Inhibition of Cellular MEK/ERK Signaling Suppresses Murine Papillomavirus Type 1

Replicative Activities and Promotes Tumor Regression

Adrian J. Luna[1,*], Jesse M. Young[1,**], Rosa T. Sterk[1], Virginie Bondu[1], Fred A. Schultz[2],

Donna F. Kusewitt[2,4], Huining Kang[3,4], Michelle A. Ozbun[1,4§]

[1] Department of Molecular Genetics & Microbiology, The University of New Mexico School of Medicine, Albuquerque, NM

87131, USA

[2] Department of Pathology, The University of New Mexico School of Medicine, Albuquerque, NM 87131, USA

[3] Department of Internal Medicine, Division of Epidemiology, Biostatistics and Preventive Medicine, The University of New

Mexico School of Medicine, Albuquerque, NM 87131, USA

[4] The University of New Mexico Comprehensive Cancer Center, Albuquerque, NMo, USA

*Present address: University of Michigan, Ann Arbor, MI

**Present address: TriCore Reference Laboratories, Albuquerque, NM

§ Corresponding Author

Abstract (300 words)

Human papillomaviruses (HPVs) are a significant public health concern due to their widespread

transmission, morbidity, and oncogenic potential. Despite efficacious vaccines, millions of unvaccinated

individuals and those with existing infections will develop HPV-related diseases for the next two decades.

The continuing burden of HPV-related diseases is exacerbated by the lack of effective therapies or cures

for infections, highlighting the need to identify and develop antivirals. The discovery of the mouse

papillomavirus type 1 (MmuPV1) and the development of experimental *in vivo* infection models in

laboratory mice has provided opportunities to study papillomavirus pathogenesis in cutaneous

epithelium, the oral cavity, and the anogenital tract. However, the MmuPV1 infection model has not been

used to evaluate potential antivirals. We previously reported that inhibitors of cellular MEK/ERK signaling

suppress oncogenic HPV early gene expression *in vitro*. In this report, we adapted the MmuPV1 infection

model to determine whether MEK inhibitors have anti-papillomavirus properties *in vivo*. We demonstrate

that oral dosage of the MEK1/2 inhibitor trametinib promotes papilloma regression in immunodeficient

mice that otherwise would have persistent infections. Moreover, our quantitative histological analyses

revealed that inhibition of MEK/ERK signaling reduces E6/E7 mRNAs, MmuPV1 DNA, and L1 protein

expression within the MmuPV1-induced lesions. These data suggest that MEK1/2 signaling is essential

for both early and late MmuPV1 replication events supporting our previous findings with oncogenic HPVs.

We also provide evidence that MEK inhibitors protect from the development of secondary tumors. Thus,

our data suggest that MEK inhibitors have potent anti-tumor properties in a preclinical mouse model and

merit further investigation as papillomavirus antiviral therapies.

Introduction

Human papillomavirus (HPV) infections are highly prevalent and cause a variety of epithelial neoplasms (i.e., tumors) ranging in severity from benign cutaneous warts to intraepithelial neoplasia to cancers [1]. Over 200 HPV genotypes have been identified and sequenced [2] with low-risk mucosotropic HPVs causing 90% of anogenital warts and all laryngeal papillomas and high-risk HPV infections etiologically linked to anogenital and oropharyngeal cancers [3]. Despite effective prophylactic vaccines, millions of unvaccinated people and those with existing infections are projected to develop HPV-related diseases for the next two decades [4]. Current HPV treatments involve lesion excision or ablation, cryotherapy, chemotherapy, and radiation, each risking long-term morbidities with reduced quality of life [5-8]. Additionally, recurrence rates can be >50% [9, 10]. To date, there are no effective antiviral HPV therapies and no cure for HPV infections.

Like all PVs, HPVs are highly host specific and cannot be productively transmitted to animals. Although this has inhibited detailed studies of HPV pathogenesis and immunology, experimental infections using a variety of vertebrate animal PVs have provided valuable models for understanding viral gene functions, tissue tropism, regression and persistence, cancer progression, vaccine efficacy, and potential therapeutic agents [11].   Despite differences in epithelial tropisms and disease manifestations, mammalian PVs have similar genome organization, protein functions, and reliance on epithelial differentiation for productive replication [1]. The murine PV type 1 (MmuPV1) mouse model is a major advancement in preclinical models of PV-induced infection and disease [12]. However, to our knowledge, this model has not been used to evaluate antiviral agents.

In all mammalian PVs tumorigenesis is primarily driven by the E6 and E7 proteins [13, 14]. Although E6 and E7 from different PV genera interact with different cellular targets, E6 and E7 expression reprograms cells in the para- and supra-basal layers to maintain cell cycle progression and proliferative capacity [13, 15, 16]. This promotes a cellular environment where viral genomes are amplified for packaging by the capsid proteins into new virions [15]. As E6 and E7 proteins are the key factors for PV persistence and

oncogenesis, they are ideal therapeutic targets [17, 18]. Genetic knockdown of oncogenic HPV E6 and

E7 expression restores cell cycle checkpoint (e.g., p53 and pRb) functions, inhibits cell proliferation, and

leads to cellular apoptosis and/or senescence [19-27]. Yet, genetic approaches have not been robustly

adaptable to human clinical studies. A handful of small molecules have been investigated for their

abilities to inhibit PV protein activities [28], but none so far show promise *in vivo*.

We recently reported that cellular MEK/ERK signaling is a key modulator of high-risk HPV E6/E7

transcription [29]. The RAS-RAF-MEK-ERK signaling pathway is evolutionarily conserved, has been

extensively investigated in mammalian cells, and is the best understood signaling cascade in tumor cell

biology [30]. MEK signaling is tightly controlled in normal epithelium where proliferative signals from

growth factor receptors are restricted to promote epithelial homeostasis, including cellular contact

inhibition and differentiation [31-34]. Thus, MEK signaling is normally limited to the lower epithelial cell

layers. MEK signaling is effected by the MEK1 and MEK2 isoforms, which are structurally similar and

share activation mechanisms. Upon activation by RAF, they function as dual-specificity tyrosine and

serine/threonine kinases, phosphorylating their only known *in vivo* substrates ERK1 and ERK2 on specific

tyrosine and threonine residues [35]. MEK1 and MEK2 exhibit extensive functional redundancy and form

functional homo- or hetero-dimers *in vivo* [36]. However, increasing evidence suggests that MEK1 and

MEK2 have distinct activities that may be controlled by specific modulation of their activity levels [37, 38],

differential binding to cellular proteins [39-43] and disparate outcomes when the genes are knocked out

in mice [36, 44, 45]. Despite an incomplete understanding of the distinct functions of MEK1 and MEK2,

particularly in the epithelium, MEK/ERK activation has long been recognized to play a key role in cell

proliferative diseases and neoplastic progression. For example, p-ERK1/2 levels are increased in the

upper epithelial layers in several proliferative skin diseases, including HPV-driven cervical neoplasia [46].

We found, in a cohort of 580 biopsies from normal cervix, low-, and high-grade cervical intraepithelial

neoplasia, a significant correlation (p<0.001, X^2=212.7) between increasing levels of p-ERK and E7

protein activity during disease progression [29]. Mechanistically, using high-risk HPV-infected 3D

organotypic (raft) epithelial tissues and monolayer cultures, we showed that MEK-induced

phosphorylation of ERK1/2 robustly governs HPV E6/E7 mRNA transcription. Importantly, we demonstrated that small molecule inhibitors of MEK and ERK potently inhibit HPV E6/E7 transcription, at least in part by blocking the activation of AP-1 transcription factors [29] whose binding sites are conserved in the long control region (LCR) enhancer/promoter of all PV genomes [47].

The combined conservation of PV genome structure, epithelial differentiation-dependent PV gene regulation, and MEK/ERK signaling in mammalian epithelium prompted us to hypothesize that inhibitors of MEK signaling would suppress E6/E7 gene transcription and tumor growth in the preclinical MmuPV1-induced tumor model that recapitulates key aspects of HPV-induced tumorigenesis [12]. We investigated two FDA- and European Medicines Agency-approved MEK inhibitors, trametinib and cobimetinib [48]. Both drugs have similar *in vitro* inhibitory concentration 50 (IC_{50}) efficacies for preventing activation of MEK1 (0.7 nM and 0.95 nM, respectively) and trametinib is equivalently inhibitory of the MEK2 isoform (IC_{50} = 0.9 nM). However, cobimetinib is ≈200-fold less potent against MEK2 (IC_{50} = 199 nM) [48]. After inducing tumors on the tails of Hsd:Athymic-*FoxN1^{nu}* mice that lack T cells, mice were treated orally with drug dosages based on previous studies [48]. Both drugs effectively inhibited tumor growth, but trametinib led to significant tumor regression beginning about 1 week post treatment initiation. Furthermore, the MEK inhibitors prevented overt lesion formation at secondary sites, suggesting diminished MmuPV1 transmission. Both drugs display mechanisms of action consistent with reduced viral gene expression and genome replication and suppressed cellular proliferation as expected from our prior *in vitro* study [29]. Our results show that both MEK1 and MEK2 are important for PV tumorigenesis, and that further investigations of MEK1/2 inhibitors are warranted for the treatment of PV-induced diseases in humans and animals.

Methods

MmuPV1 infections, tumor growth and treatments. All animal work was approved by the University of New Mexico's IACUC (protocol # 20-201020-HSC). Female Hsd:Athymic Nude-*Foxn1^{nu}* outbred mice (Envigo) 6-8 weeks of age were inoculated with MmuPV1 virions (a kind gift from Prof. Paul Lambert, Univ. of Wisconsin-Madison). Specifically, the mice were anesthetized and maintained in anesthesia using 3% isoflurane in O_2. Prior to inoculation, the tail of each mouse was scarified using a 27.5-gauge needle. To standardize infection area and papilloma growth the scarification was initiated 0.5-cm distal to the tail base and continuing for 1-cm toward the tip. Each mouse tail was superficially scarified by scratching over the epithelial surface 20-30 times as described [49]. Scarification and viral inoculations were carried out in a biosafety cabinet. MmuPV1 virions (2×10^8 viral genome equivalents [VGE] in 2 µl) were applied across the entirety of each wound site using a siliconized pipette tip. The MmuPV1 inocula were allowed to penetrate the wound before returning mice to microisolator (biocontainment) cages. Mice were monitored weekly for weight and the appearance of warts. Tumor volumes were determined with digital calipers (Bel-Art Products) using the formula (length*width*height): length was measured from the sagittal plane, width from the transverse plane, and height was measured from the base to the highest peak. When mice had developed papillomas with a volume of ≥ 17 mm^3, the animals were stratified by papilloma size and assigned into five groups with similar average tumor volumes (≈ 40 mm^3). Trametinib (Selleckchem) and Cobimetinib (Selleckchem) in vehicle mixture (30% PEG-300 + 5% DMSO + 5% Tween-80 in dH$_2$O) were administered by oral gavage and tumor dimensions and body weights were recorded every 48 h. Efficacy was measured as percent tumor growth inhibition (TGI) relative to the vehicle-treated group. TGI was calculated by the equation [1-(*T/C*) x 100], where *T* and *C* represent the mean tumor volumes on day 30 in the MEK inhibitor-treated (T) and vehicle control (C) groups, respectively. A TGI of >50% is considered to be efficacious. On day 30, mice were euthanized by CO_2 exposure and whole tail sections receiving the MmuPV1 inoculation were excised to include ≈ 0.5 cm of uninfected length on each side of the wart growth. Tail sections were fixed in 4% paraformaldehyde (PFA) in PBS overnight at 4°C. Thereafter, each tail section was rinsed twice with sterile PBS and incubated

with Versenate decalcifying reagent (StatLab) at 4°C until the tail bone became pliable. Tail sections

were rinsed with sterile PBS and stored in 70% ethanol at 4°C until paraffin-embedding. Muzzle

papillomas were excised and stored in 4% PFA in PBS overnight before washing twice with PBS and

storing in 70% ethanol until paraffin-embedding.

MmuPV1 infections *in vitro*. HaCaT cells were seeded at 10^4 cells per plate in DMEM with 10% fetal

calf serum and allowed to adhere overnight at 37°C in 5% CO_2. Cells were pretreated for 1h with medium

containing vehicle (0.1% DMSO) or 1.0 to 100 nM trametinib prior to and during MmuPV1 exposure at

1000 VGE per cell. Infections proceeded for 48h before harvesting for total DNase I-treated RNA.

Following reverse transcription (RT), qPCR was performed using primers to amplify spliced MmuPV1

E1^E4 cDNA and normalized to ribosomal protein 18s mRNA levels as previously described [29, 49, 50].

Tissue Staining and Immunohistochemistry (IHC). FFPE tail sections and muzzle specimens 4-5 μm

in thickness were baked at 60°C for 1 h. The Ventana Discovery platform was used for deparaffinization,

rehydration and H & E staining or blocking of endogenous peroxidases for IHC. Antigens were unmasked

by boiling in RiboCC buffer (Ventana 760-107; for keratin 10 and myeloperoxidase) for 32 min at 100°C.

Antibodies to cytokeratin 10 (abcam ab76318; 1:250), cytokeratin 5 (abcam ab52635; 1:400), and

myeloperoxidase (abcam ab208670; 1:1000) were individually diluted in Discovery PSS Diluent (Ventana

760-212), hand applied, and incubated for 16-32 min at 36°C. Antibody incubation was followed by anti-

Rb HQ (Ventana 760-4815), anti-HQ HRP (Ventana 760-4820), and DAB CM (Ventana 760-4304)

detection. Iimmunohistochemical detection of p-ERK1/2 (Cell Signaling #4370; 1:500) required the

tyramide signal amplification (TSA) biotin system following the manufacturer's protocol (AKOYA

Biosciences #NEL 700A001KT). Slides were counterstained with hematoxylin (Ventana 760-2021) and

Bluing solution (Ventana 760-2037) or with Gill No.1 Hematoxylin solution (Sigma-Aldrich #GHS132-1L)

followed by acid alcohol and lithium carbonate rinse. Following dehydration, coverslips were mounted

using Permount (Fisher Scientific SP15-500). Stained slides were scanned at 20X using the Leica Versa

200 digital slide scanner (Leica Biosystems, Buffalo Grove, IL).

DNA and RNA *in situ* hybridization (ISH). FFPE tail sections were stained according to the

RNAscope manufacturer's protocol (2.5 HD Detection Kit-Red, Advanced Cell Diagnostics [ACD]) using

probes to detect MmuPV1 E6/E7 RNA (ACD). DNA ISH employed probes to the noncoding MmuPV1

LCR Probe (ACD) using the chromogenic DNAscope HD Kit. Slides were counterstained with 50%

Gill's hematoxylin solution number 1 (G Biosciences), mounted using EcoMount (BioCare Medical), and

digitally imaged as above.

Immunofluorescence. FFPE tail sections were deparaffinized, rehydrated, and subjected to heat-

induced antigen retrieval for 30 min using pH 9 target retrieval solution (Dako). Endogenous

peroxidases were blocked with 3% hydrogen peroxide in methanol for 10 min. Tissues were blocked

with 5% goat serum in PBS containing 0.1% Tween-20 (PBS-T) for 1 h at room temperature, then

incubated at 4°C overnight with rabbit sera against MmuPV1 L1 (a kind gift form Chris Buck, NIH;

1:2500) and chicken anti-keratin 14 (BioLegend 905301; 1:500) diluted in 5% goat serum in PBS-T.

The sections were then washed three times in PBS-T followed by incubation with secondary antibodies

(1:500) AF488 goat anti-rabbit IgG (ThermoFisher A32731) and AF647 goat anti-chicken IgG

(ThermoFisher A32933) for 1 h at room temperature. Coverslips were mounted using ProLong

Diamond Antifade DAPI Mountant (Thermo Fisher). Images were acquired using a Leica TCS SP8

confocal microscope with fixed data acquisition settings. L1-positive foci were counted using Huygens

essential software object analysis tool (Scientific Volume Imaging, The Netherlands, http://svi.nl).

Morphometric Tissue Analysis. Tissue morphometry was performed on digitally acquired images from all tumors using HALO software (Indica, Albuquerque, NM), under the supervision of a board-certified veterinary pathologist (Kusewitt). The thickness of the epithelium within each lesion was determined using H&E sections. The linear length of the lesion was measured, and HALO was trained to recognize all epithelial elements lying above the dermis, then the area of epithelium within the lesion was determined. The epithelium within each region was selected using the bucket tool; the selection was refined using the line and scissors tools to include all nucleated cells and to eliminate artifacts. Within the identified epithelium, stroma was identified and eliminated from consideration. Epithelial thickness was expressed as the ratio of epithelial area to lesion length (mm). Using the CytoNuclear algorithm, individual epithelial cells were identified and cytoplasmic staining for each marker was categorized as negative, low, medium, or high. The total number of cells examined was enumerated and the percentage of epithelial cells staining at each intensity was determined (e.g., *SI Appendix* Fig. S3A-C). As the ISH staining lacked sufficient nuclear demacation, total areas positive for ISH signals were determined. Neutrophil infiltration was quantified by selecting all lesional epithelium and underlying dermis by hand. The percentage of that area occupied by myeloperoxidase-positive neutrophils was determined using HALO software to identify and quantify the area of positive staining. IHC stained slides were excluded from analysis (no more than one per treatment group) if they lacked clear evidence of tail features that ensured the tumor was adequately represented.

Statistical Analyses. Morphometry analyses included data from 5-6 tumors per group subjected to one-way analysis of variance (ANOVA) with Tukey's multiple comparison test. RT-qPCR data were analyzed by one-way ANOVA with Dunnett's multiple comparisons test. Biomarker level correlation coefficients (r) were calculated from morphometry data using Pearson's correlation analysis and computing a two-tailed p value. Tumor measurements among the five treatment groups were analyzed at each time point using the generalized least square (GLS) method to account for the unequal variances among the groups (*SI Appendix* Table 1). Differences among tumor groups at 30 days post

treatment were evaluated by ANOVA with the Tukey HSD (honest significant difference) pairwise

comparisons (*SI Appendix* Table 2). The rates of tumor volume changes were estimated and

compared using the linear mixed-effects model (LMM) analysis (*SI Appendix* Tables 3 and 4).

Results

MEK Inhibitors Suppress MmuPV1-Induced Tumor Growth and Reduce Papillomatous

Morphology. After MmuPV1 inoculation and 6 weeks of papilloma growth, mice were randomized into

treatment groups; the average tumor volume of each group was ≈40 mm^3 (Fig. 1A) with no significant

size differences among the groups (*SI Appendix* Table 1). Mice were orally administered either vehicle,

the MEK1 inhibitor cobimetinib (7.5 mg/kg or 15 mg/kg), or the MEK1/2 inhibitor trametinib (1.0 mg/kg or

2.0 mg/kg) every 2 days. As visualized in Fig. 1B, C and detailed in *SI Appendix* Table 1, tumor volumes

significantly differed among the five groups after 8 days of treatment (p=0.042) and the difference became

increasingly pronounced as time passed. Over the 30-day treatment period, tumors of vehicle-treated

mice increased in size by an average of 2.59-fold, resulting in a final average tumor volume of 101.7

mm^3. Comparatively, mice treated with 7.5 mg/kg or 15 mg/kg of cobimetinib demonstrated significantly

impaired papilloma growth resulting in final average tumor volumes of 42.4 mm^3 (58% TGI) and 45.4 mm^3

(55% TGI), respectively. More strikingly, trametinib treatment resulted in papilloma regression over the

same period, reducing tumor volumes to an average of 25.0 mm^3 for 1 mg/kg trametinib and 25.2 mm^3

for 2 mg/kg trametinib (both 75% TGI). Pairwise comparisons revealed significant differences between

vehicle-treated and each of the drug treatment groups (adjusted p-value <0.05), but no significant

differences when comparing each of the four groups that received the MEK inhibitors (*SI Appendix* Table

2). Similarly, the rates of tumor volume change (mm^3/day) among the treatment groups estimated by

linear mixed-effects model analysis showed that the vehicle-treatment group significantly increased over

time while the trametinib-treated groups significantly decreased, and the cobimetinib-treated groups did

not have a significant change (*SI Appendix* Table 3). Furthermore, trametinib demonstrated significant

superiority over cobimetinib in promoting tumor regression as demonstrated by comparing the rates of

tumor volume change among the MEK inhibitor treated groups (p-value = 0.0334; *SI Appendix* Table 4).

The visual characteristics of the tail papillomas on mice treated with MEK inhibitors were distinct

compared to papillomas on vehicle-treated mice (Fig. 1D; *SI Appendix* Fig. S1). Specifically, vehicle-

treated mice bore florid and irregular papillomas. Whereas mice treated with both cobimetinib doses

exhibited smaller tumors with less florid appearance, mice treated with both trametinib doses generally

displayed more flattened and smoother papillomas (Fig. 1D; *SI Appendix* Fig. S1). Note that only one

animal, in the high dose trametinib treatment group, showed significant weight loss suggesting toxicity

(*SI Appendix* Fig. S1F-H). These data indicate that MEK inhibitors have profound TGI effects *in vivo* using

the MmuPV1 preclinical model; compared to the MEK1 inhibitor cobimetinib, the MEK1/2 inhibitor

trametinib, demonstrated superior TGI.

MEK Inhibitor Effects on Tissue Morphology and Cellular Biomarkers. Serial sagittally-sectioned

tails were analyzed histologically after H&E staining, focusing on the mice treated with vehicle and those

treated with the higher doses of the two MEK inhibitors (Fig. 2A; *SI Appendix* Fig. S2). Papillomas from

vehicle-treated mice showed extensive fibrillary projections throughout the tumor cross-sections. In drug-

treated mice, particularly those treated with the MEK1/2 inhibitor, the extent of papillary projections was

considerably reduced (Fig. 2A). Consistent with this observation, morphometric analyses of all tumors

revealed significantly reduced epithelial thickness in the papillomas from mice treated with the MEK

inhibitors compared to vehicle-treated mice (Fig. 2B). Tumor sections from all three groups revealed

dysplastic epithelium and hyperkeratosis, albeit with noticeable differences depending upon the

treatment (*SI Appendix* Fig. S2). Koilocytes, epithelial cells characterized by perinuclear haloes

(cytoplasmic vacuolation) surrounding condensed nuclei, are pathognomonic of HPV infections [51] and

were scattered irregularly throughout the differentiating epithelium in all MmuPV1 lesions.

The MEK inhibitors suppressed the levels of phosphorylated-ERK1/2 (p-ERK1/2), the only recognized

signaling effector of MEK, in the tumors (Fig. 2C-D); moreover, p-ERK1/2 levels correlated significantly

with tumoral epithelial lesion thickness (p=0.00185; *SI Appendix* Fig. S5A). p-ERK1/2 was most

prominent in the papillomas of vehicle-treated mice, localizing primarily to basal and lower suprabasal

layers of all papillomas. These data indicate that the systemically delivered MEK inhibitors reached the

tail epithelium to suppress MEK/ERK signaling. Further, the findings suggest that MEK signaling is an

important contributor to papilloma growth and maintenance in the MmuPV1 mouse model.

As MEK/ERK signaling is integral to epithelial proliferation and differentiation [52], we evaluated the

papillomas for differentiation-associated epithelial markers, keratin 5 (K5) and keratin 10 (K10). K5 pairs

with K14 and these proteins are characteristic of mitotically active, undifferentiated basal cells of the

epithelium; their expression is downregulated as cells begin to differentiate [53]. In contrast, K10 is an

established early marker of keratinocytes entering terminal differentiation [54]. As expected, strong K5

staining was prominent in the cells nearest the basement membranes of all tumors. The vehicle-treated

mice displayed an expansive network of undifferentiated cells throughout the thickness of the fibrillary

papillomas (Fig. 2E; *SI Appendix* Fig. S3A-D), as previously reported for MmuPV1 tail lesions [16].

However, MEK inhibitors counteracted basal cell expansion and the number of K5-positive cells was

reduced (Fig. 2F) and correlated significantly with both p-ERK1/2 levels (p=0.0249) and lesion thickness

(p=0.000569; *SI Appendix* Fig. S5B-C, respectively). Likewise, the number of differentiating K10-positive

cells was significantly lower in the smaller papillomatous lesions of the drug-treated mice compared to

those in vehicle-treated mice (Fig. 2G-H). Interestingly, there were no significant differences amongst the

treatment groups in the percentages of lesional cells that expressed p-ERK1/2, K5, or K10 (*SI Appendix*

Fig. S3E-G). These findings indicate that while MEK inhibition and suppressed p-ERK1/2 signaling

reduced the number of proliferative cells, there were no net changes in the overall proportion of cells

proliferating or differentiating within the papillomas.

Infection with MmuPV1 or oncogenic HPVs leads to increased expression of Ki67, a basal cell

proliferation marker [55-58] and Sundberg et al. showed similar staining patterns between Ki67 and K5

in MmuPV1-induced tail tumors [55]. Furthermore, MEK inhibition is known to reduce Ki67 staining in

epithelial tumors [59, 60]. Although we attempted to detect Ki67 by IHC in the tumor sections, we were

unable to obtain robust and quantifiable Ki67 staining (data not shown). This is likely because tissue

decalcification has been found to impair the detection of nuclear biomarkers [61].

MEK Inhibitor-Induced Papilloma Regression does not Involve T Cells or Neutrophils. Whereas

various data indicate that CD4+ and CD8+ T cells play a major role in papillomavirus-induced lesion

regression [55, 62-65], there also are indications that neutrophils might contribute to MmuPV1 disease

control in immunocompetent models [66]. As the Hsd:Athymic-$FoxN1^{nu}$ mice used in this investigation

lack CD4+ and CD8+ T cells but have an intact innate immune system, we investigated if MEK inhibition

resulted in increased neutrophil infiltration in the MmuPV1-induced papillomas. Quantification of tumor-

proximal myeloperoxidase staining revealed no significant differences in neutrophil infiltration amongst

treated and control papillomas (Fig. 3A-B). Thus, the data suggest that MEK inhibitors suppressed tumor

growth and trametinib caused regression *via* a mechanism independent of T cells and neutrophils.

The MmuPV1 Vegetative Replication Cycle is Dependent on MEK Signaling. Our recent publication

demonstrated that HPV early gene expression relies on MEK/ERK signaling and that MEK1/2 inhibition

results in reduced viral early gene transcription and protein expression [29]. As robust PV genome

amplification leading to late gene expression depends on sufficient PV early gene expression [67], we

determined the effect of MEK inhibition on key aspects of the complete MmuPV1 replicative cycle. We

first strove to quantify the tumor levels of E6/E7 oncogene mRNA, which should be present predominantly

in the cytoplasm of infected epithelium (Fig. 3C). Despite various DNase treatment methods to remove

viral genomes, the E6/E7 probes consistently bound to nuclear targets, particularly evident in the vehicle-

only tumors (*SI Appendix* Fig. S4A). Thus, the data in Fig. 3C-D likely represent detection of MmuPV1

genomes and E6/E7 mRNAs; yet the morphometric analyses demonstrate the MEK inhibitors significantly

reduced the levels of MmuPV1 nucleic acids in the tumors. Consistent with this interpretation, the ISH

probe specific to the MmuPV1 noncoding long control region (LCR), revealed ISH staining patterns with

obvious overlap in serial sections (Fig. 3, compare panels C and E; *SI Appendix* Fig. S4). Morphometric

quantification of ISH data showed overall lower levels of LCR-targeted viral genomes compared to the

E6/E7 ISH results in each treatment group (Fig. 3F and D, respectively). There was a highly significant

correlation between E6/E7 ISH and LCR ISH (p<0.00001; *SI Appendix* Fig. S5J). Furthermore, both

RNA ISH and DNA ISH levels correlated strongly with p-ERK1/2 levels (p<0.001; *SI Appendix* Fig. S5E-

F). Together, the data indicate significantly decreased viral genome levels and imply reduced E6/E7

mRNAs in tumors from mice receiving the MEK inhibitors. Lastly, IF detection of MmuPV1 major capsid

protein L1 along with K14 staining of undifferentiated basal cells in the tumor sections revealed

significantly fewer L1-positive foci in the differentiating layers of tumors of the cobimetinib and trametinib

treatment groups (Fig. 3G,H). Additionally, viral LCR and E6/E7 ISH correlated strongly with detected L1-

foci (p<0.0015 and p<.000001; *SI Appendix* Fig. S5L-M). These data strongly support the idea that the

MEK inhibitors suppressed the MmuPV1 replicative cycle *in vivo*.

MEK Inhibitor Treatment Reduces MmuPV1 Transmission *in vivo*. Over the treatment course, we

observed that all (6/6) vehicle-treated mice developed papillomas on their muzzles (Fig. 4A; Table 1). In

contrast, the only mouse from the MEK inhibitor treatment cohorts to develop a visible facial wart (1/24)

was in the group receiving the lower dose (7.5 mg/kg) of cobimetinib (Table 1). This mouse was co-

housed with other animals receiving cobimetinib (i.e., it was not co-housed with vehicle-treated mice).

H&E staining and E6/E7 ISH confirmed that the facial lesions arose from MmuPV1 infections (Figure 4B).

As the snouts were not experimentally scarified or infected, the secondary muzzle-arising infections were

likely transmitted from tail grooming. The most obvious explanation for lack of secondary muzzle

infections in MEK inhibitor-treated mice is that their tail papillomas produced fewer virions due to

suppressed viral replication as shown in Fig. 3C-H. We reported that MEK/ERK signaling stimulates HPV

early gene expression *via* activation of cellular fos/jun family transcription factors [29], which bind to AP-

1 factor binding sites that are highly conserved in papillomavirus LCRs [68]. Thus, it is also possible that

MEK inhibition would result in lower viral early gene transcription after infection-mediated delivery of viral

genomes to the cell nucleus. To test this prospect, we exposed HaCaT keratinocytes to MmuPV1 virions

in the presence of increasing doses of trametinib. Indeed, MEK inhibition resulted in significantly

decreased levels of spliced MmuPV1 E1^E4 mRNAs compared to vehicle treated cells (Fig. 4C).

Combined, our data suggest that MEK inhibition is likely to impede new MmuPV1 infections by both

reducing virion shedding from existing lesions and by suppressing early viral transcription during infection

establishment at new sites.

Discussion

Herein we demonstrate the potent antiviral and tumor suppressive properties of MEK1/2 inhibitors in a

preclinical model of HPV disease. To our knowledge, this is the first report to assess antiviral candidates

in the MmuPV1 preclinical model. This work confirms and extends our recent study showing that

inhibiting MEK/ERK signaling has antiviral effects, specifically reducing early gene transcription and

oncoprotein functions, against oncogenic HPVs in three dimensional organotypic epithelial tissue cultures

[29]. The conservation of MEK/ERK signaling in mammalian epithelium coupled with the conservation of

MEK/ERK activated AP-1 transcription factor binding sites in the LCRs of animal PVs indicates that this

pathway is both critical for controlling PV early gene transcription and a prime target for PV antivirals.

Thus, our work suggests that targeting this pathway will have antiviral effects for all mammalian PV

infections. Importantly, in our prior work and in this study, the antiviral and tumor suppressive effects of

MEK inhibitors on PV infections occurred in the absence of T cells, which has critical implications for

treating PV infections in individuals lacking functional T cells.

A major strength of this study is the use of pathologist-guided, quantitative tumor tissue analyses of tumor thickness and a battery of biomarkers relevant to PV-induced tumorigenesis. Coupled to robust statistical analyses, our objective quantification of biomarkers revealed clearly that MEK inhibitors accessed the epithelium to suppress p-ERK1/2 levels, basal cell expansion, and tumor thickness without affecting overall epithelial differentiation. Whereas it is most likely that MEK inhibition suppressed tumor growth *via* both blunting ERK-mediated cellular proliferative signals and reducing MmuPV1 early gene transcription leading to cell proliferation, the precise contribution of each of these interdependent activities to the overall decreased tumor growth will be challenging to dissect. To our knowledge this is the first study to use quantitative histological analyses of PV-induced pathology.

The MmuPV1 tumor growth inhibitory effect of the MEK1/2 inhibitor, trametinib, was superior to that of cobimetinib, which preferentially targets the MEK1 isoform. Despite the functional redundance of MEK1 and MEK2 in many assays [36], our understanding of their distinct activities and differential regulation is expanding. For example, MEK1 contains a site (Thr292) for ERK-mediated feedback phosphorylation; MEK2 lacks this site [37, 38]. Additionally, several scaffold proteins specifically bind to and enhance the activation of MEK1, but not MEK2 [39-42]. MEK1 knockout in mice is embryonic lethal [36, 44], whereas MEK2 knockout animals are viable, fertile, and phenotypically normal [45]. MEK2, but not MEK1, phosphorylates the tumor suppressor GCIP (Grap2- and cyclin D1-interacting protein), promotes its degradation, and decreases its tumor suppressor function [43]. Our work suggests that inhibition of both MEK1 and MEK2 is crucial for controlling PV disease. However, MEK2 has distinct functions important for MmuPV1 tumor growththat will require futher dissection. .

The tumor suppressive properties of MEK1/2 inhibition by trametinib became evident only four days post treatment, when the mean tumor volumes in the drug-treated groups were smaller than the group's mean starting tumor volumes (Fig. 1C, *SI Table 1*). While the tumors in the trametinib-treated groups continued to decrease in size over the next two weeks, the growth reduction seemed to plateau thereafter. This raises the question as to whether continued trametinib treatment would eventually cure the infections, or whether the drug had reached its maximum effects. It seems likely that ceasing treatment with the drugs

prior to complete MmuPV1 clearance would result in regrowth of the tumors, but this has yet to be tested

and it would also be useful to do so in the context of functional T cells.

The mechanisms by which the MEK inhibitors exerted their effects in this MmuPV1 infection and

tumorigenesis model are consistent, in part, with those observed in other non-PV-related cancer models.

In a variety of cancer cell types *in vitro*, trametinib and cobimetinib have been shown to reduce p-ERK1/2,

modulate cyclin D1 and p27 levels in a manner aligned with a G1/S cell cycle arrest, and induce caspase-

dependent apoptosis [60, 69, 70]. Unfortunately, a limitation of our study wss the inability to detect

nuclear antigens in the lesions due to Versenate treatment of the tails before fixation. Because Sundberg

et al. showed similar staining patterns between Ki67 and K5 in MmuPV1-induced tail tumors [55], and we

found a significant correlation between p-ERK1/2 levels and strong K5 staining (p=0.025; Fig. S5B), we

infer that MEK inhibitors suppressed cellular proliferation. Additionally, the highly significant correlations

between p-ERK1/2 levels and MmuPV1 E6/E7 mRNA (p= 6.85e-5) and between strong K5 staining and

MmuPV1 E6/E7 mRNA (p= 9.995e-5) highlight the interdependency of the biomarkers p-ERK1/2, K5 and

MmuPV1 E6/E7 mRNA transcription (Fig. S5B, E, I). Future studies evaluating markers of proliferation,

apoptosis, and senescence will be needed to clearly delineate the antiproliferative effect of MEK inhibition

in mammalian PV tumors.

In our previous study and in this work, the antiviral and tumor suppressive effects of MEK inhibition

occurred in the absence of T cells [29]. This has important clinical implications for treating PV diseases

in those who are immunocompromised [71]. For example, people living with AIDS have increased HPV

acquisition, prevalence, persistence, high tumor burdens, and cancer progression [72] and would greatly

benefit from effective HPV antiviral treatments. Herein, neither T cells nor neutrophils were implicated

tumor regression despite reports that immune mediated cell death is an important characteristic of tumor

reduction (reviewed in [73]). Whether immune cell populations are involved in the MEK-inhibitor induced

regression of PV neoplasia will require further investigation. Importantly, use of MEK1/2 inhibitors as a

therapeutic for PV diseases must be tested in the context of functional T cells as MEK signaling is induced

by T cell receptor signaling [74]. While this could be a disadvantage to tumor clearance, recent evidence

indicates that MEK inhibitors can lead to a shift from a Th2 to a Th1 response [75], a reduction of

regulatory T cells (Tregs) [76], and reprogramming of CD8+ T cells into memory stem cells with antitumor

activities [77]. Lastly, we provide strong evidence that MEK inhibitors reduced productive MmuPV1

infection measured by both the reduced levels of the viral capsid protein, L1 in tumors, and the lack of

secondary muzzle infections observed in the MEK inhibitor-treated mice. In total, our work suggests that

MEK1/2 inhibitors warrant further investigation for treatment of mammalian PV infections *in vivo*; such an

approach might also reduce PV transmission to new susceptible epithelial sites or between individuals.

Acknowledgements

This study was supported by the American Cancer Society Mission Boost Grant MBG-18-207-01-COUN

(M.A.O.); and the US National Institutes of Health Grants: R21DE028652 (M.A.O.); T32AI07538,

F31CA232536, UNMCCC Matching Support (A.J.L.); P30CA118100 (M.A.O.). We acknowledge support

by the following University of New Mexico Comprehensive Cancer Center shared resources (NCI

2P30CA118100): Human Tissue Repository and Tissue Analysis, Animal Models, Biostatistics.

We are grateful to Dr. Paul Lambert and members of his lab for generously providing infectious stocks of

MmuPV1, to Dr. Nagayasu Egawa for sharing his protocols for mouse tail scarification and infection, and

Dr. Christopher Buck for sharing his rabbit sera against MmuPV1 L1.

Figure 1. MEK inhibition impairs MmuPV1-induced papilloma growth. (A) Immediately after epithelial tail
scarification, female Hsd:Athymic Nude-*Foxn1^{nu}* mice were exposed to 2×10^8 vge of MmuPV1. Papillomas were
allowed to grow for 6 weeks before assigning the animals into vehicle or treatment groups with similar average
tumor volumes (n=6 animals per group). Mice were treated by oral gavage treatment every 48h before harvesting
the tumor-bearing tail sections on day 30 post treatment. Image created with BioRender.com. (B, C) Mean tumor
volumes tracked over the treatment period with (B) cobimetinib or (C) trametinib (the vehicle group was the same
for both drugs). The dotted horizontal line marks the mean starting volumes. Data were analyzed comparing all
treatment groups together using ANOVA with the generalized least square method (*p<0.05 and **p<0.01; *SI
Table 1*); the treatments were graphed separately for clarity. Error bars represent SE. Mean TGI for the MEK
inhibitors were 58% and 55% for the 7.5 mg/kg and 15 mg/kg cobimetinib, respectively and 75% for both doses of
trametinib. (D) Representative images of the MmuPV1 induced papillomas for each treatment group at day 30
post treatment initiation.

Figure 2. Histological and immunohistochemical analysis of MmuPV1-induced papillomas. Representative images of papilloma histology from mice treated with vehicle (i),15 mg/kg cobimetinib (ii), or 2.0 mg/kg trametinib (iii). Tails were fixed with paraformaldehyde, paraffin embedded, sectioned, and stained: (A) H&E; (C) IHC for p-ERK1/2; (E) IHC for keratin 5 (K5); (G) IHC for keratin 10 (K10); dotted lines mark the basement membrane. (B, D, F, H) Morphometric quantification of tail tumors from each mouse (4-5 per group) for papilloma thickness (height, B); p-ERK1/2 (D), K5 (F), and K10 (H) IHC staining expressed as positive cells per tumor length (mm); vehicle (V), 15 mg/ml cobimetinib (C), 2.0 mg/kg trametinib (T). Data were analyzed using one-way ANOVA with Tukey's multiple comparison test (*p<0.05, **p<0.01; ***p<0.001).

Figure 3. Histological analysis of immune and viral markers in MmuPV1-induced papillomas. Representative images of fixed histological papilloma sections for mice treated with vehicle (i),15 mg/kg cobimetinib (ii), or 2.0 mg/kg trametinib (iii). Tissues were stained *via*: (A) IHC for neutrophil marker, myeloperoxidase (MPO); (C) ISH for MmuPV1 E6/E7 mRNA; (E) ISH for MmuPV1 genomic DNA (note serial sections in panels C and E for comparison); (G) IF for MmuPV1 L1 protein (green) and keratin 14 (red). The brightness of the photos in panel G was enhanced equivalently to better illustrate L1 staining. (B, D, F, H) Morphometric quantification of each tumor section (vehicle, V; 15 mg/ml cobimetinib, C; 2.0 mg/kg trametinib, T) on raw images (n = 5-6/group) for the percent of MPO positive cells in the tumor (B), region of positive E6/E7 ISH staining per mm of papilloma (D), region of positive LCR ISH staining per mm of papilloma (F), and number of L1 positive foci per tumor (H). Data were analyzed using one-way ANOVA with Tukey's multiple comparison test (*p<0.05, **p<0.01).

Figure 4. MEK inhibition provides protection against MmuPV1 transmission to secondary epithelial sites. (A) Mice that were co-housed throughout the 30-day treatment period; arrows indicate papillomas that developed on the muzzles of vehicle-treated mice. (B) Histological images of facial papillomas harvested on day 30 post treatment. Tissue sections were stained with H&E or by MmuPV1 E6/E7 ISH. Smaller boxes in upper panels indicate regions of increased magnification (lower panels). (C) Relative MmuPV1 infection in untreated cells compared to those treated with increasing concentrations of trametinib. Data summarize three independent infections analyzed by one-way ANOVA with Dunnett's multiple comparisons test (**** $p < 0.0001$).

481 **TABLES**

483 **Table 1. Summary of animals developing visible muzzle warts**

Group	Wart positive mice / group total	Percentage
Vehicle	6/6	100%
7.5 mg/kg Cobimetinib	1/6	16.7%
15 mg/kg Cobimetinib	0/6	0%
1.0 mg/kg Trametinib	0/6	0%
2.0 mg/kg Trametinib	0/6	0%

488 **Supplemental Information Fig. S1.** Visual phenotypes of MmuPV1-induced papillomas at day 32 post treatment
489 (prior to harvest). MmuPV1-induced papillomas after treatment with vehicle (A), 7.5 mg/kg cobimetinib (B), 15
490 mg/kg cobimetinib (C), 1 mg/kg trametinib (D), or 2 mg/kg trametinib (E). The labels at the left identify animal
491 numbers in each treatment group. (F-H) Mouse weights during treatment period. Note that only one animal (mouse
492 4 of the 2 mg/kg trametinib treatment arm) showed substantial weight loss (>20% of starting weight).

Vehicle   **15 mg/kg Cobimetinib**   **2.0 mg/kg Trametinib**

495 **Supplemental Information Fig. S2. Histologic features of MmuPV1-induced papillomas**. High-magnification
496 images of H&E-stained papillomatous tissue sections from animals treated with vehicle (A), 15 mg/kg cobimetinib
497 (B) or 2.0 mg/kg trametinib (C). Regions of hyperkeratosis are denoted with green stars. Koilocytes, a hallmark of
498 papillomavirus infections, are encircled in yellow.

Supplemental Information Fig. S3. Example of pathologist-guided morphometric analysis using a HALO algorithm to identify and quantify the areas of strong positive K5 staining and comparisons of % biomarker signals amongst the tumor groups. (A-B) Tumor-bearing areas were selected (blue) and defined as nuclei-containing epithelium; the boxed area in B was subject to increased magnification in panel C. (C) Using the CytoNuclear algorithm, individual epithelial cells were identified *via* marking nuclei blue and cytoplasmic staining for each marker was categorized as negative (clear), low (yellow), medium (orange), or high (red). (D) Increased magnification of the boxed area in panel C. Because cells gradually loose K5 expression as they begin to differentiate and express K10, only the strong K5 positive cells were enumerated. (E-G) Summary of morphometric analyses for the percentage of MmuPV1-induced tumors cells expressing the cellular proteins p-ERK1/2 (E), strong K5 (F), and K10 (G) for mice treated with vehicle (V), 15 mg/ml cobimetinib (C), 2 mg/kg trametinib (T). Data were analyzed using one-way ANOVA with Tukey's multiple comparison test (ns = not significant).

Supplemental Information Fig. S4. Magnified images of ISH using probes specific for the MmuPV1 E6/E7
coding region (A) and the noncoding genomic LCR segment (B) in adjacent tumor sections from a
vehicle-treated mouse. Note that both probes strongly stained nuclei in koilocytes and suprabasal cells likely to
be amplifying viral genomes. Whereas the E6/E7 probes demonstrated cytoplasmic punctate signals expected for
viral mRNAs (A, yellow arrows), the LCR probe produced little cytoplasmic signal (B).

Supplemental Information Fig. S5. MEK inhibitor reduced tissue levels of p-ERK1/2 correlate with cellular and viral biomarkers in MmuPV1-induced tail tumors. Scatter dot plot correlations analyses between selected biomarkers were calculated using Pearson correlation coefficient (r) analysis and two-tailed (p values).

529   **SI Table 1. Mean and Standard Error (SE) of Tumor Volumes (mm^3)**

Time (days)	Vehicle Mean (SE)	7.5 mg/kg Cobimetinib Mean (SE)	15 mg/kg Cobimetinib Mean (SE)	1.0 mg/kg Trametinib Mean (SE)	2.0 mg/kg Trametinib Mean (SE)	p-value[a]
0	39.2 (8.1)	39.8 (6.3)	40.8 (6.3)	39.3 (8.0)	41.6 (7.5)	0.998996
2	46.8 (7.1)	42.1 (5.4)	48 (11.6)	40.1 (6.1)	46.1 (7.5)	0.906252
4	56.1 (9.0)	42.6 (5.8)	41.9 (7.9)	31.1 (5.5)	37.8 (8.7)	0.20922
6	61.2 (12.8)	47.0 (4.4)	41.1 (6.0)	40.9 (8.3)	34.3 (6.3)	0.27487
8	65.8 (11.6)	41.5 (7.5)	33.5 (9.2)	30.9 (5.9)	25.5 (4.3)	0.041988
10	65.8 (11.2)	34.9 (5.9)	37.8 (8.3)	29.5 (5.1)	26.0 (5.4)	0.069824
12	78.9 (12.2)	36.9 (4.6)	35.5 (9.3)	29.1 (7.7)	24.5 (6.0)	0.023779
14	84.5 (10.6)	40.3 (5.7)	36.0 (9.2)	24.1 (4.0)	25.9 (6.2)	0.001759
16	82.9 (16.0)	38.5 (5.3)	35.7 (11)	23.5 (4.4)	20.9 (4.4)	0.005515
18	92.3 (16.0)	34.0 (6.6)	32.7 (9.5)	30.3 (3.7)	21.8 (4.3)	0.016097
20	80.7 (17.1)	38.3 (6.9)	39.0 (10.7)	24.8 (5.1)	22.4 (3.7)	0.015508
22	84.7 (17.3)	43.2 (6.2)	40.0 (10.0)	24.4 (4.5)	20.7 (6.1)	0.004064
24	95.2 (22.1)	44.4 (7.3)	37.7 (9.8)	22.5 (2.6)	21.4 (4.5)	0.004354
28	109.2 (19.2)	51.4 (10.7)	36.4 (8.8)	22.6 (4.6)	23.2 (5.8)	0.002729
30	101.7 (19.1)	42.4 (8.0)	45.4 (13.2)	25.0 (4.4)	25.2 (4.8)	0.00718

530
531   [a] p-value for the significance of the difference in tumor volume among the five groups obtained using GLS to
532   account for unequal variances.
533

 SI Table 2. Pairwise Comparisons of Final Tumor Volumes Among Treatment Groups at 30 Days of
Treatment

Treatment 1	Treatment 2	Difference[a]	Lower[b]	Upper[c]	p-value adj[d]
1.0 mg/kg Trametinib	Vehicle	-76.7042163	-88.255000	-65.15343	0.0005834
2.0 mg/kg Trametinib	Vehicle	-76.4767450	-88.027529	-64.92596	0.0006047
7.5 mg/kg Cobimetinib	Vehicle	-59.2767633	-70.827547	-47.72598	0.0087560
15 mg/kg Cobimetinib	Vehicle	-56.2683900	-67.819174	-44.71761	0.0137132
2.0 mg/kg Trametinib	1.0 mg/kg Trametinib	0.2274713	-11.323313	11.77826	1.0000000
7.5 mg/kg Cobimetinib	1.0 mg/kg Trametinib	17.4274530	5.876669	28.97824	0.8121645
15 mg/kg Cobimetinib	1.0 mg/kg Trametinib	20.4358263	8.885042	31.98661	0.7095422
7.5 mg/kg Cobimetinib	2.0 mg/kg Trametinib	17.1999817	5.649198	28.75077	0.8192129
15 mg/kg Cobimetinib	2.0 mg/kg Trametinib	20.2083550	8.657571	31.75914	0.7178020
15 mg/kg Cobimetinib	7.5 mg/kg Cobimetinib	3.0083733	-8.542411	14.55916	0.9997039

[a] The difference in tumor volumes between the pair of the groups
[b] The lower bounds of the 95% confidence interval (CI)
[c] The upper bounds of the 95% confidence interval (CI)
[d] The adjusted p-value for testing the significance of the difference between the two treatments in columns one
and two. The results indicate that the difference between Vehicle and each of the groups with the MEK inhibitor
is significant (adj. p-value < 0.05). But there is no significant difference when comparing between any of the
groups that received the MEK inhibitor, as none of the corresponding p-values is less than 0.05.

SI Table 3. Estimates for Rates of Change of Tumor Volumes (Slope)

Group	Estimate[a]	SE[b]	DF[c]	t-value[d]	p-value[e]
Vehicle	1.849	0.615	445	3.01	0.0028
1 mg/kg Trametinib	-0.4739	0.2262	445	-2.09	0.0368
2 mg/kg Trametinib	-0.5325	0.254	445	-2.1	0.0366
7.5 mg/kg Cobimetinib	0.1011	0.2795	445	0.36	0.7178
15 mg/kg Cobimetinib	0.1168	0.3679	445	0.32	0.7509

[a] Estimates for the rate of change (mm^3/day) derived from the slopes of the linear equations
[b] The standard error (SE)
[c] The degree of freedom (DF)
[d] The value of t-test (t-value) where the t-test investigates whether the corresponding slopes are zero.
[e] The p-value investigates whether the rate of change significantly differs from zero.

SI Table 3 shows the estimates for the rate of change (mm^3/day), the slopes of the linear equations of the five
groups, along with the SE, DF, t-value and p-value. The t-test here investigates whether the corresponding slopes
are zero. The p-values in the first three rows are all smaller than 0.05, suggesting that the rate of change of
tumors in the vehicle-treated mice and of tumors in mice treated with trametinib significantly differ from zero. The
tumor volumes in vehicle-treated mice significantly increased over time (because the corresponding slope is
positive), and that of groups treated with trametinib significantly decreased over time (as the corresponding slopes
are negative). The tumor volumes in groups treated with cobimetinib have the smallest estimates for the slopes
(in the sense of the absolute value), and the corresponding p-values are very large, indicating that the rate of
change is not significantly different from zero (i.e., the tumor volumes, on average, did not have a significant
change over time).

565   **SI Table 4. Difference in Rates of Change of Tumor Volumes (Slope)**

Difference in Rate of Change	Estimate[a]	SE[b]	DF[c]	t-value[d]	p-value[e]
Between Vehicle and 1 mg/kg Trametinib	2.3229	0.6553	445	3.54	0.0004
Between Vehicle and 2 mg/kg Trametinib	2.3816	0.6654	445	3.58	0.0004
Between Vehicle and 7.5 mg/kg Cobimetinib	1.7479	0.6756	445	2.59	0.01
Between Vehicle and 15 mg/kg Cobimetinib	1.7322	0.7167	445	2.42	0.016
Between Vehicle and Overall Treatment	2.0462	0.6315	445	3.24	0.0013
Between Two Doses of Trametinib	0.05866	0.3402	445	0.17	0.8631
Between Two Doses of Cobimetinib	-0.01576	0.462	445	-0.03	0.9728
Between Trametinib and Cobimetinib	-0.6122	0.2869	445	-2.13	0.0334

566
[a] Estimates for difference in the rate of change (mm^3/day) between the two groups of interest obtained based on
the LMM
[b] The standard error (SE)
[c] The degree of freedom (DF)
[d] The value of t-test (t-value) where the t-test investigates whether the corresponding differences are zero.
[e] The p-value investigates whether the rate of change significantly differs between the groups of interest.
573

SI Table 4 shows the analysis of the individual tumor rates of change for each treatment group using the linear
mixed-effects model (LMM). Based on the fitted LMM, we estimated the differences in the rate of change for
comparisons of interest. The first four rows provide the estimates for the difference in the rate of change between
the Vehicle and each MEK inhibitor treatment group. The fact that the p-values are smaller than 0.05 indicates
that the rate of change differs significantly between each pair of the groups. The fifth row shows the comparison
between the Vehicle and overall treatment group (the union of all the treatment groups), and a small p-value
implies that the difference in the rate of change is significant. These results provide statistical evidence for the
considerable effect of MEK inhibitors on tumor growth. In rows six and seven, we compared the dose effect on
the rate of change among the same drug, and the large p-values indicate that the dose effect is insignificant.
Lastly, we compared the difference in the rate of change between the two drugs regardless of the dose. The
result indicates a significant difference in the rate of change between those treated with the two drugs (p-value =
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