A Multicenter, Open-Label Phase II Clinical Trial of Combined MEK Plus EGFR Inhibition for Chemotherapy-Refractory Advanced Pancreatic Adenocarcinoma

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Abstract

Purpose—Based on preclinical evidence of synergistic activity between MEK and EGFR inhibitors in pancreatic ductal adenocarcinoma (PDAC), we evaluated the safety and efficacy of selumetinib, a MEK1/2 inhibitor, plus erlotinib in patients with previously treated advanced PDAC.

Experimental design—In this single-arm phase II trial, eligible patients received the combination of erlotinib 100 mg plus selumetinib 100 mg daily in 3-week cycles. Study assessments included measurement of clinical outcomes, with a primary endpoint of overall survival, and exploration of potential molecular predictors of treatment benefit.

Results—46 patients were enrolled and received a median of 2 cycles (range, 1-7). While no objective responses were observed, 19 patients (41%) showed evidence of stable disease for 6 weeks, and 13/34 patients (38%) had a CA19-9 decline 50%. Median progression-free survival was 1.9 months (95% CI, 1.4-3.3 months), with a median OS of 7.3 months (95% CI, 5.2-8.0 months). Common adverse events included rash, diarrhea, and nausea/vomiting. Patients with tumors exhibiting an epithelial phenotype (demonstrated by high level of E-cadherin expression) were more likely to be sensitive to study treatment. Tumor-derived DNA was detectable in plasma from the majority of patients using next-generation digital DNA sequencing, and its relative abundance correlated with tumor burden.

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Conclusions—A therapeutic strategy of dual targeted inhibition of the MEK and EGFR pathways shows modest antitumor activity in pancreatic cancer. Specific molecular subtypes may derive greatest benefit from this combination. Further exploration, both with more potent MEK inhibitors and in molecularly enriched patient subsets, is warranted.

Keywords

pancreatic cancer; EGFR; MEK; clinical trial; molecular subtype

Introduction

Genetic alterations in the KRAS signaling pathway are found in approximately 90% of pancreatic ductal adenocarcinomas (PDAC) (1,2). While directly targeting KRAS itself has proved elusive as a therapeutic strategy, two of the effector pathways downstream of KRAS, the mitogen-activated protein (MAP) kinase (RAF-MEK-ERK) and phosphoinositide 3-kinase (PI3K-AKT) signaling cascades, are each independently amenable to pharmacologic inhibition. However, due to cross-talk and pathway convergence, targeting one or the other shows limited efficacy in PDAC as well as other solid tumors (3,4). We have demonstrated a negative regulatory feedback loop whereby pharmacologically inhibiting MEK induces feedback activation of PI3 kinase, with this feedback mechanism mediated by hyperactivation of the epidermal growth factor receptor (EGFR) (5,6). Recognition of this fact suggests the potential therapeutic benefit of employing a dual inhibitor strategy, and synergistic activity has been demonstrated between EGFR and MEK inhibitors in a number of pre-clinical models, including PDAC (5,7-9). Indeed, EGFR is essential for the initiation of PDAC by oncogenic *KRAS* (10,11), underscoring the extensive interplay between these two molecules.

New chemotherapy combinations such as FOLFIRINOX (infusional 5-FU, leucovorin, irinotecan, and oxaliplatin) (12) and gemcitabine plus nab-paclitaxel (13) have produced improved clinical outcomes in patients with metastatic PDAC. However, once patients progress on these regimens, therapeutic options become less certain, with no universally accepted standard of care in this salvage setting. Targeted therapies have been disappointing in this disease, with only erlotinib showing a statistically significant but marginal improvement in survival when added to gemcitabine as first-line treatment (14). Predictive biomarkers that can help guide therapeutic decision-making are likewise lacking. Based on the preclinical rationale that the EGFR fosters escape from and resistance to MEK inhibition in PDAC, we performed a phase II clinical trial to assess the safety and efficacy of combining selumetinib, a selective, allosteric inhibitor of MEK1/2, together with erlotinib, in patients with advanced PDAC who had progressed on first-line chemotherapy. We simultaneously examined potential predictive biomarkers and explored the feasibility of monitoring molecular events in the tumor through analysis of cell-free DNA (cfDNA) in plasma.

Patients and Methods

Study design

This trial was a non-randomized single arm phase II study conducted at the University of California San Francisco and Ohio State University Comprehensive Cancer Centers. Institutional Review Board approval was obtained at each site. All participants provided written informed consent.

Primary study objective was to assess overall survival (median survival and proportion of patients alive at 24 weeks) in all patients receiving at least one dose of the combination of selumetinib and erlotinib. Secondary objectives included progression-free survival (median PFS and proportion of patients with PFS at 12 and 24 weeks); CA19-9 biomarker response (defined as 50% decline in serum CA19-9 level if elevated at baseline); objective radiographic response by RECIST 1.0 criteria; and safety and toxicity profile of the study combination.

Main eligibility criteria

Patients were eligible for the study if they had histologically-confirmed inoperable PDAC (either locally advanced or metastatic) for which they had received exactly one prior line of systemic therapy (excluding adjuvant chemotherapy completed > 6 months previously). Prior radiation therapy for resectable or locally advanced disease was permitted. Other key eligibility criteria included evidence of either, or both, RECIST-defined measurable disease or an elevated serum CA19-9 at baseline (2× the upper limits of normal (ULN)); an Eastern Cooperative Oncology Group performance score of 0-1; life expectancy greater than 8 weeks; and adequate bone marrow and organ function, as defined by ANC 1500/uL, platelet count 100,000/uL, total bilirubin 2.0 mg/dL, AST and ALT 2.5 × ULN, INR 1.5, and creatinine 2.0 mg/dL. Exclusion criteria included prior therapy with either a MEK or EGFR inhibitor; mandatory use of a QT-prolonging medication; or any of the following: central nervous system metastases; HIV infection; a QTc interval >450 milliseconds or other factors known to increase the risk of QT prolongation or arrhythmic events; refractory nausea/vomiting, malabsorptive or inflammatory bowel conditions; or any other co-morbidities that would increase risk for treatment-related complications.

Study Treatment and Assessments

Enrolled patients orally self-administered selumetinib 100 mg plus erlotinib 100 mg, the recommended phase 2 dose (RP2D) of this combination, with both agents taken once-daily in 21-day cycles without any scheduled treatment interruption. Selumetinib was provided by the Cancer Therapy Evaluation Program (CTEP), while erlotinib was commercially prescribed. Subjects were instructed to take both drugs at the same time on an empty stomach with a glass of water, and to keep a medication diary to monitor compliance.

Patients were assessed in-person at the start of every treatment cycle. Tumor assessments consisted of CT scans performed at the end of every 2 treatment cycles, as well as serial measurements of serum CA19-9 every cycle (if elevated at baseline). Treatment was

discontinued at the time of disease progression, unacceptable toxicity, patient withdrawal of consent, or noncompliance to study treatment.

Correlative Analyses

Immunohistochemistry (IHC) for E-cadherin was performed on 5 μm formalin-fixed, paraffin-embedded (FFPE) sections. Following antigen retrieval, sections were incubated with an anti E-cadherin mouse monoclonal antibody (Invitrogen #13-1700; Clone #HECD-1; 1: 150 dilution), followed by the secondary antibody incubation (Envision + Dual Link System- HRP Dako #K4063). The Dako # K3468 Liquid DAB+ substrate-chromogen system was used as peroxidase substrate. Slides were counterstained with hematoxylin. E-cadherin staining was scored on a scale of 0-2 for intensity (0=absent staining, 1=weak staining, 2=strong staining) and further characterized by the percent of tumor cells demonstrating positive staining by an experienced pathologist experienced (N.J.).

KRAS mutation analysis was performed on FFPE tissue samples. Following macrodissection, *KRAS* hotspot (codon 12,13,61) mutations were detected using the SNaPshot Assay (Life Technologies) which PCR-amplifies *KRAS* (NM_004985.4) exons 2 and 3 from genomic DNA (adapted from (15)). The PCR product was subjected to a fluorescent nucleotide extension step of oligonucleotides specific for single nucleotide changes in KRAS codons 12 (c.34, c.35), 13 (c.37, c.38) and 61 (c.181, c.182, c.183). The lower limit of detection is 10% (16).

For detection and quantitation of circulating tumor cells (CTCs), we used a non-EpCAM based, immunofluorescent, morphologic approach to quantify CTCs as described previously (17). CTCs were identified by immunofluorescence microscopy for cytokeratins, DAPI, and CD45 with automated morphometric analysis followed by manual validation by a pathologist-trained technician (M.S.L.). The technologist, microscopes and automated imaging system were constant throughout the study.

The study protocol was amended partway through enrollment to include analysis of cell-free DNA (cfDNA) on pre- and post-therapeutic plasma samples using Guardant360 Digital Sequencing™ technology (Guardant Health, Redwood City, CA), which allows sequencing of all exonic basis of 18 genes and sequencing of cancer-relevant exons of an additional 36 genes. The Guardant360 panel is an advanced laboratory diagnostic test (ADLT) that converts cell-free DNA molecules into digital sequences pre-sequencing, then decodes/ reconstructs the post-sequencing signal such that over 50 genes (78,000 base pairs) can be sequenced without the false positive results that accompany such long read lengths at very low concentrations of circulating tumor DNA (ctDNA) in plasma. Summarizing the method, cell-free DNA is extracted from plasma and genomic alterations are analyzed by massively parallel sequencing of amplified target genes utilizing an Illumina Hi-Seq platform complemented by systematic end-to-end process optimization including conversion of cell-free DNA fragments into digital sequences, improvements in the Illumina next generation sequencing process itself, followed by bioinformatics algorithms which enable ctDNA to be measured as a quantitative percentage of total cell-free DNA. The lower limit of detection is

a 0.1% frequency of single nucleotide variant (SNV) mutant alleles in a wild-type cfDNA background (18).

Statistical Considerations and Analysis

Using a minimax design, 46 evaluable patients were required to provide 80% power to detect a true 24-week survival rate of at least 51%; with at least 95% probability of a negative result if the true 24-week survival rate was no more than 33%. This 24-week survival rate difference is equivalent to a 67% increase in the median OS (25 vs. 15 weeks). If at least 20 patients (at least 43.5%) were observed to survive 24 weeks among the 46 evaluable patients, this regimen would be considered worthy of further evaluation. A two-stage design was used, with plans to terminate the study early if no more than 8 of the first 25 patients enrolled were alive at 24 weeks.

Data were summarized with respect to demographic and baseline characteristics, safety observations and measurements, and efficacy observations and measurements. Overall and progression-free survival, defined from the time of starting study treatment, was summarized according to the method of Kaplan and Meier. Any patients lost to follow-up prior to 24 weeks were censored at the date of last contact. The frequencies of patients with adverse events were summarized by body system and by major adverse event codes (system/organ/class). Fisher's Exact Test was used to assess statistical significance of differences in biomarker frequencies. Spearman's Rho was calculated to assess a possible correlation between allele frequencies and changes in serum CA19-9 levels. Allele frequencies of alleles undetectable in on-treatment biopsies were set to the smallest number in the dataset (-1).

Results

Patients

Enrollment to this study took place between January 2011 and January 2013, with follow-up data collected through April 2014. Almost all patients had metastatic disease at the time of study entry, and the majority had an ECOG performance status of zero. Baseline characteristics are shown in Table 1.

The threshold for moving on to the second stage of the study, according to Simon's two-stage design, was met once the 15th patient enrolled on the study became the 9th patient to remain alive at the 24-week mark. Overall, 15 of the first 25 enrolled patients were alive at 24 weeks. Therefore, the study continued accrual to reach its final planned sample size of 46 patients.

Treatment administration

Patients received a median of 2 cycles of selumetinib plus erlotinib (range, 1-11 cycles). Eighteen patients (39%) required dose reduction of one or both agents during the course of their study treatment. Reasons for study discontinuation included disease progression (39 patients), disease-related complications (3 patients), treatment-related toxicity (2 patients),

decrease in quality of life (1 patient), and development of a second primary tumor (1 patient).

Adverse events

The most common adverse events (any grade) occurring during study treatment are highlighted in Table 2. Cutaneous (maculopapular and acneiform rash, dry skin, pruritis) and gastrointestinal toxicities (nausea, vomiting, and diarrhea) were the most common categories of adverse events probably or definitely related to study medication. While a variety of ocular disorders were reported by study patients, ophthalmologic evaluation did not reveal any cases of central serous retinopathy. In total, 36 patients (78.2%) experienced at least one grade 3 or higher adverse event, although in many instances (abdominal pain, fatigue, thromboembolic events) it was difficult to assign clear attribution to study treatment versus underlying disease. Of the two patients who discontinued study treatment due to drug-related toxicity, one experienced grade 3 rash and refractory hypertension necessitating a prolonged treatment delay and, ultimately, study discontinuation after cycle #5. The other patient had grade 3 nausea/vomiting/diarrhea, leading to dehydration and hyponatremia, during cycle #1; she was rechallenged at reduced doses, but due to persistent gastrointestinal side effects, had to discontinue study treatment. Four patients died while on or within 30 days of completing study treatment, but these were all attributed to disease progression rather than direct toxic effects from therapy.

Efficacy

Nineteen patients (41%) demonstrated stable disease for greater than 6 weeks, including 12 (26%) with stable disease for at least twelve weeks. There were no objective responses by formal RECIST criteria, although 12 (26%) did demonstrate minor radiographic response (Supplemental figure 1). A waterfall plot of best response to study treatment is shown in Figure 1. Thirteen of 34 patients (38%) with an elevated baseline CA19-9 level had a decline in this serum marker of 50% or greater. Median progression-free survival in the entire cohort was 1.9 months (95% CI, 1.4-3.3 months), with a median overall survival of 7.3 months (95% CI, 5.2-8.0 months) (Figure 2). 58% of patients were alive 6 months from starting study treatment, including 23% alive at one year. Of note, these outcomes met our prespecified definition of a "positive result" with this study regimen, in which we defined a 24-week overall survival rate of at least 43.5% as indicative of promising activity.

Twenty-seven patients (58.7%) went on to receive additional chemotherapy after discontinuing study treatment, including a fluoropyrimidine/platinum-based combination (FOLFOX or CapOx) in 8 patients; gemcitabine plus nab-paclitaxel in 12 patients; FOLFIRINOX in 2 patients; and capecitabine monotherapy in 2 patients. Fifteen patients did not undergo any further treatment, while follow-up treatment data were not available in the remaining 4 patients.

Correlative studies

Molecular analyses of tumor samples—Point mutations in *KRAS*, a well-established and central pathogenic feature in this disease (2,19), were identified in 24 of 26 (92%) tumor samples, including both FFPE tissue samples and fine-needle aspirates. A wide spectrum of

KRAS mutations were observed, the most common being G12D (42%), followed by G12V (25%).

We also assessed E-cadherin expression in 23 patients in whom sufficient archived tumor material was available for immunohistochemical analysis. Most tumors demonstrated a heterogeneous staining pattern with varying fractions of E-cadherin-expressing cells (Supplemental Figure 2). Based on our preclinical studies, we expected pancreatic cancers containing a higher proportion of E-cadherin expressing cells, reflecting an epithelial phenotype, to be more sensitive to treatment with dual MEK plus EGFR inhibition, than those with more mesenchymal-type cells (lacking E-cadherin expression). Indeed, 7 of 11 patients whose tumors contained a higher percentage of E-cadherin-expressing cells experienced a 50% or greater CA19-9 decline, compared to 0 of 9 patients whose tumors had a lower proportion of E-cadherin-expressing cells (p=0.0047) (Figure 3).

Circulating tumor cells—Enumeration of CTCs was assessed in 33 patients before and on treatment. Mean CTC concentrations were 2.71 and 2.94 cells/mL in pre- vs. on-treatment samples, respectively, while the number of samples with CTC concentrations greater than 1 cell/mL were 10 and 7, respectively (data not shown). No clear association between CTC concentration and treatment effect was observed.

Cell-free DNA analyses—Plasma samples were collected from 32 patients for digital sequencing of cfDNA using the Guardant360 assay. DNA sequence germ-line single nucleotide polymorphisms (SNPs) were detected at 100% or near-to 100% allele frequency (homozygous variants), or 50% or near-to 50% allele frequency (heterozygous variants), in all samples. Additionally, sequence variants likely originating from the tumor (based on allele frequency and absence in the above-mentioned germ-line variants) were found in 27 (84%) pre-treatment and 25 (78%) on-treatment samples. Average relative frequencies of tumor-derived mutant alleles were 4.59% (range, 0.1%-57.2%) and 3.95% (range, 0.1%-78.4%) pre- and on-treatment, respectively. Supplemental Table 1 lists all mutations found for the entire study cohort. After filtering results for mutations with known biological function and those likely to impact on the functionality of the affected protein, 17 genes were found to be mutated at least once in pre-and/or on-treatment plasma samples (Supplemental Figure 3). As expected, the most frequently mutated gene in pre-therapeutic plasma samples, in which circulating tumor fraction is > 0.4%, was *KRAS* (85%), followed by *TP53* (60%), *ATM* (30%), and *CDKN2A* (15%). *KRAS* mutations in plasma were uniformly concordant with those found in tumor in all 11 cases for which paired samples were available. Interestingly, a decline of CA19-9 of 50% or greater was observed in 7 of 10 patients (70%) in whom pre-treatment mutant *KRAS* was not detected in plasma, compared to 4/15 patients (26%) with detectable *KRAS* mutations at baseline (p=0.0486).

The majority of mutations (66%) identified in pre-treatment plasma samples were also present in on-treatment samples. A decrease in relative frequency for those alleles across these two time points showed a statistical trend toward positive correlation with CA19-9 decline (R^2=0.1369, p=0.08) (Figure 4).

Discussion

Activated KRAS is an important driving force promoting and maintaining the malignant phenotype in PDAC (1,20). Among the potential targets for novel therapeutic development for PDAC are effector pathways of KRAS signaling, including members of the mitogen-activated protein (MAP) kinase pathway (RAF-MEK-ERK). However, to date, MEK inhibitors have shown limited single-agent anti-tumor activity in PDAC (21,22). For example, selumetinib (AZD6244; ARRY-142886), a selective, allosteric inhibitor of MEK1/2, has previously been evaluated in a randomized phase II study of selumetinib vs. capecitabine monotherapy in advanced PDAC in which similar overall and progression-free survival was seen between these two agents (22).

The motivation for this trial emanated from work performed by our group identifying a novel negative regulatory feedback loop that help explain the limitations of a MEK inhibitor administered as monotherapy. In both breast and pancreatic cancer cell lines, pharmacologic inhibition of MEK results in markedly enhanced phosphorylation of EGFR and activation of the PI3K-AKT cascade (6),(20). This feedback signal can be fully abolished by concomitant inhibition of EGFR kinase activity. The combination of MEK and EGFR inhibitors show synergistic effects on cell growth in PDAC cell lines (irrespective of KRAS mutational status), and additive or synergistic antitumor activity in pancreatic tumor xenografts (20). Other groups have similarly reported synergistic activity in various preclinical models (9).

In the current study evaluating dual MEK/EGFR inhibition in patients with advanced chemotherapy-refractory PDAC, this combination conferred modest evidence of antitumor activity in a subset of patients, including prolonged disease control, minor radiographic responses, and significant declines in serum CA19-9 levels. While the study did meet its primary survival endpoint suggesting promising activity of this combination, the limitations of a non-randomized, single arm trial need to be recognized in terms of interpreting the results. Certainly, an inherent patient selection bias was likely in this study in terms of enrollment of patients with more favorable disease biology, including a relatively high proportion of patients (30 percent) who had undergone prior resection; patients with metachronous metastatic disease tend to fare better overall when compared to those who present with stage IV disease at original diagnosis. Further indication of this selection bias was reflected by the fact that median overall survival for the study cohort (from the time of original pancreatic cancer diagnosis to death) was 18.9 months (range, 5.2 – 86.4 months), which far exceeds what one would normally expect for this patient population. We also note that more than half of patients did receive additional chemotherapy after discontinuing study treatment, although the benefit of third-line therapy in this disease context is unclear in terms of its impact on survival results.

The second-line setting for advanced pancreatic cancer, the clinical context in which this study was performed, is one in which there currently remains no accepted standard of care, with conventional chemotherapy regimens producing median survival times in the range of 6 months or less (reviewed in (23)). The current *de facto* approach for patients who have progressed following first-line gemcitabine-based chemotherapy has been to use a combination of oxaliplatin plus a fluoropyrimidine, based on results from a phase III

German study (Charité Onkologie [CONKO] 003) (24), although a subsequent Canadian trial of similar sample size did not suggest any benefit of FOLFOX (5-FU, leucovorin, and oxaliplatin) when compared to 5-fluorouracil/leucovorin alone (25). A more recent international phase III trial showed that the addition of a nanoliposomal formulation of irinotecan to fluoropyrimidine-based therapy in gemcitabine-pretreated patients conferred a significant survival benefit (26), and may offer a new reference standard for future studies of second-line treatment in which randomized design is desirable to avoid the aforementioned selection biases.

While it may now be possible to offer patients two or more lines of chemotherapy, a non-cytotoxic, completely orally bioavailable regimen holds conceptual appeal in a patient population often characterized by inanition and declining performance status, for whom the side effects of chemotherapy may be considerable and potentially life-threatening. However, to date, "targeted therapy only" strategies have been met with fairly dismal outcomes in phase II trials (27,28). A recently reported Southwest Oncology Group phase II trial (SWOG S1115) randomizing patients who had progressed on gemcitabine-based therapy to either selumetinib plus the AKT inhibitor MK-2206 or traditional chemotherapy (FOLFOX) found that survival was shorter in the targeted-therapy group, albeit in a molecularly unselected patient population (29). Moreover, while patients may wish to avoid the side effects associated with classical cytotoxic therapy, it is important to recognize the unique toxicities associated with molecularly targeted agents that may limit treatment administration and affect patients' quality of life. For example, in the current study a relatively high proportion of patients required dose modifications of one or both agents, most commonly due to cutaneous or gastrointestinal adverse events. These observations highlight the challenges of administering multiple targeted therapeutic agents in pharmacologically relevant doses; furthermore, they raise important questions regarding the feasibility of merging this combinatorial approach with traditional cytotoxic agents in earlier lines of therapy, where the additive toxicities would likely be prohibitive.

A key component of our study was to identify molecular features of PDAC that might predict clinical benefit to combined EGFR/MEK inhibition. Our group previously defined three molecular subtypes of PDAC (classical/epithelial, quasi-mesenchymal, and exocrine-like) based on distinct transcriptional profiles derived from primary tissues and represented in preclinical models (30). These subtypes show differential responses to both cytotoxic and targeted therapies *in vitro*. Specific to dual MEK/EGFR inhibition, genes representative of the epithelial-like subtype (in particular E-cadherin) were highly expressed in sensitive cell lines, whereas each of the cell lines most resistant to this combination fell into the mesenchymal subtype (5). For this clinical study, we analyzed available archived tumor samples to assess for subtype-specific differential responses. In agreement with published data (31,32), the majority of tumors showed substantial intratumoral heterogeneity, harboring both epithelial- and mesenchymal subtypes at various ratios (as reflected by E-cadherin expression). Acknowledging sample size limitations, it is noteworthy that epithelial-type tumor cell fraction was significantly associated with treatment sensitivity, reflected by CA19-9 decline. It has been previously reported that cancer cells maintaining epithelial differentiation remain addicted to K-Ras (whereas epithelial to mesenchymal

transition leads to reduced K-ras dependency), with a K-Ras dependency gene expression signature associated with greater sensitivity to EGFR kinase inhibitors (33). A separate study showed, similarly, that restoring E-cadherin expression in lung cancer cell lines increased sensitivity to this same class of drugs (34). Our study supports these findings and is the first to suggest an association between an epithelial-predominant subtype (as characterized by E-cadherin expression) and drug sensitivity in patients with pancreatic cancer. While it may be premature to propose routine E-cadherin immunohistochemistry testing on all tumors prior to initiation with erlotinib or other EGFR inhibitors, such testing could be embedded as part of correlative analyses within future clinical trial design where these agents are being tested.

We also explored the utility of blood-based biomarkers to monitor molecular events over the course of treatment. Measurements of CTC concentration using an advanced high-content image analysis system revealed significantly lower levels than observed in a prior pilot study (17), with no significant association with clinical response parameters observed. More promise was observed from digital sequencing of solid tumor cfDNA in plasma using a commercial assay that enabled the sequencing of 54 tumor-associated genes. We were able to detect tumor DNA in plasma in a remarkably high fraction (84%) of patients, suggesting this method could provide valuable molecular information for both predictive and monitoring purposes in this patient population. While our results do not necessarily demonstrate on-target treatment effects specific to the particular EGFR/MEK inhibitor combination used for this study, we posit that shifts in frequency and type of mutations over the treatment course may reflect dynamic alterations in the composition of molecularly defined sub-clones within the tumor. Further preclinical and clinical studies will be necessary to elucidate such clonal dynamics and to understand the mechanisms behind treatment failure and tumor progression. Intriguingly, we found an association between changes in allele frequencies of the most frequent mutations identified in cfDNA and indicators of disease burden (notably CA19-9 levels) that almost reached statistical significance. It is conceivable that such quantitative changes in allele abundance could provide early information on therapeutic benefit or, conversely, development of resistance. Incorporation of both baseline and serial measurements of cfDNA throughout the course of treatment has potential utility for patient selection and treatment decision-making in future clinical studies of this or related combination therapies, although establishing the concordance between mutations identified in cfDNA and tumor tissue will be important to ensure that this "liquid biopsy" is a reliable surrogate. Indeed, several groups have already shown high concordance rates between the two platforms in small series of patients (35,36). Our group, for example, recently reported high levels of sensitivity and specificity of blood-based sequencing results across five genes examined (KRAS, TP53, APC, FBXW7, and SMAD4) (36). Reassuringly, in the current study, 100% concordance in KRAS mutations was observed between tumor and plasma where paired samples were available, with the performing clinical laboratory blinded to the tissue-based SNaPshot sequencing results.

In summary, the combination of MEK and EGFR inhibitors evaluated in this clinical trial showed evidence of modest anti-tumor activity and offers proof of principle regarding both the feasibility and promise of this strategy. Successor studies could be developed using more potent MEK inhibitors and/or combining these agents with inhibitors of alternative signaling

nodes, and ideally be evaluated in the context of a randomized trial design comparing a "targeted-only" approach to cytotoxic therapy, especially as second-line chemotherapy becomes more widely accepted as standard of care. Such studies would also ideally incorporate quality of life endpoints given the unique and often substantial toxicities associated with each of these therapeutic approaches.

Perhaps the most critical issue of all to address is whether the findings in our study convincingly define a particular subset of individuals most likely to benefit from this specific combination of targeted agents. One might reasonably ask whether a future study employing a similar treatment strategy, for example, should limit patient enrollment to those with epithelial-type tumors. While our clinical findings certainly have to be considered preliminary, they do corroborate our preclinical observations suggesting a subtype-specific sensitivity to this combination of agents. As such, we submit that it would be entirely appropriate to develop a study in which E-cadherin expression, clearly predefined and measured under CLIA-certified laboratory conditions, could be used as an integral biomarker for determining patient eligibility. This would represent an important next step in bringing the treatment of pancreatic cancer more squarely into the era of precision medicine.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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Statement of Translational Relevance

Recent improvements in combination chemotherapy for metastatic pancreatic cancer have not been mirrored by similar advances in molecularly targeted therapies. Due to feedback signaling mechanisms and cross-talk between signaling pathways -- for example, those downstream of KRAS -- pathway-targeting agents may need to be administered not as monotherapies, but in rational combinations balancing toxicity concerns with pharmacodynamically relevant dosing. In this report, we describe results from a non-randomized phase II clinical trial combining EGFR and MEK inhibition in patients with chemotherapy-refractory pancreatic cancer, a clinical context in which there is still great unmet need. In addition to the clinical findings, we present preliminary but provocative findings indicating certain molecular subtypes of pancreatic cancer that may be more sensitive to this dual-targeted therapeutic approach than others. Future studies should prioritize identification of molecular predictors of therapeutic response, either through tissue-based samples or preferably more accessible sources of surrogate material.

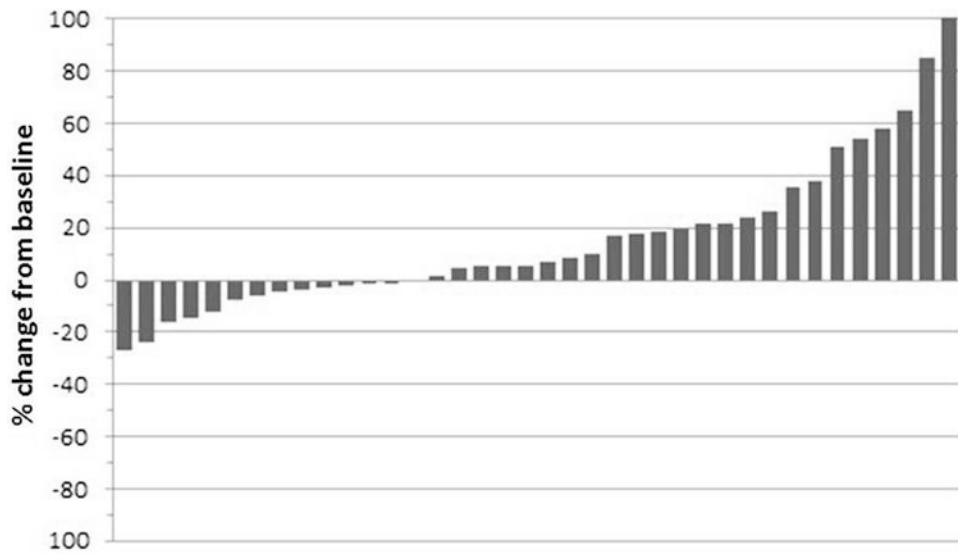**Figure 1.**
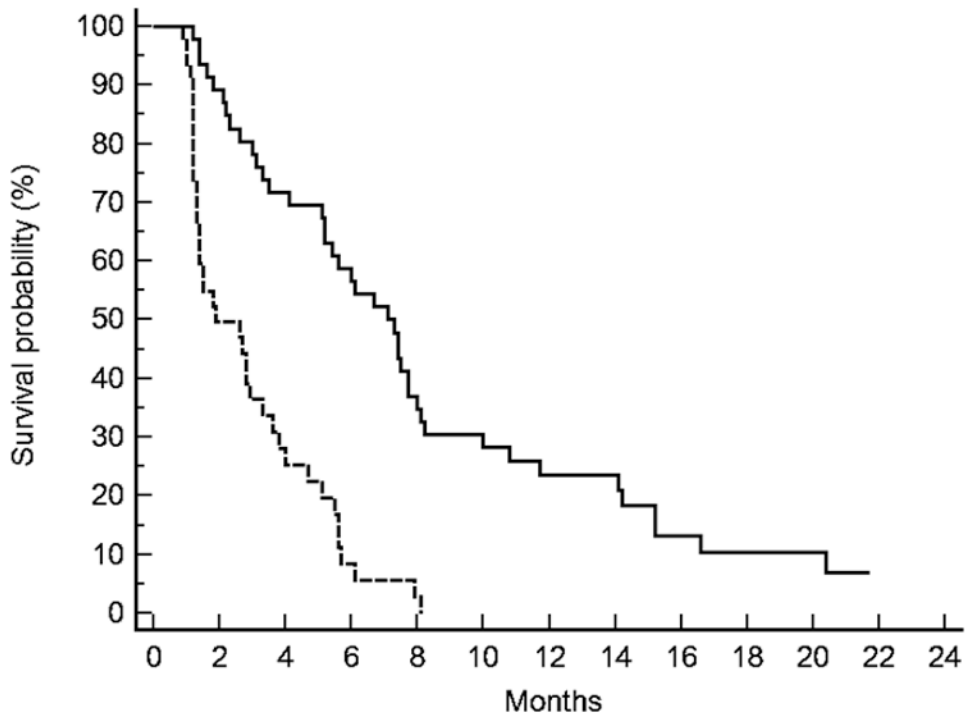Waterfall blot showing best response to treatment as determined by RECIST measurements for all patients.

Figure 2.
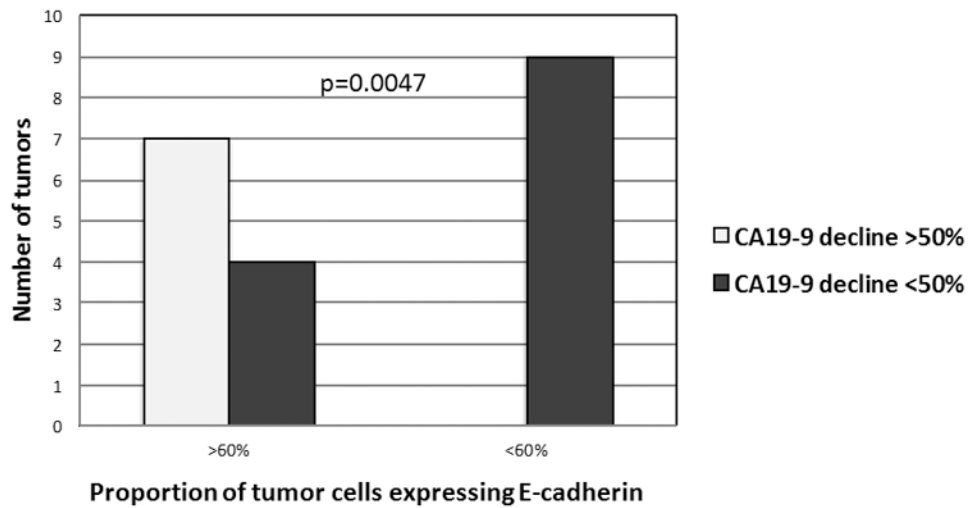Kaplan-Meier analysis of progression-free (dotted line) and overall (solid line) survival.

Figure 3.
Correlation of tumor marker response and E-cadherin expression. The proportion of E-cadherin-expressing cells in pre-therapeutic biopsies was determined by immunohistochemistry. Light-gray bars represent patients with significant decline in serum CA19-9 levels while black bars indicate patients lacking significant decline in CA19-9 levels. Statistical significance was determined using Fisher's Exact Test.
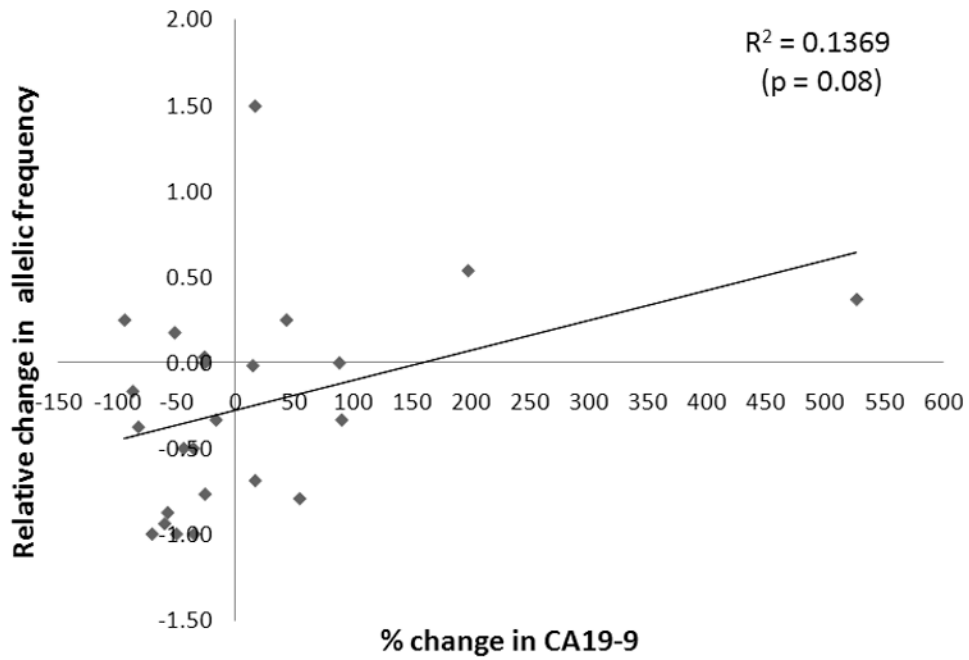
Figure 4.
Scatter plot showing correlation between CA19-9 changes (x-axis) and relative changes in frequency of the most frequent mutant allele in cfDNA as determined by the Guradant360 assay (y-axis). Spearman's Rho was calculated to assess for correlation.

Table 1

Patient characteristics at baseline

N	46
Dates of enrollment	Jan 2011 – Jan 2013
Age (median)	67 y.o. (range, 40-84)
ECOG performance status (0/1)	32/14 (70%/30%)
Stage (metastatic/locally advanced)	44/2 (96%/4%)
Prior chemotherapy	
Gemcitabine-based	34 (74%)
FOLFIRINOX	10 (22%)
Other	2 (4%)
Prior surgery	14 (30%)
Prior radiation	7 (15%)
Elevated baseline CA19-9 > 2× ULN	34 (74%)

Table 2

Treatment-related adverse events (maximum grade, all cycles).

Adverse event	Any grade, No. (%)	Grade 3-4, No. (%)
Rash	35 (76%)	10 (22%)
Diarrhea	35 (76%)	6 (13%)
Nausea/vomiting	27 (59%)	4 (9%)
Fatigue	26 (57%)	3 (7%)
AST/ALT elevation	22 (48%)	4 (9%)
Anorexia	15 (33%)	0 (0%)
Anemia	14 (30%)	5 (11%)
Dysgeusia	11 (24%)	0 (0%)
Eye disorders[1]	9 (20%)	0 (0%)
Pruritis	9 (20%)	0 (0%)
Hypertension	8 (17%)	6 (13%)
Thrombocytopenia	5 (11%)	1 (2%)
Leukopenia/neutropenia	4 (9%)	1 (2%)
Thromboembolic event[2]	4 (9%)	3 (7%)
Elevated creatinine	4 (9%)	0 (0%)

[1] Including blurry vision, eye pain, floaters, and dry or watery eyes.

[2] Including cerebrovascular event (1).