YGHLSIGTMS 170 LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 470 SIGHTGTVS 520 RSRAEDPON 70 YMDFPPTDTL 770 PVGSDSTGLA	PSLGFPAQMA 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 PNGVTRRAS 680 GYGGPEGAAA 780 PCLNAHPSEG	HQKGPSPSFG 190 GCSQEPDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RKSSFFGF 590 DPAQAADRPA 690 EPYGARGPGS 790 PPHPQPLFSH	VQPCGPHDSA 200 QLVHHINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYIVSRKSE 600 PARVQRFKSL 700 LPLGPGPPTN 800 YPQPSPPQYL
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10 SCTEGPLFSS 110 RGGMIPHPQS 210 IHGERKEFVC 310 TDSGVENTON TDSGVENTON LASPFPCSP 610 GCUTFPFVA 410 TDSGVENTON 10 GCUTFPFVA 910 VGPNPCPQQA 810 QSGPTYOPP	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGGCSKELR 320 AGGSTEDLSS 520 PENGASLPS 520 PENGASLPS 520 PENGASLPS 520 S20 S20 S20 S20 S20 S20 S20 S20 S20 S	RALSISPLSD 130 SELDMLVGKC 230 PFKAQYMLVV 330 KHVKTVHCPD 430 LDEGPCIAGT 530 LMPAQHYILR 630 PTSVYSPQPP 730 GEFPSHSGLY 830 LDFDSPTHST	ASLDLQTVIR 140 REEPLECCMS 240 HMRRHTGEKP 340 AHVTKRHRGD GLSTLRRLEN 540 GLSTLRRLEN 540 SITENAMDA 740 PGPKALGTY 840 GQLKAQLVCN	TSPSSLVAFI 150 SPNSTGIODP 250 HKCTFEGCRK 350 GPLPRAPSIS LRLDQLHQLR 550 LRLDQLHQLR 550 RGLQEEDEVG 750 SQCPRLEHYG 850 YVQSQQELLW	NSRCTSPGGS 160 LLGHLDGRED 260 SYSRLENLKT 360 TVEPKREREG 460 PIGTRGLKLP 560 RIGGLPMFPW 660 TSMVGSGLNP 760 QVQVKPEQGC 860 EGGGREDAPA	YGHLSIGTMS 170 LEREEKREPE LEREEKREPE 270 HLRSHTGEKP 370 GPIREESRLT 570 870 WADPPTDTL 770 PVGSDSTGLA 870 QEPSYLØPKF	PSLGFPAQMA 180 SVYETDCRWD 280 YMCEHEGCSK 380 VPEGAMKPQP 480 RRVGPPVSLE 580 PNGVTRAS 680 GYGGPEGAAA 780 PCLNAHPSEE 880 LGGSQVSPSR	HQKGPSPSFG 190 GCSQEPDSQE 290 AFSNASDRAK 390 SPGAQSSCSS 490 RFGAGSSCS 590 DPAQAADRPA 690 EPYGARGPGS 790 PPHPQPLFSH 890 AKAPVNTYGP	VQPCGPHDSA 200 QLVHEINSEH 300 HNRTHSNEK 400 SAY VSRRS5 700 LPLGPCPFTN LPLGPCPFTN 800 YPQPSPPQYL 900 GFGPHLPHHK
10 SCTEGPLESS 110 RGGNTPHC9S 210 IHGERKEFVC 410 PYVCKLPGCT 410 TSGVEHTPTN 550 GCVHTPTN GCVHTPTN 40 GCVHTPTN 40 GCVHTPTN 40 GCVHTPTN 40 910 910	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGCCSRELR 320 KRYTDPSSLR 420 AGGSTFDLSS 520 PENGASTPLSS 520 PENGASTPLS 620 GGGQNFDPYL 720 SYPDPTCETW 820 DYLFSERPC 920	RALSISPLS 130 SELDMLVGKC 230 PFKAQYMLVV PFKAQYMLVV 430 LDEGPCIAGT 530 LMPAQHYLLR 630 PTSVYSPQPP 730 GEFPSHSGLY 930	ASLDLQTVIR 140 REEPLECOMS 240 HMRRHTGEKP HMRRHTGEKP 440 GLSTIRRLEN S40 ARVASARGGG 640 SITENAAMDA 740 PGPKALGTY 940	TSPSSLVAPI 150 SPNSTGIODP 250 HRCTFEGCRK HRCTFEGCRK 450 LRLDQLHQLR SR GPLPRAPSIS RGLOEEPEVG 750 SQCPRLEHYG SQCPRLEHYG 950	NSRCTSPGGS 160 LLCMLDGRED 260 SYSRLENLKT 360 TVEPKRRREG 460 PIGTRGLKLP 560 RIGGLPMPPW 660 QVQVKPEQGC QVQVKPEQGC EGGGRDAPA 960	YGHLSIGTMG 170 LEREEKREPE 270 GPIRESRLT GPIRESRLT 470 GPIRESRLT 520 RSRAEPGON 670 YMDFPPTDTL 770 QUESTCIA 970 QEPSTCIA 970	PSLGFPAQMA 180 SVYETDCRWD 280 VPCEHEGCSK WPCEHEGCSK 480 RRVGPPVSLE 580 PNAGVTRRAS 680 GYGGPEGAA 780 PCLNAHPSEG 921 LGGSQFPSR 580	HQKGPSPSrc 190 GCSQEFDSQE 290 AFSNASDRAK 490 SPGAQSSCSS 490 DPAQAADRPA 690 DPAQAADRPA 690 DPAQAADRPA 690 PPHPQPLFSH 990 AKAPVNYYGP 990	VQPCGPHDSA 200 QLVHEINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYTVSRRS5 600 PARVQRFKSL 700 PARVQRFKSL 700 LPLGFGPPTN 800 90 GFGPNLPNHK 1000
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10 SCTEGPLESS 210 HGERKEFVC 310 PVVCKLPGCT 410 TDSGVEHIGN LASPFPGS 510 GCVHTPFTVA 710 GCVHTPFTVA 810 QSGPYTOFPD QSGPYTOFPD 910 SGSYPTPSPC 1010	20 PRSAVKLTKK 120 RGPFPTCQLK 220 HWGCCSRELR 320 AGGSTEDLSS 520 PENCASSPE 620 GGGQNFDPYL 720 SYPDPTQETW 820 DYLPSEPRPC 920 HENFVVGANR 1020	RALSISPLS 130 SELDMLVGKC 230 PFRAQYHLVV PFRAQYHLVV PFRAQYHLVV 430 LDBCPCIAGT 530 LMPAQHYLLR 630 PTSVYSPQPP 730 GEFPSHSGLY 830 LDFDSPTHST 930 ASHRAAAPPR 1030	ASLDLQTVIR 140 REEPLECOMS 240 HNRRHTGEKP 340 AHVTKRIRGD 440 GLSTLRRLEN 540 GLSTLRRLEN 540 SITENAAMDA 740 PGPRALGTY 940 CQLKAQLVCN 1LPPLPTCYG	TSPSSLVAPT 150 SPNSTGTODP 250 GPLPRAPSIS GPLPRAPSIS IRLDQLHQLR 550 CRLQEPEVG 750 SQCPRLEHYG 850 VVQSQQLLW 950 PLKVGCTNPS 1046	NSRCTSPGGS 160 LLCMLDGRED 260 SYSRLENLKT 360 TVEPKRRREG 460 PIGTRGLKLP 560 RIGGLPMPPW 660 QVQVKPEQGC QVQVKPEQGC EGGGRDAPA 960	YGHLSIGTMG 170 LEREEKREPE 270 GPIRESRLT GPIRESRLT 470 GPIRESRLT 520 RSRAEPGON 670 YMDFPPTDTL 770 QUESTCIA 970 QEPSTCIA 970	PSLGFPAQMA 180 SVYETDCRWD 280 VPCEHEGCSK WPCEHEGCSK 480 RRVGPPVSLE 580 PNAGVTRRAS 680 GYGGPEGAA 780 PCLNAHPSEG 921 LGGSQVGPSR 580	HQKGPSPSrc 190 GCSQEFDSQE 290 AFSNASDRAK 490 SPGAQSSCSS 490 DPAQAADRPA 690 DPAQAADRPA 690 DPAQAADRPA 690 PPHPQPLFSH 990 AKAPVNYYGP 990	VQPCGPHDSA 200 QLVHEINSEH 300 HQNRTHSNEK 400 DHSPAGSAAN 500 SAYTVSRRS5 600 PARVQRFKSL 700 PARVQRFKSL 700 LPLGFGPPTN 800 90 GFGPNLPNHK 1000

Figure 7. Phosphorylation status of GLI1 in absence or presence of MEKK1. Aminoacidic sequence of GLI1 showing phosphorylated residues (highlighted in red). Mass spectrometric analysis was performed on 293T cells transfected with plasmid encoding Flag-GLI1 C-terminal region (AA 424-1106), with or without MEKK1. Cell lysates were immunoprecipitated with anti-Flag antibody and analyzed.

whereas only one residue was found phosphorylated in the absence of the kinase (Fig. 7). We also found that a few proteins

co-purified with immunoprecipitated GLI1 + MEKK1, but not with GLI1 alone. Mass spectrometric analysis of these

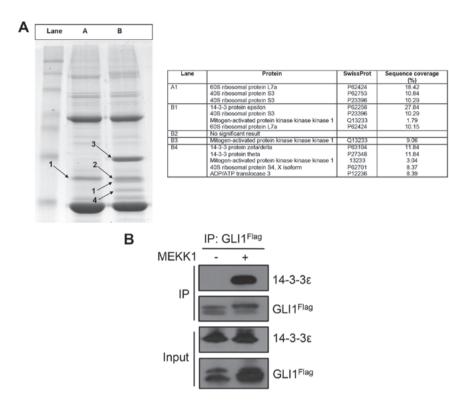


Figure 8. (A) Left panel, Coomassie-blue stained SDS-PAGE gel, showing proteins associated to Flag-GL11(424-1106), in the absence or presence of MEKK1 in 293T cells. Lane A, proteins associated with Flag-GL11(424-1106); lane B, proteins associated with Flag-GL11(424-1106) + MEKK1. Numbered black arrows indicate bands cut out from the gel and processed. Right panel, mass spectrometry results for the selected gel bands. (B) Co-immunoprecipitation assay of Flag-GL11 with endogenous 14-3-3 ϵ proteins in 293T cells, with or without MEKK1. Lysates were immunoprecipitated with anti-Flag antibody and endogenous 14-3-3 ϵ proteins binding is shown.

bands revealed that 14-3-3 $\varepsilon,\zeta/\delta,\tau$ were specifically detected in the GLI1 + MEKK1 lane (Fig. 8A, lane B). These data were further validated by a co-immunoprecipitation experiment that revealed the association between Flag-GLI1 and endogenous 14-3-3 ε (Fig. 8B). Furthermore, we found that MEKK1 also co-purified with immunoprecipitated GLI1 (Fig. 8A, lane B), confirming the previously described binding assay (Fig. 5A).

MEKK1 exerts an inhibitory effect on cultured medulloblastoma cells. To determine the effects of the MEKK1/GLI1 regulation on tumor growth and viability, we performed colony formation and MTT assays. We utilized the Med1-MB cells, a SHH medulloblastoma cell line derived from a tumor originated in a *PTCH1*^{+/-} mouse. The mutation of the *PTCH1* gene in these cells causes an upregulation of the signaling pathway and hence high levels of GLI1, but not of the other GLIs. Thus, selective GLI1 inhibitors prevent the growth of these cells (19,20).

We stably transfected the Med1-MB cells with MEKK1 or control vectors and analyzed cell proliferation and viability. As shown in Fig. 9A and B, the Med1-MB cells expressing MEKK1 exhibited a number of colonies and a percentage of viable cells which were significantly lower than those of the cells transfected with the control vector, indicating that this kinase efficiently counteracted the growth and viability of HH-dependent tumor cells.

We also examined the effect of the MEKK1 agonist, Nocodazole, on medulloblastoma cells and found that this drug significantly decreased the number of viable cells compared to the control (Fig. 9C). Collectively, these data indicate that the activation of MEKK1 exerts significant anticancer effects by inhibiting GLI1 function.

Discussion

HH signaling is found aberrantly activated in a number of tumors and is considered an attractive target for cancer therapy (26). The limited efficacy of the SMO inhibitor, Vismodegib, has prompted efforts to identify novel drugs with the ability to directly target the GLI transcription factors or GLI-regulated pathways.

In this study, we provide evidence that the kinase MEKK1 has the ability to bind and promote GLI1 phosphorylation, resulting in inhibition of its activity. MEKK1 is a member of the MAP3K family, the most upstream components of the mitogen-activated protein kinase (MAPK) phosphorylated modules, consisting of MAPK, MAPK kinase (MKK) and MAPK kinase kinase (MKKK) (27). MKKKs phosphorylate and activate MKKs, which in turn phosphorylate and activate MAPKs. Twenty different MAP3Ks have been characterized and each of these is regulated by various cues, such as growth factors, cytokines, antigens, stress insults, changes in extracellular matrix and cell-cell contacts.

MEKK1 is a 196 kDa protein that activates both the JNK and ERK pathways, although JNK appears to be preferentially regulated. MEKK1 is activated by a variety of stimuli, including growth factors, microtubule disruption, heat shock, hypermolarity and UV irradiation (28). Previous studies

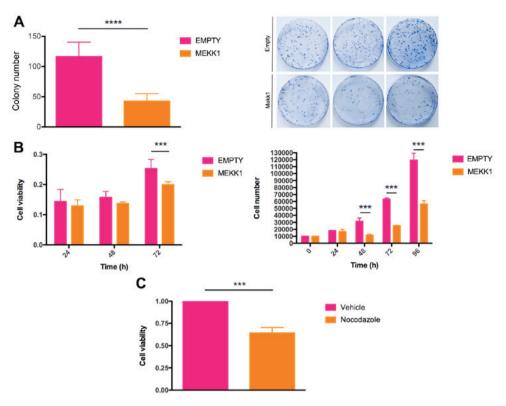


Figure 9. MEKK1 counteracts *in vitro* medulloblastoma cells growth and viability. (A) Colony formation assay on Med1-MB cells stably transfected with expression plasmids encoding MEKK1 or empty vector. Left panel, colonies were quantified with ImageJ software (Version 1.50i), using 4 images per dish. The bar graph represents the average of three biological replicates. Right, representative colony formation assay. (B) Left panel, MTT assay measuring cell proliferation activity of Med1-MB cells expressing MEKK1 or control plasmids at 24 h, 48 h and 72 h in each group. Right panel, growth curve on Med1-MB cells expressing MEKK1 or empty vector. (C) MTT assay on Med1-MB cells treated with Nocodazole (0.1 μ g/ml) for 48 h. Results are expressed as the means ± SD of 3 independent experiments, each performed in triplicate. ***P<0.001 and ****P<0.0001 [calculated by a Student's t-test (A and C) or ANOVA with Tukey's post hoc test (B)].

have documented a crosstalk between the HH and MAPK cascades (29) and its role in various tumors, including cancers of the skin, gastrointestinal, pancreas, liver, breast and brain (30).

It has been demonstrated that a positive synergy exists between the two signaling pathways, mainly mediated by ERK1/2 kinases, which have been shown to induce GLI1 phosphorylation and activation, thus implying that a proper combination of specific pathway inhibitors could be a possible therapeutic options for these type of tumors (28). In contrast to these observations, in this study, we provide evidence that MEKK1, which has the ability to activate both ERK and JNK, inhibits GLI1 function through multiple phosphorylation events, occurring at the C-terminal domain of the transcription factor. Mass spectrometric analysis revealed almost 30 sites in the C-term of GLI1 were phosphorylated in cells expressing MEKK1. Unfortunately, our attempts to identify a phosphorylation-defective mutant failed and we could not mutagenize all the modified residues, due to stability issues and generation of unreliable data. However, we observed that upon MEKK1 phosphorylation, GLI1 associated with 14-3-3 proteins, suggesting that this binding may be responsible, at least in part, for the observed inhibitory effect. In support of this hypothesis, a previous study described an association between GLI and 14-3-3 upon PKA phosphorylation that was associated by transcriptional inhibition (31), although the underlying mechanism was not fully elucidated.

In addition to its kinase activity, it has been observed that MEKK1 may also ubiquitylate some substrates such as c-JUN and promote their degradation (32), suggesting that a proteolytic-mediated effect could also account for the observed GLI1 inhibition. However, the steady state levels of GLI1 do not appear reduced in the presence of this kinase, thus ruling out degradation-dependent mechanisms. Recently it has been described that two other mitogen-activated protein kinase kinase (MAP3Ks), MEKK2 and MEKK3, play a critical role in regulating HH signaling. MEKK2/MEKK3 are conserved for the 55% in the amino-acid sequence and 95% in the kinase domain, both are co-expressed in many cell type and they share substrate specificity (16). MEKK2/3 are activated in response to the FGF signaling and directly phosphorylates GLI1 resulting in the suppression of GLI1 transcriptional activity and the suppression of HH-dependent medulloblastoma tumor cell growth (16). In contrast to these findings, we did not observe an involvement of MEKK1 in the response to FGF stimulation (data not shown), indicating the differential recruitment of these MAP3Ks in response to various cues.

Finally, a relevant finding of this study was the significant antitumor effect of ectopically expressed MEKK1 observed in medulloblastoma cells. This evidence suggests that MEKK1 can be now included among the druggable targets with the ability to turn off HH signaling at a post-receptor level in tumors. The ability of Nocodazole to inhibit HH signaling and to counteract SHH-MB growth supports this hypothesis and opens the door to future studies aimed at analyzing the potential of Nocodazole and other MEKK1 agonists as novel therapeutic options for this type of malignancies.

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Availability of data and materials

All data generated or analyzed during this study are included within the manuscript or are available from the corresponding author on reasonable request.

Authors' contributions

LA and LaDM designed and performed experiments, analyzed the data and edited the manuscript. DD, SM, SMS, FDP, RB, ZNY, MC and MP performed the experiments. AG, MES and JRYIII performed the mass spectrometry experiments and analyzed the data. LuDM, EDS, SCh, CC, EA and MM analyzed the data and edited the manuscript. SCo and GC designed the experiments, analyzed the data and wrote the manuscript. All authors have read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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