FGFR1 is Essential for Prostate Cancer Progression and Metastasis

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Abstract

The fibroblast growth factor receptor FGFR1 is ectopically expressed in prostate carcinoma cells, but its functional contributions are undefined. In this study, we report the evaluation of a tissue-specific conditional deletion mutant generated in an ARR2PBi(Pbsn)-Cre/TRAMP/\textit{fgfr1}^{loxP/loxP} transgenic mouse model of prostate cancer. Mice lacking \textit{fgfr1} in prostate cells developed smaller tumors that also included distinct cancer foci still expressing \textit{fgfr1} indicating focal escape from gene excision. Tumors with confirmed \textit{fgfr1} deletion exhibited increased foci of early, well-differentiated cancer and phyllodes-type tumors, and tumors that escaped \textit{fgfr1} deletion primarily exhibited a poorly differentiated phenotype. Consistent with these phenotypes, mice carrying the \textit{fgfr1} null allele survived significantly longer than those without \textit{fgfr1} deletion. Most interestingly, all metastases were primarily negative for the \textit{fgfr1} null allele, exhibited high FGFR1 expression and a neuroendocrine phenotype regardless of \textit{fgfr1} status in the primary tumors. Together, these results suggest a critical and permissive role of ectopic FGFR1 signaling in prostate tumorigenesis and particularly in mechanisms of metastasis.
Introduction

Prostate cancer is the most commonly diagnosed cancer in males in the United States and the third leading cause for male cancer patient death (1). Localized prostate tumors can be treated and are not a common cause for patient death. However, prostate cancer patients may develop metastatic tumors in different organs, such as bone, lung, brain and liver etc, and die from metastasis. Currently there is no cure for locally advanced and metastatic prostate cancer. Accordingly, understanding the molecular mechanisms and biology that mediates prostate cancer progression and metastasis is critically important in the search for novel therapeutic approaches.

In the normal human prostate gland, expression of fibroblast growth factor receptor 1 (FGFR1) is restricted to stroma and is not expressed in epithelial cells (2). In contrast, foci of prostate cancer exhibit aberrant expression of FGFR1 in epithelial carcinoma cells (3, 4). In addition, FGF-2, a cognate ligand for FGFR1, is also overexpressed in stromal fibroblasts and endothelial cells immediately associated with prostate cancer cells (3). Accordingly, human prostate cancer evolves with both the aberrant expression of FGFR1 in prostate carcinoma cells coincident with elevated expression of FGF-2 in the adjacent stroma microenvironment. The elevated expression of ligand in stroma together with ectopic expression of receptor in carcinoma cells suggests that the FGF ligand / FGFR1 signaling axis may be a critical mediator of prostate cancer progression and metastasis.

Previous studies have shown that engineered ectopic expression of constitutively active FGFR1 in mouse prostate epithelial cells in a transgenic model resulted in hyperplasia and evolution of pre-malignant prostatic intraepithelial neoplasia (PIN) (5), and that ectopic expression of FGFR1 in prostate epithelium affected expression of matrix degrading enzymes, including matrilysin (MMP-7) (6), implicating FGFR1 in matrix turnover and cell invasion. Our
studies have shown that overexpression of FGF-2 in prostate stromal cells drives elevated angiogenesis, and promotes human prostate cancer xenograft growth (7). Furthermore, studies using chemical inducers of dimerization (CID) drugs to induce dimerization and activation of an engineered FGFR1 in mouse prostate epithelium resulted in the induction of hyperplasia and PIN (8) that was initially reversible, but progressed over time to adenocarcinoma (9). In xenograft studies using urogenital sinus mesenchyme recombined with adult prostate epithelial cells, overexpression of dominant negative FGFR1 in epithelial cells led to a reversal of the induction of PIN and prostate cancer by FGF-10 expressed in the mesenchyme (10). However, since FGFR1 can also form heterodimers with other FGFRs, the specificity of this dominant negative approach remains to be determined. In summary, previous studies have primarily used gain of function approaches with models driven by activation of FGF signaling cascades. Moreover, no studies have yet addressed the role of FGFR1 in prostate cancer progression to metastasis.

In order to address the significance of FGFR1 in prostate cancer progression and metastases we have used a loss of function knockout approach in the metastatic TRAMP transgenic model of prostate cancer. The TRAMP model exhibits a well-documented step-wise progression of primary tumor to metastatic phenotype with distant metastases to lymph node, lung, liver, and bone (11-13). Although this model represents more of a neuroendocrine phenotype at late stages of progression, the model is useful in defining component regulators of metastatic spread. Important for the present study, the TRAMP model exhibits aberrant expression of FGFR1, detected in cancer cells (14), similar to human prostate cancer. Moreover, the evolution to a neuroendocrine phenotype appears to be important in the emergence of castration resistant disease in human prostate cancer (15) and these evolve to particularly aggressive tumors. Hence, owing to the tendency of the TRAMP model to evolve a
neuroendocrine and metastatic phenotype, understanding FGFR1 action in this model will aid in understanding mechanisms that promote particularly aggressive and metastatic human prostate cancers (16). It is possible that ectopic expression of FGFR1 is important in acquiring an aggressive neuroendocrine phenotype associated with metastasis. The role of FGFR1 in this context is understudied.

In the present study, we demonstrate that conditional ablation of fgfr1 in TRAMP mouse prostate epithelium results in attenuation of primary tumor growth, extended lifespan, and altered histopathology to a less aggressive phenotype. Moreover, mice with primary tumors that evolve foci that escape fgfr1 excision produced metastases that were homogeneously positive for FGFR1 expression. These results suggest that ectopic FGFR1 expression strongly correlates with the development of poorly differentiated tumors and that continued FGFR1 signaling is a key component of prostate cancer metastasis within the context of a neuroendocrine tumor type.

Materials and Methods:

Animals. C57BL/6 and FVB mice were purchased from Harlan Laboratories. TRAMP transgenic mice (in C57BL/6 background), ARR2PBi-Cre mice (in FVB background) have been described before (12, 17, 18). The fgfr1loxP/loxP mice (in ICR background) were kindly gifts from Dr. Juha Partanen (19-21) and were re-derived in local transgenic mice facility. All experiments were carried out in compliance with the NIH Guide for the Care and Use of Laboratory Animals and according to Baylor College of Medicine institutional guidelines and IACUC approval.

Genomic DNA PCR. ARR2PBi-Cre, fgfr1loxP, and fgfr1wt alleles were PCR screened as previously described (17, 21). TRAMP mice were identified by PCR using primer 5’
CCGGTCGACCGGAAGCTTCCACAAGTGCATTTA 3’ and primer 5’ CTCTTTCAAGACCTAGAAGGTCCA 3’. \(fgfr1^{KO}\) allele was identified by genomic PCR using primers 5’ ACCTCAGGAACCTCGAATAAGCCACCAC 3’ and 5’ AGGTTCCTCCTCTTGGATGACTTTAG 3’. PCR was done using genomic DNA from mouse tails and tumors, including microdissected tumors when it was visually possible to separate tumor tissue from surrounding tissue.

Histology, Immunohistochemistry, and \textit{In situ} Hybridization. Tissues were fixed in 4\% paraformaldehyde and paraffin embedded. Sections (5 \(\mu\)m) were mounted onto ProbeOn Plus slides (Fisher, Pittsburgh, PA, USA) for H&E staining, immunohistochemistry, and \textit{In situ} Hybridization. Immunostaining were performed with the MicroProbe Staining System (Fisher) following a general protocol published previously (22). Antibodies used are anti-AR (1:100, Santa Cruz sc-816), anti-Ki67 (1:200, Neomarkers, clone SP6, RM-9106), and anti-CD31 (1:400, Epitomics 2530-1). Where applicable, antigen retrieval consisted of incubation in citrate buffer (pH 6.0) for 20 minutes under steam conditions. TUNEL staining was performed using an In Situ Cell Death Detection Kit, Fluorescein (Roche, 11 684 795 910) following the recommended protocol. For in situ hybridization, DIG labeled riboprobes were prepared using \textit{in vitro} transcription kit (Promega) with DIG RNA labeling mix (Roche). The antisense riboprobe of FGFR1 was generated by \textit{in vitro} transcription using T3 RNA polymerase on the pKS+\(\Delta\)FGFR1 vector linearized with XbaI (kindly provided by Dr. Juha Partanen) (21). Control sense riboprobe was similarly generated but using T7 RNA polymerase on pKS+\(\Delta\)FGFR1 linearized with HindIII. The \textit{In situ} hybridization for FGFR1 was performed following a general protocol as previously described (18). To further confirm the FGFR1-specific ISH signal, a
fragment of human FGFR1 cDNA was cloned into pBlueScript SK vector between EcoRI and PstI sites. A second set of riboprobes for FGFR1 was similarly generated based on this construct. Antisense riboprobe was generated by in vitro transcription using T3 RNA polymerase on vector linearized with EcoRI, and sense riboprobe using T7 RNA polymerase on vector linearized with BamHI. Both sets of probes produced the same ISH signal. Sense riboprobes exhibited no significant staining patterns (Supplementary Fig. S3).

Statistics. Tumors from each group were analyzed. Average tumor weight was compared between groups for statistical relevance using the Mann-Whitney test (nonparametric). The correlation of tumor genotype with tumor pathology was analyzed using the Fisher’s exact test. The difference of mouse survival was analyzed using the Gehan-Breslow-Wilcoxon test. Statistical analyses were generated using Graphpad Prism 5.0 (GraphPad Software). \( P < 0.05 \) was considered statistically significant.

Results:

Conditional ablation of \( fgfr1 \) in prostate tumors in TRAMP model.

\( In situ \) hybridization showed that FGFR1 message was localized exclusively in prostate stromal cells with no apparent expression in epithelial cells in normal neo-natal (day 3 postnatal, Fig. 1A) and adult prostate gland (12-week old, Fig. 1B). Accordingly, conditional ablation of \( fgfr1 \) in embryonic urogenital sinus / prostate progenitor cells did not affect prostate development, morphology and androgen receptor action (Supplementary Fig. S1).

In contrast, foci of high grade PIN in the TRAMP transgenic prostate tumor model exhibited positive expression of FGFR1 (Fig. 1C). The signal intensity was elevated in foci of
well-differentiated prostate carcinoma cells and was particularly notable in foci of poorly
differentiated carcinoma (Fig. 1D) and in metastatic foci (as shown, to liver, Fig. 1E). Therefore,
we concluded that ectopic expression of FGFR1 in epithelial carcinoma cells is a feature of
TRAMP prostate carcinoma cells, which is consistent with previous findings.

To determine how \(fgfr1\) ablation affects prostate tumor progression and metastasis,
\(fgfr1^{\text{loxP/loxP}}\) mice (19-21), ARR2PBi-Cre mice (17), and TRAMP mice (12) were used to produce
the target population of ARR2PBi-Cre/TRAMP/\(fgfr1^{\text{loxP/loxP}}\) mice, which resulted in knockout of
\(fgfr1\) specifically in the prostate epithelial cells of TRAMP model. To minimize the complex
effects of mouse strain background difference on tumor progression, \(fgfr1^{\text{loxP/wt}}\) mice in an ICR
background were first backcrossed four generations into FVB background as well as four
generation into C57BL/6 background (Supplementary Fig. S2). The \(fgfr1^{\text{loxP/wt}}\) mice (four
generations into FVB background) were then crossed another two generations with ARR2PBi-
Cre mice (FVB) to produce the ARR2PBi-Cre/\(fgfr1^{\text{loxP/wt}}\) mice (six generations into FVB
background). Similarly, the \(fgfr1^{\text{loxP/wt}}\) mice (four generations into C57BL/6 background) were
crossed another two generations with TRAMP mice (C57BL/6) to generate the
TRAMP/\(fgfr1^{\text{loxP/wt}}\) mice (six generations into C57BL/6 background). As a final step, the
ARR2PBi-Cre/\(fgfr1^{\text{loxP/wt}}\) mice and the TRAMP/\(fgfr1^{\text{loxP/wt}}\) mice were crossed to generate the
target ARR2PBi-Cre/TRAMP/\(fgfr1^{\text{loxP/loxP}}\) mice along with ARR2PBi-Cre/TRAMP/\(fgfr1^{\text{loxP/wt}}\),
ARR2PBi-Cre/TRAMP/\(fgfr1^{\text{wt/wt}}\) and all other control mice in an approximately 50% C57BL/6
and 50% FVB background, which is most optimal for prostate carcinoma development and
metastasis in the TRAMP model (11-15). Necropsy was done in cohorts of mice at either 22
weeks (22-week study) or when prostate tumors evolved to equal 10% of body weight, or the
mice develop hunched posture, immobility and/or moribund appearances following specific IACUC-approved criteria (survival study).

**fgfr1 ablation inhibits prostate cancer progression.**

Cohorts of *ARR2PBi-Cre/TRAMP/fgfr1^wt/wt* and *ARR2PBi-Cre/TRAMP/fgfr1^loxP/loxP* mice at 22 weeks of age were evaluated for efficiency of *fgfr1* knockout in prostate tissues and alterations in histopathology as an initial evaluation of phenotype. Genomic DNA from prostate tissue was evaluated by PCR to assess the presence of *fgfr1^KO* alleles to assess the efficiency of *fgfr1* knockout in prostate tissue (Fig. 2A). Of the 36 *ARR2PBi-Cre/TRAMP/fgfr1^loxP/loxP* mice in this study, 28 mice exhibited the *fgfr1* knockout allele in prostate tissue (referenced here as KO+), whereas 8 mice exhibited no detectable *fgfr1* knockout alleles in prostate tissue (KO-) although each of the 8 was confirmed as a *ARR2PBi-Cre/TRAMP/fgfr1^loxP/loxP* genotype (based on tail DNA). Of these two groups, the *fgfr1* KO+ mice primarily exhibited PIN and carcinoma regions with non-detectable FGFR1 message as determined by *in situ* hybridization (Fig. 2B and 2C, asterisk), although some well-differentiated cancer foci were positive (Fig. 2C, arrow). However, some regions of poorly differentiated foci with positive expression of FGFR1 mRNA were observed in 3 of these 28 KO+ mice (Fig. 2D and 2E). Together, these data suggest focal escape from Cre-mediated excision in some regions of KO+ prostate glands. In contrast, prostate carcinoma cells in the 8 *ARR2PBi-Cre/TRAMP/fgfr1^loxP/loxP* mice designated as *fgfr1* KO- (no detectable *fgfr1* knockout alleles in prostate tissue by genomic PCR), were universally positive for FGFR1 mRNA and all tumors universally exhibited a poorly differentiated carcinoma phenotype (Fig. 2F, 2G, and 2I).
Expression of wild type FGFR1 message correlated with tumor phenotype, mass, and histopathology (Fig. 2H and 2I). At 22 weeks, wild type (ARR2PBi-Cre/TRAMP/fgfr1wt/wt) tumors exhibited a mean mass of 1.94 (+/-0.47) grams (n=48) (Fig. 2H). In contrast, the 28 mice with knocked out fgfr1 in prostate tissue (ARR2PBi-Cre/TRAMP/fgfr1loxP/loxP, fgfr1 KO+) exhibited significantly smaller tumors, with a mean wet weight of 0.22 (+/-0.03) grams (n=28) (p=0.0010, Mann Whitney Test). The 8 tumors that escaped Cre mediated fgfr1 excision altogether (ARR2PBi-Cre/TRAMP/fgfr1loxP/loxP mice without detected fgfr1KO alleles in prostate, fgfr1 KO-) exhibited nearly a 10-fold increase in mass at 2.81 (+/-1.18) grams (n=8) (p = 0.0005). Interestingly, cohorts of mice with loss of just one fgfr1 allele (ARR2PBi-Cre/TRAMP/fgfr1loxP/wt) also resulted in a trend to decreased mass at 0.80 (+/-0.20) grams (n=81) (compared to wild type, p=0.1116), however this was a significant increase of mass as compared with the fgfr1 KO+ tumors at 0.22 (+/-0.03) grams (n=28) (p=0.0079).

The fgfr1 KO status also correlated with histopathology, as scored by a pathologist in a genotype-blinded manner (Fig. 2I). Prostatic intraepithelial neoplasia (PIN), a premalignant phenotype, was detected in 100% of fgfr1 KO+ tumors. Well-differentiated carcinoma foci were detected in 78% of KO+ tumors, phyllodes foci were detected in 15%, and poorly differentiated foci were observed in only 11% of fgfr1 KO+ tumors respectively. In contrast, the fgfr1KO- tumors were positive for PIN in only 25% and well-differentiated cancer foci was detected in only 25% of tumors. Poorly differentiated foci were detected in all (100%) of the fgfr1 KO- tumors. The phyllodes phenotype was not observed in any of the fgfr1 KO- tumors. The phenotypic differences between fgfr1 KO+ and fgfr1 KO- tumors in the categories of PIN, well-differentiated tumor, and poorly differentiated tumor, were each statistically significant (P < 0.05, Fisher’s Exact Test for correlation) (Table 1). Wild type tumors (fgfr1wt) exhibited a
histopathology somewhere between the \(fgfr1\) KO+ and \(fgfr1\) KO- extremes in most categories (Fig. 2I and Table 1). Furthermore, while 50\% of \(fgfr1\) KO- and 24\% of control \(fgfr1^{\text{wt}}\) tumors were exclusively poorly differentiated, none of the \(fgfr1\) KO+ tumors were exclusively poorly differentiated. In addition, metastases were observed in all mice with \(fgfr1\) KO- primary tumors, whereas few mice with KO+ primary tumors exhibited metastases.

Control TRAMP tumors, \(fgfr1\) KO+, and KO- tumors exhibited differential patterns of Ki67 immunoreactivity that was associated with different histopathology. The more aggressive \(fgfr1\) KO- tumors with no detectable \(fgfr1\) knockout allele, and some of the control TRAMP tumors exhibit a dense pattern of Ki67 staining that are associated with regions of poor differentiation that are non-necrotic (Fig 3B and 3D). In contrast, regions of well-differentiated lesions in control TRAMP tumors and all of the \(fgfr1\) KO+ tumors examined, exhibited a focal and heterogeneous staining pattern (Fig. 3A and 3C). TUNEL staining showed no apparent apoptotic changes in any of the tumor types with exception of the larger and poorly differentiated \(fgfr1\) KO- tumors, which exhibited some regions of focal necrosis (Supplementary Fig. S4). Immunohistochemistry for CD31 showed no apparent differences in vessels (data not shown).

**\(fgfr1\) ablation prolongs survival**

A longitudinal survival study was conducted in another cohort of mice. Mice were evaluated for time-to-death and histopathology of primary and metastatic tumors was determined at time of death. All mice eventually developed prostate tumors and metastatic disease progression irrespective of the \(fgfr1\) genotype in prostate tissue. No significant differences in time-to-death was observed between the wild type control mice and the ARR\(2\)PBi-Cre/\textit{TRAMP}/\textit{fgfr1}^{\text{loxP/loxP}} mice when analyzed as a group \((p > 0.05\), data not shown\). However,
upon death and necropsy, two groups, \(fgfr1\) KO+ and \(fgfr1\) KO- were also identified as before within the ARR2PBi-Cre/TRAMP/\(fgfr1^{loxP/loxP}\) cohort (n=22) as assessed by \(fgfr1^{KO}\)-specific genomic DNA PCR on prostate tumors. Mice with \(fgfr1\) KO+ prostate tumor tissue (n=11) exhibited a 38 week mean time-to-death as compared with a mean 26.3 week time-to-death of mice with \(fgfr1\) KO- tumor tissue (n=11) (\(p=0.0172\), Gehan-Breslow-Wilcoxon test, Fig. 4A). Histopathology of recovered tumors at time of death showed that poorly differentiated tumor foci was observed in 100% of \(fgfr1\) KO- tumors, whereas only 38% of \(fgfr1\) KO+ tumors exhibited poorly differentiated foci (Fig. 4F). The presence of poorly differentiated foci was negatively associated with \(fgfr1\) KO+ tumors (KO+ vs. KO-, \(p=0.0090\), \textit{odds ratio}= 0.0335, Fisher’s exact test). In addition, 89% of \(fgfr1\) KO- tumors were exclusively poorly differentiated, whereas only 12.5% of \(fgfr1\) KO+ tumors were exclusively poorly differentiated.

In situ hybridization for FGFR1 message revealed a pattern similar to the 22-week study. \(fgfr1\) KO+ tumors exhibited foci with either no reactivity or some isolated foci with positive reactivity showing some focal escape from excision (Fig. 4B and 4C). In contrast, \(fgfr1\) KO-tumors were mostly poorly differentiated and all strongly expressed FGFR1 message (Fig. 4D and 4E). Of interest, phyllodes-like foci (observed in Fig. 4B and 4C) were observed in 75% of \(fgfr1\) KO+ tumors, including 38% that were exclusively phyllodes-like. In contrast, none of the \(fgfr1\) KO- tumors were exclusively phyllodes-like, and only one carried minimal phyllodes-like foci among mostly poorly differentiated foci (Fig. 4D and 4E). The phyllodes-like pathology was strongly associated with \(fgfr1\) KO+ tumors (KO+ vs. KO-, \(p=0.0152\), \textit{odds ratio}= 24.0, \textit{Fisher’s exact test}). As expected, PIN and well-differentiated tumor foci were minimally observed in the prostate tumors in the time-to-death study and there was no association with the \(fgfr1^{KO}\) status in prostate tumors (\(p>0.05\), data not shown).
FGFR1 expression in metastases.

An important observation in this study was that metastases exhibited expression of FGFR1 message irrespective of genotype. Metastasis to lymph node, lung, liver and kidney was observed at necropsy in ARR$_2$PBi-Cre/TRAMP/fgfr1$^{loxP/loxP}$ mice in the time-to-death study. However, the fgfr1$^{KO}$ knockout alleles were not detected in any of the metastatic tumors (multiple metastatic locations per mouse, PCR of genomic DNA in tissue) in 15 out of 16 mice examined, irrespective of the status of fgfr1$^{KO}$ alleles in the primary tumors (Fig. 5A). In concordance with PCR data, in situ hybridization in a subset of samples showed that FGFR1 message was observed in all cancer cells throughout the metastasis (Fig. 5E and 5G) and metastatic cells were near universally positive for Ki67 (Fig. 3F). Also of interest, all metastatic tumors exhibited a neuroendocrine phenotype, typical of poorly differentiated TRAMP tumors (16). Together, these results suggest that FGFR1 signaling is requisite for metastatic spread as no cancer cells with knockout alleles were present in metastases even though many cancer cells with knockout alleles were present in the primary tumors in these same mice.

Discussion

FGF signaling has been implicated in development and cancer progression. Compared to the numerous FGF ligands, there are only four major FGF receptors (FGFR1 - FGFR4). FGFR1 signaling is particular interesting since FGFR1 expression is low in normal prostate epithelium, but is elevated in human prostate cancer epithelium (3, 4). Previous studies have shown an association of FGFR1 with a more aggressive phenotype: overexpression of FGFR1 was
associated with both the evolution of androgen independent tumors (23) and with a higher preoperative serum PSA level (24).

Use of a conditional \textit{fgfr1} knockout approach in a mouse prostate cancer model has permitted us, for the first time, to pinpoint the key biology that is regulated by FGFR1 signaling in a tumorigenesis model that is not specifically driven by engineered and elevated FGFR1 signaling. Data reported here confirms that the TRAMP model exhibits ectopic expression of FGFR1 in carcinoma cells and this is similar to human prostate cancer. Conditional knockout of \textit{fgfr1} in the TRAMP mouse prostate gland epithelium resulted in significantly smaller primary tumors that exhibited less aggressive and more well-differentiated phenotypes. Moreover, \textit{fgfr1} knockout mice exhibited a lower rate of tumor growth, and an extended time-to-death. Interestingly, the \textit{fgfr1} knockout mice developed a similar extent of metastasis as controls in the time-to-death study where the primary prostate tumors in all mice evolved to a similar size (equal 10\% of body weight). Further analysis revealed a significant degree of incomplete Cre-mediated excision and a resultant focal escape within primary tumors. Clearly defined foci of carcinoma cells positive for FGFR1 message was obvious by in situ hybridization. Of most importance, metastases in 15 of 16 \textit{fgfr1} conditional knockout mice evaluated in the study were universally negative for the \textit{fgfr1} knockout alleles and exhibited universal expression of FGFR1. All metastases exhibited the same poorly differentiated neuroendocrine phenotype typical of wild type TRAMP tumor metastases. Hence, incidence, tissue pattern, and histopathology of multiple metastases per mouse under \textit{fgfr1} knockout condition, were identical to wild type TRAMP mice.

These data suggest that ectopic expression of FGFR1 in carcinoma cells in the TRAMP model is requisite for progression to metastasis. Furthermore, these data suggest that TRAMP
carcinoma cells within primary tumors that have undergone successful excision and replacement with \( fgfr1 \) knockout alleles are either not capable of metastasis or do not efficiently survive and/or expand to a secondary tumor after they have successfully metastasized. Moreover, since the metastatic secondary tumors exhibited a neuroendocrine phenotype, these data suggest that expression of FGFR1 and signaling may be important for the genesis of this more aggressive phenotype. Of interest, the neuroendocrine phenotype is associated with castration resistant prostate cancer. Hence, FGFR1 signaling may be very important in progression of prostate cancer to castration resistant disease. Understanding mechanisms that drive resistance is critically important for the design of new therapeutic strategies to treat more advanced tumors.

ARR2PBi-Cre mice have been previously shown to efficiently drive Cre recombinase expression in normal prostate epithelial cells. Consistent with this, we did not observe FGFR1 expression (escape) in most of the pre-malignant PIN foci in the prostate of the ARR2PBi-Cre/TRAMP/\( fgfr1^{loxP/loxP} \) mice, indicating similar high knockout efficiency during early tumorigenesis. However, some foci of well differentiated cancer and especially poorly differentiated carcinoma cells exhibited escape. These data suggest that ARR2PBi-Cre may not drive expression quite as efficiently during the stages for overt carcinoma development from carcinoma progenitor/stem cells. These data may also mean that carcinoma progenitor/stem cells that are restricted from ectopic expression of \( fgfr1 \) due to excision, are not as capable of forming an adenocarcinoma lesion and hence, are selected against during the evolution of the carcinoma. Specific mechanisms are not known. However, it is clear from this study that poorly differentiated tumors in the ARR2PBi-Cre/TRAMP/\( fgfr1^{loxP/loxP} \) mice all expressed high levels of FGFR1. Interestingly, \( fgfr1 \) KO- tumors exhibited particularly aggressive growth and histopathology. At 22 weeks, all KO- tumors were classified as poorly differentiated, whereas
40% of control TRAMP tumors were poorly differentiated. It is possible that tumors which escape *fgfr1* knockout have a significant growth advantage and naturally evolve to a poorly differentiated phenotype. We suspect that escape from *fgfr1* knockout resulted in pre-selection of tumor cells that have a more rapid proliferation and are prone to poor differentiation. This may result in an enrichment of the poorly differentiated phenotype (to 100%).

Although specific mechanisms of FGFR1 signaling in prostate cancer cells and the role of this signaling on tumor progression is not yet fully understood, our study clearly suggests that FGFR1 signaling is a key regulator of prostate cancer proliferation, histopathological phenotype, and cancer progression to metastasis. Accordingly, understanding the biology of FGFR1 action and associated signaling pathways in prostate cancer will likely be important in designing novel therapeutic approaches to control evolution of aggressive cancer and the neuroendocrine phenotype, particularly in the context of castration-resistant disease.

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**Figure Legends**

**Figure 1.** In situ hybridization for localization of FGFR1 message in mouse prostate gland. FGFR1 message is localized exclusively in stroma in day 3 postnatal prostate gland (Panel A) and in normal prostate gland (shown as 12 week old, 200X, Panel B). Panel C: Elevated FGFR1 message in prostate epithelium in high grade PIN in the TRAMP prostate cancer mouse model (200X). Panel D: Elevated FGFR1 message in carcinoma cells in TRAMP tumors (200X). Panel E: Elevated FGFR1 message in carcinoma cells in metastatic TRAMP tumors (red arrow) as opposed to adjacent tissue (black arrow) (200X).

**Figure 2.** Conditional ablation of *fgfr1* results in attenuated tumorigenesis and altered phenotype in the TRAMP mouse model. Panel A: an example of four mice where the prostate tissues / tumors from two are positive (KO+) and two are negative (KO-) for the *fgfr1*KO allele. Panel B and C show an example histopathology (H&E section) and the corresponding in situ hybridization for FGFR1 message in a serial section respectively at foci PIN and well differentiated cancer exhibiting some focal escape from Cre-mediated excision (arrow) in a 22-week KO+ mouse (200X). Panels D and E show an example of escape of excision in foci of poorly differentiated cancer that are positive for FGFR1 message in the same mouse (200X). Panels F and G show universally positive FGFR1 message in poorly differentiated cancer in a 22-week KO- mouse (200X). Panel H: Knockout of *fgfr1* results in a significant reduction in tumor mass in mice with detected *fgfr1* KO allele (KO+) as compared to mice with undetected KO allele (KO-) or wild type controls. Numbers of mice (n) in each cohort are shown above the bars. Asterisks indicate significant changes (p<0.05). No TRAMP: mice that do not carry TRAMP transgene. Panel I shows the percent of mice in each cohort that contain the indicated histopathology phenotype (open bars are wild type controls).

**Figure 3.** Immunohistochemistry for Ki67. Panel A: Regions of well differentiated carcinoma in TRAMP control mice show a focal and diffuse pattern of Ki67 immunoreactivity. Panel B: Regions of poor differentiation in control TRAMP tumors exhibit a dense pattern of Ki67 immunoreactivity. Panel C: Mice with detected *fgfr1* KO allele (KO+) exhibit an intermittent and diffuse pattern similar to control TRAMP mice with no regions of dense staining. Panel D: Mice with no detectable *fgfr1* KO allele (KO-) exhibited poorly differentiated tumors that exhibited a dense Ki67 staining pattern, similar to the poorly differentiated tumors in the TRAMP control mice. Panels E and F. Primary tumor with a KO+ genotype (Panel E) showing intermittent and focal staining in comparison to a liver metastasis (Panel F) in this same mouse with dense and near universal staining of carcinoma cells. (100X all panels).

**Figure 4.** Ablation of *fgfr1* results in altered mean time to death in TRAMP mice. Panel A: Mice with *fgfr1* KO+ tumors (n=11) showed a significantly increased mean time-to-death (38 weeks) as compared to mice with *fgfr1* KO- tumors (26.3 weeks) (n=11) (p=0.0172, Gehan-Breslow-Wilcoxon test). Panels B and C: HE staining and in situ hybridization for FGFR1 message show that *fgfr1* KO+ tumors (shown as a phyllode tumor) exhibited foci with either no reactivity or some isolated foci with positive reactivity for FGFR1 (arrow) (200X). Tumors with a phyllodes histopathology were differentially observed in 75% of the *fgfr1* KO+ tumors. Panels D and E: *fgfr1* KO- tumors were poorly differentiated and universally positive for *fgfr1* (200X).
Only one of the KO- tumors carried minimal phyllodes-like foci and most were poorly differentiated. (200X). Panel F: Respective histopathology of tumors at time of death. Poorly differentiated tumor foci were observed in 100% of fgfr1 KO- tumors, whereas only 38% of fgfr1 KO+ tumors exhibited poorly differentiated foci.

**Figure 5.** Metastatic tumors do not exhibit the fgfr1 KO allele. Panel A: PCR of genomic DNA from metastatic tumors in 15 out of 16 ARR2PBi-Cre/TRAMP/fgfr1loxP/loxP mice examined in the survival study showed no fgfr1 KO allele in any of the metastatic tumor sites. Mouse No. 1201 is a representative mouse exhibiting no KO allele in primary tumor (fgfr1 KO-). Mice No. 1204, 1237 and 2288 are representative samples of mice with the KO allele in the primary tumor (fgfr1 KO+). Regardless, no KO allele was detected in metastases to lymph node, liver or lung. PCR for ARR2PBi-Cre transgene was used as control. Panel B and C shows representative in situ hybridization for FGFR1 message in primary tumors in fgfr1 KO+ mouse No. 2288 (200X). Note some focal escape from Cre excision shown in Panel C. Panels D and E shows the H&E section (D) and the corresponding in situ hybridization (E) from an adjacent serial section from a metastatic tumor to liver from the same mouse (200X). Panels F and G shows a similar association with metastatic tumor to the lung in the same mouse (200X). PT: primary prostate tumor, LN: lymph node metastasis, LUM: lung metastasis, LIM: liver metastasis, SV: seminal vesicle.

**Table 1:**

<table>
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<th>fgfr1 KO+ vs. fgfr1 KO-</th>
<th>fgfr1 KO+ vs. wt</th>
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<tr>
<td></td>
<td>p value</td>
<td>Odds ratio</td>
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<td>PIN</td>
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<td>Well-differentiated</td>
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<td>10.50</td>
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<tr>
<td>Poorly differentiated</td>
<td>&lt; 0.0001*</td>
<td>0.0084</td>
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<td>Phyllodes-like</td>
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Table 1. Fisher’s exact test for association of TRAMP prostate tumor pathology with FGFR1 status at 22-week. fgfr1 KO+ : Tumors with confirmed fgfr1\textsuperscript{KO}; wt: wild type tumors; fgfr1 KO-: Tumors escaped Cre-mediated fgfr1\textsuperscript{KO}. *: Statistically different; \textsuperscript{N}: Non-statistically different.

**Literature Cited:**

Fig. 1
**Fig. 2**

**A**

KO+ prostate

KO- prostate

fgfr1KO prostate

ARR2PBi-Cre

**B**

**C**

Foci of PIN* and well differentiated PCa (arrow)

**D**

**E**

Foci of poorly differentiated PCa

**F**

Poorly differentiated PCa

**H**

Prostate Weight (g)

- wt/wt
- loxP/loxP

**I**

Percent

- PIN
- Well diff.
- Poorly diff.
- Phyllodes

*wt/wt fgfr1 KO+ prostate not detected*
Fig. 3
Fig. 4

A) Graph showing percent survival over survival time (weeks) with lines for KO+ and KO-.

B) H&E stained section of tissue labeled fgfr1 KO+.

C) H&E stained section of tissue labeled fgfr1 KO-.

D) H&E stained section of tissue labeled H&E.

E) H&E stained section of tissue labeled In Situ FGFR1.

F) Bar graph showing percent survival for PIN, Well diff., Poor diff., and Phyllodes.

KO+ and KO- bars for each category.
FGFR1 is Essential for Prostate Cancer Progression and Metastasis

Feng Yang, Yongyou Zhang, Steven J. Ressler, et al.

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