Integrating Murine and Clinical Trials with Cabozantinib to Understand Roles of MET and VEGFR2 as Targets for Growth Inhibition of Prostate Cancer

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Abstract

**Purpose:** We performed parallel investigations in cabozantinib-treated patients in a phase II trial and simultaneously in patient-derived xenograft (PDX) models to better understand the roles of MET and VEGFR2 as targets for prostate cancer therapy.

**Experimental Design:** In the clinical trial, radiographic imaging and serum markers were examined, as well as molecular markers in tumors from bone biopsies. In mice harboring PDX intrafemurally or subcutaneously, cabozantinib effects on tumor growth, MET, PDX in which MET was silenced, VEGFR2, bone turnover, angiogenesis, and resistance were examined.

**Results:** In responsive patients and PDX, islets of viable pMET-positive tumor cells persisted, which rapidly regrew after drug withdrawal. Knockdown of MET in PDX did not affect tumor growth in mice nor did it affect cabozantinib-induced growth inhibition but did lead to induction of FGFR1. Inhibition of VEGFR2 and MET in endothelial cells reduced the vasculature, leading to necrosis. However, each islet of viable cells surrounded a VEGFR2-negative vessel. Reduction of bone turnover was observed in both cohorts.

**Conclusions:** Our studies demonstrate that MET in tumor cells is not a persistent therapeutic target for metastatic castrate-resistant prostate cancer (CRPC), but inhibition of VEGFR2 and MET in endothelial cells and direct effects on osteoblasts are responsible for cabozantinib-induced tumor inhibition. However, vascular heterogeneity represents one source of primary therapy resistance, whereas induction of FGFR1 in tumor cells suggests a potential mechanism of acquired resistance. Thus, integrated cross-species investigations demonstrate the power of combining preclinical models with clinical trials to understand mechanisms of activity and resistance of investigational agents. *Clin Cancer Res; 1–15. ©2015 AACR.*

**Introduction**

The planned integration of clinical and murine investigations can overcome the limitations of each and efficiently link mechanisms to therapeutic benefit. Furthermore, this strategy can provide mechanistic insights into clinical observations (1–3). This approach is particularly relevant in cancers in which “drivers” that account for important clinical phenotypes have not been identified, such as bone metastatic castrate-resistant prostate cancer (mCRPC). This limited understanding of the biology of the disease and mechanisms of resistance hamper development of targeted therapeutic strategies for mCRPC. An example of the difficulty of objectively linking clinical observations to inhibition of specific signaling pathways has occurred with cabozantinib, an oral multikinase inhibitor with potent activity against MET and VEGFR2 (4) which, in phase II clinical trials, led to striking improvements in bone scans, associated with reduced pain and soft-tissue/visceral tumor responses and reduction in circulating tumor cells (5, 6). A major caveat of these studies is that the mechanisms leading to these responses, despite a corresponding decline in serum prostate-specific antigen (PSA), are not fully understood.
Nevertheless, the initial excitement from cabozantinib responses led to a recent phase III clinical trial studying the effects of cabozantinib monotherapy in late-stage mCRPC (COMET 1). This phase III study showed a significant lengthening of progression-free survival but not prolongation of overall survival compared with patients treated with prednisone (7).

The inability to prolong survival in a large-scale phase III clinical trial illustrates a central problem in therapy development. Neither preclinical models nor phase I and II clinical trials alone have been sufficient to predict success of novel therapies in phase III clinical trials. In mCRPC, serial sampling and molecular–pathologic analyses of tumors via transilicace bone marrow biopsies have facilitated the discovery of predictive biomarkers of response and resistance. However, an inherent problem with examining markers in human bone biopsies from patients with prostate cancer in phase II clinical trials is intratumoral heterogeneity, both within individual biopsy samples and over time, leading to sampling bias (8–11). While preclinical models allow more complete examination of markers, they often overestimate the success of novel therapies. To overcome these limitations, we have used the approach of running parallel investigations on well-defined, representative patient-derived xenografts (PDX) in conjunction with a phase II clinical trial as a strategy to provide insights into the unanticipated clinical findings. Studies in PDX are suited to defining mechanisms as they lack limitations as to the time course over which specimens can be collected and allow the collection of large amounts of material for analyses. In addition, PDX can be genetically manipulated to assess the effects of specific gene products on therapy response, thus allowing mechanistic studies on drug targets and resistance. For these reasons, mouse models complement clinical investigations.

Our parallel studies provided insights into the mechanism of action of cabozantinib that are of general relevance to targeted agents for the treatment of prostate cancer. Specifically, we demonstrate: (i) MET in tumor cells is not a sustained therapeutic target for established, late-stage tumors, but MET in the microenvironment is; (ii) genetic and pharmacologic inhibition of MET leads to induction of FGFR1 expression in tumor cells; (iii) vascular heterogeneity represents one source of primary resistance when VEGFR2 is targeted; (iv) inhibition of osteoblast proliferation and induction of differentiation is responsible for the compelling bone scan changes in cabozantinib-treated patients and mice bearing PDX; and (v) biologically optimized dose and scheduling of therapy may be important for maximizing the efficacy of microenvironment targeting agents.
platform (Aushon BioSystems), and data were analyzed with Aushon’s PROarray Analyst Software.

**Primary patient-derived prostate cancer xenografts**

The development and characterization of primary xenograft models have been described elsewhere (15, 16). Between 2009 and 2012, 35 PDX models were developed from 96 attempted (36%). For this study, we used fresh-frozen tumors from stock of PDX models that have been well-characterized and represent different spectra of prostate cancer progression. Briefly, the MDA PCa-180-30 xenograft has morphologic features of conventional adenocarcinoma and expresses high levels of androgen receptor. The MDA PCa-144-13 xenograft has morphologic features of mixed adenocarcinoma and small cell prostate cancer. The MDA PCa-118b xenograft when implanted in the mouse femur exhibits a strong osteogenic phenotype similar to that of the human prostate cancer from which it was derived (17). Importantly, the MDA PCa-118b induces new bone formation even at subcutaneous sites (17, 18). Histologic analysis of subcutaneous MDA PCa-118b implants indicates that they have all of the cellular elements, including osteoblasts and osteoclasts, of human bone lesions (19).

**Development of the sh-c-met–expressing MDA PCa-144-13 xenograft**

To develop xenografts in which MET expression was reduced, a single-cell suspension of MDA PCa-144-13 cells from a fresh tumor was maintained in tissue culture plates for 3 days. Cells were infected with lentivirus directing the expression of sh-c-met or a nontargeting sequence (Supplementary Table S2). NT and sh-c-met MDA PCa-144-13 cells were sorted for GFP and injected into the flanks of SCID mice.

**Reagents**

Cabozantinib (XL-184) is a small-molecule tyrosine kinase inhibitor that potently targets MET, VEGFR2, and several other receptor tyrosine kinases implicated in tumor pathobiology, including RET, TIE2, AXL, FLT3, and KIT (14). Cabozantinib was provided by Exelixis. For the parallel mouse experiments, cabozantinib was formulated in sterile H2O/10 mmol/L HCl. Anti–c-erbB-2 antibodies used in the study are listed in Supplementary Table S3.

**Treatment of MDA PCa-180-30, MDA PCa-118b, and MDA PCa-144-13 xenograft tumors**

Primary xenograft experiments were performed in accordance with regulations and standards of the U.S. Department of Agriculture, the U.S. Department of Health and Human Services, the NIH, and The University of Texas MD Anderson Cancer Center Institutional Animal Care and Use Committee guidelines. Mouse treatment schedules are described in the Supplementary Methods. Tumor volumes were calculated with the formula \( V = (W/2) \times (L)^2 \). Mice were killed when tumor volume reached 1,500 mm\(^3\), when weight loss exceeded 30%, or at the times specified in Results. After the mice were killed, tissue samples were preserved for hematoxylin and eosin (H&E) staining, immunoblotting, immunohistochemical (IHC) staining, and immunofluorescent staining as described elsewhere (16, 20, 21).

**Statistical methods**

Differences among groups were assessed by the Student t tests or ANOVA followed by Fisher exact tests for multiple comparisons. Tumor growth was compared by repeated-measures ANOVA and survival by the log-rank (Mantel–Cox) test. \( P < 0.05 \) was considered significant. Error bars show means ± SEM. For human studies, descriptive statistics were used to summarize maximum changes in bone-specific alkaline phosphatase (BAP), urine N-telopeptides (uNTx), and cytokines that occurred during treatment.

**Results**

**Responses to cabozantinib in a phase II clinical trial and PDX**

MDA PCa-118b grown intrafemurally

Sixteen of 20 patients in the phase II trial (80%) showed greater than a 30% reduction in BSLA, a measure of tumor response, at 6 weeks after treatment (Fig. 1A). Four representative bone scans are shown in Fig. 1B, 1 from a nonresponder, 2 from partial responders, and 1 from a patient showing complete bone scan resolution. Patient characteristics are shown in Supplementary Table S1. To determine whether the responses of PDX grown in the bone were consistent with what was observed in patients in the trial, we injected MDA PCa-118b (1 × 10\(^6\) cells) into the femur of immunodeficient mice and obtained baseline MRI scans 10 days later. After randomization of mice based on both tumor size and growth of tumor inside the bone, half the mice were treated with cabozantinib starting 10 days after the MRI, and the other half were treated with vehicle alone. Untreated tumors grew exponentially (as estimated by MRI), whereas tumor growth was strongly inhibited by cabozantinib. Representative MRI scans are shown in Fig. 1C (left). Tumor volumes (Fig. 1C, right) were calculated as described in Materials and Methods.

Next, to examine bone turnover in mice, we used a functional bone imaging technique involving NaF-18 PET scans as described in Materials and Methods. Changes in signal intensity in control bones were apparent in the PET (Fig. 1D, left). The standard uptake value (SUV; calculated as described in Materials and Methods) demonstrated decreased bone turnover in cabozantinib-treated mice relative to untreated mice (Fig. 1D, right). Representative PET scans of whole mice including an intensity scale are shown in Supplementary Fig. S1. These results demonstrate that responses to cabozantinib in the MDA PCa-118b intrafemoral model correspond with initial responses in the clinical trial.

**Responses to cabozantinib in subcutaneous models mimic response to tumors growing in the bone**

We next examined the effects of cabozantinib on the subcutaneous growth of MDA PCa-118b and 2 other PDX models, the androgen receptor–positive MDA PCa-180-30 PDX and the androgen receptor–negative MDA PCa-144-13 (the latter 2 PDX can only be grown subcutaneously). Tumor stabilization was observed in all 3 PDX as estimated by tumor volume (Fig. 2A–C) and was comparable to that observed in tumors grown intrafemurally. Relative growth in control and cabozantinib-treated mice was similar in each model (Supplementary Fig. S2A–S2C). Animal weights were maintained throughout treatment (Supplementary Fig. S2D–S2F). Cabozantinib-treated mice also had a substantially prolonged survival time (i.e., time until tumor volume reached 1,500 mm\(^3\)) relative to control mice in each model (Supplementary Fig. S2G–S2I). Thus, the results from xenograft models parallel the clinical responses of our patient population and of patients reported by others (6).
Although tumor volume was stabilized, massive tumor necrosis was observed in the PDX models after 3 weeks of cabozantinib treatment (Fig. 2D). Occupancy of viable tumor cells was determined in the tumor mass (as measured by H&E in 10 tumor sections, 4× magnification) and significantly decreased in all xenografts (Fig. 2D, quantified in 2E). Areas of necrosis exceeded 70% of total tumor section area (Fig. 2E). Thus, these PDX studies demonstrated regression in tumor burden.

Furthermore, a characteristic pathologic finding in these PDX specimens after cabozantinib treatment was the presence of multiple, well-defined islets (80–160 μm radius) of viable tumor cells with a central blood vessel. The patient studies included transiliac bone marrow biopsies collected at baseline and after 6 weeks of daily cabozantinib treatment. Similar-sized foci of viable tumor cells (65–150 μm radius) were seen in both patient biopsies and in treated MDA PCa-118b tumors grown intrafemurally (Fig. 2F and Supplementary Fig. S3), as well as PDX grown...
Figure 2.
Growth inhibition and tumor islets of viable cells following cabozantinib treatment in xenografts and human bone metastases. Xenograft tumors were grown subcutaneously to 100 to 400 mm³, and mice were randomized to vehicle- and cabozantinib-treated groups. A–C, growth of PDX treated 6 d/wk by oral gavage with 30 mg/kg cabozantinib or H2O for indicated times (\(P < 0.01; \text{**}; P < 0.001; \text{***}; P < 0.0001\)). D, representative H&E (4× magnification) of above xenograft tumors before and after 3 to 4 weeks of cabozantinib treatment. *, necrotic areas; arrows indicate live tumor cells. b, bone; live tumor cells (\(^*\)). E, quantitation of occupancy of tumor mass by viable tumor cells at baseline and after 3 weeks of cabozantinib treatment. F, H&E showing bone (b), necrotic tumor cells (\(^*\)) in MDA PCa-118b xenograft model (top) and human bone metastases (bottom) at baseline and end of cabozantinib treatment. (Continued on the following page.)
subcutaneously (Fig. 2G and Supplementary Fig. S3). Cells in the islets were actively dividing at rates comparable with untreated tumors, as determined by phospho-histone H3 staining (Fig. 2H, top; H&E shown in insets; quantification shown in bottom). Thus, residual, viable tumor cells were a common characteristic of patient samples and all xenograft models examined. A schematic representation of the features of islets is shown in Fig. 2I.

**MET activation persists in human and mouse tumors treated with cabozantinib**

We next determined whether cabozantinib inhibited MET phosphorylation in viable tumor cells. We performed IHC staining for total MET and activated pMET on pretreatment and cabozantinib-treated tumor specimens from both humans (after 6 weeks of daily cabozantinib, when steady-state levels of cabozantinib were achieved; ref. 13) and mice after 3 weeks of treatment. Mice were sacrificed 2 to 4 hours after the final cabozantinib treatment. Bone scan images, CT scans, H&E staining, MET, and pMET are shown for representative patients with partial improvement (Fig. 3A) and complete improvements (Fig. 3B) on bone scans. In all 9 patients in which tumor was evident in pre- and posttreatment biopsies, pMET expression was observed at baseline, although staining intensity was variable. Eight of those 9 patients showed no decrease in MET phosphorylation in 6-week biopsies relative to baseline biopsies. A 30% decrease in pMET was observed in the ninth patient. In parallel, PET scans, H&E staining, and MET and pMET stainings were performed for intrafemoral MDA PCA-118b PDX (Fig. 3C). Images of the excised tumor, H&E, and MET and pMET stainings for subcutaneously grown MDA PCA-180-30 tumors are shown in Fig. 3D. Cabozantinib effectively controlled tumor growth in both PDX, and the treated MDA PCa-180-30 tumors appeared to be reduced in angiogenesis as gauged by their white appearance (Fig. 3D); however, as was true for human specimens, pMET staining was not inhibited in islets of viable tumor cells.

**PDX reveal initial, but not sustained, pMET inhibition by cabozantinib**

The unexpected presence of pMET (by IHC) after cabozantinib treatment raised several possibilities: (i) the drug was not hitting the target, (ii) inhibition of pMET occurred only at earlier time points than tested in patients, and (iii) inhibition of pMET was not required for sustained growth inhibition by cabozantinib. As part of our parallel approach, we evaluated the effect of cabozantinib on pMET expression over time in MDA PCA-144-13 xenografts. Mice were sacrificed and tissue obtained at intervals that could not be done clinically: 0, 2, 4, 6, 9, and 21 days after cabozantinib treatment. Findings from H&E, MET, and pMET stainings are shown in Supplementary Fig. S4A. By IHC, pMET was nearly completely inhibited within 2 days of treatment, indicating cabozantinib was capable of inhibiting one of its principal targets. Thus, initial inhibition of tumor growth may be due, in part, to pMET inhibition in tumor cells. However, pMET was readily detectable after 9 days of treatment (Supplementary Fig. S4A). The unanticipated MET reactivation explains the presence of MET phosphorylation in the islets of viable cells identified after 21 days, in which MET was phosphorylated to the same level as in control tumors.

(Continued) G, islets of viable tumor cells in cabozantinib-treated tumors after 3 weeks (20× magnification). H, H&E and phospho-histone H3 IHC in control and cabozantinib-treated tumor islets after 3 weeks (20× magnification); bottom, quantitation of phospho-histone H3 staining. Inset, H&E staining of the same area. Graph shows the percentage of phospho-histone H3–positive cells relative to total number of viable cells (data represent mean and SEM). I, diagrammatic representation of islets: (a) live cells growing in proximity to the central vessel, (b) live cells on the periphery of the islet, (c) apoptotic and necrotic cells, (1) axial plane, (2) coronal plane showing red blood cells in center of islet.

**Figure 3.** Response to cabozantinib and MET activation in human tumors and PDXs. Bone scan, CT scan, H&E staining, and MET and pMET IHC for patients with mCRPC at baseline and 6 weeks after cabozantinib treatment for a patient with (A) partial response and (B) complete response. Arrows indicate area of bone biopsy. Response in MDA PCA-118b grown in the bone (C) or MDA PCA-180-30 grown subcutaneously (D). Left, PET scan of bone tumors; right, macroscopic appearance for subcutaneously grown tumors. Panels below H&E staining, MET, and pMET IHC.
To further examine mechanisms of tumor inhibition, immunoblotting was performed on tissue lysates from PDX specimens (control and cabozantinib-treated). These experiments were performed after 4 days of treatment, before extensive necrosis occurred. In the MDA-Pca-144-13 tumors, both pMET and pVEGFR2 were inhibited after treatment, as expected (Supplementary Fig. S4B, left). Cabozantinib treatment also led to inhibition of phosphorylation of the downstream targets, c-Src and Akt, but not their expression (Supplementary Fig. S4B, right). These results confirm that cabozantinib inhibited primary and downstream signaling intermediates at early times after treatment.

**MET signaling is not required for sustained growth of prostate cancer cells in vitro and in vivo**

We next determined the relevance of pMET in the islets of viable cells that persisted after cabozantinib treatment. For this study, we short-term cultured MDA-Pca-144-13 cells and assessed the effect of cabozantinib on these cultures. Both intrinsic pMET (Fig. 4A) and hepatocyte growth factor (HGF)-induced pMET (Fig. 4B) were inhibited. Next, we infected cultured MDA-Pca-144-13 cells with a lentivirus directing the expression of an sh-c-met or an NT sequence as described in Materials and Methods. Infecting MDA-Pca-144-13 cells with an sh-c-met lentivirus resulted in more than 90% decreased expression of MET protein, as determined by immunoblotting (Fig. 4C), and decreased c-met mRNA by 92%, as determined by qRT-PCR (Supplementary Fig. S5). However, no change was observed in downstream signaling, including p-Akt, and p-Erk1/2 (Fig. 4C). Knockdown of MET also had no effect on apoptosis, as determined by cleaved PARP (Fig. 4C), or on proliferation (Fig. 4D). We next examined the effect of cabozantinib on proliferation of MDA-Pca-144-13 cells transfected with an NT vector or sh-c-met vectors in vitro. As shown in Fig. 4E, cabozantinib at 100 nmol/L, a concentration that completely inhibited MET phosphorylation, had no effect on proliferation of both NT and MET knockdown variants after 96 hours. Similarly, cabozantinib concentrations from 10 nmol/L to 1 mmol/L had no effect on proliferation of cells transfected with an NT vector (Fig. 4F) or on sh-c-met knockdown cells (Fig. 4G) relative to untreated controls after 96 hours. Therefore, lack of inhibition by cabozantinib suggests no “off-target” effectors of proliferation were affected in tumor cells in this dose range.

**Cabozantinib induces a sustained inhibition of MET phosphorylation in endothelial cells**

In the MDA-Pca-144-13 sh-c-met tumors, MET and pMET staining is almost entirely confined to the mouse vasculature (Fig. 4K and Supplementary Fig. S6B), consistent with efficient knockdown of MET in tumor cells. The macroscopic appearance of both NT and sh-c-met cells was similar, with the characteristic white tumors (similar to those described in Fig. 3D, right), an indication of inhibition of angiogenesis (Fig. 4K). To further assess angiogenesis in NT and sh-c-met–derived tumors, we used immunofluorescent staining and confocal microscopy and observed reduction of vasculature in both tumor types. However, as described above, pMET-positive vessels (derived from mouse) were observed in the sh-c-met–derived untreated tumors. The near-complete lack of MET expression in tumor cells allowed us to examine the effect of cabozantinib on pMET in the vasculature. As shown in Fig. 4K, bottom right, pMET was inhibited in the CD31+ cells, suggesting that cabozantinib inhibits pMET in the endothelial cells for long time periods. However, after 120 days of treatment, when MDA-Pca-144-13 cells are resistant to cabozantinib, pMET is observed in some vessels, suggesting partial reactivation (not shown).

**Antiangiogenic effects precede induction of apoptosis in cabozantinib-treated xenografts**

Previous preclinical studies have shown that cabozantinib has strong antiangiogenic and proapoptotic effects (4, 22, 23). Our xenograft models allowed us to examine whether changes in vasculature and cellular apoptosis occurred simultaneously with pMET and pVEGFR2 inhibition. For these studies, we performed CD31 immunofluorescence at baseline and after 2, 4, 6, 9, and 21 days of cabozantinib treatment. Figure 5A shows H&E staining (to show tumor structure), terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling (TUNEL; to examine extent of apoptosis), CD31+ (to identify vasculature), and 4′,6-diamidino-2-phenylindole (DAPI; to stain nuclei). We observed decreases in the vasculature by day 2, and these decreases continued throughout treatment (Fig. 5A, bottom). In contrast, apoptosis was observed only after 6 days of treatment and continued to increase thereafter. Quantification of changes in CD31 expression is shown in Fig. 5B and for TUNEL in Fig. 5C. The spatial distribution of apoptotic cells changed over time: at 21 days of treatment, apoptosis occurred only at the periphery of the previously described islets, whereas cells in close proximity to the central vessel were TUNEL-negative (Fig. 5A, middle and bottom). These results suggest that cabozantinib treatment does not induce apoptosis in tumor cells in islets, in accord with the positive phospho-histone H3 cells observed in Fig. 2H. However, the time–dependent changes in the CD31+, TUNEL+ cells indicate that cabozantinib continues to induce sustained apoptosis in endothelial cells outside of the islets. To examine the effects of cabozantinib specifically on VEGFR2, we used immunofluorescence (VEGFR2 + CD31 + DAPI) to test cells at baseline and at 21 days after cabozantinib treatment. As shown in Fig. 5D and quantified in Fig. 5E, most, but not all, CD31+ vessels in control tumors costained for VEGFR2 (VEGFR2-negative vessels are indicated with arrows). Central vessels in islets of viable cells are CD31+, VEGFR2+, and pMET+ (see Fig. 4K), suggesting that combined inhibition of pMET and VEGFR2 contributes to the antiangiogenic effect of cabozantinib. Vessel density was also examined in biopsy samples from human bone metastases and MDA
MET and VEGFR2 as Targets for Prostate Cancer Therapy

Confocal microscopy of immuno

Expression and phosphorylation of MET were determined by immunoblotting. B, MDA PCa-144-13 cells were pretreated with cabozantinib for 2 hours.

Role of pMET in cabozantinib inhibition of xenograft growth. A, MDA PCa-144-13 cells were treated with cabozantinib at indicated concentrations for 2 hours.

Figure 4.

Continuous cabozantinib treatment is required to control tumor growth.

An observation from the clinical trial was that in patients where therapy was discontinued because of toxicity, tumors rapidly progressed. We therefore used PDX models to determine whether an intermittent approach was sufficient to sustain response or whether continuous treatment was required for optimal response. For this experiment, mice with xenograft tumors were treated for 21 days and then randomly assigned to continuous treatment or withdrawal arms. In the continuously treated mice, minimal changes in tumor volume were observed for 50 days, indicating that cabozantinib effectively inhibits xenograft growth for relatively long treatment periods. In contrast, cabozantinib withdrawal led to rapid, immediate exponential regrowth of all tumors (Fig. 6A). These results demonstrate that continuous treatment is required to inhibit tumor regrowth. Next, we compared tissues stained for H&E, MET, pMET, and phospho-histone H3 from untreated and cabozantinib-withdrawal specimens. As shown in Fig. 6B, pMET expression and proliferation are nearly identical in these specimens. Phospho-histone H3 staining is quantified in Supplementary Fig. S10.

Development of acquired resistance

Finally, we examined the effect of even longer cabozantinib treatment in the 2 PDX, MDA PCa-144-13. After about 120 days treatment, treated PDX grew exponentially in the presence of cabozantinib, at rates similar to untreated tumors. After reimplantation of tumors into SCID mice for 3 generations, resistance to cabozantinib was maintained (Fig. 6C), and pMET levels, as
Figure 5.
Effects of cabozantinib on tumor vasculature. A, time-dependent cabozantinib-induced changes in vasculature and apoptosis in MDA PCa-144-13 xenograft models. Inset (bottom right) indicates CD31-positive cells undergoing apoptosis (arrows). Broken line indicates border between islets of viable cells and TUNEL-positive cells. B, quantitation of CD31 staining. C, quantitation of TUNEL staining. Values shown are mean and SEM (ns, not statistically significant; **, P < 0.01; ***, P < 0.001). D, confocal microscopy showing immunofluorescence of DAPI, VEGFR2, and CD31 in control and cabozantinib-treated MDA PCa-144-13 tumors. Arrows indicate CD31-positive, VEGFR2-negative vessels. Broken line indicates borders of the islets. E, quantitation of CD31 and VEGFR2 immunofluorescence (data represent mean and SEM; ***, P < 0.0001). F, changes in tumor vasculature in MDA PCa-118b model (top) and human bone metastases (bottom), insets, 20× magnification. Changes in angiogenesis markers in the serum of patients 6 weeks after cabozantinib treatment relative to baseline for (G) VEGF and (H) VEGFR2.
determined by IHC, were equivalent to those of untreated tumors (Fig. 6D). Genomic sequencing showed no amplification or mutation of c-met in resistant tumors (data not shown).

Downregulation of MET signaling is associated with upregulation of FGFR1 expression

Numerous reports have demonstrated that acquired resistance to tyrosine kinase inhibitors targeting growth factor receptors arises from overexpression or amplification of nontargeted receptor kinases that perform overlapping signaling (27–33). Therefore, we evaluated the expression of several growth factor receptors that might contribute to acquired cabozantinib resistance. Treatment with cabozantinib did not lead to substantial changes in the expression of IGF1R, EGFR, or VEGFR1 in tumor cells (data not shown) but did lead to increased expression of FGFR1, as shown by immunoblotting (Fig. 6E) and IHC (Fig. 6F) in cabozantinib-resistant MDA PCa-118-b tumors. To further determine whether MET inhibition led to increased FGFR1 expression, we examined the effect of continuous cabozantinib treatment in vitro in the expression of these receptors. As shown in Fig. 6G, treatment with cabozantinib for 4 weeks led to upregulation of FGFR1 expression relative to untreated controls. In contrast, the expression of EGFR was unchanged relative to untreated cells. Next, we examined FGFR1 expression 10 days following MET knockdown in 144-13 and PC3 cells. As shown in Fig. 6H, the expression of FGFR1 is significantly higher in MET-knockdown cells relative to cells expressing the NT vector, with no change in EGFR or IGFR1. Thus, inhibition of MET activity or expression corresponds to increased FGFR1 expression in 2 prostate cancer models in vitro and in vivo.

Discussion

Results from parallel studies of investigational therapeutic agents in well-characterized PDX and clinical trials can provide unanticipated insights into mechanisms of clinical efficacy and development of resistance. We applied this approach to studying the effects of cabozantinib, a multitargeted pMET, p-VEGFR2 inhibitor that had promising activity in phase I and II clinical trials in prostate cancer. In a recent phase III trial in mCRPC,
cabozentinib prolonged progression-free but not overall survival (6, 14, 34–36). The advantage of our parallel approach is that by using models of tumor growth in mice that closely mimic response in humans, mechanistic studies could be performed that lead to an understanding of therapeutically relevant targets, mechanisms of resistance, and dosing schedules that affect the efficacy of targeted therapies that should dictate development of future clinical trials.

First, we showed that responses in PDX by pathology and radiographic imaging closely mimicked responses in human patients. In most patients and mice harboring PDX, cabozantinib treatment initially resulted in tumor stabilization or regression. However, we demonstrated in both human patients and PDX models that primary resistance occurs, as cabozantinib fails to inhibit tumor cell growth at physiologically relevant concentrations. This result is manifested in the presence of similar-sized islets of viable resistant tumor cells found in both PDX and in the phase II clinical trial. Strikingly, while pMET is initially inhibited and may account for initial growth inhibition, these islets of resistant cells were pMET-positive, suggesting that MET phosphorylation is reactivated by an HGF-independent mechanism, as serum levels of the ligand for MET, HGF, remain unchanged. Several mechanisms have been reported for non-ligand-induced MET activation that could account for these results (21, 22, 37–40).

To directly examine the role of pMET in tumor growth and response to cabozantinib, we derived MDA PCA-144-13 xenografts in which MET expression was reduced by more than 90%. Surprisingly, downregulation of MET had no effect on MDA PCA-144-13 cell proliferation, either in vitro or in vivo. Similar conclusions regarding the role of MET in proliferation of SW1736 thyroid cancer cells were reached by Zhou and colleagues, who transfected these cells with c-met–targeted siRNAs and demonstrated that neither cell-cycle arrest nor apoptosis was observed in vitro (41). More strikingly, our studies demonstrated that in the near-complete absence of MET expression in xenografts, cabozantinib was equally effective in inhibiting tumor growth as in NT-infected cells with robust MET expression. In contrast to our studies, those of Dai and colleagues demonstrated that concentrations of 2 to 5 μmol/L cabozantinib did lead to growth inhibition, but these concentrations are above what can be achieved clinically (23). Thus, the ability of cabozantinib to inhibit pMET in the tumor cells appears unlinked from a sustained antitumor response, at least in established mCRPC. Our results agree with several clinical studies that demonstrate that inhibition of the HGF/MET axis alone has modest clinical benefit. Specifically, in mCRPC, the addition of monoclonal anti-MET antibodies to conventional chemotherapy failed to show significant increases in overall survival (42).

These results do not preclude a role for MET signaling in prostate cancer at earlier stages of progression. MET expression increases with prostate cancer stage, with the highest levels found in bone metastases (43); however, it should be noted that in primary tumors, expression and activation of MET did not correlate with disease recurrence (44, 45). An inverse correlation between androgen receptor activity and MET expression also has been described (46). Recently, Chu and colleagues demonstrated a feed-forward loop between RANK and MET, and in their studies, blocking MET expression inhibited the development of bone metastases after intracardiac injection (45). Thus, MET may play an important role in the establishment of metastases, but not in the continued growth of tumors once metastasis has occurred. Furthermore, studies in genetically engineered mouse models suggest that MET might be a therapeutic target when it is amplified in tumor cells (47). Thus, understanding at which stages of disease MET may drive tumor progression will be critical to finding efficacy for drugs like cabozantinib that target this receptor tyrosine kinase.

Our results suggest that the mechanism of action of cabozantinib is primarily through microenvironment targeting, with VEGFR2 being a principal target. Unlike pMET in tumor cells, both p-VEGFR2 and pMET are inhibited long term in endothelial cells, corresponding with inhibition of angiogenesis in both patients from the phase II trial and PDX. Numerous studies have shown that combining pMET inhibition with p-VEGFR2 inhibition is superior to anti-VEGF therapy alone (48, 49). This result supports studies demonstrating that inhibition of both MET and VEGFR2 is superior in inhibiting vasculature to inhibiting either receptor alone (49, 50). However, our results provide insights as to how vascular heterogeneity contributes to the formation of islets of resistant cells. As observed in Fig. 5, most tumor-associated vessels in untreated tumors were VEGFR2-positive. However, islets of MET-positive tumor cells surrounded large VEGFR2-negative vessels. Thus, the recognized heterogeneity of tumor-associated vasculature may account for the emergence of resistance to cabozantinib and other therapeutic agents that target VEGFR2 (51) and islets of viable cells that grow in close proximity to mature vessels, which Dvorak and colleagues have shown to express low levels of VEGFR2 and are therefore resistant to angiogenesis inhibitors (52). An alternative approach that may lead to improved tumor control is to add a vascular-targeting agent that would affect VEGFR2-negative vessels to cabozantinib to achieve a more complete vascular suppression.

Despite the profound inhibition of VEGFR2+ vessels by cabozantinib, leading to tumor cell apoptosis and tumor volume stabilization, therapy withdrawal led to rapid and exponential growth of tumor cells. This characteristic regrowth of tumor cells has been associated with other angiogenesis-targeted agents, and as discussed above, was observed in patients in the phase II clinical trial. This result is not surprising, as we demonstrate that residual tumor cells in the islets continue to proliferate at similar rates as control tumors. Thus, continuous exposure to cabozantinib that is sufficient to suppress angiogenesis may therefore be required to maximize its antitumor effect. This approach is in contrast to cabozantinib dosing strategies in medullary thyroid cancer where RET may be an important target (34, 53) that favor maximal tolerated doses and necessary imposition of rest periods when toxicity occurs. This result demonstrated an advantage to parallel use of PDX in conjunction with an early-stage clinical trial and may account for the failure of the phase III cabozantinib trial in prostate cancer, as many patients were withdrawn from therapy due to toxicity.

In addition to its effects on vasculature, cabozantinib directly affects bone formation and turnover. Decreases in serum alkaline phosphatase and urinary N-telopeptides, as found in the phase II clinical trial, are characteristic of inhibition of bone remodeling. In mice with intratremoral MDA PCA-118b cells, cabozantinib caused a pronounced decrease in NaF-18 accumulation, consistent with reduced bone turnover, as was also observed by Graham and colleagues (23, 54). In our model, we were able to examine bone volume and density in the same animals before and at the end of treatment. Although we found no change in gross bone
volume or density, intramedullary bone formation occurred only in untreated tumors. Viable osteoblasts were observed in cabozantinib-treated MDA PCs-118b tumors. We therefore examined the effects of cabozantinib in POMs and found that proliferation was decreased and differentiation was induced, as determined by increased osteocalcin and alkaline phosphatase expression. We speculate that cabozantinib-mediated prostate cancer cell death leads to reduction of prostate cancer−induced new bone formation. Our in vitro results on effects of cabozantinib on osteoblasts from mouse calvaria, in which proliferation was inhibited and differentiation was induced, demonstrate a direct effect of cabozantinib in osteoblasts, as was also shown by Dai and colleagues (23). These effects provide an explanation for the improvement in bone scans and reduction in bone pain observed in patients who respond to cabozantinib. For this reason, bone scan changes alone are not sufficient to predict an antitumor response.

Finally, our results provide further evidence that inhibition of a single growth factor receptor in tumor cells is rapidly compensated by derepression of a growth factor receptor with overlapping function. We demonstrate, for the first time, that inhibition of either MET activity or expression leads to increased expression of FGFR1. This result agrees with signaling network models described by Wagner and colleagues (55) who predicted that increased abundance of an RTK might be induced by pharmacologic inhibition of another RTK within the same class/cluster. Of note, FGFR1 and MET are grouped within the same cluster on the basis of these signaling network models (55). Whether overexpression of FGFR1 mediates acquired resistance to MET inhibition will require further study.

Our integration of clinical and murine studies, conducted in parallel, led to new insights about the effects of cabozantinib on mCRPC that could not be ascertained by either type of study in isolation and demonstrate the power of this approach for future investigational agents. Our studies also suggest that the evolving concept of “co-clinical” trials should be expanded. As initially conceived by Pandolfi and colleagues (1), the co-clinical aspect constitutes the use of genetically engineered mice with driving mutations characteristic of the human tumor or PDX derived from the same patients undergoing a clinical trial. Our results illustrate the power of integrating datasets from complex PDX to efficiently prioritize observations of interest. This cross-species iterative process gains strength when identical conclusions arise from complex PDX, thus reducing the inherent bias of commonly used models. Because the distance between cancer genotypes and clinical phenotypes remains large for informing clinical decisions, parallel investigations involving PDX representative of the spectrum of mCRPC may rapidly lead to more biologically informed clinical trials.

Disclosure of Potential Conflicts of Interest
C.J. Logothetis reports receiving speakers bureau honoraria from Helsinn Healthcare, Johnson & Johnson, Novartis, and Pfizer and is a consultant/advisory board member for Astellas, Bristol-Myers Squibb, Exelixis, Helsinn Healthcare, Johnson & Johnson, Novartis, and Pfizer. No potential conflicts of interest were disclosed by the other authors.

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