MEK plus PI3K/mTORC1/2 Therapeutic Efficacy Is Impacted by TP53 Mutation in Preclinical Models of Colorectal Cancer

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Abstract

**Purpose:** PI3K pathway activation occurs in concomitance with RAS/BRAF mutations in colorectal cancer, limiting the sensitivity to targeted therapies. Several clinical studies are being conducted to test the tolerability and clinical activity of dual MEK and PI3K pathway blockade in solid tumors.

**Experimental Design:** In the present study, we explored the efficacy of dual pathway blockade in colorectal cancer preclinical models harboring concomitant activation of the ERK and PI3K pathways. Moreover, we investigated if TP53 mutation affects the response to this therapy.

**Results:** Dual MEK and mTORC1/2 blockade resulted in synergistic antiproliferative effects in cell lines bearing alterations in KRAS/BRAF and PIK3CA/PTEN. Although the on-treatment cell-cycle effects were not affected by the TP53 status, a marked proapoptotic response to therapy was observed exclusively in wild-type TP53 colorectal cancer models. We further interrogated two independent panels of KRAS/BRAF- and PIK3CA/PTEN-altered cell line- and patient-derived tumor xenografts for the antitumor response toward this combination of agents. A combination response that resulted in substantial antitumor activity was exclusively observed among the wild-type TP53 models (two out of five, 40%), but there was no such response across the eight mutant TP53 models (0%). Interestingly, within a cohort of 14 patients with colorectal cancer treated with these agents for their metastatic disease, two patients with long-lasting responses (32 weeks) had TP53 wild-type tumors.

**Conclusions:** Our data support that, in wild-type TP53 colorectal cancer cells with ERK and PI3K pathway alterations, MEK blockade results in potent p21 induction, preventing apoptosis to occur. In turn, mTORC1/2 inhibition blocks MEK inhibitor-mediated p21 induction, unleashing apoptosis. Clin Cancer Res; 21(24): 5499–510. ©2015 AACR.

Introduction

Metastatic colorectal cancer (mCRC) is the third leading cause of cancer-related deaths worldwide. Currently, the standard of care for mCRC is chemotherapy (fluoropyrimidin and oxaliplatin/irinotecan combinations). Target-specific agents against the EGFR—cetuximab and panitumumab—or against the VEGF pathway—bevacizumab and aflibercept—as well as the multitarget kinase inhibitor regorafenib, are also approved for the treatment of mCRC (1–3). However, the efficacy of anti-EGFR compounds is often limited by mutations that activate downstream signaling pathways, rendering targeted therapy ineffective (4–6).

The landscape of somatic mutations in colorectal cancer has been defined during the last years (7). According to The Cancer Genome Atlas Network (8), 42% of primary colorectal cancers display activating mutations of the KRAS oncogene, 10% in BRAF and an additional 10% in NRAS, being typically mutually exclusive mutations. Mutations in this pathway result in hyperactivation of the mitogen-activated protein kinase kinase 1 (MAP2K1 or MEK1) and the downstream mitogen-activated protein kinases p42/p44 (p42/p44 MAPK or ERKs; ref. 9). Activation of the phosphatidylinositol-3-kinase/Akt/mammalian target of the
Translational Relevance

The utmost objective of targeted therapies is to achieve selective cancer cell death by specifically targeting the driver oncogenes. Equally important is the identification of poten-
tially responding patients by means of biomarkers, in order to
avoid overtreatment and to maximize response rate. A signif-
icant proportion of patients with colorectal cancer carry muta-
tions in both the ERK (Ras/Raf) and PI3K pathways and are
therefore potentially susceptible to dual pathway blockade.
Nonetheless, half of the tumors harboring alterations in
KRAS/BRAF and PIK3CA/PTEN have a TP53 mutation along.
In this work, we show that mutant TP53 tumor cells are unable
to engage apoptosis upon MEK plus mTORC1/2 blockade.
Our results are of interest for the design of future cancer
therapies targeting the ERK/MEK and PI3K/mTORC1/2 sig-
naling cascades in colorectal cancer.

Materials and Methods

Cell lines and reagents

All the colorectal cancer cell lines were obtained from the ATCC,
with the exception of LIM2405, which was obtained from the
Ludwig Institute for Cancer Research (Switzerland). All cell lines
were authenticated using DNA profiling by the ATCC/Ludwig
archive. DLD-1 was maintained in RPMI-1640 (Invitrogen),
HT-29 and HCT116 in McCoy’s 5A (Modified) Medium (Invi-
trogen), and SW948, RKO, and LIM2405 in DMEM, all were
supplemented with 10% FBS and 2 mmol/L L-glutamine
(Life Technologies) at 37 °C in 5% CO2. PD0325901 and
MLN0128 were obtained from Takeda California. General
labatory supplies were acquired from Sigma-Aldrich, Invitro-
gen, or Merck.

Western blot analyses

Cells were grown in 60-mm dishes and treated with
PD-0325901 (referred to as PD-901), MLN0128 (formerly known
as INK-128), or a combination of both for the indicated con-
centrations and times. Cells were washed with ice-cold PBS
and scraped into ice-cold lysis buffer (Tris–HCl pH 7.8 20 mmol/L,
NaCl 137 mmol/L, EDTA pH 8.0 0.2 mmol/L, NP40 1%,
glycerol 10%, supplemented with NaF 10 mmol/L, Leupeptin 10 μg/mL,
Na3VO4 200 μmol/L, PMSF 5 mmol/L, and Aprotinin (Sigma-
Aldrich)]. Lysates were cleared by centrifugation at 13,000 rpm
for 10 minutes at 4°C, and supernatants removed and assayed for
protein concentration using the Pierce BCA Protein Assay Kit
(Termo Scientific). Thirty micrograms of total lysate was
resolved by SDS-PAGE and electrophoretically transferred to
nitrocellulose membranes. Membranes were then hybridized
using the following primary antibodies: pAkt (S473), Akt, pS6
(S240/244), pS6 (S235/236), p4EBP1 (S65), 4EBP1, pERK
(T202/Y204), ERK, cleaved PARP, PARP, cleaved caspase-7 and
p53 (Cell Signaling Technology), tubulin (Sigma-Aldrich),
c-Myc (Santa Cruz Biotechnology), p21 (Neomarkers, Thermo-
Fisher Scientific Inc.) in 5% BSA in Tris Buffered Saline (Tris
50 mmol/L, NaCl 150 mM) + 0.1% Tween 20 (TBST) (Sigma
Aldrich) and GAPDH (Cell Signaling Technology) in 1% nonfat
dry milk in TBST. Mouse and rabbit horseradish peroxidase-
conjugated secondary antibodies (Amersham Biosciences) were
used at 1:2,000 in TBST-T 1% nonfat dry milk. Protein–antibody
complexes were detected by chemiluminescence with the Immo-
bilon Western HRP Substrate (Millipore), and images were cap-
turnered with a FUJIFILM LAS-3000 camera system.

Determination of inhibitory concentration 50 and
combination index

Cells were seeded in 96-well plates and treated with 1:10 serial
dilutions of PD-901 and MLN0128 within the 10 μmol/L to
1 pmol/L range as single agents or in 1:1 combinations. After
4 days of treatment, cell proliferation was analyzed with the
CellTiter-Glo Luminescent Cell Viability Assay (Promega) as
described by the manufacturer. Proliferation curves were calcu-
lated using GraphPad Prism (GraphPad Software), and the
combination index (CI) was determined using CompuSyn
(CompuSyn Inc.; ref. 23). CI < 1 indicates synergism, CI = 1 indicates
additive effect, and CI > 1 indicates antagonism. Experiments were
performed in triplicate.

Determination of cell cycle and apoptosis

Cell cycle and hypodiploid (sub-G1) cells were quantified by
flow cytometry. Briefly, cells were washed with PBS, fixed in cold
70% ethanol, and then stained with propidium iodide while
treating with RNase (Sigma-Aldrich). Quantitative analysis of
sub-G1 cells was carried out in a FACScan calibur cytometer using
the Cell Quest software (BD Biosciences). Annexin V–positive
cells were quantified using the Guava Nexin Reagent (Millipore)
according to the manufacturer’s recommendations. Briefly, cells
were harvested in 1% BSA/PBS and diluted 1:1 in the Guava Nexin Reagent. After 20 minutes at room temperature, cells were analyzed in the Guava System (Millipore).

RNA extraction and quantitative PCR (qPCR)
RNA was extracted using the PerfectPure RNA Tissue Kit (5Prime), according to manufacturer’s instructions. QRT-PCR was performed using TaqMan probes (Applied Biosystems) according to the manufacturer’s recommendations. Reactions were carried out in an ABI7000 sequence detector (Perkin Elmer), and results were expressed as fold change calculated by the ΔΔCt method relative to the control sample. The β-glucuronidase gene GUSB mRNA was used as internal normalization control.

Overexpression of p53-R248W, p21, and RNA interference
p53-R248W was synthesized and cloned into a pBABE backbone vector (GenScript). The pINDUCER20-HA-p21<sup>591</sup>plasmid was kindly provided by Stephen J. Elledge (Perkin Hughes Medical Institute and Department of Genetics, Harvard Medical School, Boston, MA; ref. 24). siRNAs against p21 and nontargeting siRNAs control were synthesized by Sigma-Aldrich. Cells were transfected with the indicated siRNAs at 50 mmol/l during 24 hours using a DharmaFECT1 transfection agent (Dharmacon Research), as described by the manufacturer. The shTP53 construct was obtained from The RNAi Consortium (Broad Institute, MA).

Establishment of cell line–derived tumor xenografts in nude mice
Mice were maintained and treated in accordance with the institutional guidelines of the Vall d’Hebron University Hospital Care and Use Committee. Six-week-old female athymic nude mice HsdCpb:NMRI– were purchased from Harlan Laboratories. Mice were housed in air-filtered laminar flow cabinets with a 12-hour light cycle and food and water ad libitum. HT-29, HCT116, or LIM2405 cells were resuspended in sterile PBS before subcutaneous injection at a final concentration of 2 × 10<sup>6</sup> cells/100 μl per mouse.

Establishment of colorectal cancer patient–derived xenografts
Human colon carcinoma models were used and grown as described by Puig and colleagues (25). Experiments were conducted following the European Union’s animal care directive (86/609/EEC) and were approved by the Ethical Committee of Animal Experimentation of the Vall d’Hebron Research Institute and patient consent. Patient-derived xenograft (PDX) models from passages 5 to 8 were established by implantation of enzymatically digested surgical colon cancer biopsies in NOD/SCID mice (NOD.CB17-Prkdc<sup>scid</sup>/NcrCrl). PDXs recapitulated the same histopathologic and genetic features as the original patients’ carcinomas. For drug-efficacy studies, a total of 1 × 10<sup>5</sup> patient-derived tumor cells were obtained from an established tumor, suspended in PBS 1:1 with Matrigel (BD Bioscience) and injected subcutaneously into both flanks of NOD/SCID mice, as previously described (26, 27). After 3 to 8 weeks, when palpable tumors matched 200 ± 50 mm<sup>3</sup>, treatments started and tumor size was evaluated twice weekly by caliper measurements.

PDXs from the Candiolo Cancer Institute (18) were established following procedures approved by the local Ethical Commission and by the Italian Ministry of Health. Briefly, 25-mm<sup>3</sup> Matrigel-coated tumor material derived from liver metastectomies were implanted in the flank of NOD/SCID mice, as previously described (18). For treatment-efficacy experiments, established tumors (~400 mm<sup>3</sup>) were treated with 40 mg/kg of BEZ235 (Selleck Chemicals) or 25 mg/kg of AZD6244 (SEQUOIA Research Products). Tumor size was evaluated once weekly by caliper measurements.

**In vivo treatment study**
Animals were divided into four groups, consisting of 6 to 10 mice per group. Animals were treated with PD0901 6 q.d./week (2 mg/kg in 5% NMP, 95% PEG in water, oral gavage) and/or MLN0128 6 q.d./week (0.3 mg/kg in 5% NMP, 15% PVP in water, oral gavage). Tumors were measured with digital calipers, and tumor volumes were determined using the formula (length × width<sup>2</sup>) × (π/6). At the end of the experiment, animals were euthanized using CO<sub>2</sub> inhalation. Tumor volumes are plotted as mean ± SE of 6 to 10 mice. For Western blot analysis, whole-protein lysates from two to four different tumors derived from each treatment were processed as described above.

**Patient selection and genotyping of tumor samples**
All patients with pathologically confirmed mCRC refractory to standard therapy referred to phase I clinical trials at the Molecular Therapeutic Research Unit of Vall d’Hebron Institute of Oncology had archived formalin-fixed paraffin-embedded (FFPE) tumor samples analyzed for targeted molecular aberrations: KRAS/ NRAS/BRAF/PIK3CA mutations were identified using the Thermus aquaticus molecular diagnostic assay (Dxs) or the OncoCarta Panel v1.0 Sequenom MassARRAY, by the Pathology Service from the Vall d’Hebron University Hospital or the Cancer Genomics Group at Vall d’Hebron Institute of Oncology (VHIO), respectively. For three patients, KRAS was sequenced at the hospital of origin using the commercial PCR kit (Dxs). PTEN expression by immunohistochemistry was determined by the Molecular Oncology Group at VHIO. The three laboratories are UNE ISO 15189 accredited (28). Patients’ informed consent was obtained at baseline. In total, from 2011 to 2013, 14 patients with double pathway aberrations participated in early clinical trials, with MEK plus PI3K pathway inhibitors based on the results of tumor profiling as well as logistic factors, including study availability and eligibility criteria (19).

Patients achieved clinical benefit if their cancer was controlled for a minimum of 16 weeks, the time point for the second response evaluation by computerized tomography (28). Tumor specimens from primary colorectal cancer or metastasis and from the established PDX were subjected to capture-based massive parallel sequencing (MiSeq, Illumina). Briefly, to avoid false negatives, only tumor samples with a tumor area above 30% were analyzed. DNA was extracted from 5 × 10<sup>5</sup> tumor slices using the Maxwell FFPE Tissue LEV DNA Purification Kit (Promega). An initial multiplex-PCR with a proofreading polymerase was performed on samples. An in-house–developed panel of more than 600 primer pairs targeting frequent mutations in oncogenes plus several tumor suppressors, totaling 57 genes, was applied (Supplementary Table S1 and primer pairs available upon request). The panel includes the entire coding sequence of TP53 (NM_005546). Indexed libraries were pooled and loaded onto a MiSeq instrument, and paired-end 100-bp-read-length sequencing was performed (2 × 100 bp). Initial alignment was performed with the Burrows–Wheeler Aligner after primer sequence clipping, and variant calling was done with the Genome Analysis Toolkit Unified Genotyper and VarScan2 followed by ANNOVAR annotation.
Clinical Cancer Research

Mutations were called at a minimum 3% allele frequency. SNPs were filtered out with the SNP database (dbSNP; ref. 29) and 1,000 genome datasets (30). All detected variants were manually inspected.

PDx from the Candiolo Cancer Institute were genotyped as described (18), by capillary electrophoresis (3730 ABI Applied Biosystems) using exon-specific and sequencing primers, which were designed with Primer3 software.

**Immunohistochemistry**

Xenograft tumors were fixed immediately after excision in 10% buffered formalin solution for a maximum of 24 hours at room temperature before being dehydrated and paraffin-embedded under vacuum conditions (FFPE). Tissue microarrays (TMA) were constructed, including duplicate cores from each tumor. TMA slides underwent deparaffinization and antigen retrieval using PT Link system (DAKO) following manufacturer's instructions. Immunohistochemical staining against cleaved caspase-3 or p53 (DAKO) was performed as follows: 4-μm sections from FFPE material were deparaffinized and hydrated. Antigen retrieval was performed using a T/T Mega microwave system following manufacturer's instructions and DAKO reagents. After peroxide blocking, slides were incubated with primary antibody, secondary antibody, and developed with freshly prepared 0.05% 30,3-diaminobenzidine and counterstained with hematoxylin. Positive and negative controls were run along with the tested slides per each marker. Images were acquired using Aperio ImageScope software (Aperio), and a pathologist blinded to the identity of the samples quantified the percentage of positively stained cells.

**p53 status**

We analyzed the p53 status of tumor samples from archival tissue primarily upon the TP53 mutation status (MiSeq). Only when tumor sample was scarce (tumor area <30%) or the coverage of the genomic assay was insufficient we used IHC to provide a surrogate of TP53 mutation. Those tumors that markedly stained for nuclear p53 (≥50% of tumor cell positivity) were considered p53 mutant (31).

**Statistical analysis**

Two-way ANOVA with a Bonferroni post-test was performed using GraphPad Prism (GraphPad software). Error bars represent the SE. All experiments were repeated at least three times. A log-rank test is performed with the clinical data (R software).

**Results**

Combined MEK and mTORC1/2 inhibition synergistically suppresses colorectal cancer cell proliferation

To test the biochemical effects of dual MEK and mTORC1/2 blockade in vitro, we treated six colorectal cancer cell lines bearing concomitant alterations in KRAS/BRAF and PIK3CA/PTEN (Supplementary Table S2), three of which were also harboring TP53 mutations, with the MEK inhibitor PD901, the catalytic mTOR inhibitor MLN0128, or the combination of both. After 24 hours of treatment, PD901 markedly suppressed ERK phosphorylation (Fig. 1A). Treatment with MLN0128 resulted in a reduction of p-Akt-S473 and downstream mTORC1 targets phospho-S6 ribosomal protein, p-S6-S240/244, and phospho-4E binding protein-1, p-4EFP1-S65, accompanied by minor increases in ERK activation. As expected, the combination of PD901 and MLN0128 suppressed both ERK and PI3K pathways in all the cell lines.

The antiproliferative response of combined PD901 and MLN0128 treatment was synergistic (CI < 1) in five out of six cell lines, irrespective of the TP53 mutational status (Fig. 1B).

When examining the cell cycle, we found that the TP53 mutational status did not discriminate the combination response (% of S-phase; Supplementary Fig. S1A). Moreover, cell-cycle biomarkers were markedly reduced in all cell-cycle–sensitive cell lines, independently of the TP53 mutational status (see Supplementary Fig. S1B; transcription factor E2F1 and the phosphorylation levels of the retinoblastoma tumor suppressor, pRB). Thus, the presence of a TP53 mutation did not affect the antiproliferative activity of combined MEK and mTORC1/2 inhibition in colorectal cancer cells harboring activating RAS/BRAF and PI3K pathway alterations.

**Combined MEK and mTORC1/2 blockade promotes apoptosis in TP53 wild-type but not in TP53 mutant colorectal cancer cell lines via activation of BAX**

We next investigated whether combined PD901 and MLN0128 induced apoptosis in our panel of colorectal cancer cells. We observed a clear-cut difference in terms of apoptosis induction between colorectal cancer cell lines harboring wild-type or mutant TP53. In wild-type TP53 cell lines (HCT116, RKO, and LIM2405), PD901 or MLN0128 treatment increased cell death, as measured by sub-G1 DNA accumulation (Fig. 2A). The combination treatment synergistically increased the sub-G1 population in all three models, reaching profound levels of cell death (45%, 32%, and 79%, respectively) with concomitant caspase-7 and PARP cleavage (Fig. 2B). In contrast, TP53 mutant cell lines (DLD-1, HT-29, and SW948) showed only minor combination response compared with single agents, achieving relatively limited cell death (5%, 15%, and 15%, respectively), with no detectable biochemical readouts of apoptosis. These results were supported by the significantly higher induction of Annexin V in TP53 wild-type versus mutant cells treated with the combination of agents (Fig. 2C).

We further studied which p53 targets are involved in the response to dual MEK and mTORC1/2 blockade. We found that, although the levels of NOXA remained relatively stable across treatments, the levels of PUMA increased in all cell lines upon MEK and/or mTORC1/2 blockade, regardless of the p53 status (Supplementary Fig. S1B and S1C). Interestingly, BAX levels increased following MEK inhibition exclusively in the p53 wild-type cell lines. These results suggest that BAX may be mediating apoptosis in p53 wild-type colorectal cancer treated with MEK and mTORC1/2 inhibitors.

**Combined MEK and mTORC1/2 suppression promotes antitumor responses in TP53 wild-type colorectal cancer xenografts**

In vivo, xenografts derived from one mutant (HT-29) and two wild-type TP53 (HCC116 and LIM2405) colorectal cancer cell lines exhibited biochemical ERK or PI3K/mTOR signal inhibition with PD901 and MLN0128, respectively, and inhibition of both pathways when treated with the combination of both agents (Fig. 3A). However, detection of PARP and caspase-3 cleavage was evident only in TP53 wild-type tumors upon combination treatment (Fig. 3A and B and Supplementary Fig. S1D). We then expanded our panel of models with five PDx that harbored
alterations in KRAS and PIK3CA/PTEN, in addition to the three cell line–derived models. Single-agent antitumor activity was variable across the eight colorectal cancer models; yet the combination of PD901 and MLN128 resulted in tumor growth stabilization in one out of three TP53 wild-type colorectal cancer models (PDX-T77), and in none of the TP53-mutant ones (Fig. 3C). We confirmed our results with an independent sample set (18), namely, five colorectal cancer PDX models that harbor hotspot mutations in KRAS and PIK3CA, using different MEK and PI3K/mTORC1/2 inhibitors. A combination response of AZD6244 (MEK inhibitor) plus NVP-BEZ235 (PI3K/mTORC1/2 inhibitor) that resulted in tumor growth stabilization was
observed in one of two wild-type TP53 PDX and in none of the three TP53-mutant ones (Supplementary Table S3). Altogether, an antitumor combination response was observed in two out of five (40%) TP53 wild-type colorectal cancer models, while there was no such response across the eight TP53-mutant models (0%).

These data suggest that TP53 mutational status could affect the antitumor activity of combined MEK and mTORC1/2 inhibition in colorectal cancer.

p53 status in patients with colorectal cancer treated with MEK plus PI3K/mTORC1/2 therapy

We next investigated whether the p53 status of tumors from patients with colorectal cancer treated with the combination of MEK and PI3K/mTORC1/2 could predict for response to therapy (Fig. 3D). Assessment of the p53 status was possible in 13 cases using DNA sequencing or immunohistochemistry (when the genomic assay failed or when tumor tissue was scarce; Supplementary Table S4 and Supplementary Fig. S2). In this cohort, three patients stopped therapy due to toxicity. For the remaining 10 cases, we observed no significant correlation between p53 mutations and progression-free survival. This was not surprising given the small number of cases and the overall short time of response to therapy in these heavily pretreated patients. However, we noted that the two patients with the longest (32 weeks) responses to dual MEK and mTORC1/2 blockade had tumors with wild-type p53 (Fig. 3D).

Because our results in multiple colorectal cancer models supported an association between TP53 mutation status and sensitivity to combined MEK and mTORC1/2 inhibition, we sought to further elucidate the role of p53 as a possible determinant of therapy response. We stably overexpressed a mutant variant of TP53 (p53-R248W) or GFP (control) in the TP53 wild-type cell lines HCT116 and LIM2405. The p53-R248W mutation has been described as a dominant-negative variant that represses p53 transcriptional functions by interacting with the endogenous wild-type p53 (32, 33). Upon treatment, both cell line models exhibited the expected reduction in p-ERK and p-AKT/p-S6 upon PD901 and MLN0128, respectively, both downstream target of MEK, mTORC1/2, and p53, we hypoth-

Figure 2.

MEK and mTOR inhibition induces apoptosis in p53 wild-type colorectal cancer cells. The indicated colorectal cancer cell lines were treated with DMSO (control), 50 nmol/L PD901, 50 nmol/L MLN0128, or the combination of both inhibitors (901+128). A, apoptosis was measured after 72 hours of treatment as the percentage of cells with sub-G1 DNA content by flow cytometry and analyzed with FCS Express 4 Flow software. Data, mean ± SE from three independent experiments. B, whole-cell protein extracts were analyzed after 24 hours of treatment by Western blot with the indicated antibodies. Tubulin antibody was used as a loading control. Figures are representative of three independent experiments. C, apoptosis was measured after 72 hours of treatment by quantification of the Annexin V-positive cells (Guava Nexin Reagent; Millipore). n.s., not significant. *, P < 0.05; **, P < 0.001.

p53 function is necessary for apoptotic and antitumor effects of MEK and mTORC1/2 blockade in colorectal cancer cells

Given that the cell cycle and apoptosis inhibitor p21 is a downstream target of MEK, mTORC1/2, and p53, we hypothesized that expression of p21 could limit cell death mediated by the combination of PD901 and MLN0128 in p53-R248W xenografts compared with the p53 wild-type counterparts (Supplementary Fig. S3C). Similarly, knockdown of TP53 in HCT116 cells resulted in significant attenuation of the proapoptotic response upon combined treatment with PD901 and MLN128 (Fig. 4B). These data support the hypothesis that p53 function is necessary for the induction of apoptosis and antitumor response to combined MEK and mTORC1/2 inhibition in colorectal cancer.

MEK blockade promotes p21-dependent upregulation of p21 in TP53 wild-type colorectal cancer

Figure 4A and Supplementary Fig. S3A and S3B. However, expression of p53-R248W suppressed caspase-3/7 and PARP cleavage induced by combined MEK and mTORC1/2 inhibition (Fig. 4A and Supplementary Fig. S3A and S3B). This resulted in reduced sensitivity to combined PD901 and MLN0128 in p53-R248W xenografts compared with the p53 wild-type counterparts (Supplementary Fig. S3C). Similarly, knockdown of TP53 in HCT116 cells resulted in significant attenuation of the proapoptotic response upon combined treatment with PD901 and MLN128 (Fig. 4B). These data support the hypothesis that p53 function is necessary for the induction of apoptosis and antitumor response to combined MEK and mTORC1/2 inhibition in colorectal cancer.
reverted (posttranscriptionally) by mTOR blockade (Fig. 5A and B). These data are in agreement with p21 being negatively regulated by c-Myc, a downstream target of MEK (36), and with mTORC1 regulating p21 stability at the translational level (34). In contrast, p21 mRNA and protein levels remained unaffected in the TP53-mutant models (DLD-1, HT-29, and SW948) treated equally.

To confirm the role of wild-type p53 in modulating p21, we made use of the HCT116-GFP and HCT116-p53-R248W cell lines described above. In GFP-transfected cells, treatment with PD901 resulted in induction of p21. In agreement with the previous data, expression of p53-R248W prevented p21 upregulation consequent to MEK inhibition (Supplemental Fig. S3F). We next confirmed that p21 upregulation upon MEK inhibition was p53 dependent by downregulating p53 in two TP53 wild-type cell lines, HCT116 and LIM2405 (Supplementary Fig. S3G). In both models, p53 knockdown counteracted PD901-mediated induction of p21. In summary, we show that MEK blockade results in increased p21 mRNA and protein expression in TP53 wild-type colorectal cancer cells.

p21 upregulation prevents apoptosis mediated by MEK blockade in TP53 wild-type colorectal cancer cells

Finally, we sought to investigate whether p21 upregulation following treatment with PD901 alone precludes the induction of apoptosis in TP53 wild-type colorectal cancer cells. Specific downmodulation of the mRNA of CDKN1A (the gene encoding for p21) in two TP53 wild-type cell lines, HCT116 and LIM2405, resulted in increased induction of apoptosis by PD901, as shown by caspase-7 and PARP cleavage as well as accumulation of the sub-G1 cell fraction (Fig. 6A and B). In addition, overexpression of p21 in p53 wild-type cells mimicked the effect of MEK inhibition...
and prevented PARP cleavage upon the combination of PD901 and MLN0128 treatment (Fig. 6C). In summary, our results show that the apoptotic response following MEK and mTORC1/2 blockade in colorectal cancer models is p53 dependent. As a consequence of mTOR blockade, PD901-induced upregulation of p21 is blunted, which likely precipitates apoptosis.

**Discussion**

Agents targeting MEK have shown limited activity used as monotherapy in colorectal cancer (37), with PI3K pathway activation being a potential bypass mechanism (38, 39). Several clinical trials were initiated to ask whether concomitant MEK and PI3K/mTORC1/2 blockade is efficacious in various diseases (19, 20), including colorectal cancer. In this study, we investigated the effectiveness of these agents in colorectal cancer and whether TP53 mutation status affects the antitumor response.

We focused on colorectal cancers with concomitant alterations of RAS/BRAF and PIK3CA/PTEN, which entitles for approximately 8% of the overall colorectal cancer population (8), to show that wild-type TP53 is associated with preferential response to combined MEK and PI3K/mTOR inhibition. In our *in vitro* and *in vivo* models, wild-type TP53 mediates an apoptotic outcome following MEK plus mTORC1/2 blockade. These preclinical observations need to be validated in a larger cohort of patients.

The inhibition of MEK and mTORC1/2 has previously been explored in other settings, including lung (14), pancreatic (15), breast (16, 17), and colorectal tumors (18). However, the present study is the first one in which TP53 status has been associated with treatment outcome. Particularly, the study by Migliardi and colleagues (18) highlighted the limitations of simultaneously targeting MEK and PI3K/mTORC1/2 in colorectal cancer PDXs, with limited antitumor responses across a panel of 40 models. Our study focused on KRAS/BRAF and PIK3CA/PTEN double mutants, and we similarly observed that minor response was the best therapeutic outcome in PDX, or resulted in disease stabilization in patients. In addition, our study identified TP53 mutation as a potential predictive
When tissue is scarce or quality is compromised, as in some of our specimens, IHC remains as the unique test available to assess TP53 status.

Disappointingly, MEK plus PI3K/Akt/mTORC1/2 inhibitor combinations have shown limited clinical activity even in retrospectively selected, molecularly defined populations (19, 20, 48). The overlapping dose-limiting toxicities of these combinations have prevented the achievement of dose levels similar to the single-agent maximum tolerated doses, which compromises pathway inhibition and precludes substantial clinical benefit over single-agent strategies (48). Alternative scheduling, with noncontinuous/pulsatile dosing of either agent, might be an option to increase tolerability of these regimens and likely to induce a proapoptotic response (49).

Currently, clinical trials explore further combinations, namely, blockade of mutant BRAF with selective BRAF<sup>V600E</sup> inhibitors (±MEK inhibitors) and EGFR inhibitors in patients with colorectal cancer harboring BRAF<sup>V600E</sup> mutations or targeting MEK in combination with anti-IGF-1R (in KRAS mutant colorectal cancer). It remains to be understood if these strategies will be efficacious in colorectal tumors with concomitant activation of the PI3K pathway. Our work prompts to investigate if patients with wild-type p53 colorectal cancers obtain higher benefit than those with mutant p53 tumors, from therapeutic combinations that directly or indirectly target Ras/Raf and PI3K. This interrogation should be feasible, as the institutions conducting these studies have implemented prescreening strategies that allow massive parallel capture.

**Figure 5.**

MEK inhibition induces p21 upregulation in p53 proficient colorectal cancer cells. A, colorectal cancer cell lines were treated with DMSO (control), 50 nmol/L PD901, 50 nmol/L MLN0128, or the combination of both for 16 hours. p21 mRNA levels were analyzed by qRT-PCR, normalized to GUSB mRNA levels, and expressed as fold change compared with control. B, colorectal cancer cell lines were treated with DMSO (control), 50 nmol/L PD901, 50 nmol/L MLN0128, or the combination of both for 24 hours and whole-cell protein extracts were analyzed by Western blotting with the indicated antibodies. GAPDH antibody was used as a loading control. Figures are representative of three independent experiments.
based sequencing of many cancer-related genes of many cancer-related genes, including TP53.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors’ Contributions
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30. 1000 Genomes Database. Available from: http://www.1000genomes.org/
Correction: MEK plus PI3K/mTORC1/2 Therapeutic Efficacy Is Impacted by TP53 Mutation in Preclinical Models of Colorectal Cancer

In this article (Clin Cancer Res 2015;21:5499–510), which was published in the December 15, 2015, issue of Clinical Cancer Research (1), the grant support is listed incorrectly. It should read as follows: “J. Baselga was recipient of a FIS Grant Award (PI09/00623 and RD06/0020/0075), a ‘Tumor Biomarkers Collaboration’ supported by the Banco Bilbao Vizcaya Argentaria (BBVA) Foundation and a private donation from the Orozco family through the Oncology Research Foundation (FERO). In addition, this study was supported in part by the NIH/NCI Cancer Center Support Grant P30 CA008748. V. Serra is recipient of an Instituto de Salud Carlos III (ISCIII) grant FIS PI13/01714 and a GHD/FERO grant. This work was also supported by the FP7-HEALTH-2010 COLTHERES grant (to J. Tabernero); the PI11/00917 Instituto de Salud Carlos III grant (to J. Tabernero); the AIRC (Associazione Italiana per la Ricerca sul Cancro) Investigator Grant 14205 and AIRC 2010 Special Program Molecular Clinical Oncology 5×1000, project 9970 (to L. Trusolino); the AACR, American Association for Cancer Research—Fight Colorectal Cancer Career Development Award (to A. Bertotti); the AIRC Investigator Grant 15571 (to A. Bertotti); and the unrestricted help of the Cellex Foundation. R. Dienstmann is a recipient of ‘La Caixa International Program for Cancer Research & Education.’” The authors regret this error.

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