Biomarker and pharmacological evaluation of the γ-secretase inhibitor PF-03084014 in breast cancer models

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Abstract

Purpose: We aimed to assess the biological activity of PF-03084014 in breast xenograft models. The biomarkers for mechanism and patient stratification were also explored.

Experimental design: The in vitro and in vivo properties of PF-03084014 were investigated. The mRNA expressions of 40 key Notch pathway genes at baseline or after treatment were analyzed to link with the anti-tumor efficacy of PF-03084014 in a panel of breast cancer xenograft models.

Results: In vitro, PF-03084014 exhibited activity against tumor cell migration, endothelial cell tube formation and mammosphere formation. In vivo, we observed apoptosis, anti-proliferation, reduced tumor cell self-renewal ability, impaired tumor vasculature and decreased metastasis activity after the treatment of PF-03084014. PF-03084014 treatment displayed significant antitumor activity in 10 of the 18 breast xenograft models. However, the antitumor efficacy in most models did not correlate with the in vitro anti-proliferation results in the corresponding cell lines, suggesting the critical involvement of tumor microenvironment during Notch activation. In the tested breast xenograft models, the baseline expressions of the Notch receptors, ligands, and the cleaved Notch1 failed to predict the antitumor response to PF-03084014, whereas several Notch pathway target genes, including HEY2, HES4, and HES3, strongly corresponded with the response with a p-value < 0.01. Many of the best molecular predictors of response were also significantly modulated following PF-03084014 treatment.

Conclusions: PF-03084014 demonstrated antitumor and antimetastatic properties via pleiotropic mechanisms. The Notch pathway downstream genes may be used to predict the anti-tumor activity of PF-03084014 and enrich for responders among breast cancer patients.

Translational Relevance
Aberrant Notch signaling, which requires the constitutive activation of \( \gamma \)-secretase, is implicated in the disease progression of breast cancer. PF-03084014 is a small molecule \( \gamma \)-secretase inhibitor (GSI) that is currently under phase 1 clinical investigation. To aid the clinical development of PF-03084014 in breast cancer, we characterized the diverse biological properties of PF-03084014 and evaluated the biomarkers in the preclinical setting. By impairing Notch signaling, PF-03084014 demonstrated significant antitumor efficacy in a subset of breast cancer xenograft models via various mechanisms such as apoptosis induction, the inhibition of cancer stem cell self-renewal, antiproliferation and antiangiogenesis. The Notch pathway target gene expressions correlated with the antitumor efficacy and can potentially serve as biomarkers for proof of mechanism and patient enrichment. This work provides guidance for the clinical investigation of PF-03084014 therapy for breast cancer patients.
Introduction

In mammalian cells, Notch signaling is activated when the Notch family receptors (Notch1–4) bind to the membrane-bound ligands (Jagged1, Jagged2, Delta-like1, Delta-like3 and Delta-like4) on neighboring cells. Upon ligand binding, the Notch receptor undergoes a series of proteolytic cleavage steps. The constitutively active γ-secretase complex catalyzes the final step, which results in the release of the Notch intracellular domain (NICD). The NICD subsequently translocates to the nucleus, where it acts as a transcriptional co-activator of the Notch target genes. In human breast cancers, aberrant Notch signaling has been reported to promote disease progression and is associated with significantly poor overall survival (1) (2). Notch1 and Notch2 fusion proteins have been recently reported in breast cancer cell lines and patient specimens (3), and the treatment of breast cancer cell lines that harbor these fusions with the γ-secretase inhibitor, DAPT, have demonstrated robust growth inhibition when the γ-secretase cleavage site is present. NUMB, a negative regulator of the Notch signaling, is lost in approximately 50% of human mammary carcinomas, and its expression is inversely correlated with tumor grade and proliferation rate (4). Notch signaling also drives cancer progression via crosstalk with many other oncogenic pathways, such as EGFR and TGFβ signaling (5) (6).

During malignant progression, Notch signaling affects a broad range of the cellular activities of tumor cells and their microenvironment, including cell proliferation, differentiation, apoptosis, angiogenesis and invasion (5) (7). Notch is also known for the maintenance and survival of tumor-initiating cells. Notch signaling directs endothelial cell fate during new vessel formation via the Notch ligands Dll4 and Jag1 (8) (9), thereby mediating tumor angiogenesis, progression and metastasis. Notch signaling is also triggered when tumor cells interact with neighboring endothelial cells and promotes neovascularization (10). In stromal cells, in which Notch
receptors and ligands are expressed (11), Notch signaling regulates cell migration and controls smooth muscle cell growth and apoptosis (12). Elevated expression levels of Jagged1 promote the spread of breast cancer cells to the bone by activating stromal cell Notch signaling (13). These findings highlight the critical role that of Notch signaling plays in tumor-stromal cell communication during solid tumor disease progression and suggest that therapeutic assessment of a Notch inhibitor should involve both the tumor cells and the corresponding microenvironment.

The complexity of Notch pathway activation during cancer development provides numerous opportunities for the development of targeted therapies; several proteins involved in the Notch signaling pathway are therapeutic targets for the treatment of various types of cancers (14), including anti-Dll4 antibodies (15) and γ-secretase inhibitors (GSI) (16) (17). PF-03084014 is a potent and selective GSI, which is currently under clinical phase 1 development. By blocking Notch signaling, PF-03084014 exhibited anti-tumor efficacy in human T-ALL xenograft models (18). In this report, we evaluated the pharmacological properties of PF-03084014 in breast cancer xenograft models and investigated the candidate biomarkers.

**Materials and Methods**

All cell lines and fine chemicals were purchased from ATCC (Rockville, MD) and Sigma-Aldrich (St. Louis, MO), respectively, unless noted otherwise. MDA-MB-231Luc was purchased from Xenogen (Caliper Company). HUVEC and cancer-associated fibroblast (CAF) lines were obtained from Clonetics Corp. (San Diego, CA) and Asterand (Detroit, MI), respectively. The anti-cleaved Notch1 (NICD1), anti-Notch1, CD31, cleaved caspase 3 and γH2AX antibodies
were purchased from Cell Signaling Technology. The anti-BrdU antibody was obtained from BD Pharmingen.

**In vitro cell-based assays**

The *in vitro* proliferation assays were performed by treating exponentially growing cells for seven days, followed by an MTT assay to measure cell viability. Real-time measurement of cell migration was performed using the CIM-Plate 16 package (Roche Applied Science) according to the manufacturer’s instructions. The rate and onset of cell migration were quantified by a xCELLigence Real-Time Cell Analyzer (Roche Applied Science) for 24 hr.

**Mammosphere formation assay**

The mammospheres were generated by plating viable cells in 96-well ultra-low attachment plates (Corning) using Mammo Cult™ complete medium (Stem Technologies) supplemented with 4 µg/ml heparin and 0.5 µg/ml Hydrocortisone. The mammospheres were collected on day 6 and dissociated to yield a single-cell suspension. The treatment effect was evaluated when cells were re-seeded for second-generation mammospheres. After a six-day treatment, the cells were quantified and the images were analyzed using an Olympus 1X51 inverted microscope. The *in vitro* angiogenesis tube formation assay was performed as previously described (19). For the *ex vivo* mammosphere test, the collected tumors were dissociated into individual cells before performing the assay (20). After a 12-day treatment, the images were captured using Cellomics (Thermo Scientific) and quantified using Image-Pro® Plus (Media Cybernetics).

**In vivo studies and drug administration**

All experimental animal procedures conducted internally were performed in compliance with the Guide for the Care and Use of Laboratory Animals (Institute for Laboratory Animal Research, 1996) and were approved by the Pfizer Global Research and Development Institutional Animal
Care and Use Committee. Two million cells were implanted into the dorsal region of either athymic NCr-nu/nu or SCID-beige mice (Charles River Breeding Laboratories). Studies using human patient-derived xenograft models, including the HBCX1, HBCX6, HBCX7, HBCX9, HBCX12B and HBCX17 models, were performed using athymic nude mice (Harlan Laboratories) at Xentech (France). The studies of BT474 in CB-17 SCID mice (Harlan) and SKBR3 in BALB/c nude mice were conducted at Piedmont Research Lab (Charles River) and Crown Bio, respectively.

To evaluate efficacy, the mice were randomly assigned to different groups when the tumors reached a volume of 100-200 mm³, such that the mean value of the tumor size was matched between the groups. Either vehicle or PF-03084014 was administered p.o. to mice twice daily for 12 days. Tumor growth inhibition (TGI) was calculated after the treatment ended. Statistical analyses were conducted using GraphPad Prism for one-way ANOVA analysis followed by the Dunnett's t test (p < 0.05 was considered statistically significant).

**Pharmacodynamic endpoints assessment**

The endogenous levels of NICD1 were assessed either by Western blot or using an ELISA Sandwich Kit (Cell Signaling) according the manufacturer's instructions. The tumors were snap-frozen and pulverized in a liquid nitrogen-cooled mortar prior to being lysed. For Western blotting, 100 μg of cell or tumor lysates was loaded per lane for analysis.

For functional tumor vasculature assessment, tumor-bearing mice received an i.v. injection of 5 mg/kg FITC-lectin (Vector Labs) 15 min prior to euthanasia. The tumor samples were frozen in OCT® medium, manually sectioned into 100 μm slices and stained with anti-CD31 antibody. The fluorescence images were captured using a Nikon Eclipse TE2000 fluorescent microscope with Q-Capture software, and the analysis was performed using Image Pro Plus 5.1 (Media
Cybernetics, Silver Spring, MD). For in vivo metastasis measurements (21), the tumor-bearing mice were i.v. injected with MMPSense 680 (PerkinElmer, Inc.) 24 hrs prior to fluorescence imaging (FMT 2500, PerkinElmer, Inc.).

RNA Isolation

Xenograft tumors were collected and preserved in RNAlater RNA stabilization reagent (Qiagen, Germantown, MD). RNA was isolated using an RNeasy kit (Qiagen, Germantown, MD) according to manufacturer’s protocol with an additional DNA digestion step. The RNA concentration and integrity were measured using a NanoDrop (Thermo Fisher Scientific, Waltham, MA) and a 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA), respectively.

nCounter™ Gene Expression Assay

nCounter probes were designed and obtained from NanoString Technologies (Seattle, WA). The human probe sequences, which are listed in supplementary Table 1S, were screened against mouse RefSeq to eliminate potentially cross-hybridizing probes. Each assay was performed using at least two biological replicates. Total RNA (100 ng) was hybridized to nCounter™ capture and reporter probes at 65°C for 16 hrs. The hybridized products were purified and processed using an automated sample prep station, and the images were prepared using the NanoString Digital Analyzer according to the company’s standard gene expression assay protocol [http://www.nanostring.com].

nCounter™ Data Analysis

The counts were first normalized to six spiked-in positive controls to correct for experimental variability. A reference normalization factor was determined by first calculating the geometric mean of the positive controls for each sample and then computing the arithmetic mean across all
samples. The gene count for each sample was then normalized by dividing by the ratio of the geometric mean of the positive controls for the sample to the reference normalization factor. To account for the variability in RNA content, the normalized gene counts were further normalized against four endogenous control genes. This was performed by calculating the geometric mean of the endogenous controls for each sample, averaging across all samples, and generating an endogenous normalization factor by computing the ratio of the geometric mean of the endogenous controls to the average value as described above. Each target gene count was divided by this endogenous normalization factor to compute the final normalized target gene count reflective of the transcript level. The detailed gene expression analysis guidelines can be found on the NanoString Technologies website [http://www.NanoString.com]. The final normalized data are available in the supplementary Table 2S, and a detailed sample description is provided in supplementary Table 3S.

**Data analysis**

Replicates of xenograft mRNA profiling experiments were summarized using median values and log2 transformed for subsequent analyses. The comparison between tumor growth inhibition and the log2 vehicle-treated expression values was performed using the Pearson linear correlation coefficient implemented in R. The analysis of genes modified after PF-03084014 treatment was performed using the paired moderated t-statistic in limma (22). Both the nominal p-values and the p-values corrected for multiple comparisons using Benjamini and Hochberg's method (23) are shown. All gene expression analyses, figures, and statistical tests were performed in R. For reproducibility (24), the input files and the full R code are available in the supplementary methods as a Sweave transcript (25).
Results

PF-03084014 impairs Notch pathway signaling in tumor and HUVEC cell lines and results in cellular functional changes

We tested the in vitro activity of PF-03084014 against tumor cell proliferation, migration and self-renewal as well as endothelial cell proliferation and tube formation.

The growth inhibition mediated by PF-03084014 was assessed in a panel of 35 breast cancer cell lines using an MTT assay. In most lines (33/35), the 7-day treatment of 2 µM PF-03084014 had no effect. PF-03084014 induced significant growth inhibition exclusively in the HCC1599 (Notch1MUT) and MDA-MB-231Luc cell lines after 5-7 days of treatment with IC50 values of 0.1 and 0.9 µM, respectively. In HUVEC, treatment with PF-03084014 for seven days reduced cell proliferation with an IC50 value of 0.5 µM. To further assess the effect of PF-03084014 against the early steps of angiogenesis, HUVECs were co-cultured with human skin fibroblast cells in fibrin gels to generate sprouts with a clear lumen-like structure. The treatment with PF-03084014 for 14 days decreased the lumen formation with an IC50 value of 50 nM (Figure 1A).

The effect of PF-03084014 on the function of tumor-initiating cells was evaluated. Non-adherent mammospheres were established under serum-free conditions. Treatment with 1 µM PF-03084014 reduced mammosphere-forming efficiency by 50% in both HCC1599 and SUM149 cell lines (Figure 1B), suggesting that the compound inhibits the ability of tumor cells to self-renew. In contrast, PF-03084014 (1 µM) treatment showed no anti-proliferative effect in adherent SUM149 cells and 100% cell killing in the HCC1599 cells cultured in serum-containing medium.

The effect of PF-03084014 on tumor cell migration was assessed in MX1 and MDA-MB-231Luc cell lines. Treatment with 1 µM PF-03084014 had no anti-proliferative effect in MX1 cells;
however, it nevertheless inhibited migration by 95% (Figure 1C), and a similar result was observed in MDA-MB-231Luc cells.

To confirm the biological relevance of the functional changes, cells were treated with 1 µM PF-03084014 for 48 hrs and then harvested to assess the levels of cleaved Notch1 (NICD1) via ELISA (Figure 1D). PF-03084014 robustly suppressed NICD1 in HUVEC cells, cancer-associated fibroblasts and multiple tumor cell lines, although suppressing NICD1 failed to elicit anti-proliferation in vitro in several cell lines including the MX1, HCC1806 and SUM149PT cells.

**Diverse mechanisms of PF-03084014-induced anti-tumor efficacy in breast xenograft models**

The dose-dependent anti-tumor efficacy of PF-03084014 was evaluated in HCC1599 cells. Mice with palpable tumors were administered PF-03084014 p.o. twice daily for 12 days (Figure 2A). PF-03084014 treatment at 45, 90 and 120 mg/kg resulted in TGI of 95%, 115% and 120% and a significant growth delay of 20, 30 and 60 days, respectively. Using this dosing schedule, the maximum tolerated dose (MTD) was 120 mg/kg in SCID-bg mice.

To assess the biological relevance of PF-03084014 treatment in vivo, mice bearing HCC1599-derived tumors were treated (p.o.) with 120 mg/kg PF-03084014 twice daily and the tumors were harvested on day 3 for pharmacodynamic assessment. A robust modulation of NICD1 (Figure 2B) was observed along with significant expression alterations of Notch down-stream genes that impact cell cycle and apoptosis, including MYC, CCND1, BIRC5, CDKN1A and NOXA1 (Figure 2C). The tumors displayed decreased BrdU uptake as well as increased γH2AX and cleaved caspase 3 levels as assayed by IHC (Figure 2C, D), suggesting that impairing Notch signaling with PF-03084014 results in anti-proliferative activity and induces apoptosis in tumor cells.
The effect of PF-03084014 on the tumor-initiating cells was examined. Treatment with PF-03084014 (120 mg/kg, BID) in HCC1599 tumor-bearing mice was performed for 12 days prior to tumor harvest. Tumor cells were then dissociated for mammosphere formation assays under stem cell selective culture conditions. As shown in Figure 2E, PF-03084014 induced a drastic reduction in mammosphere forming efficiency.

Given the essential role of Notch signaling in vascular development, we assessed whether the efficacy of PF-03084014 was associated with vessel functional change in vivo. A fluorescently conjugated FITC-lectin was injected i.v. into HCC1599 tumor-bearing mice after a 7-day continuous treatment. Tumors were harvested for immunofluorescence co-staining to assess FITC-lectin and CD31 positivity. PF-03084014 (120 mg/kg) had a minimal impact on CD31-positive endothelial cells, whereas the treated tumors lacked functional lumens as demonstrated by the marked decrease in co-staining with FITC-lectin, which indicates the presence of vascular defects (Figure 2F). Similar results were observed in both the MX1 and MDA-MB-231Luc models.

**PF-03084014 displays anti-metastasis activity in breast cancer models**

The in vivo assessment of PF-03084014 against spontaneous metastasis was performed in MDA-MB-231Luc and MX1 mammary fat-pad implanted tumor models. Size-matched tumor-bearing mice were administered with PF-03084014 p.o. twice daily for 12 days. Secondary tumor burden was assessed using an FMT system via injection of MMPsense 680 (Visen) at 24 hr prior to imaging.

Figure 3A depicts representative fluorescence images of the lung tumor burden in the vehicle- and PF-03084014-treated MX1 mice on day 22 following dosing commencement. On day 23, and the lungs were harvested. H&E staining of the lungs revealed marked reductions in the
infiltrated tumor foci in PF-03084014-treated groups compared with the vehicle controls, which is in agreement with the FMT imaging readout (Figure 3B). The TGI of PF-03084014 (90 mg/kg) was 31% and 68% in the primary and secondary tumors, respectively (Figure 3C). Notably, a greater efficacy against tumor cell infiltration into lung than against primary tumor growth was observed in the MX1 model. The anti-metastasis activity of PF-03084014 was also observed in the MDA-MB-231Luc tumor model.

In solid tumors, aberrant Notch signaling between tumor cells and the host microenvironment was shown to induce neovascularization and metastasis thus promote disease progression via a non-cell autonomous effect (13) (26). In multiple tumor models, including the HCC1599, MX1 and MDA-MB-231Luc models, treatment with PF-03084014 (120 mg/kg, BID) for two days reduced the expression of the Notch stroma target genes Notch3, Hey2 and HeyL (Figure 3D). The robust decrease in HeyL expression is consistent with the antiangiogenic and antimetastatic effects of PF-03084014, as elevated levels of HeyL were found in the vasculature of invasive breast carcinomas (27).

**PF-03084014 demonstrates antitumor activities in a panel of breast cancer models**

The *in vivo* efficacy of PF-03084014 was evaluated in subcutaneously implanted breast cancer xenograft models at or near the MTD level (120 mg/kg). In 10 of the 18 tested breast cancer models (Figure 4A), PF-03084014 displayed a TGI value of at least 50% (p < 0.05). Interestingly, the *in vivo* sensitivity (TGI > 50%) of PF-03084014 in breast cancer models did not correlate with the 7-day proliferation assay (MTT) results (Figure 4B) in which PF-03084014 only inhibited the growth of the HCC1599 and MDA-MB-231Luc cultures with IC50 values of 0.1 µM and 0.9 µM, respectively. The disconnect between the *in vitro* and *in vivo* efficacies is not simply due to differences in exposure as the highest concentration of PF-03084014 tested in
the *in vitro* anti-proliferation assay (2 μM) exceeded the steady-state concentration achieved *in vivo* (1.2 μM) at the MTD.

Using an ELISA assay, we assessed the baseline expression levels of the Notch1 intracellular domain as a marker of Notch pathway activation; NICD1 levels did not vary significantly between the sensitive and resistant tumors (Figure 4C). We were unable to develop assays for NICD2, NICD3, and NICD4 due to the limited supply of commercially available antibodies; therefore, we used a different biomarker approach to predict sensitivity to PF-03084014.

The NICD1 levels in the Notch1*mut* HCC1599 cells were relatively high both *in vitro* and *in vivo*. In contrast, NICD1 was below the detection limit *in vitro* in the MDA-MB-361, MDA-MB-231 and MDA-MB-436 cell lines, whereas was significantly elevated in the corresponding *in vivo* tumors (Figure 4D). These results suggest that because of the stroma activated Notch signaling, PF-03084014 was significantly more active *in vivo.*

In a subset of responding tumor models (TGI > 50%) with high baseline levels of NICD1, pharmacodynamic studies were performed. Tumor-bearing mice were treated with 120 mg/kg PF-03084014 twice daily for two days and the tumors were harvested on the third day for NICD1 analysis. Treatment with PF-03084014 suppressed NICD1 (Figure 4E), suggesting that PF-03084014 efficacy is in part mediated by the blockade of Notch1 signaling.

**Expression of Notch pathway target genes corresponds to the response to PF-03084014 in vivo**

To establish the correlation of the PF-03084014-induced efficacy with Notch pathway biomarkers in 17 *in vivo* models, we analyzed the expression of 40 genes selected primarily from the Notch pathway, including receptors, ligands, and regulators such as NUMB, as well as canonical target genes such as the Hes and Hey gene families. We also selected cell cycle genes
associated with the Notch pathway (28). In total, 45 probes from 40 genes were profiled using NanoString technology.

We first analyzed the correlation between the vehicle-treated gene expression profiles and the PF-03084014 in vivo activity. The expression of 11 probes from 8 genes positively correlated with tumor growth inhibition at the nominal p < 0.05 (Figure 5A). The most significant genes included the three canonical Notch pathway targets, HEY2, HES4, and HES3 (correlated at nominal p < 0.01 and a false discovery rate (FDR) adjusted p < 0.15). Notch2 represented the only Notch receptor expression profile that significantly correlated with compound activity; the expression of the other three notch receptors, Notch1, Notch3, and Notch4, did not significantly correlate with response. We also identified 4 unique genes, CDKN1B, HEYL, DTX1, and CDKN1A, with which the expression negatively correlated with PF-03084014 activity (defined R < -0.1), although none of these correlations was significant. In addition to the correlation tests, we also performed differential gene expression analysis between the most sensitive (defined by TGI > 70%) and resistant (models with TGI < 30%) models. This analysis (Figure 1S and supplementary methods) confirmed that HEY2 was the most significantly upregulated gene and that CDKN1B was the most significantly downregulated gene in the most sensitive models.

Next, we analyzed the modulation of the 40 selected genes after treatment. For 15 in vivo models, we assessed the modulation upon PF-03084014 treatment compared with vehicle treatment. In both cases, RNA was collected 2 days after treatment and profiled using the NanoString assay. We identified 12 different probes from 10 unique genes that were significantly modulated upon PF-03084014 treatment (univariate p < 0.05, paired t-test) as shown in Figure 5B. The most significant genes (nominal p < 0.001) were HES1, HES4, NOTCH1, and HEY2. A majority of the significantly modulated genes were downregulated upon treatment, including
several canonical Notch pathway targets (HES, HES4, HEY2, NRARP, and HEY1) and the three Notch receptors, Notch1, Notch3 and Notch4. Interestingly, high baseline levels of HES4 and HEY2 expression correlate with efficacy, and these genes are among the most downregulated mRNAs post-treatment. NOXA1 and CLEC4A were the only genes that were significantly upregulated after treatment.

The HCC1599 model was the only model in which PF-03084014 treatment led to tumor regression. Therefore, we investigated the genes that were differentially expressed between the HCC1599 model and the other models to characterize the treatment-induced molecular changes in HCC1599 cells (supplementary Figure 2SA). Several genes, many of which represented cell cycle and/or apoptosis factors, differed significantly in the magnitude of modulation; MYC, BIRC5/survivin, and CCND1/cyclin D1 were downregulated more than four-fold (log2 fold change < -2) post-treatment in the HCC1599 model compared with other models. Unsupervised clustering of all assayed cell cycle genes revealed a distinct modulation pattern in HCC1599 cells (supplementary Figure 2SB).

We also compared the magnitude of mRNA modulation after treatment with the baseline gene expression levels and the anti-tumor efficacy. Table 1A lists the mRNAs for which the extent of post-treatment modulation correlated with the baseline expression levels in vehicle-treated samples (for more details, see supplementary Figure 3S). In all of the significant cases, there was a negative correlation between the baseline expression level and the magnitude of modulation. In other words, the higher the relative expression level of a gene, the more it was downregulated after treatment (for down-regulated genes) or the less it is upregulated (for up-regulated genes). The genes that were downregulated by treatment with GSI include the Notch target genes HES4, NRARP, HES3 and HEY2. In contrast, the models with low baseline CDKN1B expression, which
are sensitive to PF-03084014, displayed CDKN1B upregulation upon treatment. We found that following treatment with PF-03084014, the Notch target genes of the Hes and Hey families were downregulated, while the negative regulator CDKN1B was upregulated, and the changes were more pronounced in the sensitive models. Table 1B and Figure 4S show the genes for which the magnitude of modulation after treatment correlated with the antitumor efficacy. Strong downregulation of several genes including NOTCH4, NRARP, HES4, DLL3 and HEY2 was associated with increased tumor inhibition as was the upregulation of NCSTN and CDKN1B.

**Discussion**

In this report, we examine the preclinical properties of PF-03084014, a γ-secretase inhibitor, in breast cancer cell lines and breast cancer models. PF-03084014 impairs the Notch pathway and demonstrates antitumor and anti-metastasis activities. Using a panel of breast xenograft models, we investigated different biomarker approaches for patient stratification and proof of mechanism (POM). This work provides insight into the mechanism of PF-03084014 activity and may potentially aid the clinical development in breast cancer patients.

Treatment with PF-03084014 *in vivo* resulted in antitumor activity (TGI > 50%) in 10 of the 18 breast xenograft models. These results did not correlate with the *in vitro* growth inhibition assay using the corresponding cell lines despite the modulation of NICD1 levels by PF-03084014 in many of the cell lines. Among the 12 evaluable cell lines, only two displayed growth inhibition following treatment with 2 μM PF-03084014, which represents a concentration above the steady-state plasma concentration (Css = 1.2 μM) at the *in vivo* MTD. One of these cell lines was the HCC1599, which harbors an activating Notch1 mutation (3), and was highly responsive to PF-03084014 treatment in both *in vitro* and *in vivo* conditions. Notch1 and Notch2 gene rearrangements have recently been reported in ER-negative breast tumors and cell lines [3].
lines with Notch fusions that retain the γ-secretase cleavage site are sensitive to GSI. In addition, we also observed PF-03084014-induced antitumor efficacy in other ER-positive models, thereby suggesting that the GSI responsive population in breast cancer is not restricted to ER-negative patients or those with Notch gene fusions.

Notch signaling mediates breast cancer disease progression via both cell-autonomous and non-autonomous interactions. We observed elevated NICD1 levels in some of the GSI-responding models in vivo compared with the corresponding cell lines in culture, suggesting that the absence of a stromal compartment may be responsible for the overall lack of the in vitro anti-proliferative activity of PF-03084014. In agreement with previous reports, the Notch pathway activation in solid tumors often depends on ligand-receptor interactions via tumor and stroma cell-to-cell contact (5).

Biomarkers were assessed by correlating the in vivo TGI with the mRNA expression of Notch pathway genes. We profiled both the baseline (estimated by vehicle-treated profiles) and post-treatment expression of 40 selected pathway genes. Given the relatively modest number of models, we focused on a small set of genes to mitigate the risk of over-fitting. This hypothesis-driven approach revealed that neither expression of Notch receptors nor their ligands significantly correlated with PF-03084014-induced antitumor activity with the possible exception of Notch2, while the expression of several Notch pathway target genes, including HEY2, HES4 and HES3, clearly correlated with increased sensitivity to the inhibitor. These three genes were also significantly downregulated after treatment. Interestingly, the baseline expression of the most significantly modulated gene, HES1, failed to correlate with the compound sensitivity results in vivo. Our results suggest that the expression of select downstream Notch pathway targets better reflects the overall status of pathway activation than
the Notch receptors and, in turn, sensitivity to GSIs. Similar results have been previously reported for other GSIs (28). The lack of a correlation between PF-03084014 activity and the mRNA expression of the Notch receptors and ligands may be due to exclusive activation of the Notch receptors and/or the post-transcriptional regulation of the proteins.

It has been previously reported (28) that a 10-gene Notch signature score corresponds with the response to the GSI, MRK-003, in T-cell acute lymphoblastic leukemia (T-ALL) cells. The 10-gene Notch score predicted PF-03084014 activity in our in vivo breast cancer models, albeit with borderline significance (p = 0.05; Figure 5S). Two of the predictive markers that we identified, HEY2 and HES4, along with two genes significantly modulated by PF-03084014, HES1 and NRAPR, were among the 10 Notch pathway targets reported (28). These results suggest that while the biological processes associated with GSI sensitivity are similar and linked to the activation of downstream Notch signaling, the expression of key effector genes may differ between different tissues. For certain genes, the magnitude of expression modulation after short-term treatment correlates with the subsequent antitumor efficacy of PF-03084014 during long-term treatment. One can speculate that the expression changes of these genes after the initial dose may represent the early readout of PF-03084014 efficacy in breast tumors; this hypothesis would require confirmation in independent samples.

PF-03084014 reduced proliferation and induced apoptosis in the HCC1599 (Notch1mut) model in a dose-dependent manner, and the efficacy significantly correlated with the depletion of NICD1, thus suggesting that the efficacy was driven at least in part by Notch1 pathway impairment. Consistently, we observed a robust treatment-induced modulation of Notch down-stream genes that are associated with cell cycle and apoptosis, including Myc, CCND1, BIRC5 and Noxa1, which may be due to pan-Notch inhibition by PF-03084014.
Notch is one of the signaling pathways that mediates breast cancer cell self-renew (29). The \textit{in vivo} efficacy of PF-030841014 may be partly derived from the reduction of tumor-initiating cells. Indeed, PF-03084014 significantly suppressed mammosphere formation efficiency in HCC1599 residual tumor cells after a 12-day treatment period \textit{in vivo}. An \textit{in vitro} mammosphere formation assay using HCC1599 and SUM149 cells also confirmed the ability of PF-030841014 against tumor cell self-renewal. For both SUM149 and HCC1599 cells, PF-03084014 triggered differential responses against cell growth and maintenance under high- and low-serum conditions. This maybe explained by that the signaling pathways for regulating differentiated cell to proliferate are not necessarily same as those for cancer stem cell self-renewal.

PF-03084014 also caused less functional vasculature \textit{in vivo} at a high dose level (120 mg/kg) as displayed with a lectin perfusion assay. However, the changes in CD31 staining were marginal, which could be a net outcome of concurrent suppression inDll4- and Jagged 1-mediated angiogenesis, as Jagged 1 and Dll4 exert opposing effects on endothelial cells and blocking either pathway would yield less functional tumor vasculature (9). A decrease in endothelial cell proliferation has also been reported using other \(\gamma\)-secretase inhibitors (30). In contrast to an anti-VEGF inhibitor, PF-03084014 only impaired tumor vasculature at a high dose level (>100 mg/kg), whereas target-associated efficacy was observed at a much lower dose (45 mg/kg). These results indicate that the antiangiogenic effect is not a dominant mechanism responsible for the therapeutic response to PF-03084014 in breast cancer.

In PF-03084014-treated MX1 tumor-bearing mice, we observed higher levels of antimetastatic activity than antitumor efficacy. \textit{In vitro}, 1 \(\mu\)M PF-03084014 inhibited MX1 cell migration by 95% but failed to exert any growth inhibitory effect. When primary tumor cells disseminate to distant organs, secondary tumor formation requires both a malignant cell with high invasive and
migratory capabilities and a permissive microenvironment in which the tumor cell interacts with nearby stromal cells to establish a secondary tumor. Notch signaling is implicated throughout this metastatic cascade via EMT (31) (32), TGF-β signaling (13), neovascularization and other mechanisms. In addition to the treatment-induced decrease of tumor cell motility, impairing Notch signaling in the stromal compartment may also contribute to the antimetastatic activity of PF-03084014. Supporting this notion, cell-autonomous Notch signaling was modulated by PF-03084014 in cultured HUVECs and cancer-associated fibroblasts. In vivo, PF-03084014 treatment led to a marked decrease in the expression of the stromal gene, HeyL, a Notch target gene that is highly expressed in invasive breast cancer vasculature and drives neovascularization (27). Notably, PF-03084014-induced modulation of HeyL expression was not observed in HUVEC culture in vitro. These results highlight the potential therapeutic uses of PF-03084014 to combat both primary tumor growth and tumor metastasis to distant sites.

As breast orthotopic models rarely develop efficient metastases, we were unable to generate sufficient data to draw a correlation between the antimetastatic effect and Notch pathway biomarkers. One of the caveats of using TGI as an endpoint to generate predictive biomarkers is that primary tumor growth may not necessarily reflect comprehensive human disease progression, as clinical metastases account for a large percentage of breast cancer-associated deaths. Another limitation of xenograft-derived biomarkers is that aberrant Notch signaling can occur between the tumor-stroma cell interactions, while the mouse stromal microenvironment may not fully recapitulate the situation in patient tumors.

Taken together, these data highlights that PF-03084014 exhibits efficacy against breast tumor growth and metastasis through pleiotropic mechanism. In a panel of breast xenografts, we identified a Notch gene signature that is predictive of the sensitivity to PF-03084014. This gene
signature could serve as a biomarker for patient stratification and aid in personalized therapeutic
treatment strategies for PF-03084014. In recent years, a large body of evidence has shown that
Notch signaling crosstalks with many other oncogenic pathways to drive cancer progression.
Future work is warranted to identify a rational combination strategy to reach the full potential for
the clinical development of PF-03084014.

Acknowledgements

The authors would like to thank Stephanie Shi for assisting all the external studies. We also
would like to acknowledge Chassidy Hall (Piedmont Research Center), Yanmei Sun (Crown
Bioscience), Myriam Lassalle (XenTech), Truong-An Tran (XenTech) and Jean-Gabriel Judde
(XenTech) for conducting the external in vivo xenograft studies.
References


Tables

Table 1 The Notch target gene analyses and the biomarker identifications of PF-03084014 in breast cancer xenograft models

Table 1A - Correlation between gene modulation after treatment and baseline expression

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* Benjamini and Hochberg's correction
Table 1B – Correlation between modulation after treatment and TGI

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* Benjamini and Hochberg's correction
**Figure legend**

**Figure 1.** *In vitro* characterization of PF-03084014.  
**A.** Inhibition of Notch signaling by PF-03084014 (100 nM) blocks HUVEC-fibroblast lumen formation. **B.** Treatment with 1 µM PF-03084014 results in a 50% reduction of non-adherent HCC1599 and SUM149 mammosphere formation. The second-generation mammospheres were generated by plating 500 and 2000 viable cells/well using SUM149 and HCC1599 cells, respectively, in 96-well ultra-low attachment plates (Corning). The imaging analysis was performed after a 6-day treatment with PF-03084014. **C.** In MX1 cells, treatment with 1 µM PF-03084014 leads to a significant suppression of NICD1 and tumor cell migration but fails to exert an anti-proliferative effect. **D.** The decrease in NICD1 levels after treatment with 1 µM PF-03084014 for 48 hr in tumor cells, HUVECs and cancer-associated fibroblasts (CAF). NICD1 levels were assessed by ELISA. Each data point represents triplicate assays. Value = mean ± SEM.

**Figure 2.** Antitumor efficacy and pharmacodynamic assessment of PF-03084014 in the HCC1599 xenograft model. **A.** PF-03084014 exhibits dose-dependent antitumor efficacy in a HCC1599 model. Mice bearing palpable tumors were administered P-F03084014 p.o. twice daily at the indicated dose levels for 12 days. N =10 mice/group; **B.** Western blot measurement of NICD1 expression levels upon treatment. **C.** The Notch down-stream gene modulations correlate with the cell phenotypic changes observed after treatment with PF-03084014. The mRNA expression profile of Notch target genes was normalized to GAPDH. The semi-quantitative measurement of BrdU and yH2AX staining was performed by a board-certified pathologist. **D.** The representative staining of BrdU, yH2AX and cleaved caspase 3 in vehicle and treated tumors. Here, 50 mg/kg BrdU was administered i.p. to mice 2 hrs before harvesting the tumors.
The graph represents the value relative to vehicle-treatment (= 1). E. Treatment of PF-03084014 results in 65% reduction of mammosphere formation. F. PF-03084014 impairs functional vasculature as measured by the lectin-perfusion assay. Before tumor collection, mice were injected i.v. with 5 mg/kg FITC-lectin (Vector Labs) 15 min prior to tumor collection. The tumors were collected after the mice were treated with either vehicle or 120 mg/kg PF-03084014 twice daily for 2 days (B, C, D), 12 days (E) and 7 days (F). N = 5 mice/group (B, C, D, E and F). Value = mean ± SEM.

**Figure 3.** The antitumor and antimetastatic properties of PF-03084014 in the MX1 orthotopic model. Size-matched tumor-bearing mice were administered 90 mg/kg PF-03084014 p.o. twice daily for 12 days. A. Representative fluorescence tomographic images of lung metastasis at 22 days after dosing commencement. MX1 tumor-bearing mice received i.v. injections of MMPsense 680 (5 nmol/mouse) 24 h before analyzing the images using an FMT 2500 system. B. H&E staining of tumor cell infiltration into lungs 24 hr after the FMT imaging analysis. C. PF-03084014 treatment displayed greater antimetastatic efficacy than antitumor efficacy. The primary tumor size under the mammary fat-pad was assessed with calipers. N =10 mice/group (A, B and D); N = 5 mice/group (C). Value = mean ± SEM. D. PF-03084014 suppresses stromal Notch target gene expression in multiple models. The tumors were collected after the mice were treated with either vehicle or 120 mg/kg PF-03084014 twice daily for 2 days. The graph represents the value relative to vehicle treatment (= 1).

**Figure 4.** The antitumor efficacy of PF-03084014 in breast cancer cells and xenograft models. A. The effect of PF-03084014 on tumor growth in a panel of breast cancer xenografts. Size-matched tumor-bearing mice were administered 120 mg/kg PF-03084014 p.o. twice daily for 12 days. The relative tumor size change = 100*ΔT/ΔC. The ΔC (ΔT) value was measured by
subtracting the mean tumor volume for the vehicle (treated) group on the first day of treatment from the mean tumor volume on the evaluation day. The relative tumor size changes were assessed after the treatment ended. *: p < 0.05. B. In an MTT assay, 2 µM PF-03084014 treatment for 7 days displayed no anti-proliferative activity in most of the breast cancer cell lines. C. The baseline NICD1 levels were variable across different breast cancer models. D. The differences in NICD1 levels between the in vitro and in vivo settings suggest the activation of Notch1 signaling by the in vivo microenvironment (loaded 100 µg protein). E. Treatment with 120 mg/kg PF-03084014 for 2 days led to a decrease in NICD1 levels in the efficacious tumor models. NICD1 levels were assayed by ELISA.

**Figure 5.** Gene expression correlated with PF-03084014 sensitivity and treatment modulation. A. Top genes with baseline expression correlated with tumor growth inhibition. Vehicle-treated expression levels were taken as a baseline and compared to anti-tumor efficacy. Samples were sorted from most resistant on the left to most sensitive on the right (top panel). The heatmap (bottom panel) shows relative baseline expression of each gene; red means that gene is over-expressed compared to average in a given sample, blue under-expressed. On the top are gene most significantly over-expressed in sensitive models, the bottom 5 genes are negatively correlated (R < -0.1) with sensitivity. The panel on the right shows the linear correlation coefficient (R) between tumors inhibition and expression values, the corresponding nominal p-value and Benjamini and Hochberg's corrected p-values (FDR). Genes with positive R values (up in sensitive models) are highlighted in blue, and the 5 genes negatively correlated with sensitivity are in red. B. Expression modulation after PF-03084014 treatment compared to vehicle treated samples. Samples were again sorted from resistant on the left to sensitive on the right (top panel). The heatmap shows relative expression modulation of each gene, red means
that gene is over-expressed post PF-03084014 treatment compared to the vehicle control, blue
down-regulated by the PF-03084014 treatment. The panel on the right shows log2 of fold change
(LogFC) between PF-03084014 and vehicle treated samples, moderated t-test statistics p-values
and Benjamini and Hochberg's corrected p-values (FDR). Genes highlighted in blue are
significantly down-regulated post treatment across the panel of models, the two red rows
correspond to mRNAs up-regulated after PF-03084014 treatment.
Figure 1

A. Control

EC-Tube

PF-4014 (100 nM)

B. Control

HCC1599

PF-4014 (1 µM)

SUM149

C. Relative Value

Control

PF-4014 (1µM)

NICD

Migration

Proliferation

D. NICD1 (OD450nm)

Tumor Cells

Non-Tumor

Control

PF4014 1µM

HCC1599

HCC1806

MX-1

SUM149

MDA-MB-231

HUVEC

CAF
Figure 2

A. Tumor volume (mm³) over days post 1st dosing for different doses of PF-4014.

B. Immunohistochemistry images showing NICD and Actin expression in Veh and PF-4014 groups.

C. mRNA and protein fold change for various genes in Veh and PF-4014 groups.

D. Immunohistochemistry images showing BrdU, γH2AX, and Cleaved Caspase 3 expression in Vehicle and PF-4014 groups.

E. Mammosphere images comparing Vehicle and PF-4014 groups.

F. Immunofluorescence images showing Lectin, CD31, and Merge for Vehicle and PF-4014 groups.
Figure 3

(A) Vehicle and PF-4014 treated MX1 tumors imaged by FMT. (B) Representative H&E images of MX1 tumors. (C) Relative tumor size in HCC1599 tumors treated with PF-4014. Antitumor TGI = 31%, anti-met TGI = 64%. *p < 0.05. (D) mRNA expression levels of Notch3, Hey2, and HeyL in HCC1599, MDA-MB-231, and MX1 tumors. Veh value = 1.
Figure 4

A. Relative Tumor Size Change (% of Control)

B. IC50 (µM)

C. NICD1 (OD Value)

D. NICD1 Level (OD Value)

E. NICD1 (OD Value)

(A) TGI < 50% and TGI > 50%

(B) IC50 values for different BC types.

(C) NICD1 levels for different cell lines.

(D) NICD1 levels in vivo and in vitro.

(E) NICD1 levels with different treatments.
### Figure 5

#### A

**Tumor size (% of control)**

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**Log2 Tx/vehicle ratio**

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Cathy C. Zhang, Adam Pavlicek, Qin Zhang, et al.

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