PEST Domain Mutations in Notch Receptors Comprise an Oncogenic Driver Segment in Triple Negative Breast Cancer Sensitive to a $\gamma$-Secretase Inhibitor

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Abstract

Purpose: To identify and characterize novel, activating mutations in Notch receptors in breast cancer and to determine response to the gamma secretase inhibitor (GSI) PF-03084014.

Experimental Design: We used several computational approaches, including novel algorithms, to analyze next generation sequencing data and related omic data sets from The Cancer Genome Atlas (TCGA) breast cancer cohort. Patient-derived xenograft (PDX) models were sequenced and Notch mutant models were treated with PF-03084014. Gene expression and functional analyses were performed to study the mechanism of activation through mutation and inhibition by PF-03084014.

Results: We identified mutations within and upstream of the PEST domains of NOTCH1, NOTCH2 and NOTCH3 in the TCGA data set. Mutations occurred via several genetic mechanisms and compromised the function of the PEST domain, a negative regulatory domain commonly mutated in other cancers. Focal amplifications of NOTCH2 and NOTCH3 were also observed as were heterodimerization or extracellular domain mutations at lower incidence. Mutations and amplifications often activated the Notch pathway as evidenced by increased expression of canonical Notch target genes and functional mutations were significantly enriched in the triple negative breast cancer subtype (TNBC) subtype. PDX models were also identified that harbored PEST domain mutations and these models were highly sensitive to PF-03084014.

Conclusions: This work suggests Notch altered breast cancer constitutes a bona fide oncogenic driver segment with the most common alteration being PEST domain mutations present in multiple Notch receptors. Importantly, functional studies suggest this newly identified class can be targeted with Notch inhibitors including GSIs.

Translational Relevance
While the Notch pathway is reportedly activated in breast cancer, the molecular mechanisms leading to its aberrant activation are poorly understood, hampering the clinical development of Notch inhibitors. In this study, we demonstrate the Notch pathway is activated via multiple mutational mechanisms primarily involving the PEST domain of NOTCH1, NOTCH2 and NOTCH3. Collectively, approximately 13% of TNBC exhibits a genetic alteration coupled with pathway up-regulation and these alterations may serve as biomarkers to identify patients most likely to respond to Notch inhibitors.
Introduction

The Notch pathway is a highly conserved developmental pathway responsible for a variety of cell fate decisions (1-3). The pathway is activated during normal breast development and has been implicated as a key driver in breast cancer (4-7). This has motivated the development of Notch inhibitors including GSIs as the gamma secretase (GS) complex is required to cleave and activate all four Notch receptors (8). However, pinpointing where and how this complex pathway that has redundancy at several nodes is activated and identifying robust biomarkers of response represent a critical gap. Integrated omic data sets have recently been generated on hundreds of human tumors and relevant pre-clinical models which now provide an opportunity to explore this question in detail. Within breast cancer, there is an urgent need to identify new therapeutic strategies for TNBC in particular, which is associated with a poor prognosis, lacks effective therapies and does not have a well-established catalogue of oncogenic drivers (9).

Notch is normally cleaved at the S1 site while trafficking in the Golgi and forms a bipartite receptor held together by non-covalent interactions within the heterodimerization (HD) domain. This domain is close to the membrane on the extracellular side of the cell and is flanked by site2 (S2) towards the C-terminus and a negative regulatory region (NRR) towards the N-terminus. In the unstimulated state, the NRR prevents access to and cleavage of the S2 site by an ADAM metalloprotease. Upon binding by a ligand expressed on an adjacent cell, a conformational change of the NRR exposes the S2 site thus allowing its cleavage. The gamma secretase complex then mediates S3 cleavage within the transmembrane domain liberating the Notch intracellular domain (NICD), which translocates to the nucleus and regulates the transcription of target genes. An important mechanism of NICD regulation is protein turnover. It is normally degraded quickly due to the PEST domain located at the C-terminus (1, 10).

There is a growing list of mechanisms whereby Notch is activated by mutation or complex genetic rearrangements in cancer and human diseases. In T cell acute lymphoblastic leukemia (T-ALL), translocations that remove a large portion of the extracellular domain (ECD) and HD domain mutations
involving NOTCH1 disrupt the normal function of the ECD/NRR and effectively lead to ligand
independent Notch activation (11, 12). Inactivating PEST domain mutations in NOTCH1 that increase
NICD1 half-life and Notch signaling are also frequently observed in T-ALL as well as chronic
lymphocytic leukemia (CLL), splenic marginal zone lymphoma (SMZL) and mantle cell lymphoma (13-
15). Similar NOTCH2 PEST domain mutations are present in diffuse large B-cell lymphoma (DLBCL),
SMZL and Hadju-Cheney syndrome (16-20). More recently, chromosomal rearrangements involving
NOTCH1 and NOTCH2 were identified in breast cancers (21). The common feature across the genomic
rearrangements that were shown to activate Notch signaling was the removal of a large portion of the
ECD leading to ligand independent activation, which is reminiscent of translocations and HD domain
mutations in T-ALL. However, mutations or rearrangements involving the PEST domain have not been
previously characterized in breast cancer.

**Materials and Methods**

**Cell lines and antibodies**

All cell lines were obtained from the American Type Culture Collection (Manassas, VA) before 2009
(over 5 years ago, exact date not known). The HCC1599 cell line was STR authenticated by the authors
May, 2013 using the StemElite assay (Promega) at the University of Arizona Research Lab. The other cell
lines used in this study were not STR authenticated as most of the samples were from older studies. The
HCC1599 and HPB-ALL cells were grown in RPMI-1640 medium and supplemented with 10% FBS, 50
IU/ml penicillin/0.05 mg/ml streptomycin. The remaining cell lines were grown in media recommended
by the suppliers with supplements including HEPES buffer, sodium pyruvate, non-essential amino acids,
Pen-Strep, ITS, and glutamine.

The primary antibodies used included anti-NICD1 (CST #4147), anti-Notch1 (CST #3608) and anti-
GAPDH (CST #2118) antibodies (Cell Signaling Technology, Danvers, MA).

**in vivo studies**
All in house in vivo studies were conducted in compliance with the Guide for Care and Use of Laboratory Animals and were approved by the Pfizer Global Research and Development Institutional Animal Care and Use committee. The authorization to use animals in the CERFE facilities at XenTech (Evry, France) for the HBCx PDX model was obtained by The Direction des Services Vétérinaires, Ministère de l'Agriculture et de la Pêche, France (agreement No. B-91-228-107). The animal care and housing were in accordance with European Convention n° STE123. All experiments were performed in accordance with French legislation concerning the protection of laboratory animals and in accordance with a currently valid license for experiments on vertebrate animals, issued by the French Ministry for Agriculture and Fisheries to Dr. Truong-An Tran (No. A 91-541 dated 21 December 2010; validity: 5 years). Tumor-bearing athymic nude mice were dosed twice daily at 140 mg/kg on a 12 day on, 4 day off schedule for 2 cycles. The MAXF1162 model was run at Oncotest and all experiments were approved by the local authorities and were conducted according to all applicable international, national and local laws and guidelines. Tumor-bearing nude mice were dosed twice daily at 140 mg/kg on a 10 day on 4 day off schedule for 3 cycles. The AA1077 patient-derived and HCC1599 cell line xenograft models were run at Pfizer in SCID-Bg mice. Mice were dosed at 110 mgs/kg twice daily for 9 days (AA1077) or at 120 mgs/kg twice daily for 12 days (HCC1599). To evaluate efficacy, mice with palpable tumor sizes were randomly assigned to different groups, and the mean value of the tumor size was matched between the groups. Differences between the vehicle and PF-03084014-treated groups were statistically significant by the student’s t-test. Percent tumor regression was calculated using the following formula 100*(1 - (Treated final volume/Treated initial volume)) and percent tumor growth inhibition was calculated using the following formula 100*(1 - (Treated final volume – Treated initial volume)/(Vehicle final volume – Vehicle initial volume)). For pharmacodynamic studies, tumor-bearing mice received 100 - 140 mg/kg PF-03084014 twice daily for two days before terminal collection. Some pharmacodynamic groups received one dose on the second day. The tumors were harvested 4-6 hours after the last dose, snap-frozen and pulverized in a liquid nitrogen-cooled mortar prior to analysis.
DNA/RNA analysis

Genomic DNA and total RNA were prepared from cell pellet or frozen tumor tissue with Qiagen DNeasy Blood and Tissue Kit (Cat. #69504) and Qiagen RNeasy Mini Kit (Cat. 74104), following manufacture’s protocol. Junction PCR was then performed to verify the break point of genomic DNA. Primer sequence for each particular sample is listed in the supplementary material. Total RNA were subjected to direct Quantitative RT-PCR (see below), or treated with Calf Intestinal Phosphatase (CIP) and Tobacco Acidic Pyrophosphatase (TAP) and then reverse transcribed to amplify the 5’ end messenger RNA sequence of NOTCH1 in HCC1599. CIP and TAP were included in FirstChoice® RLM-RACE Kit from Life Technologies (Cat. # AM1700).

Transcriptomic sequencing (RNA-seq) of PDX models

RNA-seq was performed on PDX models with 100 bp paired-end reads. Raw RNA-seq reads were filtered using Xenome (22) to remove potential reads from contaminating mouse cells. Non-mouse reads were then aligned to human reference genome using TopHat2 (23). 226.2, 253.9 and 298.3 million mapped reads were generated for HBCx14, AA1077 and MAXF1162, respectively.

TCGA data acquisition

Tier-2 mutation, somatic copy number and mRNA expression data (RNA Seq V2 RSEM) from the TCGA invasive breast carcinoma cohort were obtained from the TCGA data portal and Memorial Sloan-Kettering Cancer Center’s cBio portal (35). Raw Affymetrix SNP 6.0 array data were also downloaded from the TCGA data portal. Pre-aligned RNA-seq data (in BAM format) were downloaded via The Cancer Genomics Hub (36), dbGaP accession number PHS000178, version phs000178.v8.p7. A total of 956 tumors with complete mutation, copy number and gene expression data were analyzed (Supplementary Table 1).

Gene Expression Analysis
Gene expression profiles of the external PDX panel were generated using Affymetrix U133Plus2 arrays. CEL files were provided by the vendor (Xentech). Raw intensity data were processed by GC Robust Multi-array Average (GCRMA) background adjustment, quantile normalization, and median-polish summarization to generate the probe-level data in R. Normalized probe level data were further summarized into gene-level using the GSEA CollapseDataset function.

Differential expression analysis of the Notch pathway genes in the TCGA breast cancer cohort were performed on the RNA-seq based Transcript per Million metric from the RSEM results provided in the TCGA tier-3 data. Of the 100 TNBC tumors included in this cohort, 12 were selected as Notch altered that include patients with simple mutations or complex alterations in the HD or PEST domain of NOTCH1, NOTCH2 or NOTCH3, and those with focal amplification of NOTCH2 or NOTCH3 (inferred copy number >4). The Notch non-altered group included 41 TNBC tumors with no mutation, nor alteration, nor amplification (inferred copy number <2.5) in all Notch receptors. Note that we did not include in this analysis TNBC tumors that harbor mutations or alterations in non-hotspot regions, and those with mild or broad copy number gains, as they represent a “grey zone” that may blur the signal differentiating the two groups. Differential expression was calculated using a two sample t-test. Multiple hypothesis testing was controlled by False Discovery Rate using the Benjamini–Hochberg method.

**Nanostring Analysis**

Nanostring technology (24) was used to measure the RNA transcript levels using the nCounter assay according to manufacturer’s recommended protocols. Briefly, transcript specific capture and detection probes were designed and manufactured by the Nanostring Technologies and 100 ng of total RNA was hybridized to nCounter probe sets for 16 hours at 65°C. Samples were processed using an automated nCounter Sample Prep Station (NanoString Technologies, Inc., Seattle, WA). Cartridges containing immobilized and aligned reporter complex were subsequently imaged and counted on an nCounter Digital
Analyzer (NanoString Technologies, Inc.) set at 1155 fields of view. Reporter counts were analyzed and normalized using NanoString’s nSolver analysis software version 1.

Quantitative RT-PCR

Total RNA was isolated using miRNeasy Mini kit (Qiagen). 2 ug of RNA per reaction were used to generate cDNA using High Capacity cDNA Reverse Transcription Kit (Life Technology, CA). Q- PCR was performed in triplicate by using ABI PRISM 7900HT Sequence Detection System with Taqman Universal PCR Master Mix (Life Technology, CA). Primer/probes for Hes4, Hey1, Hey2, HeyL, Myc, NRARP, CCND1 and Notch3 were purchased from Life Technology. The expression level was normalized to Glyceraldehyde-3 phosphate dehydrogenase (GAPDH). Data normalized using Hypoxanthine-guanine phosphoribosyltransferase (HPRT) and Peptidylprolyl isomerase E (PPIE) yielded similar results.

Results

Identification of Notch receptor mutations and focal amplifications in TCGA breast cancer dataset

To identify potential patient selection biomarkers for the gamma secretase inhibitor PF-03084014, we mined the TCGA breast cancer data for mutations and alterations involving Notch receptors (25). A number of mutations were reported by the standard TCGA pipeline or discovered internally in each receptor (Supplementary Fig. 1 and 2 and Supplementary Table 1). Of the 956 tumor samples analyzed with complete gene expression, copy number and mutation data, there were 42 mutations in NOTCH1, NOTCH2, or NOTCH3, 25 of which either clustered in the HD domain or lead to a disruption of the PEST domain (Fig. 1a and Table 1). The PEST domain is a negative regulatory domain that is responsible for degrading the active Notch intracellular domain (NICD) and, when disrupted, leads to an increase in the NICD half-life. While PEST domain mutations in Notch are established oncogenic events in leukemias
and lymphomas, they have not been characterized in breast cancer. The majority of PEST domain mutations were nonsense mutations or frameshifting indels and were therefore predicted to truncate the normal protein sequence. The HD mutations on the other hand, occurred at highly conserved amino acid residues (26). Similar mutations are present in NOTCH1 in T-ALL and activate Notch signaling (12). While no mutations in this cohort were recurrent, several other mutations disrupted the protein at the same amino acid location as in other established Notch-driven cancers as well as Hadju-Cheney Syndrome, a genetic disorder characterized by pathway-activating NOTCH2 PEST domain mutations (Table 1).

More complex structural variants were not provided by the standard TCGA pipelines. We therefore obtained the pre-aligned RNA-seq data from the TCGA breast cancer study and applied a suite of in-house algorithms, collectively called TopNotch, that are based on a local, de novo transcript assembly approach. This analysis identified six additional candidate alterations in five tumors predicted to activate the Notch pathway. Four alterations disrupted the PEST domains in NOTCH1, NOTCH2 or NOTCH3 (Table 1, Fig. 1a and Supplementary Fig. 3). In terms of molecular mechanisms, three tumors harbored large deletions while one tumor harbored a translocation, all of which were predicted to remove the entire PEST domain (Table 1). One tumor harbored both a large PEST domain-disrupting deletion as well as a fusion with the BRD4 gene where exons 26-33 of NOTCH3 (which encode NICD3) were fused downstream of exon 1 of a non-canonical BRD4 transcript (Ensembl transcript ID: ENST00000360016). The fusion was predicted to lack the entire NOTCH3 ECD and produce an in-frame NICD3 with an intact GS site. Furthermore, we identified a tumor harboring a deletion of exons 21-27 in NOTCH1 which removes the NRR and HD domain. The PEST domain breakpoints identified from this analysis were further validated in the whole exome sequencing data from the same patients since they were all located within the last exon of the Notch genes, including the matched normal samples to confirm their somatic status (see Methods, Supplementary Fig. 4-6 and Supplementary Table 2).
We also analyzed the somatic copy number alteration (SCNA) data for amplifications of Notch receptors and found a number of tumors with focal amplification of NOTCH2 or NOTCH3 (Fig 1b, Supplementary Fig. 1 and Supplementary Table 1). Focal amplification often led to over expression of the receptor. Notably, similar to mutational patterns observed in other well-established oncogenic drivers, 37% of Notch mutations co-occurred with copy number gain > 3 at the locus (Table 1). Furthermore, 67% of the mutations exhibited very high expression of the Notch receptor (93rd percentile or greater) including all but one of the mutations that were co-incident with copy number gain. The mutation and expression pattern is most striking for NOTCH3 where out of seven mutated tumor samples, four exhibit copy number gain, two of which are focal, and all have either 97th or 99th percentile expression of NOTCH3. In contrast to NOTCH1, NOTCH2, and NOTCH3, no compelling mutations or amplifications were found in NOTCH4 (Supplementary Fig. 2). In summary, we identified 43 breast cancers in the TCGA cohort that carry either somatic mutations in a hotspot domain (ECD/HD or PEST) of NOTCH1-3, or somatic focal amplification of NOTCH2 or NOTCH3 with concomitant increase in receptor expression (collectively referred to as “Notch altered” hereafter). Our analysis demonstrates a broad spectrum of potentially activating genetic alterations in Notch receptors is present in breast cancer, most often involving the PEST domain.

Notch mutant and amplified cancers are associated with the triple negative subtype and pathway activation

To determine whether these potentially activating Notch alterations were associated with a breast cancer subtype, TCGA data was analyzed for Notch, ESR1, PGR and ERBB2 status. Of the 956 tumor samples analyzed, 130 (or 13.6%) were determined to be TNBC (see Methods). Strikingly, 21 of the 43 Notch altered BCs are TNBCs (a 3.6-fold enrichment, \( p = 6.89\times10^{-6} \) by Fisher’s exact test, Table 1 and Fig. 1d). This strong enrichment and the high unmet medical need in TNBC prompted us to focus our subsequent analyses in this subtype. To determine whether Notch alteration resulted in increased Notch pathway activity, we compared Notch pathway gene expression in the 21 Notch altered TN tumors with Notch
wild type TN tumors (Fig. 1c and Supplementary Table 3). Overall, a subset of Notch pathway and target genes, including NOTCH3, HES1, HEY2, MYC, CCND1, HES4, NRARP and NOTCH1, exhibited significant over-expression (false discovery rate <0.05) in the Notch altered tumors, and were among the top 4% most up-regulated genes in Notch altered TNBCs when all genes were queried (Supplementary Table 3). One of the more provocative results in this data set is the strong up-regulation of the Notch pathway target genes MYC and CCND1 in the Notch altered breast tumors, providing insight into both the mechanism whereby Notch activation may lead to an oncogenic phenotype, as well as how these classical breast cancer genes are, in fact, up-regulated in this subset of breast tumors (27, 28). Additionally, mutations in PTEN or FBXW7, which have been shown to confer resistance to a GSI in NOTCH1 mutant T-ALL (29, 30), do not co-occur with Notch alterations in this data set.

As canonical Notch target genes HES4 and HEY2 were differentially expressed between the Notch altered and wild type TN tumors, we used over-expression of one or both of these target genes as an indicator of Notch pathway activation (Supplementary Fig. 7). Of the 21 TNBCs with Notch alterations of interest, 17 showed evidence of Notch pathway activation. Outside TNBC, however, only 8 of the 22 Notch altered tumors showed evidence of pathway activation (Fig. 1d). This suggests Notch alterations are more likely to be functionally relevant in the TNBC subtype and we estimate 13% of TNBC falls into this newly identified Notch altered oncogenic driver class.

**Patient-derived xenograft models harboring Notch receptor PEST mutations are sensitive to PF-03084014**

To determine whether in vivo models harboring Notch receptor PEST domain mutations are sensitive to PF-03084014, we sequenced patient-derived xenograft (PDX) models using RNA-seq and whole genome sequencing. We identified three PDX models all of which had distinct genomic rearrangements that truncated the PEST domain of NOTCH1 or NOTCH2 (Fig. 2a, Supplementary Fig. 8 and 9, and Supplementary Table 4). The MAXF1162 model harbored a translocation that fused the last exon of
NOTCH2 with intronic sequence from NBPF8, which disrupted the NOTCH2 PEST domain at amino acid 2320. Similar to several Notch receptor mutations in the TCGA data, this model also harbored a focal amplification of the NOTCH2 locus (Supplementary Fig. 8). The AA1077 model harbored a transcript that fused part of the last exon of NOTCH1 with intronic sequence from NOTCH1 between exons 30 and 31 and disrupted the PEST domain at amino acid 2249. Using WGS data from this model we confirmed that this was due to a tandem duplication between intron 30 and exon 34 of NOTCH1 (Supplementary Fig. 8). Lastly, the HBCx-14 PDX model harbored a heterozygous 10 base pair (frameshift) deletion in the PEST domain (disrupting the coding sequence beginning at amino acid 2462) and a homozygous ECD deletion (Supplementary Fig. 9 and Supplementary Table 4). While the ECD was deleted, the GS site was still present in the mutated protein. All three models were highly sensitive to PF-03084014, including over 50% tumor regression in the MAXF1162 model which was similar to the NOTCH1 ECD deleted HCC1599 cell line xenograft model previously known to be sensitive to GSI (31, 32) (Fig. 2b). The MAXF1162 model was characterized as a HER2 amplified model whereas the other models were triple negative (TN).

To compare these responses in Notch mutant models to Notch wild type models, we analyzed a panel of eight xenograft models that were previously tested for sensitivity to PF-03084014 and for which we had treated and untreated samples that could be used for sequencing and pharmacodynamic gene expression analyzes (31) (Supplementary Fig. 10). No activating Notch hotspot domain alterations were found in RNAseq or whole genome sequencing data from four PDX models (HBCx-5 (HER2+), HBCx-17 (TN), HBCx-12B (TN), and AA0869 (TN)) and four cell line xenograft models (HCC1937 (TN), HCC1806 (TN), BT-474 (HER2+), and MDA-MB-231 (TN)). Responses in these Notch wt models were very heterogeneous ranging from little to no effect to slight tumor regression. On the other hand, all Notch mutant models responded to PF-03084014 including greater than 50% tumor regression in two out of four models. In summary, we identified mutations in PDX models representative of the TCGA mutations in terms of location, predicted functional consequence, spectrum of molecular mechanisms and co-incidence...
of multiple events. These data therefore confirm and extend our findings from the TCGA analysis and importantly, demonstrate that relevant pre-clinical models harboring Notch alterations are particularly sensitive to PF-03084014.

We next explored the functional consequences of the NOTCH1 mutations on NICD1, the activated form of the receptor. Mutations that remove the ECD domain are predicted to result in ligand independent activation of the receptor. Indeed, similar to the HCC1599 model, the HBCx-14 model exhibited robust NICD1 expression that was inhibited by PF-03084014 and lacked full length NOTCH1 (Fig. 3a - c). On the other hand, PEST domain truncating mutations in the AA1077 and HBCx-14 models produced a lower molecular weight NICD1 species as predicted. In contrast, NOTCH1 wt models did not exhibit strong expression of NICD1 nor were lower molecular weight species present (Supplementary Fig. 11).

We further explored the consequence of the PEST domain mutation in the HBCx-14 PDX model. In this model, 2 day treatment with PF-03084014 dramatically reduced the wt NICD1 band. In contrast, the mutated NICD1 band appeared to be only slightly reduced (Fig. 3d). This is consistent with the prediction that PEST mutant NICD1 has a longer half-life. To quantify this effect, we measured the average intensity of wt and mutated NICD1 bands in the HBCx-14 model from three animals treated for either 2 or 12 days with PF-03084014. Short term treatment reduced the wt band to ~50% of untreated levels whereas the mutated band was not significantly reduced (Fig. 3d and e). In 12 day treated mice, wt NICD1 was reduced to less than 3% of untreated wt levels whereas mutant NICD1 was present at ~15% of untreated mutant levels. These data demonstrate that mutations truncating the PEST domain in breast cancer models can increase the protein half-life of NICD1.

Activating alterations in Notch receptors would be predicted to up-regulate direct transcriptional targets of the pathway including the Hes and Hey family transcription factors similar to the TCGA gene expression analysis. Indeed, in an initial survey of gene expression levels of Notch pathway genes across the panels of in vivo models, we observed strong over-expression of HES4, HEY2, HEY1 and/or HEYL in
three of the four Notch mutant models (Fig. 4a). The MAXF1162 and HBCx-14 models both harbored multiple genetic events in the altered Notch receptor and in both cases the mutated receptor itself exhibited the highest mRNA expression among the panel of the xenograft screened (Fig 4a and b). We next used quantitative RT-PCR to analyze Notch target gene expression between Notch mutated and Notch wt xenograft models treated with or without PF-03084014. Treatment with drug reduced the expression of nearly all Hes and Hey target genes in the Notch altered models that exhibited strong over-expression at baseline demonstrating Notch alterations indeed drive the Notch pathway in these models and that PF-03084014 can effectively repress this hyperactivated transcriptional program (Fig. 4c and Supplementary Fig. 12). In addition, the Notch target genes MYC, NRARP, CCND1 and NOTCH3 were also nearly always down regulated by PF-03084014 (Fig. 4c and Supplementary Fig. 13). In contrast, in Notch wild type models, Notch target genes very rarely exhibited strong over expression at baseline. Moreover, while treatment with PF-03084014 down regulated Notch target genes in some Notch wild type models, the number of targets regulated by PF-03084014 and the magnitude of down regulation was less, on average, than in the Notch altered models (Fig. 4c and Supplementary Fig. 12 and 13). Taken together, these functional studies in pre-clinical in vivo models demonstrate PEST domain mutations in Notch receptors activate the Notch pathway, confer sensitivity to PF-03084014 and provide strong rationale for a personalized medicine strategy for Notch inhibitors in Notch altered TNBC.

Discussion

In this study, a broad spectrum of activating mutations were discovered in NOTCH1, NOTCH2 and NOTCH3 including missense mutations, nonsense mutations, small indels, large deletions and chromosomal translocations that disrupt either the ECD/HD or PEST domains. This repertoire of mutational mechanisms involving the PEST domains is in contrast to the molecular mechanisms of previously known PEST domain mutations in leukemias and lymphomas which primarily consist of point mutations and small indels (13-15, 17-19). We also found evidence for HD or ECD mutations similar to
what have been previously reported, however, these mutations appear to have a lower prevalence compared to mutations involving the PEST domain.

An interesting observation from this study is the nature of the Notch mutations and alterations. Typically, activating oncogenic mutations are restricted to a few hotspots within a gene and inappropriately activate a signal transduction cascade: for example, mutations in KRAS at codons 12, 13 or 61, or the L858R mutation or exon 19 deletion of EGFR. Conversely tumor suppressor genes such as TP53 are often altered at multiple locations along the gene. Notch receptors are somewhat unique in that the PEST domains and ECD / HD, in essence, negatively regulate the active form of Notch, the NICD. Therefore inactivation by mutation or deletion of either domain activates the Notch pathway.

The co-incidence of mutations with amplification and over expression of the Notch receptor is similar to other established oncogenes and suggests there is pressure to select for high levels of Notch pathway activity. Increased receptor expression may be important given the unique mechanism of Notch activation which lacks a true signal amplification step. GS cleavage generates the active NICD molecule which directly translocates to the nucleus and activates a downstream transcriptional program. Therefore, the maximal activity of the pathway is directly linked to Notch receptor concentration. In the case of the MAXF1162 model that harbors a PEST domain mutation and focal amplification, the receptor amplification may be required to boost the baseline signaling, whereas the PEST domain mutation would be predicted to further increase the duration of the active Notch signal.

The number and complexity of Notch mutations may preclude a definitive immediate interpretation for every alteration observed in the TCGA breast cancer data set. Reliable functional studies capable of measuring Notch pathway activation, transformation potential, and sensitivity to pathway inhibition will be required to better understand all of the mutations and alterations examined in this study. However, the observation that many of these mutations are recurrent in other cancers or diseases in which pathway activation is an established pathogenic event provides strong evidence that these alterations are operative
in breast cancer. Moreover, the increased expression of Notch pathway target genes in Notch altered human tumors and sensitivity to a GSI in Notch altered pre-clinical models provides compelling evidence that many of these mutations are oncogenic.

This data set is timely as several Notch pathway inhibitors that target various points in the pathway are currently in early clinical development. Given the spectrum of Notch alterations observed, it should be anticipated that each drug will produce different responses depending on the nature of the mutations. For instance, inhibitory antibodies against Notch receptors will likely only work against tumors in which the domain recognized by the antibody remains intact after the genomic alteration. On the other hand, GSIs should inhibit activating Notch alterations in which the gamma secretase cleavage site remains intact, which includes nearly all of the activating Notch alterations described in breast cancer thus far. Collectively, these data suggest an appreciable fraction of TNBC patients harbor oncogenic Notch alterations that may be effectively treated with targeted inhibitors.
Table 1. NOTCH1, NOTCH2, and NOTCH3 hotspot mutations in TCGA breast tumors.

<table>
<thead>
<tr>
<th>TCGA ID</th>
<th>Notch</th>
<th>AA change</th>
<th>HD or PEST</th>
<th>Subtype</th>
<th>Hes4/Hey2</th>
<th>Copy Number; Focal (Y/N)</th>
<th>Rec exp percent</th>
<th>AA mutated in cancer / HCS</th>
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<td>Notch1</td>
<td>V1110-S1723 IF del (exon 21-27 del)</td>
<td>HD</td>
<td>TNBC</td>
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<td>A2256fs (translocation to chr14)</td>
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<td>ER-/PR-/HER2+</td>
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<td>98</td>
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Table 1. Somatic NOTCH1, NOTCH2 and NOTCH3 mutations and alterations in the HD and PEST domains identified in the TCGA invasive breast carcinoma cohort. For complex alterations, genomic changes are indicated in parentheses following the amino acid (AA) change (details can be found in Supplementary Fig. 4). Hes4/Hey2 up-regulation defined when either gene is expressed 2-fold above median expression across the cohort. Rec exp percent, receptor expression percentile; T-ALL, T cell acute lymphocytic leukemia; MCL, Mantle Cell Lymphoma; SMZL, splenic marginal zone lymphoma, DLBCL, diffuse large B cell lymphoma; HCS, Hajdu-Cheney Syndrome. FS, frame-shift; IF, in-frame.
Figure legends

Figure 1. Notch receptor mutations and focal amplifications in TCGA invasive breast cancer dataset exhibit pathway activation and are enriched in the triple negative subtype. A, Lollipop graph depicting simple mutations and complex alterations in NOTCH1, 2 and 3 in the TCGA dataset clustered in or near the HD or PEST domains. Green dotted line indicates in frame deletion (NOTCH1) or in frame fusion (BRD4-NOTCH3), both of which are predicted to produce the NICD. Protein domains were obtained via a Pfam search (37) of the wildtype protein sequences. B, Examples of TCGA tumors harboring focal amplifications of NOTCH2 (top) or NOTCH3 (bottom) Copy number (CN) ratio in log2 were calculated using data from the matched normal sample as reference. C, Expression heatmap of Notch pathway genes in 21 Notch altered TN tumors compared to 50 non-altered TN tumors. See Method section for the selection of the two groups. Un-scaled expression was shown to the right of the heatmap where the circle indicates median expression and the line indicates the range of expression. The dotted red line indicates background expression level. D, Notch altered tumors are enriched in TNBC and Notch altered TNBC tumors are more likely to exhibit increased Notch pathway activity.

Figure 2. Breast cancer models harboring Notch alterations are sensitive to PF-03084014. A, Genomic alterations in Notch receptors in patient-derived xenograft models and the HCC1599 cell line model. The MAXF1162 model harbors a fusion that disrupts the NOTCH2 PEST domain (red lollipop) as well as an amplification of the locus. The AA1077 model harbors a partial tandem duplication of NOTCH1 that disrupts the NOTCH1 PEST domain. The HBCx-14 model harbors an ECD deletion and a PEST domain frameshifting deletion in NOTCH1. The HCC1599 harbors an ECD deletion in NOTCH1. See Supplementary Fig. 8 and 9 for details of the alterations at genomic and transcript levels. B. Notch altered models are sensitive to PF-03084014. Data shown as average tumor volume + SEM. MAXF1162 model exhibited 65% tumor regression, AA1077 model exhibited 88% tumor growth inhibition, the HBCx-14 model exhibited 60% tumor growth inhibition and the HCC1599 model exhibited 50% tumor regression. All models were statistically significant by the student’s t-test (p-value < 0.05).
Figure 3. NOTCH1 mutations alter full length and NICD1 protein and NICD1 half-life. A, NICD1 Western blot in Notch altered models treated with or without PF-03084014. “*” indicates NICD1 species of lower molecular weight than wt NICD1. HPB-ALL is a T-ALL model that is known to generate a NICD1 species of lower molecular weight due to a PEST domain mutation. To better visualize the wt and mutant NICD1 bands in the newly discovered NOTCH1 mutant models, 15 ug lysate were loaded for the HPB-ALL and HCC1599 models, 50 ug were loaded for the AA1077 model and 30 ug were loaded for the HBCx-14 model. B, NICD1 Western blot on the NOTCH1 PEST truncated HBCx-14 model (lane 6) alongside a panel of lysates from TNBC PDX models from the same collection. The HCC1599 cell line xenograft model +/- PF-03084014 for 2 days at 100 mg/kg BID was included as controls. 50 ug lysate was loaded for all lysates except 25 ug for the HCC1599 lysates. The Red arrow indicates the lower molecular weight NICD1 species in the HBCx-14 model. C, NOTCH1 Western blot using an antibody that recognizes the NOTCH1 transmembrane and full length species. Lower panel, lighter exposure. The Red arrows indicate the lower molecular weight species in the HBCx-14 model and the absence of detectable full length protein in either the HBCx-14 model or the HCC1599 model. The same amount of lysate was loaded in a separate gel as in (B) on the same day, therefore no additional loading control was included for this gel. D, 2 and 12 day treatment with PF-03084014 at 140 mg/kg BID. The PEST mutated NICD1 was less diminished after drug treatment relative to the wt band. E, Quantification of bands in (d). Data shown as average band intensity +/- SEM relative to 12 day vehicle and normalized to GAPDH.

ECD, extracellular domain; S3, cleavage site recognized by the gamma secretase complex; NICD, Notch intracellular domain; PEST, protein domain rich in proline (P), glutamic acid (E), serine (S) and threonine (T); wt, wildtype.

Figure 4. Notch mutant breast cancer models often exhibit increased Notch pathway expression sensitive to PF-03084014. A, Models rank-ordered from left to right using a HES4, HEY2 two gene signature score across an internal in vivo panel (left) and an external PDX panel (right). B, Relative NOTCH2 expression normalized against beta-actin across the panel of internal in vivo models. C, i, quantitative RT-PCR of
key Notch target genes at baseline in Notch wt and Notch altered models demonstrate Notch altered models exhibit high level expression of one or more genes, the *HES* and *HEY* family genes in particular.

C, ii, Fold change from baseline following 2 days of treatment with PF-03084014. Notch target genes were consistently down-regulated by PF-03084014 treatment in Notch mutant models and were down regulated to a greater degree compared with Notch wt models. Nanostring digital gene expression data were used for the internal *in vivo* model panel; Affymetrix microarray gene expression data were used for the external PDX model panel; q-RT-PCR data were used for panel C.

**Acknowledgments**

We thank Enhong Chen and Maruja Lira for technical assistance. We thank Chih-Hao Lee (Harvard School of Public Health) for critical reading of the manuscript. The results published here are in part based upon data generated by The Cancer Genome Atlas pilot project established by the NCI and NHGRI, available as dbGaP accession number PHS000178, version phs000178.v8.p7. Information about TCGA and the investigators and institutions that constitute the TCGA research network can be found at (38).

**Authors’ Contributions**

References


36. https://cghub.ucsc.edu/

37. http://pfam.sanger.ac.uk/search

Figure 1

(a) NOTCH1, NOTCH2, and NOTCH3 abnormalities.

(b) Genomic position (MB) of NOTCH2 and NOTCH3.

(c) TNBC patients in TCGA breast invasive carcinoma dataset.

(d) Number of tumors with and without pathway activation.

Total number:
- TNBC: 130
- Other BCs: 826

Number (%) of NA+:
- TNBC: 21 (16.2)
- Other BCs: 22 (2.7)

Number (%) of NA+ with pathway activation:
- TNBC: 17 (13.1)
- Other BCs: 8 (0.97)
Figure 2

(a) NOTCH2 wildtype
(a) NOTCH2 mutant (MAXF1162)
G2320fs

(b) NOTCH1 wildtype
(b) NOTCH1 mutant (AA1077)
S2449fs

(b) NOTCH1 mutant (HBCx-14)
1679 P2462fs

(b) NOTCH1 mutant (HCC1599)
1724

MAXF1162
AA1077
HBCx-14
HCC1599
Figure 4

(a) Heatmap showing expression levels of various genes in different cell lines. The y-axis represents different genes and the x-axis represents different cell lines.

(b) Bar graph showing relative expression of NOTCH2 across different cell lines.

(c) Table comparing Notch wild type (wt) and Notch mutant expression levels in different cell lines:

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Relative baseline expression is indicated by the color scale at the bottom of the heatmap. Log2 fold change from baseline is indicated by the color scale at the bottom right of the heatmap.
Clinical Cancer Research

PEST Domain Mutations in Notch Receptors Comprise an Oncogenic Driver Segment in Triple Negative Breast Cancer Sensitive to a \( \gamma \)-Secretase Inhibitor

Kai Wang, Qin Zhang, Danan Li, et al.

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